# Honey bee queens are vulnerable to heat-induced loss of fertility

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**Abstract**

All species need to reproduce to maintain viable populations, but heat stress kills sperm cells across the animal kingdom and rising frequencies of heatwaves are a threat to biodiversity. Honey bees (*Apis mellifera*) are globally distributed micro-livestock; therefore, they could serve as environmental biomonitors for fertility losses. Here, we found that queens have two potential routes of temperature-stress exposure: within colonies and during routine shipping. Our data suggest that temperatures of 15 to 38°C are safe for queens at a tolerance threshold of 11.5% loss of sperm viability, which is the viability difference associated with queen failure in the field. Heat shock activates expression of specific stress-response proteins in the spermatheca, which could serve as molecular biomarkers (indicators) for heat

22 stress. This protein fingerprint may eventually enable surveys for the prevalence of heat-induced loss of

23 sperm viability in diverse landscapes as part of a biomonitoring program.

24 Climate change is threatening biodiversity around the globe[1-3], and one potential driver is through heat-

25 induced reductions in fertility[4-6]. The impact of heat on fertility is far-reaching in the animal kingdom,

26 affecting mammals[7-11], birds[12], fish[13], nematodes[14], and insects[4,15-21]. At temperatures of 40-43 □C,

27 spermatogenesis is compromised[22], sperm viability drops[4,18,19], sperm are less competitive[4], and motility

28 is compromised[15,23,24]. Extreme weather events such as heatwaves are increasing in frequency and

29 severity[25-27], which could have widespread effects on populations via reduced reproductive output[4-6].

30 Insects and other ectothermic animals are especially vulnerable to changes in local temperatures

31 because, unlike mammals, they are less able to thermoregulate. Insects and are critical components of

32 ecosystems and agriculture, with economic estimates placing the global value of insect pollination at

33 approximately €153 billion annually[28]. Worryingly, declines in insect populations[29] and pollinating

34 species[30-34] have already been reported, with habitat destruction, range compression, pesticide residues,

35 diseases, and their interactions commonly reported as potential drivers[28,35,36]. However, there has been

36 relatively little research on the effects of heat on pollinating insect reproduction[18,19].

37 Young honey bee queens have one brief mating period early in life, and store the sperm they acquire for

38 the rest of their lives (up to 5 years)[37]. As the sole egg-layer, colony productivity directly depends on the

39 queen's reproductive output, which in turn depends on the viability and abundance of her stored

40 sperm[18,38,39].

41 Like other insects, individual honey bees are ectothermic, but colonies can thermoregulate and maintain

42 stable core temperatures of around 35°C in the brood nest[40]. Although colonies can persist in regions

43 with extreme heat, evidence suggests that extreme ambient temperatures (38 - 46°C) are associated

44 with colony losses[41]. Furthermore, internal hive temperatures positively correlate with ambient

temperatures above 18°C, and brood nest temperatures can rise upwards of 37°C, both under natural

conditions[42] and during simulated heatwaves[43]. Hives occasionally experience spikes of > 40°C[44],

suggesting that queens could be vulnerable to temperature extremes even inside the hive.

Honey bees have excellent potential for being temperature stress biomonitors. Although we do not

expect them to be sensitive sentinels, other attributes make honey bees amenable to a biomonitoring

program: they are a globally distributed, managed species, so they are readily available in almost any

geographic region, and they are already accepted as effective biomonitors for pollution[45]. If we begin to

observe signs of heat stress in honey bees colonies, that would signal a worrisome risk of reduced

reproductive output for ectothermic species.

Here, we begin to explore honey bees' utility as temperature stress biomonitors. We monitored

temperature fluctuations in colonies under extreme weather conditions, establishing that damaging

intra-hive temperatures can occur. Next, we tested a range of temperatures and exposure durations to

determine thresholds above which queen quality is likely to be compromised. We then investigated the

biochemical basis of heat-induced sperm viability reduction in queens and drones using quantitative

proteomics, which showed how heat stress alters protein expression of reproductive tissues. The

specific set of upregulated proteins we identified may eventually serve as diagnostic tools to elucidate

causes of queen failure and eventually enable regional surveys of heat stress as part of an

environmental temperature biomonitoring program.

**Results and Discussion**

*Sperm viability losses associated with queen failure*

To establish how much of a reduction in sperm viability is associated with field-observable reduced

reproductive output (and associated economic losses for beekeepers), we collected queens rated as

'failing' (N = 58) and 'healthy' (N = 55) by beekeepers and measured the queens' stored sperm viability

(**Fig 1a**). We found that the failed and healthy viability data were normally distributed (Shapiro test, P = 0.18 and 0.11, respectively), and that failed queens had significantly lower sperm viability (Student's t test, P = 5.8E-06, F = 28.16), with an average drop of 11.5%. We then set an 11.5% viability drop as the tolerance threshold in subsequent experiments aimed at identifying critical temperatures beyond which queens are at risk of substantial loss of stored sperm viability.

*Temperature spikes occur in colonies and shipments*

To document if routine shipping poses a threat of adverse temperature exposure to queens, we tracked the temperatures of eight domestic queen shipments (seven via ground transportation, one via air; **Fig 1b**). We found that even in these shipments, which were not deliberately timed to occur during extreme weather events, one package experienced a temperature spike to 38°C and one dropped to 4°C. Since honey bees cannot adequately thermoregulate in queen cages, extreme ambient temperatures are a hazard for shipping. However, little is known about a whole colony's ability to thermoregulate in the face of extreme heat.

To gain a more complete picture of temperature fluctuations within colonies, we recorded temperatures throughout the brood nest (loggers placed between each frame of three 10-frame hives) during extreme heat in August in El Centro, California. The ambient temperatures, measured in the shade beneath each hive, reached up to 45°C (**Fig 1c**). In all three hives, the temperature at the two outer-most frames spiked to upwards of 40°C for 2 - 5 h, and in two of the hives, temperatures exceeded 38°C even one or two frames closer to the core. Therefore, the colony's ability to thermoregulate begins to break down in extreme heat, and queens can be vulnerable to temperature stress inside the hive.

