Galleria mellonella larvae exhibit a weight-dependent lethal median dose when infected with methicillin-resistant Staphylococcus aureus

Hesketh-Best, PJ

http://hdl.handle.net/10026.1/16889

10.1093/femspd/ftab003
Pathogens and Disease
Oxford University Press (OUP)

All content in PEARL is protected by copyright law. Author manuscripts are made available in accordance with publisher policies. Please cite only the published version using the details provided on the item record or document. In the absence of an open licence (e.g. Creative Commons), permissions for further reuse of content should be sought from the publisher or author.
**Galleria mellonella** larvae exhibit a weight-dependent lethal median dose when infected with Methicillin-resistant *Staphylococcus aureus*

**Authors**

Poppy J. Hesketh-Best¹*, Michelle V. Mouritzen², Kayleigh Shandley-Edwards¹, Richard A. Billington¹, and Mathew Upton²

¹School of Biological and Marine Sciences, and ²School of Biomedical Sciences, University of Plymouth, PL4 8AA UK.

* Corresponding author: Poppy J. Hesketh Best  
  (poppy.heskethbest@plymouth.ac.uk)

**Abstract**

*Galleria mellonella* is a recognised model to study antimicrobial efficacy; however, standardisation across the scientific field and investigations of methodological components are needed. Here we investigate the impact of weight on mortality following infection with Methicillin-resistant *Staphylococcus aureus* (MRSA). Larvae were separated into six weight groups (180-300 mg at 20 mg intervals) and infected with a range of doses of MRSA to determine the 50% lethal dose (LD₅₀), and the ‘lipid weight’ of larvae post-infection was quantified. A model of LD₅₀ values correlated with weight was developed. The LD₅₀ values, as estimated by our model, were further tested *in vivo* to prove our model.

We establish a weight-dependent LD₅₀ in larvae against MRSA and demonstrate that *G. mellonella* is a stable model within 180-260 mg. We present multiple linear models correlating weight with: LD₅₀, lipid weight, and larval length. We demonstrate that the lipid weight is reduced as a result of MRSA infection, identifying a potentially new measure in which to understand the immune response. Finally, we demonstrate that larval length can be a reasonable proxy for weight. Refining the methodologies in which to handle and design experiments involving *G. mellonella*, we can improve the reliability of this powerful model.
Key Words
Methicillin-resistant Staphylococcus aureus; Galleria mellonella; antibiotic testing; LD$_{50}$; pre-clinical model; fat body

Introduction
Galleria mellonella (Greater wax moth) larvae are widely utilised for toxicity screening (Desbois and Coote 2012; Maguire, Duggan and Kavanagh 2016; Coates et al. 2019) and to study host-pathogen interactions (Peleg et al. 2009; Olsen et al. 2011; Junqueira 2012; Wojda and Taszlow 2013). Unlike many insect models, G. mellonella can be incubated at 37°C, which facilitates the investigation of human pathogens. This has included most of the ESKAPE pathogens: Enterococcus faecium (Chibebe Junior et al. 2013; Luther et al. 2014); Staphylococcus aureus (Brackman et al. 2011; Ramarao, Nielsen-Leroux and Lereclus 2012; Sheehan, Dixon and Kavanagh 2019); Klebsiella pneumoniae (Wand et al. 2013; Diago-Navarro et al. 2014); Acinetobacter baumannii (Peleg et al. 2009); and Pseudomonas aeruginosa (Jander, Rahme and Ausubel 2000; Seed and Dennis 2008). Additionally, Escherichia coli (Leuko and Raivio 2012; Alghoribi et al. 2014; Jønsson et al. 2017; Guerrieri et al. 2019), Burkholderia mallei (Schell, Lipscomb and DeShazer 2008) and several fungi (Cotter, Doyle and Kavanagh 2000; Reeves et al. 2004; Mylonakis et al. 2005) have also been studied using G. mellonella. Crucially, a positive correlation between the virulence and immune responses between mammalian models and G. mellonella has been established for P. aeruginosa (Jander, Rahme and Ausubel 2000), Cryptococcus neoformans (Mylonakis et al. 2005), and S. aureus (Sheehan, Dixon and Kavanagh 2019), demonstrating the powerful potential of this invertebrate model.

Antibiotic efficacy at dosages recommended for human use can be tested in G. mellonella, in addition to their toxicity correlating with toxicity observed in murine models (Ignasiak and Maxwell 2017). This has been shown with both natural and synthetic compounds (Gibreel and Upton 2013; Smitten et al. 2019), opening up the possibility of a rapid and cheap model for the early stages of discovery and development of natural and synthetic products, without the challenges of ethical approval, specialist training and the difficulties of using mice-models in early-stage drug development. Infections caused by antibiotic-resistant S. aureus are of global
concern and it is listed as a high priority pathogen for which new antibiotics are urgently needed (The World Health Organisation 2017). Methicillin-resistant *S. aureus* (MRSA) has been utilised with *G. mellonella* for the study of virulence (Mannala *et al.* 2018), pathogenicity (Ebner *et al.* 2016), antimicrobial efficacy of existing antimicrobials (Ba *et al.* 2015; Ferro *et al.* 2016), and for novel candidates (Gibreel and Upton 2013; Jacobs *et al.* 2013; Dong *et al.* 2017) (Table S1).

