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Dear Sir or Madam,

we are pleased to resubmit the revised version of the manuscript “***Galleria mellonella oral administration model to study commensal-induced innate immune responses***” by Anna Lange, Andrea Schäfer and Julia-Stefanie Frick to be considered for publication in “**Journal of Visualized Experiments**” in the section “**Immunology & Infection**”.

We thank the editor and reviewers for their constructive suggestions, which we have all incorporated into our manuscript.

We have the impression that our manuscript has significantly improved, thanks to the work and suggestions of the reviewers and hope that our work is now suitable for publication in “**Journal of Visualized Experiments**”.

Yours sincerely,



Julia-Stefanie Frick

TITLE:

A *Galleria mellonella* Oral Administration Model to Study Commensal-Induced Innate Immune Responses

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KEYWORDS:

Galleria mellonella, oral infection, force-feeding, intestinal commensals, insect model, immunogenic, innate immunity

SUMMARY:

Here, we provide a detailed protocol for an oral administration model using *Galleria mellonella* larvae and how to characterize induced innate immune responses. Using this protocol, researchers without practical experience will be able to use the *G. mellonella* force-feeding method.

ABSTRACT:

The investigation of the immunogenic potential of commensal bacteria on the host immune system is one essential component when studying intestinal host-microbe interactions. It is well established that different commensals exhibit a different potential to stimulate the host intestinal immune system. Such investigations involve vertebrate animals, especially rodents. Since increasing ethical concerns are linked with experiments involving vertebrates, there is a high demand for invertebrate replacements models.

Here, we provide a *Galleria mellonella* oral administration model using commensal non-pathogenic bacteria and the possible assessment of the immunogenic potential of commensals on the *G. mellonella* immune system. We demonstrate that *G. mellonella* is a useful alternative invertebrate replacement model that allows the analysis of commensals with different immunogenic potential such as *Bacteroides vulgatus* and *Escherichia coli*. Interestingly, the bacteria exhibited no killing effect on the larvae, which is similar to mammals. The immune responses of *G. mellonella* were comparable with vertebrate innate immune responses and involve recognition of the bacteria and production of antimicrobial molecules. We propose that

G. mellonella was able to restore previous microbiota balance, which is well known from healthy mammalian individuals. Although providing comparable innate immune responses in both *G. mellonella* and vertebrates, *G. mellonella* does not harbor an adaptive immune system. Since the investigated components of the innate immune system are evolutionary conserved, the model allows a prescreening and first analysis of bacterial immunogenic properties.

INTRODUCTION

The intestinal microbiome is an essential component for maintenance of homeostasis, and involves both innate and adaptive immune responses^{1,2}. The commensal microbiota community is characterized by different main commensal constituents: symbionts that confer beneficial effects by important immunomodulatory functions, and pathobionts that can have detrimental effects in genetically predisposed hosts and promote and trigger intestinal inflammation^{3,4}. Many studies on symbionts and pathobionts and their influence on the host immune system have been published mainly studying adaptive immune responses.

Since these studies involve many animals for the investigations and the protection and replacement of animals used for experimentation is of increasing public interest, we seek to find a replacement model to allow for a screening of different bacterial immunogenic properties. Insects, especially *Galleria mellonella*, are a widely used replacement model in infection research. *G. mellonella* combines different advantages such as low costs and high throughput; it allows oral administration of bacteria, which is the natural exposure route, and it allows for systemic infection^{5,6}. *G. mellonella* further enables incubation at 37 °C, which is the physiological body temperature of mammals and the optimum for bacterial virulence factor expression⁵. The main advantage of *G. mellonella* is the conserved innate immune system that enables the discrimination of self from non-self and encodes a variety of pattern recognition receptors like apolipoprotein or the opsonin hemolin^{6,7}. Upon microbe recognition, *G. mellonella* can trigger different downstream humoral immune responses. It can induce oxidative stress responses and secrete reactive oxygen species (ROS) which involves the activity of NOS (nitric oxide synthase) and NOX (NADPH oxidase)^{6,8}. In addition, *G. mellonella* activates a potent antimicrobial peptide (AMP) response, which results in the secretion of a mixture of different AMPs such as gloverin, moricin, cecropin or the defensin-like gallerimycin^{6,8-10}. Generally, AMPs have quite broad host specificity against Gram-positive and Gram-negative bacteria and fungi and have to provide a potent response since insects are lacking any adaptive response¹⁰. Gloverin is an AMP active against bacteria and fungi and inhibits outer membrane formation^{6,11}. Moricins exhibit their antimicrobial function against Gram-positive and Gram-negative bacteria by penetrating the membrane and forming a pore^{9,11}. Cecropins provide activity against bacteria and fungi and permeabilize the membrane similarly like moricins^{9,10}. Gallerimycin is a defensin-like peptide with anti-fungal properties⁹. Interestingly, it was found that the combination of cecropin and gallerimycin had a synergistic activity against *E. coli*¹⁰.