*Defining critical exposure and duration thresholds*

Previous research has shown that both cold (4°C) and hot (42°C) temperatures reduce stored sperm viability in queens[18], but refined tolerance thresholds and biologically relevant viability losses are not

known. To determine critical temperature and duration thresholds, we compared stored sperm viability

across a temperature and duration gradient (5, 10, 15, 25, 38, 40 and 42°C, exposed for 1, 2 or 4 h

followed by a 2 d recovery period) (**Fig 2a**). Not all experimental groups' data were normally distributed

(Shapiro test, P < 0.05); therefore, we analyzed it with a Kruskal-Wallis test for non-parametric data.

There was a significant effect of temperature for the 2 h ($x^2$ = 15.6, P = 0.016) and 4 h ($x^2$ = 17.9, P =

0.0065) treatments, while not at 1 h ($x^2$ = 9.12, P = 0.17). A Dunnett's post hoc test revealed that the

only temperatures that were significantly different from the control (25°C) were the 2 h, 10°C treatment

(P = 0.045) and the 4 h, 42°C treatment (P = 0.00057), at a family-wise error rate of α = 0.05. The 2 h and

4 h data were then pooled and optimally fit to a cubic polynomial regression ($R^2$ = 0.092, P = 0.012; **Fig**

**2b**) to find the temperature tolerance thresholds for queens, given a pre-defined maximum acceptable

drop in sperm viability (11.5%). This model suggests that 15.2 – 38.2°C is the suggested "safe zone" with

minimal loss of viability for 2 - 4 h exposures.

To test effects of heat on ejaculated sperm viability, we exposed single-drone ejaculates to 42°C for 0, 2,

or 4 h, followed by a 2 d recovery period at 25°C **(Fig 2c)**. These data were normally distributed (Shapiro

test, P = 0.18); therefore, we used a two-way ANOVA for analysis. We found that responses differed

depending on the colony source, but heat dramatically decreased viability by 35% after both 2 and 4 h

(factors: time and colony, $P_{(time)}$ = 1.2E-07, $F_{(time)}$ = 24 $df_{(time)}$ = 2; $P_{(colony)}$ = 0.00015, $F_{(colony)}$ = 11, $df_{(colony)}$ =

2). Heat-shock therefore affects stored and ejaculated sperm viability at similar magnitudes. Drones

could also be appropriate biomonitors of heat-stress, as their sperm is also sensitive to changes in

temperature. However, drones are not as long-lived as queens and are only seasonally available.

*Sex biases in heat-stress survival*

Sturup *et al.* previously reported that drones are mortally sensitive to heat[19]; however, queens are

typically tolerant of stressful conditions. As a biomonitor, a favourable feature would be to survive

through heat stress while accumulating a physiological and molecular record of the stress event(s). We

compared drone, queen, and worker survival over time at 25°C, 38°C, and 42°C, confirming that drones,

but not queens, are indeed mortally sensitive to heat (Log-rank test, P < 0.00001; **Fig 3a, FigS1)**. Fifty-

four percent of drones died over the course of 6 h at 42°C, whereas every queen survived. We also

found that drones are more sensitive to heat than workers, which have a similar lifespan to drones but

are non-reproductive females.

In this experiment, drones and workers were from local colonies, while queens were either from a local

origin or imported from Hawaii and Australia. If bees are to be used as a global biomonitor for

temperature stress, an important experiment will be to determine if there are differences in survival,

physiological response, or biochemical response to heat between genetic stocks that may be adapted to

hotter or cooler climates.

Honey bees' sex-biased heat sensitivity is puzzling because drones and queens spend most of their lives

inside the hive and can avoid participating in mating flights during hot weather. Therefore, they are

exposed to similar environmental conditions, and based on this, one might expect them to have similar

physiological tolerance thresholds. However, the ability of a colony to survive and produce reproductive

individuals directly depends on the survival of individual queens (there is only one per colony), and not

individual drones (hundreds per colony). Natural selection may have favoured high survivorship of

queens, as evidenced by not only their long lifespan (up to 5 y) but also their high tolerance to heat

stress, despite the death of their stored sperm. To our knowledge, sex biases in thermal tolerance for

other social insects has not yet been investigated, as critical thermal tolerance studies have focused on

workers or on male fertility alone.[46-55]

Next, we investigated sex biases in heat tolerance for two solitary insect species—fruit flies (*Drosophila*

*melanogaster*) and brown marmorated stink bugs (*Halyomorpha halys*). The stink bugs have a similar

body size and thermal tolerance range as honey bees[56] and their global distribution has expanded to

cover four continents, making them a potential candidate biomonitor. Fruit flies have a much smaller

body size but are also widely distributed, so they could be candidate biomonitors too. We found that

both male and female stink bugs and fruit flies readily die with heat (**Fig 3b and c**), meaning that they

cannot accumulate a physiological or molecular record of a heat stress event and have limited utility for

observing impacts of heat on fertility through time. However, these data do indicate another worrying

trend: that exceptionally extreme temperatures may reduce insect populations through direct kills, in

addition to reducing reproductive output if they survive. We found no difference between males' and

females' heat sensitivities for fruit flies and a slight opposite (female) biased heat sensitivity in stink bugs

($P = 0.015$, log rank test). In contrast, the high survivorship of honey bee queens makes them a good

candidate biomonitor, should they possess molecular signatures indicative of heat stress when it occurs.

*Heat activates specific proteins in the spermatheca*

Sperm longevity is enabled by molecular processes that reduce oxidative damage and maintain sperm in

a quiescent metabolic state. For example, the spermatheca is a highly anaerobic environment, which

helps prevent reactive oxygen species (ROS) formation[57]. Enzymes that further limit damage from ROS

are also upregulated in mated queens compared to virgins[58,59], and ROS damage leads to infertility in

mammals[60,61]. Heat is well known to lead to oxidative stress[62]; therefore, we hypothesized that queens

may combat heat-stress by upregulating enzymes that mitigate oxidative damage. Additionally,

glyceraldehyde-3-phosphate dehydrogenase (GAPDH) has been previously implicated in stored sperm

longevity, since metabolic activity measurements of stored sperm supplemented with its substrate

(glyceraldehyde-3-phosphate) improved viability and produced the highest molar ratio of ATP via

anaerobic catabolism[57]. Heat-induced changes in GAPDH expression could therefore also impact sperm

viability.

