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.

Materials and Methods

Experimental populations

Throughout this study, we used an outbred *D. melanogaster* population (LH$_m$ wild-type strain),

maintained under constant conditions of 25°C, 60% humidity, and a 12h:12h light:dark cycle.

First, we generated axenic (germ-free) focal flies by collecting eggs (within six hours of

oviposition) from four large population containers supplied with Petri dishes containing grape-

juice agar medium (300 mL water, 670 mL grape juice, 22 g agar, 20 g sugar, 19 g yeast, 20

mL nipagin per litre) supplemented with a smear of yeast paste. Eggs were washed off the

plates into a strainer, pooled, and dechorionated by immersion in 3.5% bleach for 2 minutes,

followed by a rinse in 70% ethanol and three rinses in sterile water.

Next, eggs were aseptically transferred to sterile glass vials containing autoclaved standard fly

food (75 g glucose, 100 g fresh yeast, 55 g corn, 10 g flour, and 15 mL nipagin antimicrobial

agent per liter food media) supplemented with antibiotics [a cocktail of following antibiotics

with their respective final concentrations: Ampicillin (50 μg/mL), Kanamycin (50 μg/mL),

Erythromycin (10 μg/mL), Tetracycline (10 μg/mL)]. Vials were then sealed with sterile plugs

and incubated under standard laboratory conditions until adult eclosion. All steps of vial

preparation were conducted in a laminar flow chamber to avoid contamination.

Upon eclosion, axenic status was confirmed using two methods on a subsample of flies. First,

homogenated flies were plated on Lysogeny Broth (LB) and de Man, Rogosa and Sharpe

(MRS) agar plates, incubated, and checked for bacterial colony growth. Second, genomic DNA

was extracted from pools of 3-5 putatively germ-free and conventional flies (positive control),

respectively, using Quick-DNA midiprep plus kit following the instructions provided by the

manufacturer. Universal primers (27F and 1492R) were used as forward and reverse primer,

respectively. To prepare the PCR master mix, 10 µL of nuclease-free water, 0.5 µL of forward

and reverse primer, 1 µL of template DNA and 13 µL Taq green master mix were mixed in a

sterile eppendorf tube. PCR conditions were: initial denaturation at 95°C for 90s, followed by

35 cycles of denaturation at 95°C for 30s, annealing at 55°C for 30s and extension at 72°C for

90s, and final extension at 72°C for 5 minutes). PCR products were visualized on a 1% agarose

gel under ultraviolet light to confirm the absence of bacterial DNA amplification in axenic

samples and its presence in controls.

Bacterial cultures and gnotobiotic associations

Axenic males were associated with defined compositions of microbial species, all originally

isolated from the gut of wild-type flies (Obadia *et al.* 2017): *Acetobacter tropicalis* (*At*),

and *Lactobacillus brevis* (*Lb*) for mono-associations based on their contrasting effects on male

reproductive investments in our previous study (Maggu *et al.* 2025). For comparison, we also

included axenic males and males inoculated with a defined five-species community consisting

of common and abundant *Drosophila* gut bacteria (*A. tropicalis*, *A. orientalis, A. pasteurianus,*

L. plantarum, L. brevis), resulting in four distinct microbial treatments.

Bacterial strains were cultured overnight in an incubator at 30°C: *Acetobacter* in MRS +

mannitol medium with shaking, and *Lactobacillus* in MRS broth under stationary conditions.

The following morning, cultures were checked for growth before measuring their optical

densities (OD) at 600 nm and centrifuging at 7000 rpm for 5 minutes. Bacterial pellets were

then resuspended in sterile phosphate-buffered saline (PBS) to a final concentration of 10^8

cells/mL, following established protocols (Koyle *et al.* 2016; Newell & Douglas 2014).

To inoculate vials, 50µL of bacterial suspension (approx. 5×10^6 CFUs) was added to sterile

food vials, with equal representation of bacterial strains in the 5-species consortia. This

bacterial density is comparable to previous reports for conventionally reared flies (Gould *et al.*

2018; Newell & Douglas 2014). Inoculated food vials were then allowed to air-dry in a laminar

flow cell before introducing ten 1-day-old axenic males to each to generate gnotobiotic flies.