Due to their easy-to-use character *G. mellonella* larvae are an often used infection model to assess bacterial pathogenicity. In particular, studies in which data obtained from *G. mellonella* correlate with data obtained from mice support the strength of this alternative host model. It was found that the most pathogenic serotypes of *Listeria monocytogenes* in a mouse infection

model lead also to higher mortality rates in *G. mellonella* after systemic infection. Further, less virulent serotypes turned out to be also less virulent in the *G. mellonella* model¹². Similar observations have been made with the human pathogenic fungi *Candida albicans*. Virulence of different *C. albicans* strains has been assessed by systemic infection and subsequent monitoring of larval survival. Mouse avirulent strains were also avirulent or exhibited reduced virulence in *G. mellonella*, whereas the mouse virulent strains lead also to high larval mortality¹³. The *G. mellonella* model could further be used to identify type 3 secretion system pathogenicity factors of *Pseudomonas aeruginosa*¹⁴.

Since most investigations involving *G. mellonella* were focused on virulence factors using the systemic infection approach we were especially interested in providing a method suitable for the analysis of intestinal commensals in an oral force-feeding model in which we can apply a distinct dosage of bacteria per larvae and not only observe the larval mortality rate but analyze different hallmarks of innate immune responses to maintain intestinal homeostasis.

Our method helps to increase the use of *G. mellonella* as a replacement model since we combine the application of bacteria and the analysis of RNA expression. It is not only useful to strengthen the meaning of bacterial pathogenesis studies when including the analysis of immune responses after oral administration and not only the observation of mortality rates after systemic infection. Our methods allows for the analysis of immunogenic properties of bacterial non-pathogenic commensals since it provides more complex conditions than cell culture by offering an intestinal barrier in a living organism.

PROTOCOL

1. *G. mellonella* rearing and preparation of the larvae for the experiments

NOTE: The cycle from egg to last instar larva takes approximately 5-6 weeks.

1.1. Transfer the eggs laid by adult moths to 2 L boxes containing wax moth substrate (22% corn grits, 22% wheat meal, 17.5% beeswax, 11% skimmed milk powder, 11% honey, 11% glycerol, 5.5% dried yeast). Perform the whole breeding at 30 °C in the dark.

1.2. Transfer 25 g of substrate containing the larvae into fresh substrate after approximately 1-2 weeks when small and tiny larvae were visible. Synchronize the larvae after 2 weeks according to their size and keep groups of 30-40 larvae in 2 L containers on wax moth substrate for additional 2 weeks.

1.3. Select the larvae for experiments by weight. Use only pale and fast moving larvae with a mass of 180-200 mg.

2. Cultivation and preparation of *Bacteroides vulgatus* and *Escherichia coli* for oral administration

2.1. Grow the obligate anaerobic bacterium *Bacteroides vulgatus* mpk at 37 °C anaerobically using jars and sachets for creating an anaerobic environment (see **Table of Materials**)^{15,16}. Cultivate *B. vulgatus* for 2 days and grow an overnight subculture in brain heart infusion (BHI) broth.

2.2. Grow the facultative anaerobic bacterium *Escherichia coli* mpk under aerobic conditions in Luria-Bertani (LB) broth at 37 °C. Cultivate *E. coli* overnight in LB broth and grow subculture for 2 h at 37 °C on the day of the experiment.

2.3. Harvest the cultures by centrifugation at 1,700 x *g* for 5 min. Resuspend the bacterial pellets in DPBS (Dulbecco's Phosphate-Buffered Saline). Determine the optical density (OD) of the bacterial cultures at OD 600 nm and calculate the bacterial concentrations. The bacterial concentrations were adjusted to 10⁹/mL.