Despite the increased popularity of *G. mellonella*, there is much variability in method application (Andrea, Krogfelt and Jenssen 2019). This includes differences in larval size, storage, infective dose, and injection intervals. In this study, we address larval size and its potential impact in experimental design. In antibiotic efficacy studies, typically the model is infected with a pathogen shortly before the candidate treatment is presented. This has not been standardised with respect to the parameters previously mentioned for *G. mellonella*. In our preliminary experimentation in determining a 50% lethal dose (LD$_{50}$) for MRSA in *G. mellonella*, it was noted that smaller larvae were more susceptible to infection than larger larvae. This was when using a broad range of larval weights (~200-300 mg), as previously reported (Jacobs *et al.* 2013). Furthermore, the larval weight has been demonstrated to positively correlate with the larval liquid volume, leading to recommendations on how *in vivo* concentrations of injected compounds and pathogens should be calculated (Andrea, Krogfelt and Jenssen 2019). This led us to hypothesise that the larvae LD$_{50}$ for a pathogen, in our case here MRSA, is directly proportional to the larvae weight and that larvae weight is an essential parameter in experimental design that must be tightly controlled.

When physical and anatomical barriers are breached, the wax moth larvae have an innate immune response relying on germline-encoded factors for the detection and clearance of microbial pathogens (Trevijano-Contador and Zaragoza 2019). There are two branches, cellular and humoral immunity. Cellular immunity is conducted by haemocytes, which are present in an open circulatory system called the haemolymph, which is analogous to vertebrate blood. There are at least six subpopulations of haemocytes which perform similar roles to those of the myeloid lineage in vertebrates (Boman and Hultmark 1987; Lavine and Strand 2002), and they are also associated with digestive system, trachea and fat body (Ratcliffe 1985). Five types of haemocytes were identified in fifth larval instar of *G. mellonella*;
prohaemocytes, plasmatocytes, granulocytes, oenocytoids and spherulocytes (Salem et al. 2014). The main immune processes include coagulation, phagocytosis and encapsulation (Tojo et al. 2000). Circulating haemocyte density increases during pathogenesis due to the release of suspended cells from the fat body (Tojo et al. 2000). Haemocyte density and subpopulation variations change with time of exposure to pathogen and pathogen virulence (Arteaga Blanco et al. 2017).

Melanisation additionally occurs in the haemolymph, the process of melanin production resulting in the darkened appearance of the larvae (Tojo et al. 2000). The humoral branch is involved in the production of lytic enzymes (Vogel et al. 2011), and antimicrobial peptides (AMPs) that are active against bacterial pathogens (Cytryńska et al. 2007; Tsai, Loh and Proft 2016). These molecules are mostly produced by the larval ‘fat body’, analogous to the mammalian liver, and are released into the haemolymph (Zasloff 2002).

A proteomic investigation has shown S. aureus infections lead to an increase in production of proteins such as AMPs and peptidoglycan recognition proteins (Sheehan, Dixon and Kavanagh 2019). Critically, the same study identified similarities between G. mellonella and mammal immune response to S. aureus infections. What has not been investigated is the physiological change in G. mellonella lipid as a result of S. aureus infections. For this investigation, we were motivated to quantify the lipid weight, a proxy for the fat body, of the larvae to observe how the fat body might have been affected as a result of MRSA infection.

The aim of the work here is to investigate methodological adjustments which may improve the reproducibility and reliability of using pet-food grade G. mellonella as an experimental model. This was achieved by (i) examining the effect of larval weight on the LD50 to MRSA infection, and (ii) characterising physiological changes occurring to lipid weight as a result of the larval immune response to MRSA.

**Materials and Methods**

**Cultivation of MRSA**

A single colony of Methicillin-resistant *Staphylococcus aureus* (MRSA) NTCT 12493 was streaked onto fresh Luria broth (LB, Fischer Scientific, UK; Tryptone 10 g/L, yeast extract 5 g/L, and sodium chloride 10 g/L) solidified with 1.5% agar (Acros
Organics, UK) 24 h before experimentation. Single colonies were suspended in Dulbecco A Phosphate buffered saline (PBS, Oxoid UK) to a range of optical density (OD) read at 600 nm (Eppendorf BioPhotometer, Netherlands). These dilutions were OD\textsubscript{600} = 0.1 - 1.0 in 0.1 increments. Viable cell counts were made of each dilution.