Males were transferred to freshly inoculated vials with the same bacterial treatment every 48h

for a total of four days to ensure stable colonization. Successful colonization with the intended

bacteria was confirmed by plating homogenates of males from each treatment and checking for

characteristic colony morphologies (see *Bacterial abundance of males*).

Stress treatments

Following the 4-day colonization period, males were transferred to vials containing sterile food

and exposed to pesticide and heat stress in a fully factorial design. Specifically, half of the

males from each microbial group were subjected to food supplemented with imidacloprid,

whilst the remaining half were maintained on uncontaminated standard food. We used a

concentration of 1 ppm (parts per million) of imidacloprid as concentrations of 0.04 to 20 ppm

have been used effectively in studies on larval or adult *D. melanogaster*, depending on the

exposure regime (Charpentier *et al.* 2014; Frantzios *et al.* 2008; Martelli *et al.* 2020). These

concentrations are low enough to avoid immediate lethality but sufficient to induce sublethal

effects on behavior, reproduction, and physiology. Males were exposed to imidacloprid for an

acute window of 18 h, following an additional thermal treatment of 4-hour in a hot water bath.

To this end, half of the males from each microbiome and pesticide treatment were subjected to

acute heat stress by transferring them to vials containing only sterile 1% agar (to prevent

dehydration) and placing these vials in a water at 36°C for 4 hours. The remaining males

(thermal controls) were treated identically but at benign 24.5°C. All males were then allowed

to recover overnight in standard food vials under standard laboratory conditions.

Hatching success and fertility

To quantify the fitness consequences of heat and pesticide exposure and their potential

mitigation by the microbiome on the morning after the stress treatments, experimental males

were individually mated to standard females of the same population. All females had been

collected as virgins (within 7 hours of eclosion) and reared under axenic conditions along with

the experimental males to minimize confounding contributions of female microbes to the

measured outcomes. After mating ended, females were allowed to lay eggs for 24 h, and

another 30 h later (allowing time for embryonic development), oviposition vials were frozen

for later quantification of the proportion of eggs hatching as a proxy of fertilization success,

and the total number of larvae estimating male-mediated fecundity. This assay was performed

in two blocks, each with 25 males per treatment combination, totaling 800 experimental males

(4 bacterial treatments × 2 pesticide treatments × 2 temperature treatments × 2 blocks × 25

males).

Sperm competitiveness

To assess male sperm competitiveness, the above experimental design was repeated, but this

time using standard females that had mated once with standard competitor males two days

before the focal mating. These standard competitors were of the same strain but genetically

modified to ubiquitously express green fluorescent protein (GFP), permitting paternity

assignment against the focal wild-type males (Lüpold *et al.* 2012, 2020). Pairs were monitored

for remating for up to 8 h. Remated females were then isolated in fresh vials for oviposition,

while pairs not mating were separated and given another 8-hour mating opportunity on the

following day. Females still not remating were excluded. Offspring paternity (focal vs.

competitor) was assessed via GFP fluorescence to calculate P_2 as the proportion of offspring

sired by the second (focal) male. The treatment design of this assay was identical to the non-

competitive experiment above, but this time with 30 trials per treatment combination in each

of the two experimental blocks (i.e., 960 trials in total).

Bacterial abundance in males

To investigate the impact of stress treatments on the bacterial load, colony forming units

(CFUs) were compared between ten random males from each experimental treatment, surface-

sterilized with 70% ethanol, and individually homogenized in 1.5 mL microcentrifuge tubes

containing sterile PBS using a pestle. Homogenates were serially diluted to different dilutions

at a final volume of 100 μL, then plated on MRS media for quantification of CFUs at

appropriate dilutions (approx. 100 CFUs/plate). For the control groups with both *Acetobacter*

and *Lactobacillus* species, MRS agar was supplemented with 10 μg/mL ampicillin to avoid the

growth of *Lactobacillus,* whilst replicate plates were incubated in a CO_2 atmosphere to exclude

the growth of *Acetobacter*. The presence of only target bacterial species on plates was

confirmed based on colony morphologies, with *A. tropicalis* producing small tan-brown

colonies and *L. brevis* producing small yellowish colonies. CFUs per fly were calculated as:

$CFU = C \times D/P \times V$, where C = number of colonies counted, D = dilution, P = volume plated,

V = volume of fly homogenate (Koyle *et al.* 2016). For control males, with all the five bacterial

species, bacterial colonies were identified by their morphology and total CFUs per fly was

obtained by adding CFUs from all the five bacterial species.

Cross-generational effects

To assess cross-generational impacts of paternal (F_0) stress exposure, we quantified hatching success and fecundity in both male and female offspring (F_1) of our experimental males. Within each experimental block, up to 20 freshly hatched larvae from each of ten randomly selected vials per parental treatment combination (i.e., 16 combinations) were transferred to rearing vials containing sterilized standard fly food. This immediate transfer minimized the potential acquisition of parental microbes via consumption of the egg chorion or contaminated food. These larvae developed under standard laboratory conditions.

Upon eclosion, 4-5 virgin F_1 male and female offspring were collected from each rearing vial, separated by sex. At 2-3 days of age, three males and three females from each lineage were individually mated with a virgin standard fly of the opposite sex reared under axenic conditions (to avoid potential confounding effects of their microbiota). Following copulation, hatching success and fecundity were measured for these F_1 flies as in their parents (see above). These offspring themselves were not subjected to any experimental treatment, thus assessing solely the cross-generational effects. This experiment was carried out in two independent blocks of 480 offspring per sex from 160 F_0 males (i.e. total of 1,920 mating trials).

Statistical analysis

All statistical analyses were performed in R version 4.4.3 (R Core Team 2025), using generalized linear models (GLMs) with a Poisson (fecundity) or binomial error distribution (hatching success, paternity shares) in the experimental generation, and the corresponding mixed-effects models (GLMMs) in the offspring generation with sire as a random effect to account for non-independence among siblings. Each model included microbiome composition (4-level factor) along with the binary thermal and pesticide treatments with all two- and three-way interactions as fixed effects, along with experimental block as a nuisance factor accounting

for inter-block variation. Given that this factor only had two levels except for the assay of CFUs

with three experimental blocks, thereby limiting estimates of random variance, we included it

as a fixed effect in all models.

The binomial model of the relative abundance of Acetobacter versus Lactobacillus exhibited

slight overdispersion (dispersion factor = 1.12), which we addressed by fitting a mixed-effects

model with an observation-level random effect. In contrast, the remaining non-linear models

showed moderate underdispersion (dispersion factors $\approx$ 0.9). Alternative model families such

as Tweedie, negative binomial, and quasibinomial did not improve model fit, so the original

models were retained for clarity and interpretability.

Model performance was checked using the performance package (Lüdecke *et al.* 2021), and

output plots were generated was plotted using ggplot2 (Wickham 2016) based on means and

95% confidence intervals estimated via emmeans (Lenth 2025).

The impact of the different experimental treatments was also analyzed for the total bacterial

abundances (CFUs) and, separately, for compositional shifts in the five-species consortia. For

the former, we used a linear mixed-effects model with block as a random effect. For

microbiome community composition in the five-species consortium, we quantified the species-

specific abundances per sample, then applied a Hellinger transformation to these count data

and computed Bray-Curtis distances using the *vegdist* function in the package vegan (Oksanen

et al. 2025). We assessed treatment effects (temperature, pesticide, and their interaction) in a

permutational multivariate analysis of variance (PERMANOVA) using *adonis2* in the same

package. To visualize compositional shifts, we further ran non-metric multidimensional scaling

(NMDS) (*metaMDS*) on the Bray-Curtis dissimilarities and fitted species vectors onto the

NMDS ordination with *envfit*, which indicates the direction and strength of each species-

specific association with the ordination space. We also compared the relative abundances at

the genus level, using a binomial GLMM with block as a random effect and accounting for

overdispersion by including an additional observation-level random effect.