3. Force-feeding of *G. mellonella* larvae with bacterial suspensions

3.1. Force-feed each larva with 10 µL of the adjusted bacterial suspension containing 10⁷ bacteria per dose. Use an insulin syringe with a blunt-ended needle for oral application of the bacterial suspension.

3.1.1. Fix the syringe was fixed into a microsyringe pump (**Figure 1**) to ensure the accuracy of the applied suspension volume to each larva (see **Table of Materials**). Insert the syringe carefully between their mandibles. Do not force the syringe between the mandibles. Wait for the larvae to open it mouthparts and insert then the syringe.

3.2. Incubate the force-fed larvae in the dark at 37 °C between 1-24 h. Use DPBS-administered larvae as mock background controls to exclude potential stress responses induced due to the handling of the larvae during force-feeding.

4. Processing of orally administered larvae and RNA isolation

4.1. Work under a hood and wear safety glasses. Clean the hood and spray reagent to prevent RNase contamination.

4.1.1. Snap-freeze the living larvae after incubation in liquid nitrogen and homogenize them. Use a mortar and pistil for homogenization. Add liquid nitrogen to the mortar and grid each larval individual until powdered homogenates are produced.

4.1.2. Pour the homogenate to a disposable weighing boat and wait for the liquid nitrogen to evaporate.

4.2. Mix the liquid nitrogen-free frozen powdered homogenates with 1 mL of Trizol in a 2 mL tube and incubate the mixture at room temperature for 1 h.

177 4.3. Centrifuge the mixture at 8,000 x *g* for 15 min at room temperature and transfer the
178 supernatant into a fresh tube and discard the pellet. Mix the supernatant with 200 µL of 1-
179 Bromo-3-Chloropropane (BCP). Incubate the mixture for 5 min at room temperature and for 10
180 min on ice.

181
182 4.4. Centrifuge the BCP-added reactions at 18,000 x *g* for 15 min at 4 °C. Transfer the upper
183 transparent layer into a new 2 mL tube and discard the rest. Precipitate the RNA of the
184 transferred upper layer with 500 µL isopropanol by mixing and inverting the tube for 5 min.

185
186 4.5. Centrifuge the tube at 18,000 x *g* for 15 min at 4 °C. Wash the precipitated RNA pellet
187 with 500 µL of 75% ethanol.

188
189 4.6. Dry the RNA pellet for 5-10 min at RT. Take care to not over dry it as it will be hard to
190 dissolve later.

191
192 4.7. Dilute ribonuclease inhibitor (1:100) in nuclease-free water and use 100 µL of the
193 solution to resuspend the dried RNA pellet. Vortex the tube carefully until the pellet is
194 completely dissolved.

195
196 4.8. Measure RNA quality and quantity. Ensure that the 260/280 ratio is approximately 2.0
197 and 260/230 ratio in the range of 2.0-2.2 (see **Table of Materials**).

198
199 4.9. Use 5 µg of the isolated RNA for DNase digestion. Mix 5 µL of 10x buffer, 1 µL of
200 ribonuclease inhibitor enzyme, 2 µL of DNase enzyme, 5 µg of RNA, and fill up with nuclease-
201 free water up to 50 µL. Incubate for 30 min at RT.

202
203 4.9.1. Add 6 µL of inactivation reagent and incubate for 2 min at RT and vortex reaction
204 occasionally. Centrifuge reaction at 10,000 x *g* for 1 min. Transfer supernatant into fresh 1.5 mL
205 tube.

206
207 NOTE: The RNA contains the larval RNA as well as the bacterial RNA of the respective strain
208 used for oral administration.

209 210 5. Quantification of the bacterial 16S copy numbers after force-feeding

211
212 NOTE: The copy numbers of the expressed bacterial 16S was determined using cDNA
213 synthesized from the RNA extracted in section 4. Final quantification is calculated with the help
214 of a standard curve of plasmid in which the 16S PCR fragment of either *B. vulgatus* or *E. coli* was
215 cloned.

216 217 5.1. Preparation of plasmid standards

218
219 5.1.1. Amplify 16S fragments from *E. coli* mpk or *B. vulgatus* mpk genomic DNA by PCR. Mix
220 10 µL of 5x buffer, 1 µL of 10 mM dNTP solution, 2.5 µL of 10 µM forward primer and 2.5 µL of

10 μ M reverse primer dilution, 1 μ L of DMSO, 1 μ L of genomic DNA template, 31.5 μ L of nuclease-free water and 0.5 μ L of proof-reading enzyme.