Determining a weight-based LD\textsubscript{50} for Galleria mellonella larvae

Larvae were purchased commercially from Livefoods UK Ltd. (Somerset, UK; www.livefoods.co.uk). On receipt, larvae were individually weighed using an accurate scale and grouped into the following weight bands: 180-200, 201-220, 221-240, 241-260, 261-280, and 281-300 mg. Larvae were stored at 4°C for up to 7 days in the dark with no food and water. Healthy larvae were identified by a uniform cream colour, with no indications of melanisation such as spots or markings (Fig. 1A) (Li et al. 2018). Larvae were euthanised by chilling them at 4°C for 1 h, before freezing them at -20°C for a minimum of 24 h.

**Figure 1:** Galleria mellonella larvae. (A) Melanisation is a visual indication of the health of the larvae, as larvae progress from none to complete melanisation as a result of stress and/or infection. (B) Larvae pupation. (C) Route of infection for larvae is by intra-haemocoelic injection at the penultimate pro-leg (arrow). Larvae diagram was adapted from Singkum et al. (2019). (D) Larvae are divided up into six weight groups.

Larvae (n = 10) from each weight band were infected by injecting 10 µl of one of the 10 dilutions of MRSA into the left penultimate pro-leg (Fig. 1C), using a 50 µl Hamilton 750 syringe (Hamilton Company, UK) with a removable needle. Injected larvae were placed into Petri dishes lined with tissue paper (KIMTECH, UK). Three
independent replicates of this experiment were carried out. Syringes were cleaned before and after each bacterial dilution. Cleaning consisted of taking up and discarding of each wash solution thrice before progressing to the next wash solution. Wash solution order was as follows: distilled H₂O (dH₂O), 70% ethanol, and dH₂O. After infection, the larvae were maintained at 37°C in the dark without food or water. A placebo control of sterile PBS was used to account for the effect of the physical trauma of injection, along with a non-manipulation (NM) control. After 24 h the live/dead counts were recorded. Larvae were recorded as dead when they met the following: (i) complete melanisation (Fig. 1A), (ii) did not respond to touch, and (iii) could not correct itself when rolled onto its back. Determining the weight-dependent LD₅₀, live/dead counts were converted into percentage mortality at 24 h for each group. For this investigation we have defined LD₅₀ as CFU of MRSA per mg of organism resulting in 50% mortality. To model the dose-response and describe the relationship between increasing the infection dose on survival for each weight group, a non-linear sigmoidal regression curve was plotted. The infection dose, represented as CFU/ mg of total weight of larva, was log-transformed. A non-linear regression curve was calculated to fit best the data generated from three independent replicas. From the equation generated from this curve, the theoretical LD₅₀ was calculated along with the standard deviation (SD). Estimated LD₅₀ from each weight groups were plotted against the mean larvae weight. A regression line was drawn, and the coefficient of determinant $R^2$ was calculated.

Correlating larval size with rate of pupation

On the day of receipt, larvae were placed into weight groups in Petri dishes. They were immediately placed at 37°C, in the dark with no food or water and permitted to pupate over 15 days. Larvae were observed daily and pupation events recorded.

Quantifying lipid weight of G. mellonella

Following investigation of the LD₅₀ for MRSA, the lipid weight for all living and dead larvae was quantified. Live larvae from treatments, the NM and PBS controls were ethically euthanised. Dead larvae were stored at -20°C until needed. Larvae were left to thaw at room temperature for 24 h and were weighed and individually placed in
Eppendorf tubes to be dried over 7 days at 55°C, and re-weighed to reveal their dry weight. Larvae were then submerged in ≥99.9% diethyl ether (Sigma-Aldrich, UK) and left for 3 days at 4°C to dissolve lipid. Diethyl ether was utilised as the lipid extraction solvent (Tzompa-Sosa et al. 2014). After, ether was left to evaporate in a fume hood for 24 h. Once dried, larvae were weighed again to acquire the post-ether weight. Quantities are then presented as followed: 'total weight' is the weight of the larvae pre-experimentation; ‘water weight’ (water weight = pre-experimentation weight – dry weight); 'lipid weight' (lipid weight = dry weight – post-ether weight).

Statistical analysis

All statistical analysis was performed using PRISM GraphPad 8.4.2 (GraphPad Software, San Diego, CA, USA). One-Way ANOVA (two-tailed), Two-Way ANOVA, and Pearson’s correlation coefficients were used when applicable to compare treatment groups. Log-rank Mantel-Cox tests compared survival curves for antimicrobial efficacy tests and pupation. A p-value of: < 0.05 (∗), < 0.01 (∗∗) or < 0.001 (∗∗∗), < 0.0001 (∗∗∗∗) was considered to be significantly different.