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 binomial GLM revealed a

significant three-way interaction between microbiome, temperature, and pesticide ($N = 650$, χ^2

$= 15.19$, $df = 3$, $p = 0.002$; 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 ($\chi^2 = 22.01$, $df = 3$, $p < 0.0001$) and microbiome ´pesticide   ($\chi^2 = 18.29$, $p <$

0.0001), as well as by all main effects (all $\chi^2 \geq 67.07$, $p < 0.001$; 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 ($\chi^2 = 0.68$, $df = 3$, $p = 0.878$) for this metric and was removed from the final model.

The simplified model revealed significant two-way interactions between microbiome and

temperature ($N = 650$, $\chi^2 = 8.06$, df $= 3$, $p = 0.042$) and between temperature and pesticide (χ^2

= 8.06, df = 1, p = 0.005; Fig. 1B, Supplementary Table S2). All main effects were again

significant (all χ^2 ³23.92, $p < 0.0001$).

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 none of the interactions were statistically significant and thus removed from the

model (N = 331, all χ^2 = ≤5.26, df = 3, $p \geq 0.15$), all experimental treatments exhibited highly

significant main effects on P_2 (all χ^2 ³99.60, p £0.0001; Fig. 1C, Supplementary Table S3).

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

(N = 120, $F_{2,106}$ = 4.78, p = 0.010; Fig. 1D, 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 F ³10.54, p £0.001)

A PERMANOVA controlling for block effects ($F_{1,35}$ = 0.20, p = 0.874) 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. 2A) 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 ³0.54, p £0.0001), in that both

Lactobacillus species showed positive (³0.68),   and all *Acetobacter* exhibited negative (£-

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 (³0.56).   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 ($N = 725$, $\chi^2 = 9.45$, df $= 1$, $p = 0.002$;

Supplementary Table S7) and female offspring ($N = 740$, $\chi^2 = 4.73$, df = 1, $p = 0.030$;

Supplementary Table S8, Fig. 3A,B), indicating that the effects of paternal stress exposure

were transmitted to the next generation. However, the paternal microbiome contributed only to

very weak and non-statistically significant trends for an interaction with temperature in either

offspring sex ($\chi^2 \pounds 6.38$, df = 3, $p = 0.10$), suggesting limited cross-generational effects on F_2

hatching.

The interactive effect of paternal temperature and pesticide exposure was also significant for

the fecundity of F_1 daughters ($N = 740$, $\chi^2 = 6.11$, df = 1, $p = 0.013$), along with a main effect

of the paternal microbiome composition ($\chi^2 = 8.91$, df = 3, $p = 0.030$; Fig. 3, Supplementary

Table S9). By contrast, the paternal effects on larval numbers in sons was limited to main

effects of temperature and pesticide exposure ($\chi^2 \geq 26.84$, df = 1, $p < 0.0001$), with no

contribution of the paternal microbiome ($\chi^2 = 0.52$, df = 3, $p = 0.915$; Fig. 3, 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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Author contributions

KM and SL conceived the study and acquired funding; KM, AM, ANDN, BE, SHS and RATS

collected the data; KM and SL conducted statistical analyses and drafted the manuscript, which

was reviewed and approved by all other authors.

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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. (D) 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.

A   B

Figure 2 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.

1006

1007 **Figure 3** Fitness consequences of paternal thermal and pesticide treatments on fitness measures

1008 in male (A, C) and female (B, D) offspring. Panels A and B depict the proportion of eggs

1009 hatched out of total number of eggs fertilized, panels C and D the fecundity either of the sons'

1010 mates (C) or of the daughters (D). Each circle represents the mean of all the replicates in that

1011 treatment combination with error bars corresponding to 95% confidence intervals.

Supplementary material

Table S1: Results from a generalized linear model on hatching success. The model assessed the impact of male microbiome (axenic, *Acetobacter tropicalis*, *Lactobacillus brevis*, control), temperature (24.5°C/36°C), and pesticide exposure (absent/present). Total sample size: $N = 650$.