5.1.2. Run the PCR (initial denaturation: 98 °C for 30 s, denaturation: 98 °C for 10 s, annealing: 60 °C for 30s, extension: 72 °C for 30 s, final extension: 72 °C for 5 min, repeat denaturation, annealing and extension for 30 cycles).

5.1.2.1. Use 16S *E. coli* primers (p_forward: GTTAATACCTTTGCTCATTGA, p_reverse: ACCAGGGTATCTAATCCTGTT¹⁷, 320 bp) or 16S *B. vulgatus* primers (p_forward: AACCTGCCGTCTACTCTT, p_reverse: CAACTGACTTAAACATCCAT¹⁸, 400 bp) for amplification.

5.1.3. Use the *E. coli* and *B. vulgatus* 16S PCR fragments for blunt-end cloning into a cloning vector. Set up ligation and mix 10 μ L of 2x buffer, 1 μ L of non-purified PCR product, 1 μ L of blunt-end cloning plasmid, 7 μ L of nuclease-free water and 1 μ L of T4 DNA Ligase. Incubate ligation for 10 min at RT.

5.1.4. Prepare *E. coli* DH5 α competent cells.

5.1.4.1. Inoculate 100 mL of LB medium in an Erlenmeyer flask with 1 mL of an overnight culture. Grow the culture until OD 600 nm is between 0.4-0.6. Split the resulting culture into two 50 mL tubes and incubate the cultures on ice for 10 min.

5.1.4.2. Centrifuge the cultures at 1,700 x *g* for 10 min at 4 °C. Discard the supernatant and resuspend each pellet carefully with 5 mL of RFI solution (30 mM CH₃COOK, 100 mM KCl, 10 mM CaCl₂, 50 mM MnCl₂, adjust pH 5.8 with glacial acid, sterile filtered). Fill each tube with additional 45 mL of RFI solution.

5.1.4.3. Centrifuge the cultures at 1,700 x *g* for 10 min at 4 °C. Discard the supernatant and resuspend each pellet carefully with 6 mL of RFII (10 mM MOPS, 15 mM CaCl₂, 10 mM KCl, 15% glycerol, autoclaved) solution. Pool both fractions and incubate the 12 mL suspension on ice for 15 min. Prepare cell suspension aliquots (200 μ L). Store the aliquots at -80 °C.

5.1.5. Transfer the ligation reaction to one aliquot of competent *E. coli* DH5 α cells and leave the reaction on ice for 15 min. Heat shock the cells for 45 s at 42 °C and add 1 mL of LB medium.

5.1.5.1. Incubate transformation for 45 min at 37 °C. Add 100 μ L of the transformation to a LB agar plate containing ampicillin and incubate overnight at 37 °C.

5.1.6. Perform colony PCR of 8 resulting transformants from the LB agar plate of step 5.1.5. Pick each colony with a toothpick, dip it onto a fresh LB plate containing ampicillin (master plate) and then dip the same toothpick into a well containing 5.5 μ L of nuclease-free water in a PCR stripe.

5.1.6.1. Add 7.5 µL of 2x PCR mix, 0.5 µL of 10 µM forward primer and 0.5 µL of 10 µM reverse primer dilution. Use the same primer pairs mentioned in section 5.1.1.

5.1.6.2. Run PCR (initial denaturation: 95 °C for 5 min, denaturation: 95 °C for 1 min, annealing: 60 °C for 30s, extension: 72 °C for 1 min, final extension: 72 °C for 7 min, repeat denaturation, annealing and extension for 35 cycles).

5.1.7. Verify the size of the 16S fragments on a 1% agarose gel. Use 0.5x Tris-Borate-EDTA (TBE) buffer to dissolve 1 g of agarose and boil it in a microwave. Add 1:50,000 dye to gel and pour it. Add the colony PCR reactions and a 100 bp DNA ladder to the gel, and run the gel for 45 min at 110 V.

5.1.8. Inoculate a 5 mL LB overnight culture containing ampicillin with one clone from the master plate (section 5.1.6) for each *E. coli* and *B. vulgatus* 16S plasmid that contains the right insert size.