To test these hypotheses, we compared expression of ROS mitigating enzymes (superoxide dismutases

(SOD1, 2, and 3) and catalase) as well as GAPDH in heat-shocked and non-heat-shocked virgin

spermathecae, mated spermathecae, and ejaculated semen. Stored sperm are reportedly

transcriptionally active in queens to some degree[57], although whether this is true in general has been a

matter of debate across species[63]. It is not known with certainty whether ejaculated sperm are

transcriptionally active; nevertheless, analyzing ejaculates, virgin spermathecae and mated

spermathecae helped us to disentangle the male versus female origins of expression in sperm-filled,

mated spermathecae. We found that heat-shock did not upregulate expression of ROS-mitigating

enzymes, nor GAPDH (**Supplementary Figure 1**); rather, all enzymes were consistently (but not

significantly) downregulated with heat (by 10-30%). Queens must therefore employ other strategies, if

any, to combat heat stress.

A multitude of other proteins could also be responsible for mitigating damage from heat—most

obviously, members of the heat-shock protein (HSP) family[24,64-66]. HSPs generally function as molecular

chaperones that stabilize proteins, refold damaged proteins, and prevent protein aggregation, but they

can have diverse functions in specific contexts and their precise role in the honey bee spermatheca is

unknown. Some HSPs contain an ATPase domain and require ATP to function (*e.g.,* HSP70s, HSP90s,

HSP110s), while others operate independently of ATP (*e.g.,* HSP10s, HSP20s, HSP60s). In addition, since

glyceraldehyde-3-phosphate yields the most ATP per unit via anaerobic catabolism of any tested

substrate and significantly increased sperm longevity[57], this implies that ATP usage economy is a critical

factor for maintaining viable sperm. Therefore, we expect that ATP-independent HSPs should be

upregulated with heat stress in spermathecae, and ATP-dependent HSPs (or a mix of ATP-dependent

and ATP-independent HSPs) should be upregulated as a result of heat stress in other tissues. In addition,

some ATP-independent short HSPs (sHSPs, typically 20-28 kDa) suppress ROS generation while

preventing protein aggregates and apoptosis[62,67]. Since molecular processes that reduce oxidative

damage favour sperm longevity, we hypothesized that heat should induce expression of sHSPs in the

spermatheca.

To determine which HSPs were upregulated with heat-shock, we compared global protein expression

profiles in heat-shocked and non-heat-shocked mated and virgin spermathecae, ejaculates, and ovaries

**(Fig 4a, Supplementary Figure 2)**. We hypothesized that the heat-shock response should both mitigate

ROS production and conserve ATP in the spermatheca, but this ATP-conservation may not be as critical

in the ovaries where the ATP economy is not expected to be as tightly controlled. Of the 2,778 protein

groups identified in the spermathecae and ejaculates, only five were significantly up-regulated with heat

(5% FDR), all of which were identified in the mated and virgin spermathecae. All five of the proteins

were unique, ATP-independent sHSPs (accessions: XP_001120194.1, XP_001119884.1, XP_395659.1,

XP_001120006.2, and XP_026294937.1) **(Fig 4b)**. In heat-shocked virgin spermathecae, two of the same

sHSPs (XP_395659.1 and XP_001120006.2) were also significantly upregulated, and all mirrored the

expression patterns in the spermathecae of heat-shocked mated queen (even if not significant),

indicating that this is a queen-derived, and not a sperm-derived, response **(Fig 4c and d)**. By contrast,

the most strongly upregulated protein in heat-shocked ovaries was HSP70—an ATP-dependent HSP—

and no sHSPs were upregulated in this tissue, supporting our initial hypotheses **(Fig 4e)**.

As expected, the significantly enriched Gene Ontology (GO) terms were all related to responses to heat

and stress in the spermathecae **(Fig 5a and b)**. However, the only significantly enriched GO term in the

semen analysis was related to the electron transfer activity **(Fig 5c)**, driven by a heat-induced down-

regulation of the proteins linked to this GO term **(Fig 5d)**, suggesting that the sperm may be less able to

produce the large amounts of ATP necessary for flagellar beating. This is consistent with the findings of

Gong *et al.*, who found that heat stress at 42°C impaired mitochondrial function, reduced electron

transport chain complexes' activities, and lowered total cellular ATP[23]. Numerous proteins (none of

which were HSPs) were downregulated in heat-shocked spermathecae, but based on the GO term

enrichment analysis and manual inspection of their functions, it is unclear what their biological

significance is. It is possible that they are degradation products of heat-killed sperm, but since these

proteins were largely absent in the semen samples, we cannot confirm this hypothesis.

Twenty HSPs were identified in spermathecae overall and 13 were identified in the semen **(Fig 6)**;

however, the precise functions of specific honey bee HSPs are largely unknown. To gain insight into

potential roles of the five differentially expressed HSPs we identified, we compared their sequences to

annotated sequences in other species and identified putative protein domains using NCBI's basic local

alignment search tool (BLAST)[68]. All five of the HSPs contain one or more alpha crystallin domains, which

is characteristic of small HSPs (sHSPs). Four of these HSPs are within the expected molecular weight

range, and one of the proteins (XP_026294937.1) is predicted to be 56.7 kDa (and contains two alpha

crystallin domains instead of one), highlighting that HSPs should not necessarily be categorized based on

molecular weight alone. All five of the honey bee sHSPs are paralogous to the *D. melanogaster* gene

*l(2)efl* (also known as CRYAB). In *Drosophila*, upregulation of this gene causes increased lifespan of

individual flies[69]. CRYAB and other sHSPs are highly conserved in both vertebrates and invertebrates,[70]

but is by far the best studied in human. In humans, sHSP upregulation is associated with anti-apoptotic

properties, as well as mitigating ROS production[62,66,71,72]. Their up-regulation in heat-shocked testes is

thought to help compensate for the damaging effects of heat[71], and we speculate that they are playing a

similar role in the spermathecae. Queens with strongly up-regulated sHSPs may therefore be better able

to counter-act ROS production, sperm death, and ultimately maintain longevity. However, it remains

unknown if the honey bee paralogs have functionally diverged from those in other species.