Results

Larval weight affects LD50

To begin testing our hypothesis, LD50 values were determined for each weight group. A sigmoidal non-linear model best fit the dose-dependent response of the data, resulting in an LD50 calculated for each weight group (Fig. 2). When adjusted to the number of cells injected into each larvae per one unit of body weight (CFU/mg), the resulting LD50 ranged from 1.19 x10⁷CFU/mg, for the 180-200 mg group, to the highest LD50 which was 8.97 x10⁷ CFU/mg for the 261-280 mg group (Table 1). The LD50 increased across weight groups except for the 281-300 mg group, which had a lower LD50 than the 261-280 mg weight group. Throughout this experiment, we encountered some difficulties when handling larvae from the two higher weight-bands (261-280 and 281-300 mg), such as high variation in mortality at the lowest infective dosages (0-40% mortality) and highest dosages (60-100% mortality). Nevertheless, we were able to calculate an LD50 with the final data.
Figure 2. Sigmoidal non-linear logistic regressions best fit the dose-dependent response observed when calculating an LD_{50} for MRSA. LD_{50} was calculated for each weight group with 10 larvae/group. Data are shown as mean ± SD (n = 10) of three independent replicates.

Table 1. Summary of the LD_{50}s as calculated by non-linear models for each weight group (N, number of replicas; R^2, coefficient of determination).

<table>
<thead>
<tr>
<th>Weight group (mg)</th>
<th>LD_{50} (CFU/mg)[a]</th>
<th>SD (CFU/mg)</th>
<th>N</th>
<th>R^2</th>
</tr>
</thead>
<tbody>
<tr>
<td>180-200</td>
<td>1.19 x10^7</td>
<td>1.47</td>
<td>30</td>
<td>0.85</td>
</tr>
<tr>
<td>201-220</td>
<td>1.26 x10^7</td>
<td>2.45</td>
<td>30</td>
<td>0.77</td>
</tr>
<tr>
<td>221-240</td>
<td>2.34 x10^7</td>
<td>1.57</td>
<td>30</td>
<td>0.80</td>
</tr>
<tr>
<td>241-260</td>
<td>4.40 x10^7</td>
<td>3.35</td>
<td>30</td>
<td>0.76</td>
</tr>
<tr>
<td>261-280</td>
<td>8.97 x10^7</td>
<td>1.46</td>
<td>30</td>
<td>0.69</td>
</tr>
<tr>
<td>281-300</td>
<td>4.19 x10^7</td>
<td>1.81</td>
<td>30</td>
<td>0.78</td>
</tr>
</tbody>
</table>

[a]Example of how this is calculated can be found in Table S3

We observed a positive correlation between weight of the larvae and LD_{50}, as calculated by Pearson correlation test (r = 0.87, p = 0.025, n = 18). A linear regression model arriving at an equation (y = 0.007966x + 5.548) was used to estimate LD_{50} (Fig. 3A). The LD_{50} values, as estimated by our model, were tested in
vivo, demonstrating an approximate 50-56% (± 5.7 – 10%) survival for four of the weight groups (Fig. 3B). Survival at 24 h for the weight groups 261-280 and 281-300 mg was 30% (± 0%) and 43% (±15.3%), respectively.

Figure 3. LD$_{50}$ as calculated by non-linear regression models positively correlated with weight and was validated in vivo for all but the two highest weight groups. (A) Calculated LD$_{50}$ by non-linear models correlation positively with total weight. (B) LD$_{50}$ value as calculated by the model was validated by injecting into larvae and observing mortality. Data are shown as mean ± SD (n=10) of three independent replicas.

MRSA infection leads to a reduction in lipid weight

With the non-manipulated (NM) group, we assessed the overall relationship between total weight, dry weight, and lipid weight and length of the larvae (Fig. 4). Determined by Pearson’s correlation test, we found a positive correlation between the total and dry weight, ($r = 0.972, p < 0.0001, n = 83$) (Fig. 4A), and total and water weight ($r = 0.989, p < 0.0001, n = 83$) (Fig. 4B). These two results support the findings of previous research (Andrea, Krogfelt and Jenssen 2019). Two additional positive correlations were observed between total weight and lipid ($r = 0.788, p < 0.0001, n = 83$) (Fig. 4C), and total weight and length ($r = 0.9944, p < 0.0001, n = 252$) (Fig. 4D).
Figure 4. Multiple correlations observed between larvae total weight and dry weight, water weight, lipid weight, and larvae length. Non-manipulated (NM) larvae were used to analyse the relationships between (A) total weight and dry weight, (B) total weight and the lipid weight after here presented as lipid weight, (C) total weight and lipid weight as proportional to the total weight, water weight, and (D) total weight and larvae length where data is presented as mean ± SD (n = 252).