5.1.8.1. Centrifuge the bacterial overnight cultures in a 2 mL tube at 1,700 x g. Discard the supernatant and resuspend the pellet in 600 µL sterile water.

5.1.8.2. Add 100 µL of lysis buffer and mix by inverting the tube 6 times. Add 350 µL of cold (4°C) neutralization solution and mix thoroughly by inverting the tube.

5.1.8.3. Centrifuge at maximum speed in a centrifuge for 3 min. Transfer the supernatant (~900 µL) to a spin column and centrifuge at maximum speed in a centrifuge for 15 s.

5.1.8.4. Discard the flowthrough and add 200 µL of endotoxin removal wash and centrifuge at maximum speed in a centrifuge for 15 s.

5.1.8.5. Add 400 µL of wash solution to the column and centrifuge at maximum speed in a centrifuge for 30 s. Transfer the column to a clean 1.5 mL tube, add 30 µL of elution buffer to the column incubate it for 1 min at room temperature.

5.1.8.6. Centrifuge at maximum speed in a centrifuge for 30 s (see **Table of Materials**).

5.1.9. Determine the plasmid DNA concentration by mixing 1 µL of plasmid DNA with 199 µL of working solution (1 µL of fluorescent dye per 199 µL of buffer for each reaction). Prepare two standards by mixing 10 µL of standard 1 or 10 µL of standard 2 with 190 µL. Vortex the sample and standard tubes and incubate reaction for 2 min. Measure the concentration (see **Table of Materials**).

5.1.10. Prepare standard concentrations in 10-fold serial dilutions in a range of 10-100,000 copies: Calculation the mass of the single plasmid ($m = (n) \times (1.096 \times 10^{-21} \text{ g/bp})$, n = plasmid size, m = mass). Calculate the mass of plasmid DNA needed to contain the desired copy

numbers of interest (copy number of interest x mass of single plasmid = mass of plasmid DNA needed).

5.2. Preparation of samples for quantification

5.2.1. Synthesize cDNA. Mix 2 µL of 7x buffer, 1 µL of DNase-digested RNA from section 4 and 11 µL of nuclease-free water. Incubate for 2 min at 42 °C.

5.2.1.1. Place reaction immediately on ice. Mix 4 µL of 5x RT Buffer, 1 µL of RT (Reverse Transcriptase) primer mix, 1 µL of RT enzyme and the reaction of step 5.2.1. Incubate for 15 min at 42 °C. Incubate for 3 min at 95°C to inactivate RT enzyme.

5.2.2. Quantify cDNA concentrations fluorometrically like described in step 5.1.9.

5.3. Measurement of bacterial load

5.3.1. Adjust cDNA concentrations to 5 ng per 12 µL reaction for quantitative PCR. Mix 2x RT-PCR mix, 0.25 µL of 100 µM forward primer, 0.25 µL of 100 µM reverse primer (5.1.1) and 12 µL of adjusted cDNA. Run qPCR (initial denaturation: 95 °C for 5 min, denaturation: 95 °C for 10 s, annealing: 60 °C for 30 s, repeat denaturation and annealing for 35 cycles, melting: 95 °C, cool down to 4 °C).

5.3.2. Plot log₁₀ concentrations of plasmid standard curve (10-100,000 copies), i.e. 1-5 (x-axis), against the corresponding ct-values (y-axis). Perform linear regression to obtain the regression equation. Solve the equation for x (concentration). Use the formula to calculate the log₁₀ of the copy numbers by inserting ct-value into the formula. Calculate the antilogarithm to obtain copy numbers.

6. Determination of innate immune marker gene using quantitative RT-PCR

6.1. Check primers for gene-specificity by PCR and subsequent agarose gel electrophoresis to verify the correct fragment size. Perform PCR like described in section 5.1.5.