Other researchers have suggested that in mammals, some ATP-dependent HSPs (*e.g.,* HSP70s and

HSP90s) may be important for maintaining male fertility via quality control of sperm[66,73]. Unlike sHSPs,

these HSPs appear to be pro-apoptotic factors and could theoretically help prevent damaged sperm

from being able to fertilize an egg. Neither queen spermathecae nor drone ejaculates provide evidence

supporting this strategy of quality control in honey bees; in this experiment, none of the HSPs that were

up-regulated with heat in spermathecae or semen contained an ATP-binding nor ATPase domain, which

are characteristics of HSP70s and HSP90s but not the sHSPs (**Figure 5 and 6**)[66]. Rather, HSP70 was only

upregulated in the ovaries, which does not directly participate in sperm maintenance.

In mammals, sHSPs are upregulated in testes after heating, but so are ATP-consuming proteins like

HSP105, HSP70-1, HSP70-2, and HSP90[74-76]. We speculate that the energetic cost associated with

ensuring high sperm quality is advantageous in mammals because it helps reduce the risk of an egg

going unfertilized, which would produce no progeny. However, the honey bee's differing strategy of

upregulating only the ATP-independent sHSPs in the spermatheca is consistent with a tightly controlled

ATP usage economy, as has been previously suggested[37,57]. The ATP-independent sHSPs have the dual

purpose of also limiting oxidative damage and conserving ATP. The significant enrichment for

differentially expressed proteins involved in multiple nucleotide metabolic processes, including ATP, in

the transition from virgin to mated spermathecae (**Supplementary Figure 2**) supports the notion that

regulating ATP production and consumption is critical for maintaining stored sperm viability.

Moreover, analyzing heat-shocked mated queen ovaries revealed that HSP70—an ATP-dependent HSP—

was uniquely upregulated in this tissue (**Fig 5 and 6**). This observation is consistent with selection for

ATP-consuming quality control mechanisms when a failed fertilization event fails to produce offspring (in

this case, when a non-viable egg meets a viable sperm). Overall, these data indicate that upregulation of

specific sHSPs is not a general indicator of cellular stress, since it was not observed in the ovaries.

Indeed, the ovaries appear not to express most sHSPs at all, whereas they were abundantly expressed

even in non-heat-shocked spermathecae.

Finally, we compared protein expression in spermathecae, fat bodies, and ovaries between 11 queens

that failed due to unknown causes and 11 age-matched, apiary-matched healthy queens. We identified

1,219, 1,640, and 1,782 proteins, respectively, but did not find any significant expression differences at

10% FDR, indicating that there is not one universal signature of failure (**Supplementary Figure 3**).

Rather, we suspect that different stressors alter protein expression in these tissues in different ways,

and that no significant differences were found because it is highly unlikely that the queens all failed from

the same cause.

We propose that the sHSP response of the spermathecae may serve as a post-queen-failure biomarker

of heat stress which could help diagnose causes of colony failure in the field and simultaneously provide

an indication of risks for heat-induced loss of fertility for other species. Beekeepers routinely replace

queens every 1-2 y, and these queens could be banked for biomarker testing as part of a surveillance

program. Future experiments should include a blind heat-shock trial to determine a) if previously heat-

shocked queens can be reliably distinguished from non-heat-shocked queens based on these

biomarkers, b) how long the heat-shock proteomic signature lasts, and c) if other stressors produce

proteomic signatures that overlap with the heat-shock signature.

**Conclusion**

Our experiments show that temperature stress deeply damages both stored and ejaculated honey bee

sperm viability, that queens are vulnerable to temperature changes both in colonies and during

transport, and that temperatures ranging between 15°C and 38°C for 2 - 4 h are generally safe for

queens. Honey bees have a strong sex bias in heat tolerance, with females being highly tolerant—a bias

which does not exist in the two solitary insect species we tested (*H. halys* and *D. melanogaster*). Future

research should investigate if this sex-biased heat tolerance is also present in other Hymenopterans in

order to better understand the evolutionary origin. Upon heat-shock, queens upregulate ATP-

independent HSPs in their spermathecae, which both minimizes ATP consumption and could provide

beneficial anti-apoptotic properties. In contrast, HSP70 (an ATP-consuming HSP) is upregulated in

ovaries. Once validated in field trials, these protein signatures could serve as biomarkers for heat stress

enabling longitudinal surveys for the prevalence of heat-induced loss of sperm viability in diverse

landscapes as part of a biomonitoring program.

**Methods**

*Sperm viability assays*

Honey bee queens (Kona Queens supplied in a single shipment) were treated at one of five different

temperatures (5, 10, 15, 25, 38, 40, and 42°C) for 1, 2, or 4 hours, then held at 25°C for 2 d. The

temperature range was chosen because previous research showed that 4°C and 8°C were sufficiently

cold to reduce sperm viability, and that 40 - 42°C was sufficiently hot.[18] Therefore, more temperatures

were chosen at the cold (5, 10, and 15°C) and hot (38, 40, and 42°C) extremes to try to capture the

critical point at which the viability begins to drop. We chose 25°C as the control temperature, rather

than 35°C, because these queens were obtained from a commercial supplier and queens are not held at

hive temperature during transport. While a 35°C treatment group would be an appropriate control, it

would not be meaningful in these circumstances.