Predictor	df	χ^2	P
Microbiome	3	215.696	**<0.001**
Temperature	1	93.332	**<0.001**
Pesticide	1	67.065	**<0.001**
Block	1	6.955	**0.008**
Microbiome × Temperature	3	22.007	**<0.001**
Microbiome × Pesticide	3	18.286	**<0.001**
Temperature × Pesticide	1	0.292	0.589
Microbiome × Temperature × Pesticide	3	15.190	**0.002**

Coefficients of the model described above.

Term	Estimate	SE	z	P
(Intercept)	0.889	0.082	10.847	**<0.001**
Microbiome[At]	1.501	0.141	10.624	**<0.001**
Microbiome[Lb]	0.855	0.133	6.442	**<0.001**
Microbiome[Control]	1.960	0.154	12.713	**<0.001**
Temperature[36°C]	-1.074	0.111	-9.661	**<0.001**
Pesticide[Present]	-0.855	0.104	-8.189	**<0.001**
Block[2]	0.107	0.040	2.637	**0.008**
Microbiome[At] × Temperature[36°C]	-0.698	0.184	-3.793	**<0.001**
Microbiome[Lb] × Temperature[36°C]	-0.500	0.171	-2.915	**0.004**
Microbiome[Control] × Temperature[36°C]	-0.717	0.189	-3.796	**<0.001**
Microbiome[At] × Pesticide[Present]	-0.704	0.173	-4.062	**<0.001**
Microbiome[Lb] × Pesticide[Present]	-0.355	0.166	-2.144	**0.032**
Microbiome[Control] × Pesticide[Present]	-0.483	0.186	-2.589	**0.010**
Temperature[36°C] × Pesticide[Present]	0.082	0.151	0.540	0.589
Microbiome[At] × Temperature[36°C] × Pesticide[Present]	0.877	0.236	3.721	**<0.001**
Microbiome[Lb] × Temperature[36°C] × Pesticide[Present]	0.542	0.226	2.400	**0.016**
Microbiome[Control] × Temperature[36°C] × Pesticide[Present]	0.576	0.239	2.405	**0.016**

Table S2: Results from a generalized linear model on the total number of larvae produced. The model assessed the impact of male microbiome (axenic, *Acetobacter tropicalis*, *Lactobacillus brevis*, control), temperature (24.5°C/36°C), and pesticide exposure (absent/present). The three-way interaction was removed due to non-significance ($P = 0.88$). Total sample size: $N = 650$.

Predictor	df	χ^2	P
Microbiome	3	207.693	**<0.001**
Temperature	1	85.063	**<0.001**
Pesticide	1	23.921	**<0.001**
Block	1	0.718	0.397
Microbiome × Temperature	3	8.223	**0.042**
Microbiome × Pesticide	3	4.264	0.234
Temperature × Pesticide	1	8.061	**0.005**

Coefficients of the model described above.

Term	Estimate	SE	z	P
(Intercept)	2.554	0.040	63.187	**<0.001**
Microbiome[At]	0.443	0.049	9.039	**<0.001**
Microbiome[Lb]	0.275	0.053	5.206	**<0.001**
Microbiome[Control]	0.652	0.047	13.873	**<0.001**
Temperature[36°C]	-0.521	0.057	-9.223	**<0.001**
Pesticide[Present]	-0.260	0.053	-4.891	**<0.001**
Block[2]	0.018	0.021	0.848	0.397
Microbiome[At] × Temperature[36°C]	0.152	0.069	2.190	**0.029**
Microbiome[Lb] × Temperature[36°C]	0.094	0.072	1.311	0.190
Microbiome[Control] × Temperature[36°C]	0.175	0.064	2.724	**0.006**
Microbiome[At] × Pesticide[Present]	0.021	0.066	0.318	0.750
Microbiome[Lb] × Pesticide[Present]	-0.054	0.069	-0.788	0.431
Microbiome[Control] × Pesticide[Present]	0.065	0.062	1.042	0.297
Temperature[36°C] × Pesticide[Present]	-0.126	0.045	-2.839	**0.005**

Table S3: Results from a generalized linear model on the proportion of second-male offspring (sperm offense ability). The model assessed the impact of male microbiome (axenic, *Acetobacter tropicalis*, *Lactobacillus brevis*, control), temperature (24.5°C/36°C), and pesticide exposure (absent/present). All interactions were sequentially removed due to non-significance ($P > 0.15$). Total sample size: $N = 331$.