We also investigated the effect of infection on the lipid weight of all the larvae used in determining the LD₅₀ for MRSA (Fig. 5). As calculated by one-way ANOVA, injection with MRSA resulted in an overall decrease in the lipid weight for both dead (18.7 mg ± 8.541, p < 0.0001, n = 573) and live larvae (22.4 mg ± 6.556, p < 0.0001, n = 524), when compared to the NM control (31.92 mg ± 8.815, n = 83) (Fig 5A). When compared to one another, live larvae had a significantly greater lipid weight compared to dead larvae (p < 0.0001). There was no significant reduction in the lipid weight between NM and PBS control (27.81 mg ± 5.825, p > 0.999, n = 50) (Fig 5A and Table S2).
Figure 5. Injection of the larvae with MRSA results in an overall decreased in the lipid weight of the larvae. (A) Statistical results from a one-way ANOVA are illustrated above the bars as compared to the NM control. Summary of multiple analysis can be found in Table S2. (B) Box-plots above and to the right of the scatter plot are to illustrate the distribution of the data. Colours are as follows: black, NM control; purple, PBS control; blue, live larvae; and red, dead larvae 24 h post-MRSA infection. Correlations of infective dose and lipid weight for (C) living and (D) dead larvae. Data is presented as Log[CFU], as the infective doses are not adjusted for larvae weight. Data presented as mean ± SD (n = 10) of three independent replicas.

Finally, we observed that at a high infective dosage of MRSA, the larvae had a lipid weight close to the mean of the NM and PBS control compared to the lower dosages (Fig. 5C-D). This was supported by a positive correlation between lipid weight and infective dose for both live ($r = 0.778$, $p = 0.008$) (Fig. 5C) and dead larvae ($r = 0.669$, $p = 0.035$) (Fig. 5D).

Pupation is unaffected by weight
To explore whether larger larvae were closer to the final instar stage (pupae) in which they begin to pupate into adult moths, an observational experiment was performed. NM larvae were left to pupate at 37°C, and it was observed that 80-100% of larvae pupated within the 15 day incubation period, independent on their weight grouping, as calculated by Log-rank (Mantel-Cox) test ($X^2(5, N = 60) = 4.004, \ p = 0.549$) (Fig. 6).

Figure 6. The weight did not influence the probability of pupation of NM larvae. NM larvae were incubated at 37°C for 15 days and observed daily for pupation events. No significant difference was found between the weight group and the probability of pupation as calculated by a Log-rank Mantel-Cox test ($p = 0.5489$). Data are shown as mean ± SD (n = 10) repeated twice.

Discussion

MRSA exhibits a weight-dependent LD$_{50}$

In this study, we have demonstrated it is possible to develop a model in which a LD$_{50}$ can be predicted based on the weight of the larvae, and that the prediction can be experimentally validated (Fig. 3). The linear model correlating total and water weight (Fig. 4B) imply that in increasingly larger larvae, the in vivo dilution of MRSA increases requiring a greater density of pathogen to reach the LD$_{50}$. Likewise for the
positive correlation confirmed with total and lipid weight (Fig. 4C), the presence of a
larger fat body that can be degraded for the production of immune factors, may well
be why we observe the weight-dependent effect on LD_{50}. The LD_{50}s (1.19 – 8.97
x10^7 CFU/mg) for the MRSA strain was not within range of infective dosages utilised
in previously investigated MRSA and Methicillin-sensitive S. aureus (MSSA) strains
(0.8 – 5.0 x10^6 CFU) (Table S1). However, a direct comparison may not be
appropriate given the variation in reporting densities as in our study the LD_{50} was
adjusted to account for \textit{in vivo} dilution in the larvae as described in Andrea, Krogfelt
and Jenssen (2019), but this is not always done.

During the process of this investigation, we found two of the largest weight groups
(261-280 and 281-300 mg) to be unreliable, which hindered progress. This was
consistent across multiple batches of larvae orders. LD_{50}, as calculated by our model
for 261-280 and 281-300 mg larvae, resulted in less than 50% survival at 24 h (Fig.
3B), indicating that our model for a weight-dependent LD_{50} had overestimated the
LD_{50}. Our first assumptions were that larger larvae were older and closer to pupation
than the smaller weight groups, as larvae increase in size until pupation (Jorjão \textit{et al.}
2018), which might somehow impact on survival. Given the difficulty in identifying an
age for each larva, it is a difficult hypothesis to test beyond quantifying the number of
days it took for NM larvae from each weight group to pupate.

When this was conducted, we found that larval size did not influence the probability
of pupation (Fig. 6), and we conclude that the larvae received from the supplier had
an 80-100% probability of pupating within 15 days if kept at 37°C, regardless of
weight. It would appear that larger larvae were not likely to be closer to pupation than
smaller ones, so the reason for our observed decrease in LD_{50} for large larvae
remains unknown. Since larvae were kept without food, this may be a reason for the
observed similar pupation times across all weight groups as lack of food source may
be forcing the larvae into pupation. Feeding regimes are not the standard protocol
when investing antibiotic efficacy, as such we feel this best represented the
conditions larvae would be exposed to at the start of experimentation.