Fourteen queens (replicates) were included in the 25°C treatment (negative control), whereas 8 or 9

queens were included in all other temperatures and exposure durations (see **Supplementary Table 1** for

specific replication information). Following this, queens were beheaded, and their spermathecae were

dissected with fine forceps. The spermathecae were gently agitated with a pipet tip in 100 µl Buffer D

(17 mM D-glucose, 54 mM KCl, 25 mM $NaHCO_3$, 83 mM $Na_3C_6H_5O_7$) to break them open and release the

sperm. Sperm viability was determined using a live/dead sperm viability kit (Thermo) following the

protocols of Collins and Donoghue[77]. Briefly, the SYBR14 dye was diluted 1:9 in DMSO. Two microlitres

of the diluted SYBR14 dye and 4 µl of propidium iodide were gently mixed with the sperm and incubated

for 15 minutes in the dark. Two microlitres of the mixture was then added to a glass microscope slide

and viewed under a fluorescent microscope. Live (green) and red (dead) sperm were counted until 100

cells were observed, covering multiple fields of view. Unless otherwise reported, all statistical analyses

were performed in R (v3.5.1). First, the data were tested for normality using a Shapiro test. The data was

not normally distributed, we used a non-parametric test (Kruskal Wallis) to investigate the effects of

temperature on viability for each duration separately. When a significant effect of temperature was

identified, we performed a post-hoc Dunnett's test to identify significant contrasts to the 25°C control.

To identify the best-fitting linear model, we pooled the 2 h and 4 h data and performed linear

regressions using temperature as a continuous variable, testing exponents 1 - 4 to identify the optimal

fit (highest $R^2$).

Drones were harvested from three different colonies headed by Kona queens with unknown

relatedness. The colonies were kept in Beaverlodge, Alberta. Semen was collected with glass capillaries

according to the methods of Collins and Donoghue[77]. Briefly, we pinched drone abdomens with a rolling

motion from the anterior to posterior end to expel the endophallus and semen. The semen was

collected by first filling glass capillaries with 1 µl Buffer D, then drawing up the semen via capillary action

(avoiding the white mucus secretions). Capillaries were then filled with a further 1 µl of Buffer D to

prevent the sample from drying out, and both ends were wrapped with parafilm. This technique

typically yielded 0.5-1.0 µl of semen per sample. Semen samples were then heat-shocked at 42°C for 0,

2, or 4 h, then allowed to recover at 25°C for 2 d. Depending on the colony, 5 or 6 drones were sampled

for each time point (see **Supplementary Table 2** for complete replication information). We chose a

lower temperature for semen recovery because ejaculated drone semen can be maintained at room

temperature for several weeks while retaining high viability[78]. Viability assays for these semen samples

was performed following the same methods as for spermathecae. Data were analyzed by a Shapiro test

and Levene's median test to confirm normal distribution and evaluate the validity of the assumption of

equal variance, respectively. The data passed both tests, so a two-way ANOVA (factors: time, colony)

was performed, followed by a Tukey HSD test.

*Recording temperatures during shipments*

We arranged seven shipments of locally produced (BC) queens via ground transportation from Kettle

Valley Queens, Nicola Valley Honey, Wild Antho, Campells Gold Honey, Heather Meadows Honey Farm,

Six Legs Good Apiaries, and Wildwood Queens (located in Grand Forks, Merrit, Armstrong, Abbotsford,

Telka, Surrey, and Powell River, respectively) to the University of British Columbia, Vancouver, in the

summer of 2019. These queens (7-8 queens per shipment) were all considered to be "good" queens by

the donating bee breeders based on their laying pattern. These queens cumulatively make up the

"healthy" queen cohort (N = 55 queens total). An additional shipment travelled from Edmonton to UBC

Vancouver via air freight. All shipments were accompanied by two temperature data loggers (B-series

WatchDog loggers, Spectrum Technologies) set to record the temperature every 10 minutes for the

duration of the shipment.

339
340    *Failed queen viability survey*
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We solicited samples of failed queens, as rated by beekeepers, from throughout BC in the summer of

2019. Reported reasons for designating the queens as 'failed' included poor brood pattern, drone laying,

poor population build-up, disease symptoms, injury, small size, and worker rejection. These queens (N =

58) make up the "failed" queen cohort. We measured the sperm viability of all failed and healthy queens

using the same live/dead sperm staining kit as described under "Sperm Viability Assays." These queens

were not age-matched. Therefore, the tolerance threshold loss of viability we set using these queens is

likely a conservative estimate.

*Hive temperature recording*

To record the internal and external temperatures of colonies, we placed temperature loggers inside

three standard, 10-frame colonies in El Centro, California, from August 23rd to September 6th, 2017. The

hottest day (the data shown) was August 26th. Loggers were set to record the temperature every 10

minutes and were placed between each frame of the hive. Hives consisted of 10 deep frames in a single

wooden Langstroth brood box with a medium depth box on top of the brood chamber and a migratory

wooden cover. The ambient temperatures were recorded with a temperature logger placed in the shade

beneath each hive.

*Heat-shock survival*

For honey bee heat-shock tests, drones and workers were collected by retrieving a frame of capped

brood from a hive and allowing the bees to emerge in an incubator. Newly emerged bees were marked

with a paint pen and returned to the colony to age for one week, at which time they were recaptured

and caged in California mini cages. For drone heat-shock tests, one drone was added per cage along with

malleable candy (icing sugar-based) and five worker attendants. A total of 199 drones were caged in the

following experimental groups: 42°C heat (50), 38°C heat (50), and 25°C (99) for six hours (all at 60%

relative humidity). Every hour, the number of drones that perished was recorded. Worker heat stress

tests were conducted independently with six workers per cage (54 workers per group) held at 42°C and

25°C.

Queens were from a variety of sources (local, Hawaii, and Australia) and their ages ranged from

approximately 3 - 5 weeks. They were kept in California mini-cages with five worker attendants each and

held at 42°C, 38°C, or 25°C for either 1, 2, or 4 h as part of other experiments (for viability

measurements and proteomics). Relative humidity varied between 40 and 80%, but this did not have an

effect of survival (100% of queens survived in both cases). Eight queens were held at 42°C for 6 h at a

constant 60% relative humidity specifically for survival analysis. See **Supplementary Figure 4** for sample

sizes and risk tables for each treatment group. No queens died in these tests; therefore it was not

necessary to account for geographic origin in statistical analyses.