Predictor	df	χ²	P
Microbiome	3	218.453	**<0.001**
Temperature	1	162.250	**<0.001**
Pesticide	1	99.596	**<0.001**
Block	1	0.827	0.363

Coefficients of the model described above.

Term	Estimate	SE	z	P
(Intercept)	0.397	0.067	5.902	**<0.001**
Microbiome[At]	0.700	0.068	10.320	**<0.001**
Microbiome[Lb]	0.356	0.068	5.252	**<0.001**
Microbiome[Control]	0.985	0.072	13.716	**<0.001**
Temperature[36°C]	-0.604	0.047	-12.738	**<0.001**
Pesticide[Present]	-0.476	0.048	-9.980	**<0.001**
Block[2]	0.043	0.048	0.910	0.363

Table S4: Results from a linear model on colony forming units. The model assessed the impact of male microbiome (axenic, *Acetobacter tropicalis*, *Lactobacillus brevis*, control), temperature (24.5°C/36°C), and pesticide exposure (absent/present). Total sample size: $N = 120$.

Predictor	df	F	P
Temperature	1	135.611	**<0.001**
Pesticide	1	146.557	**<0.001**
Microbiome	2	991.897	**<0.001**
Block	2	0.156	0.856
Temperature × Pesticide	1	11.281	**0.001**
Temperature × Microbiome	2	10.543	**<0.001**
Pesticide × Microbiome	2	43.073	**<0.001**
Temperature × Pesticide × Microbiome	2	4.778	**0.010**
Residuals	106		

Coefficients of the model described above.

Term	Estimate	SE	t	P
(Intercept)	4.530	0.010	470.489	**<0.001**
Temperature[36°C]	-0.152	0.013	-11.645	**<0.001**
Pesticide[Present]	-0.163	0.013	-12.106	**<0.001**
Microbiome[Lb]	0.166	0.013	12.706	**<0.001**
Microbiome[Control]	0.567	0.013	43.323	**<0.001**
Block[2]	0.003	0.005	0.510	0.611
Block[3]	-0.006	0.031	-0.187	0.852
Temperature[36°C] × Pesticide[Present]	0.063	0.019	3.359	**0.001**
Temperature[36°C] × Microbiome[Lb]	0.030	0.018	1.624	0.107
Temperature[36°C] × Microbiome[Control]	0.084	0.018	4.532	**<0.001**
Pesticide[Present] × Microbiome[Lb]	0.130	0.019	6.944	**<0.001**
Pesticide[Present] × Microbiome[Control]	0.166	0.019	8.851	**<0.001**
Temperature[36°C] × Pesticide[Present] × Microbiome[Lb]	-0.067	0.026	-2.559	**0.012**
Temperature[36°C] × Pesticide[Present] × Microbiome[Control]	-0.074	0.026	-2.792	**0.006**

Table S5: Results of a PERMANOVA examining the temperature and pesticide effects on relative bacterial abundances (based on colony-forming units) in the five-species consortium.

Predictor	df	Sum of squares	R^2	F	P
Temperature	1	0.004	0.263	13.882	**<0.001**
Pesticide	1	<0.001	0.022	1.157	0.314
Block	1	<0.001	0.004	0.202	0.874
Temperature × Pesticide	1	<0.001	0.048	2.553	*0.068*
Residual	35	0.011	0.663		
Total	39	0.017	1.000		

Table S6: Ordination of the Bray-Curtis dissimilarities between the relative abundances of the five bacterial species via non-metric multidimensional scaling (NMDS).