Using \textit{G. mellonella} does have drawbacks, one such being the functional equivalent
of adaptive immunity termed ‘immune priming’ (Little and Kraaijeveld 2004; Sadd
and Schmid-Hempel 2006). Individual larvae that survive infection or exposure to a
particular pathogen may exhibit increased immune resistance against the same or similar pathogens. Priming with heat-killed pathogens was observed to result in increased larval survival (Wu et al. 2014). Ultimately there will be no control over the immune history of the larvae and this should always be recognised when working with pet-food grade *G. mellonella.* Across the literature, a wide range of weight bands have been utilised: 150-200 mg (Mannala et al. 2018); 300-700 mg (Ebner et al. 2016); 200-300 mg (Jacobs et al. 2013); and in other studies this is not declared (Ba et al. 2015; Jorjão et al. 2018). Our results suggest that choosing weight ranges as wide as 300-700 mg and 200-300 mg could result in inconsistent data. While a weight range of only 20 mg is likely a conservative approach, ranges such as 100 mg or greater in our weight-dependent LD$_{50}$ model for MRSA indicates that there would be significant differences in survival (Fig. 3A).

Weighing individual larvae is a time-consuming procedure. This study also demonstrated that larval length is a reasonable proxy for the weight (Fig. 4D). Larval length has been previously used to characterise larvae for experimentation where larvae of 15-25 mm were utilised (Bazaid et al. 2018). Like total weight, a large length grouping may also encounter similar challenges. A 20 mg weight grouping would equate to roughly 1 mm, for example, 180-200 mg would be 20-21 mm. Measuring length may be a preferred alternative to accurately weighing all larvae. When sourcing larvae from our supplier, we frequently found that larvae belonging to the weight groups 201-220 and 221-240 mg were most abundant, which will inevitably be the practical determining factor in weight group selection. Our findings would support selection of larvae in this range.

*Lipid metabolism occurs in response to MRSA infection*

MRSA infection leads to a decreased lipid weight in the larvae after 24 h, whether they died or survived the infection (Fig. 5A). The reduction in lipid weight is likely the result of lipolysis during an immune response. This is to be expected, the fat body of the larvae produce many defence compounds essential to the larvae’s immune response (Cytryńska et al. 2007; Tsai, Loh and Proft 2016). This reaction can be rapid, in some models showing production of AMPs within the first 4 to 6 h post-infection (Sheehan, Dixon and Kavanagh 2019; Trevijano-Contador and Zaragoza 2019). This is supported by proteomic work, which demonstrated that at 6 and 24 h
post-S. aureus infection larvae had increased expression of AMPs (Sheehan, Dixon and Kavanagh 2019).

On exposure to the infecting pathogen, there may be a rapid metabolism of the fat body to provide the required energy to fight the infection. Larvae with larger lipid weight before infection might be more likely to survive, as seen with the surviving larvae having a greater lipid weight than dead larvae (Fig. 5A). Within this experimental design, the larvae are not fed before or during the experiment, and therefore they cannot be acquiring more lipid. Where lipid weight was seen as closer to the NM and PBS control baseline, as observed in the trend of lipid weight positively correlating with infective dose (Fig. 5C-D), it is more likely that lipid metabolism has been compromised.

What could reasonably be expected is that lipolysis of the fat body occurs to increase the production of AMPs and additional defence compounds. When Drosophila are stimulated by a systemic infection with S. aureus, signalling from the Toll receptor increases, which leads to increased production of AMPs and reduced accumulation of lipids (Liu et al. 2016; Lee and Lee 2018). This could suggest that for larvae surviving high infective dosages, there are additional immune responses that do not deplete the fat body.

We intended to quantify the larval lipid weight to aid in understanding the weight-dependent LD50 effect and the observed unreliability of the two largest weight groups (261-280 and 281-300 mg). We report several observations regarding the lipid weight and MRSA infection; however, none can fully explain the irregularity we encountered for the largest weight groups. Analysing larval lipid weight has proved some insight, but would benefit from further investigation, though alternative methods to estimate lipid mass would be required.

Overall assessment of G. mellonella as a model

There remains a lack of widely available and cheap standardised stocks of larvae reared under controlled conditions. Temperature (Mowlds and Kavanagh 2008), diet (Banville, Browne and Kavanagh 2012; Jorjão et al. 2018), past infections (Fallon, Kelly and Kavanagh 2012), and antibiotics and hormones in the feed (Büyükgüzel and Kalender 2008) are all reported to influence laboratory experimentation. Most
larvae currently used are acquired from commercial insect food providers (Andrea, Krogfelt and Jenssen 2019), where it is understood that use of antibiotics and hormones in the culture medium is common practice, and acquiring accurate information regarding the conditions in which the larvae are reared is challenging. All of which may vary between larvae suppliers, which is a challenge that warrants further investigation.