Male and female 3- to 10-day-old Canton S wild type fruit flies were held at 38°C and 25°C for six hours

in *Drosophila* vials with media (50 males and 50 females). Loss of motility was recorded every hour. We

used this as the endpoint because fruit flies will become paralyzed with heat, but recover motility after

several hours (in some cases, overnight) at cooler temperatures. Control female flies were maintained

for a further week after the experiment to confirm that the majority of them had successfully mated

prior to the heat stress tests.

Male and female stink bugs were reared in the laboratory according to standard protocols[79]. Stink bugs

which transitioned from nymphs to adults 3 - 7 d prior were transferred to ventilated 500 ml volume

plastic cages with a piece of moist paper towel (3 - 6 stink bugs per cage). They were heat stressed at

42°C (55 females and 41 males) or held at 25°C (36 females and 24 males) for 6 h. Only mated females

carrying eggs were included in the experiment, as determined by post-stress dissection.

In all cases, Kaplan-Meier survival curves were generated in R and compared using log-rank tests. See

**Supplementary Figure 3** for risk tables and sample size information for survival tests for all species.

*Heat-shock for proteomics*

Our experimental design for the proteomics experiments was to compare heat-shocked and non heat-

shocked treatments of three tissues: virgin spermathecae, mated spermathecae, and ejaculated semen

(N = 10 each for all but the semen, which was N = 5 where each N was a pooled sample of five drones

from one colony). For the mated spermathecae, expression differences induced by heat-shock would be

the sum of any expression differences that may have occurred in the queen's cells and in the sperm

cells. The virgin spermathecae, however, do not contain sperm so that response to heat-shock is purely

from the queen.

Honey bee colonies were maintained in an apiary at the University of British Columbia. During the

summer of 2018, 40 queens were reared from a single colony of local origin and half were allowed to

open mate, while the other half were kept as virgins in plastic queen cages. Two weeks after emergence,

the virgin queens were given two, eight-minute carbon dioxide treatments on sequential days, then re-

introduced to their nucleus colonies. This process stimulates virgin queens to begin laying[80], and we

conducted these treatments in order to minimize the physiological differences between virgin and

mated queens.

Virgin and mated queens were retrieved from their nucleus colonies and half of each (10) were

subjected to heat-shock (42°C, 2 h), and then maintained at 30°C for 2 d. The other half were held only

at 30°C for 2 d. Four to six weeks after mating, the queens were anesthetized with carbon dioxide,

beheaded, then their spermathecae were removed with fine forceps. Both ovaries were also removed

and weighed.

During the same summer, 200 drones from a different colony in the same apiary were collected and

maintained in the laboratory overnight at ambient temperature with excess syrup (50% sucrose). The

next day, semen was harvested with glass capillaries according to the methods described above.

Because many drones were not sexually mature, 60 semen samples (out of the 200 drones) were

collected. Capillaries were placed in petri dishes and half (30) were heat-shocked as described above,

then kept at 25°C for 2 d. The other half were only kept at 25°C for 2 d. Ten samples from each

experimental group were used for sperm viability assays as described above.

*Proteomics sample preparation*

Semen and spermatheca samples were homogenized in 2 ml screw-cap tubes containing 100 µl of lysis

buffer (6 M guanidinium chloride, 100 mM Tris, pH 8.5) and four ceramic beads. The homogenizer

(Precellys 24, Bertin Instruments) was set to 6,500 $s^{-1}$ for 30 s, then samples were centrifuged (16,000

rcf, 10 min, 4°C) to remove debris. Supernatants were transferred to a new tube and diluted 1:1 with

$dH_2O$. Protein was precipitated by adding four volumes of ice-cold acetone and incubating overnight at -

20°C. The precipitated protein was pelleted and washed twice with 500 µl of 80% acetone, then the

pellet was allowed to air dry (ca. 5 min) prior to solubilization in 50 µl of digestion buffer (6 M urea, 2 M

thiourea).

Approximately 25 micrograms of protein were reduced (0.5 µg dithiothreitol, 20 min), alkylated (2.5 µg

iodoacetamide, 30 min, dark), and digested (0.5 µg Lys-C for 3 h, then 0.5 µg trypsin overnight). Digested

peptides were acidified with one volume of 1% trifluoroacetic acid and desalted with high-capacity

STAGE tips as previously described[81]. Eluted samples were dried (SpeedVac, Eppendorf, 45 min) and

resuspended in Buffer A (0.1% formic acid). Peptide concentrations were determined using a NanoDrop

(Thermo, 280 nm) and sample orders were randomized for liquid chromatography-tandem mass

spectrometry (LC-MS/MS) analysis.

*LC-MS/MS data acquisition and analysis*

Peptides (0.5 µg for each sample) were injected on an EASY-nLC 1000 liquid chromatography system

(Thermo) coupled to an Impact II Q-TOF mass spectrometer (Bruker), essentially as previously

described[82]. The LC system included a fused-silica (5 µm Aqua C18 particles (Phenomenex)) fritted 2 cm

trap column connected to a 50 cm analytical column packed with ReproSil C18 (3 µm C18 particles (Dr.

Maisch)). The separation gradient ran from 5% to 35% Buffer B (80% acetonitrile, 0.1% formic acid) over

90 min, followed by a 15 min wash at 95% Buffer B (flow rate: 250 µL/min). The instrument parameters

were: scan from 150 to 2200 m/z, 100 µs transient time, 10 µs prepulse storage, 7 eV collision energy,

1500 Vpp Collision RF, a +2 default charge state, 18 Hz spectral acquisition rate, 3.0 s cycle time, and the

intensity threshold was 250 counts.