Species	NMDS1	NMDS2	R^2	P
A. tropicalis	-0.384	-0.923	0.920	**<0.001**
A. orientalis	-0.831	0.556	0.601	**<0.001**
A. pasteurianus	-0.751	0.660	0.539	**<0.001**
L. brevis	0.899	-0.439	0.887	**<0.001**
L. plantarum	0.678	0.735	0.826	**<0.001**

Table S7: Results from a binomial generalized linear mixed-effects model on hatching success among the eggs laid by the mates of the sons. The model assessed the impact of male microbiome (axenic, *Acetobacter tropicalis*, *Lactobacillus brevis*, control), temperature (24.5°C/36°C), and pesticide exposure (absent/present), incorporating sire to account for non-independence among siblings. The three-way interaction was removed due to non-significance ($P = 0.48$). Total sample size: $N = 725$.

Predictor	df	χ^2	P
Microbiome	3	0.903	0.825
Temperature	1	8.359	**0.004**
Pesticide	1	0.008	0.929
Block	1	5.924	**0.015**
Microbiome × Temperature	3	6.380	*0.095*
Microbiome × Pesticide	3	1.681	0.641
Temperature × Pesticide	1	9.451	**0.002**

Random effects variance components from the model described above.

Group	Term	SD	Variance
Sire	(Intercept)	0	0

Fixed effects estimates from the model described above.

Term	Estimate	SE	z	P
(Intercept)	2.163	0.103	21.076	**<0.001**
Microbiome[At]	-0.014	0.126	-0.113	0.910
Microbiome[Lb]	0.059	0.127	0.467	0.640
Microbiome[Control]	-0.052	0.127	-0.406	0.685
Temperature[36°C]	-0.337	0.117	-2.891	**0.004**
Pesticide[Present]	0.010	0.118	0.089	0.929
Block[2]	-0.125	0.051	-2.434	**0.015**
Microbiome[At] × Temperature[36°C]	0.008	0.147	0.054	0.957
Microbiome[Lb] × Temperature[36°C]	-0.192	0.143	-1.340	0.180
Microbiome[Control] × Temperature[36°C]	0.170	0.146	1.165	0.244
Microbiome[At] × Pesticide[Present]	0.072	0.147	0.489	0.625
Microbiome[Lb] × Pesticide[Present]	0.183	0.142	1.283	0.199
Microbiome[Control] × Pesticide[Present]	0.076	0.146	0.524	0.600
Temperature[36°C] × Pesticide[Present]	-0.317	0.103	-3.074	**0.002**

Table S8: Results from a binomial generalized linear mixed-effects model on hatching success among the eggs laid by the daughters. The model assessed the impact of male microbiome (axenic, *Acetobacter tropicalis*, *Lactobacillus brevis*, control), temperature (24.5°C/36°C), and pesticide exposure (absent/present), incorporating sire to account for non-independence among siblings. The three-way interaction was removed due to non-significance ($P = 0.87$). Total sample size: $N = 740$.

Predictor	df	χ^2	P
Microbiome	3	1.500	0.682
Temperature	1	17.866	**<0.001**
Pesticide	1	0.023	0.878
Block	1	7.816	**0.005**
Microbiome × Temperature	3	6.151	0.104
Microbiome × Pesticide	3	0.420	0.936
Temperature × Pesticide	1	4.733	**0.030**

Random effects variance components from the model described above.

Group	Term	SD	Variance
Sire	(Intercept)	0	0

Fixed effects estimates from the model described above.

Term	Estimate	SE	z	P
(Intercept)	2.240	0.097	23.120	**<0.001**
Microbiome[At]	0.085	0.126	0.675	0.499
Microbiome[Lb]	-0.024	0.127	-0.188	0.851
Microbiome[Control]	-0.062	0.126	-0.496	0.620
Temperature[36°C]	-0.478	0.113	-4.227	**<0.001**
Pesticide[Present]	-0.018	0.116	-0.153	0.878
Block[2]	-0.143	0.051	-2.796	**0.005**
Microbiome[At] × Temperature[36°C]	0.009	0.144	0.063	0.950
Microbiome[Lb] × Temperature[36°C]	0.085	0.144	0.591	0.555
Microbiome[Control] × Temperature[36°C]	0.319	0.146	2.184	**0.029**
Microbiome[At] × Pesticide[Present]	-0.019	0.143	-0.133	0.894
Microbiome[Lb] × Pesticide[Present]	0.069	0.144	0.480	0.631
Microbiome[Control] × Pesticide[Present]	0.008	0.146	0.054	0.957
Temperature[36°C] × Pesticide[Present]	-0.223	0.103	-2.176	**0.030**