Ultimately from our investigation, it would appear that lipid deposits are essential in G. mellonella response to MRSA. Prior investigation has evaluated the effect of nutrient deprivation on larvae (Banville, Browne and Kavanagh 2012), and the selection of diet (Jorjão et al. 2018), which both influence susceptibility to S. aureus infection. This emphasises the issues associated with a having lack of knowledge of rearing conditions used by suppliers and how they will influence experimental results. TruLarv™ (BioSystems Technology, UK) currently provide the only standardised G. mellonella in the UK. While cheap compared to murine models, it is considerably costlier (£1.20 per larvae) than purchasing larvae from commercial pet food providers.

However for pet-food grade larvae to be reliably used in research, more significant consideration should be taken over the parameters that can be controlled, and in this study, we emphasise that such experiments can be reproducible and reliable. We recommend that investigators consider the potential variability associated with using different larval weight as we have shown herein. We would recommend using weight groupings as a means to control this. Our data suggests that all larvae used should be within 10 mg of the mean weight of all larvae to provide consistency. Additionally, larvae of >260 mg should not be avoided.

In this work, we present several linear regression curves that could be used as tools to aid in experimental design, such as the linear model for LD₅₀ (Fig. 3A), weight and lipid content (Fig. 4C), and length (Fig. 4D). Finally, we demonstrate that the lipid weight is reduced as a result of MRSA infection, identifying a potentially new measure in which to understand the immune response. Similarities between G. mellonella and mammals in response to S. aureus infections can be used to study the efficacy and interactions of novel antimicrobials, even at early development stages. By refining and standardising methodologies in which to handle and select
G. mellonella for study, we can improve the reliability of this powerful model for multiple purposes.

Author Contributions

Conceptualisation, PJHB and MVM; Methodology, PJHB, MVM, KSE, RAB, and MU; Validation, PJHB, MVM, and KSE; Formal Analysis, PJHB; Investigation, PJHB and MVM; Resources, PJHB and MVM; Data Curation, PJHB and MVM; Writing – Original Draft Preparation, PJHB; Writing – Review & Editing, PHB, MVM, KSE, RAB, and MU; Visualization, PJHB; Supervision, RAB, and MU; Funding Acquisition, MU.

Funding

This study was funded in part by the University of Plymouth, School of Biology and Marine Science postgraduate research studentship and Innovate UK Antibiotic Development grant (Innovate UK 103358).

Transparency declaration

The authors declare no conflict of interests. The funders had no role in the design of the study; in the collection, analyses, or interpretation of data; in the writing of the manuscript, or in the decision to publish the results.

References


Andrea A, Krogfelt KA, Jenssen H. Methods and Challenges of Using the Greater Wax Moth (Galleria mellonella) as a Model Organism in Antimicrobial Compound Discovery. Microorganisms 2019;7:85.


Ba X, Harrison EM, Lovering AL et al. Old drugs to treat resistant bugs: Methicillin-resistant Staphylococcus aureus isolates with mecC are susceptible to a combination of penicillin and clavulanic acid. Antimicrob Agents Chemother


Dong CL, Li LX, Cui ZH et al. Synergistic effect of pleuromutilins with other antimicrobial agents against *Staphylococcus aureus* in vitro and in an experimental *Galleria mellonella* model. *Front Pharmacol* 2017;**8**:553.


Gibreel TM, Upton M. Synthetic epidermicin NI01 can protect *Galleria mellonella* larvae from infection with *Staphylococcus aureus*. *J Antimicrob Chemother* 2013;**68**:2269–73.


Jønsson R, Struve C, Jenssen H et al. The wax moth *Galleria mellonella* as a novel model system to study Enteroaggregative *Escherichia coli* pathogenesis.


Mannala GK, Koettitz J, Mohamed W et al. Whole-genome comparison of high and low virulent *Staphylococcus aureus* isolates inducing implant-associated bone


Seed KD, Dennis JJ. Development of Galleria mellonella as an alternative infection


Wojda I, Taszłow P. Heat shock affects host-pathogen interaction in *Galleria*


Supplementary

Table S1. Summary of experimental design utilised for *G. mellonella* experiments. Table adapted from Andrea, Krogfelt and Jenssen (2019) to include details of strains and a brief summary of their characteristics. (LP, left pro-leg; NA, not available, P-, privately purchased larvae from country specified).