Mass spectrometry data were searched using MaxQuant (v1.5.3.30) using default parameters, except

"match between runs" was enabled. Peptide spectral matches, peptide identifications and protein

identifications were controlled at 1% false discovery rates (FDRs). The protein search database was the

NCBI Identical Protein Groups database for *Apis mellifera* (downloaded Nov. 1st, 2018; 21,425 entries)

plus all honey bee viral proteins contained within NCBI (a further 508 entries). Differential expression

analysis was performed in Perseus (v1.6.1.1) essentially as previously described[82]. Histograms of protein

counts across LFQ intensities were first inspected for normality. Then proteins differentially expressed

between heat-shocked and non-heat-shocked samples, as well as among tissues (semen, virgin

spermathecae, and mated spermathecae), were identified using two-tailed t-tests and an ANOVA,

respectively. Only P values surviving the 10% FDR threshold (permutation-based method) were

considered significant.

*GO term enrichment analysis*

Gene Ontology (GO) terms were retrieved using BLAST2GO (v4.1.9)and subsequent enrichment analyses

were conducted using ErmineJ[83]. We used the gene score resampling (GSR) method (with P values as

scores). Unlike conventional over-representation analyses, this method does not depend on submitting

a 'hit list,' the composition of which is sensitive to arbitrary significance cut-offs. Rather, the GSR

method uses p-values as a continuous variable and looks for GO terms that are enriched in proteins with

low p-values along the continuum. More documentation about the GSR method and ErmineJ can be

found at https://erminej.msl.ubc.ca/help/tutorials/running-an-analysis-resampling/. Enrichment false

discovery rates were controlled to 10% using the Benjamini-Hochberg correction method. Protein

multifunctionality (MF) scores were also computed in ErmineJ based on the number of different GO

terms with which the protein is associated. This process generates an "MF-corrected P value" (also

limited to 10% FDR), which is the enrichment P value after correcting for multifunctionality.

*Differential expression of failed and healthy queens*

Age-matched failing and healthy queens (11 each) were obtained from a research apiary in

Pennsylvania. Queens were rated as 'failing' if they had ceased to lay eggs, were 'drone layers' (*i.e.,*

were not laying fertilized female eggs), or had otherwise inferior brood patterns. Queens were frozen on

dry ice in the field and stored at -80°C until spermatheca and ovary dissection. Proteomics analysis was

performed as described above. Sample handlers were blind to queen groups until all proteomics data

was acquired. Differential expression analysis was performed in Perseus as described above.

**Data availability statement**

All raw mass spectrometry data, protein databases, and search results are available on PRIDE

ProteomeXchange (accession: PXD013728). Figures with associated raw mass spectrometry data include

Figs. 4, 5, 6, and S4. Global protein abundances and p values for the laboratory heat-shock comparisons

are available in Table S1. Any other data that support the findings of this study are available from the

corresponding author upon request.

**Code availability statement**

No specialized code central to our conclusions was used in this manuscript. R code for standard

statistical analyses and figure generation will be provided upon request.

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**Acknowledgements**

This work was supported by an NSERC Discovery grant (311654-11) and grants from Genome Canada

and Genome British Columbia awarded to LJF, a Project Apis m grant awarded to MMG, a Project Apis m

grant awarded to JSP, a USDA-NIFA grant (2016-07962) awarded to JSP and DRT, and a Boone-Hodgson-

Wilkinson Trust grant awarded to AM and LJF. We would like to thank Alexandra Sébastien and Meghan

Jelen for providing us with stink bugs and fruit flies, respectively, for the survival experiments.

We also thank Ashurst Bee Company for help with colony heat testing and Kettle Valley Queens, Nicola

Valley Honey, Wild Antho, Campbells Gold Honey, Heather Meadows Honey Farm, Six Legs Good

Apiaries, Wildwood Queens, Cariboo Honey, and Worker Bee Honey Company for donating failed and

healthy queens for this research.

**Author contributions**

AM wrote the first draft of the manuscript and revisions, conducted all data analysis, made the figures,

and performed the proteomics experiments. AC and AM conducted the failed queen survey, with

assistance from HH and MMG. HH and MMG executed the queen shipment temperature tracking. JM

performed the survival experiments. MMG and JSP performed the drone sperm viability analyses. RU

contributed the age-matched failed and healthy queens. JSP performed the queen sperm viability

measurements across the range of temperatures and measured internal hive temperatures. Grants to

LJF, JSP, MMG, and DRT funded the research. All authors contributed intellectually.

**Competing interests**

JSP owns a honey bee consulting business. All other authors declare no competing financial interests.

**Figure Legends**

**Figure 1. Observational data on shipping temperatures, hive temperatures, and stored sperm viability.**
A) Healthy (N = 55) and failed queens (N = 58) were collected from BC beekeepers for sperm viability
analysis. Failed queens had significantly lower sperm viability (Student's T-test, F = 28.16, P = $5.8 \times 10^{-6}$),
with an average drop of 11.5%. Boxes represent the bounds between the 2st and $3^{rd}$ interquartile range
(IQR), midlines represent the median, and whiskers are extended by 1.5*IQR. B) Temperatures of eight
domestic Canadian queen shipments were recorded during the summer of 2019 (7 via ground, 1 via air
transportation). Temperature loggers were kept immediately adjacent to the queen cages. C) Internal
temperatures of three standard single-deep, wooden hives were recorded, with temperature loggers
placed between each frame. Ambient temperatures were recorded in the shade beneath each hive.