Table S9: Results from a Poisson generalized linear mixed-effects model on the total number of larvae produced by the daughters. The model assessed the impact of male microbiome (axenic, *Acetobacter tropicalis*, *Lactobacillus brevis*, control), temperature (24.5°C/36°C), and pesticide exposure (absent/present), incorporating sire to account for non-independence among siblings. The three-way interaction was removed due to non-significance ($P = 0.22$). Total sample size: $N = 740$.

Predictor	df	χ^2	P
Microbiome	3	8.911	**0.030**
Temperature	1	29.042	**<0.001**
Pesticide	1	1.776	0.183
Block	1	15.554	**<0.001**
Microbiome × Temperature	3	3.148	0.369
Microbiome × Pesticide	3	2.930	0.403
Temperature × Pesticide	1	6.106	**0.013**

Random effects variance components from the model described above.

Group	Term	SD	Variance
Sire	(Intercept)	0	0

Fixed effects estimates from the model described above.

Term	Estimate	SE	z	P
(Intercept)	2.981	0.032	94.536	**<0.001**
Microbiome[At]	0.109	0.041	2.645	**0.008**
Microbiome[Lb]	0.007	0.042	0.162	0.872
Microbiome[Control]	0.051	0.042	1.214	0.225
Temperature[36°C]	-0.219	0.041	-5.389	**<0.001**
Pesticide[Present]	-0.053	0.040	-1.333	0.183
Block[2]	-0.071	0.018	-3.944	**<0.001**
Microbiome[At] × Temperature[36°C]	-0.088	0.052	-1.698	*0.089*
Microbiome[Lb] × Temperature[36°C]	-0.068	0.052	-1.303	0.192
Microbiome[Control] × Temperature[36°C]	-0.054	0.052	-1.038	0.299
Microbiome[At] × Pesticide[Present]	-0.055	0.051	-1.069	0.285
Microbiome[Lb] × Pesticide[Present]	0.024	0.052	0.467	0.641
Microbiome[Control] × Pesticide[Present]	-0.037	0.051	-0.722	0.470
Temperature[36°C] × Pesticide[Present]	-0.091	0.037	-2.471	**0.013**

Table S10: Results from a Poisson generalized linear mixed-effects model on the total number of larvae produced by the mates of the sons. The model assessed the impact of male microbiome (axenic, *Acetobacter tropicalis*, *Lactobacillus brevis*, control), temperature (24.5°C/36°C), and pesticide exposure (absent/present), incorporating sire to account for non-independence among siblings. The interactions were sequentially removed due to non-significance ($P \geq 0.20$). Total sample size: $N = 725$.

Predictor	df	χ^2	P
Microbiome	3	0.516	0.915
Temperature	1	367.958	**<0.001**
Pesticide	1	26.840	**<0.001**
Block	1	11.132	**<0.001**

Random effects variance components from the model described above.

Group	Term	SD	Variance
Sire	(Intercept)	0	0

Fixed effects estimates from the model described above.

Term	Estimate	SE	z	P
(Intercept)	3.044	0.024	128.264	**<0.001**
Microbiome[At]	0.016	0.026	0.589	0.556
Microbiome[Lb]	-0.001	0.026	-0.042	0.967
Microbiome[Control]	0.003	0.026	0.122	0.903
Temperature[36°C]	-0.356	0.019	-19.182	**<0.001**
Pesticide[Present]	-0.095	0.018	-5.181	**<0.001**
Block[2]	-0.061	0.018	-3.337	**<0.001**