<table>
<thead>
<tr>
<th>S. aureus strain</th>
<th>Strain characteristics</th>
<th>Larva weight/size</th>
<th>Larva origin</th>
<th>Storage</th>
<th>Injection site</th>
<th>Infection</th>
<th>Reference</th>
</tr>
</thead>
<tbody>
<tr>
<td>EDCC 5455-5461</td>
<td>clinical isolates</td>
<td>150–200 mg</td>
<td>Reared</td>
<td>30°C</td>
<td>Not given</td>
<td>1.0 x10⁶</td>
<td>(Mannala et al. 2018)</td>
</tr>
<tr>
<td>EDCC 5464</td>
<td>clinical isolate, MRSA strain</td>
<td>NA</td>
<td>P-UK</td>
<td>4°C</td>
<td>Between segments</td>
<td>~1.3 x10⁶</td>
<td>(Ba et al. 2015)</td>
</tr>
<tr>
<td>RN4220</td>
<td>veterinary isolate, mecC positive</td>
<td>02.5099.D</td>
<td>P-UK</td>
<td>7 days</td>
<td>LP</td>
<td>0.8–2.6 x10⁸</td>
<td>(Bazaid et al. 2018)</td>
</tr>
<tr>
<td>ATCC 43300, Newman</td>
<td>MRSA, type culture</td>
<td>~15–25 mm long</td>
<td>P-UK</td>
<td>7 days</td>
<td>LP</td>
<td>~1.0 x10⁶</td>
<td>(Dong et al. 2017)</td>
</tr>
<tr>
<td>ATCC 29213, NCTC 13277</td>
<td>MSSA</td>
<td>2x clin. isol.</td>
<td>P-China</td>
<td>NA</td>
<td>LP</td>
<td>~1.0 x10⁶</td>
<td>(Dong et al. 2017)</td>
</tr>
<tr>
<td>ATCC 43300, N54</td>
<td>MRSA, MSSA, clinical isolate</td>
<td>USA300 JE2</td>
<td>MRSA</td>
<td>300–700 mg</td>
<td>NA</td>
<td>LP</td>
<td>1.0 x10⁶</td>
</tr>
<tr>
<td>MRSA N9</td>
<td>MRSA, clinical isolate</td>
<td>ATCC 25923, type culture</td>
<td>~200 mg</td>
<td>P-China</td>
<td>NA</td>
<td>LP</td>
<td>1.0 x10⁵</td>
</tr>
<tr>
<td>USA300-0114</td>
<td>MRSA, type culture</td>
<td>ATCC 6538</td>
<td>clinical isolates</td>
<td>NA</td>
<td>P-USA</td>
<td>4°C, 14 days</td>
<td>5.0 x10⁶</td>
</tr>
<tr>
<td>SA01-04</td>
<td>clinical isolates</td>
<td>USA300-0114</td>
<td>P-USA</td>
<td>4°C, 14 days</td>
<td>LP</td>
<td>5.0 x10⁶</td>
<td>(Jacobs et al. 2013)</td>
</tr>
<tr>
<td>UAMS-1</td>
<td>type culture</td>
<td>UAMS-1112</td>
<td>NA</td>
<td>Reared</td>
<td>28°C</td>
<td>NA</td>
<td>10⁸ CFU/ml</td>
</tr>
<tr>
<td>RN4220</td>
<td>type culture</td>
<td>ATCC 11195</td>
<td>P-UK</td>
<td>4°C, 14 days</td>
<td>NS</td>
<td>~2.5 x10⁶</td>
<td>(Gibreel and Upton 2013)</td>
</tr>
</tbody>
</table>
Table S2. Multiple comparison results for change in lipid weight 24 h post-MRSA infection described in Figure 5. (PBS; phosphate-buffered saline injection; NM, no manipulation control)

<table>
<thead>
<tr>
<th>Interaction</th>
<th>Mean rank diff.</th>
<th>Adjusted p-value</th>
<th>Summary</th>
</tr>
</thead>
<tbody>
<tr>
<td>NM vs. PBS</td>
<td>78.87</td>
<td>&gt;0.9999</td>
<td>ns</td>
</tr>
<tr>
<td>NM vs. Live</td>
<td>339.5</td>
<td>&lt;0.0001</td>
<td>****</td>
</tr>
<tr>
<td>NM vs. Dead</td>
<td>490.7</td>
<td>&lt;0.0001</td>
<td>****</td>
</tr>
<tr>
<td>PBS vs. Live</td>
<td>260.6</td>
<td>&lt;0.0001</td>
<td>****</td>
</tr>
<tr>
<td>PBS vs. Dead</td>
<td>411.8</td>
<td>&lt;0.0001</td>
<td>****</td>
</tr>
<tr>
<td>Live vs. Dead</td>
<td>151.2</td>
<td>&lt;0.0001</td>
<td>****</td>
</tr>
</tbody>
</table>

Table S3. Editable excel table that can be used in order to calculate the LD50 for MRSA based on weight-grouping.

Calculating the LD50 for MRSA NCTC 12493

Equation as given by linear model: \( y = 0.007966x + 5.548 \)

<table>
<thead>
<tr>
<th>Larvae weight (mg): ( x = 180 )</th>
<th>Insert here the median weight for the selected weight group</th>
</tr>
</thead>
<tbody>
<tr>
<td>( \text{LD}_{50} ) (Log[CFU/mg]): ( y = 9.61E+06 )</td>
<td>This is the ( \text{LD}_{50} ) for your selected weight group</td>
</tr>
<tr>
<td>( \text{LD}_{50} ) (CFU): ( 2.88E+09 )</td>
<td>This is the total density of MRSA 12493 that must be injected into larva of the selected weight-group in order to kill 50% of the population</td>
</tr>
</tbody>
</table>