**Figure 2. Viability of stored and ejaculated sperm after temperature stress.** In all cases, boxes
represent the bounds between the 2st and $3^{rd}$ interquartile range (IQR), midlines represent the median,
and whiskers are extended by 1.5*IQR. A) Honey bee queens were heat- and cold-shocked for 1 - 4
hours, then held at 25°C prior to assessing stored sperm viability. The 25°C treatment is the negative
control (the same control data is replotted in each panel). Each point represents a single queen. Data
were analyzed with a Kruskal-Wallis test followed by a Dunnett's *post hoc* test. See **Supplementary**
**Table 1** for sample sizes. B) Combined 2 h and 4 h treatments were optimally fit with a cubic model ($R^2$ =
0.092, P = 0.012). Thresholded at 11.5% loss of viability, the line y = $y_{max}$ − 11.5 intersects with
temperatures 15.2 and 38.2°C. C) Ejaculated honey bee semen from three different colonies (5-6 drones

per colony, illustrated as different boxes) was subject to heat-shock at 42°C for 2 h and 4 h, then kept at
25°C for 2 d. The total number of drones evaluated for 0, 2, and 4 h treatments were 16, 16, and 18,
respectively (see **Supplementary Table 2** for more details). Each data point represents a single drone.
Letters indicate significant differences at P < 0.05 (two-way ANOVA, factors: colony and time, followed
by a Tukey HSD post hoc test).

**Figure 3. Sex-biased heat mortality in honey bees, stink bugs, and fruit flies**. Statistical differences
were evaluated using a log-rank test. Asterisks indicate significant differences. See **Supplementary**
**Figure 4** for risk tables, including population sizes used to generate survival curves. A) Honey bees
(drones, queens, and workers) were held at different temperatures and mortality was recorded hourly.
Drones are sensitive to heat, whereas queens and workers are not. B) Fruit flies (*Drosophila*
*melanogaster*; heat-shock = 38°C) and stink bugs (*Halyomorpha halys*; heat-shock = 42°C) do not have
sex-biased heat sensitivity. For fruit flies, loss of motility was used as the endpoint.

**Figure 4. Differential protein expression comparing heat-shocked (HS) and not heat-shocked (NS)**
**reproductive tissues.** A) Samples included mated queen spermathecae, virgin queen spermathecae,
ejaculated semen, and mated queen ovaries, which were all analyzed by intensity-based, label-free
quantitative tandem mass spectrometry. For drones, 4 semen samples were pooled into one replicate,
then fractionated into eight fractions by basic reverse phase chromatography prior to analyzing by mass
spectrometry (final biological replicates: n = 5 heat-shocked and 5 non-heat-shocked). The significance
cut-off for volcano plots (B-E) was 10% FDR (false discovery rate, permutation-based). Volcano plots
represent mated queen spermathecae (B), virgin spermathecae (C), mated queen ovaries (D), and drone
semen (E). Differentially expressed HSPs are red; other differentially expressed proteins are black.
Accessions for sHSP [1-5] are XP_001120194.1, XP_001119884.1, XP_395659.1, XP_001120006.2, and
XP_026294937.1, respectively. The accession for HSP70 is NP_001153536.1. Bee silhouettes are adapted
from McAfee *et al.* (2019)[84] (CC-BY 4.0).

**Figure 5. Gene ontology (GO) term enrichment analyses**. A-C) Enrichments were performed via gene
score resampling, correcting for both multiple hypothesis testing and protein multifunctionality (MF).
The x-axes depict enrichment P values (10% FDR, Benjamini-Hochberg correction) without
multifunctionality correction. The y-axes depict enrichment P values after correction for both multiple
hypotheses and multifunctionality. The red dotted lines indicate the P value significance cut-off that
achieves 10% FDR. D) Summary of proteins associated with significantly enriched GO terms. Subscripts
refer to comparisons within drones (D), mated queens (M), and virgin queens (V). Bee silhouettes are
adapted from McAfee *et al.* (2019)[84] (CC-BY 4.0).

**Figure 6. Heat-shock protein expression profiles.** Proteins with GO terms for cellular response to heat
were retrieved from the proteomics datasets. Fold-change is relative to the non-heat-shocked state.
Proteins marked with an asterisk were significantly up-regulated in the global differential gene
expression analysis (permutation-based FDR: 10%), and error bars indicate standard deviations.

**a.** Drop:11.5%

**b.** 38 C, ground / 4 C, air

**c.** Hive 1 Hive 2 Hive 3

Frame

Ambient

**a.** Mated queen

Response to abiotic stimulus (GO:0009628)
Cellular response to stress (GO:0033554)
Cellular response to heat (GO:0034605)
Response to heat (GO:0009266)

Response to stress (GO:0006950)

Response to stimulus (GO:0050896)

Cellular response to stimulus (GO:0051716)

-Log(MF-corrected P-value)

**b.** Virgin queen

Response to abiotic stimulus (GO:0009628)
Cellular response to heat (GO:0034605)
Response to heat (GO:0009266)

Cellular response to stress (GO:0033554)

-Log(MF-corrected P-value)

**c.** Drone semen

Electron transfer activity (GO:0009055)

-Log(MF-corrected P-value)

-Log10(Enrichment P value)

**d.**

XP_624487.1
XP_392368.1
XP_026295425.1
XP_026295177.1
XP_016915999.1
XP_006572317.1
XP_006568940.1
XP_006564913.1
XP_001121362.1
XP_001120432.1
ADJ93842.1
1103243A
NP_001040234.1
XP_026296854.1
XP_026294937.1
XP_006572194.1
XP_006566003.1
XP_001120194.1
XP_001120006.2
XP_001119884.1
XP_395659.1
XP_624111.1
XP_623366.2
XP_003250526.1
XP_395614.3
XP_026297659.1
XP_026296889.1
XP_006562528.1
XP_006557811.1
XP_016919814.1
XP_006618378.1
XP_003399667.1
XP_006571335.2
NP_001171519.1
NP_001171518.1
NP_001171498.1
NP_001171492.1
NP_001153536.1
NP_001005101.1
5XZ3_A
1FCQ_A

**Electron transfer activity**
GO:0009055
$P_D$ = 4.18E-10

**Response to abiotic stimulus**
GO:0006950
$P_M$ = 3.13E-10
$P_V$ = 3.01E-10

**Response to heat**
GO:0009408
$P_M$ = 6.25E-10
$P_V$ = 6.02E-10

**Response to stress**
GO:0006950
$P_M$ = 0.013

-1.0    0.0    +1.0

Scaled difference (HS-NS)