Ubiquitin 130 bp: forward TCAATGCAAGTAGTCCGGTTC, reverse CCAGTCTGCTGCTGATAAACC¹⁹ (housekeeping)

Nox-4 159 bp: forward TGGCACGGCATCAGTTATCA, reverse ACAGCGACTGTCATGTGGAA⁸

Nos 76 bp: forward ATGAAGGTGCTGAAGTCACAA, reverse GCCATTTTACAATCGCCACAA⁸

Gst 156 bp: forward GACAGAAGTCCTCCGGTTCAG, reverse TCCGTCTTCAAGCAAAGGCA⁸

ApolII 265 bp: forward AGACTTGACGCCATCAAGA, reverse TGCATGCTGTTTGTCACTGC⁸

hemolin 267 bp: forward CTCCTCACGGAGGACAAAC, reverse GCCACGCACATGTATTACC⁸

gallerimycin 161 bp: forward GAAGTCTACAGAATCACACGA, reverse ATCGAAGACATTGACATCCA⁸

cecropin 158 bp: forward CTGTTCTGTTTCGTTGTGT, reverse GTAGCTGCTTCGCCTACCAC⁸

gloverin 101 bp: forward GTGTTGAGCCCGTATGGGAA, reverse CCGTGATCTGCTTGCTAAC⁸

morcin 124 bp: forward GCTGTACTCGCTGCACTGAT, reverse TGGCGATCATTGCCCTCTTT⁸

6.2. Assess primer efficiency to be E=2.

6.2.1. Pool 2 µL of 5-10 different positive samples (i.e., samples that are expressing the gene for which the primer pair needs to be investigated).

6.2.2. Prepare a 1:5 dilution series of the sample pool: standard 1 (S1): undiluted pool; S2: 2 µL of S1 + 8 µL nuclease-free water; S3: 2 µL of S2 + 8 µL nuclease-free water; S4: 2 µL of S3 + 8 µL nuclease-free water.

6.2.3. Apply 1 µL of S1-S4 and a non-template control (nuclease-free water) to a 96-well qPCR plate. Add 5 µL of RT master mix, 0.1 µL of each 100 µM forward and reverse primer, 3.7 µL of nuclease-free water and 0.1 µL of RT mix per well.

6.2.4. Run quantitative RT-PCR (reverse transcription: 50 °C for 10 min, initial denaturation: 95 °C for 5 min, denaturation: 95 °C for 10 s, annealing: 60 °C for 30 s, repeat denaturation and annealing for 40 cycles, melting: 95 °C, cool down to 4 °C).

6.2.5. Plot log₁₀ of relative units for S1-S4 (1, 0.2, 0.04, 0.008) (x-axis) against the corresponding ct-values (y-axis). Perform linear regression and determine the slope of the standard curve. Calculate the efficiency E: $E = 10^{-(1/\text{slope})}$.

NOTE: A slope of -3.32 indicates ideal reaction conditions and primer efficiency of E=2.00. This means: the amount of PCR product doubles during each cycle.

6.3. Use 100 ng of digested RNA (100 ng/µL) as a template for RT-PCR. Mix RT-PCR reagents and run RT-PCR like mentioned in section 6.2. Measure all bacteria- and DPBS-administered samples with both housekeeping primer pair and target primer pairs. Always run the S1-S4 dilutions with the housekeeping primer pair and S1-S4 with the target primer pair on the same plate for efficiency determination.

6.4. Calculate ratio (R) of RNA gene expression according to the following formula using the experimentally determined primer efficiency of both the housekeeping and the target primer pair. Normalize bacteria stimulated samples to mock controls²⁰.

$$R = \frac{E_{\text{target}}^{\Delta \text{ct}_{\text{target}}(\text{control-sample})}}{E_{\text{housekeeping}}^{\Delta \text{ct}_{\text{housekeeping}}(\text{control-sample})}}$$

R: ratio

E_{target}: efficiency of S1-4 measured with target primer pair

E_{housekeeping}: efficiency of S1-4 measured with housekeeping primer pair

Δct_{target}^(control-sample): Δct of (ct of DPBS-fed sample)-(ct of bacteria-fed sample) measured with target primer pair

Δct_{housekeeping}^(control-sample): Δct of (ct of DPBS-fed sample)-(ct of bacteria-fed sample) measured

with housekeeping primer pair

REPRESENTATIVE RESULTS

The *G. mellonella* hemolymph infection model is widely used to analyze the virulence factors of a huge variety of pathogens. Most measurements include the analysis of larvae mortality, which is a quite easy method. Nevertheless, this method does not allow conclusions about immune responses in general and link the results of *G. mellonella* immune responses with vertebrate immune mechanisms. The *G. mellonella* oral administration model on the other hand is only rarely used for oral infection or colonization of the larvae due to the difficulties to obtain exact infection dosage⁹. Further, only little is known about *G. mellonella* innate immune responses towards non-pathogenic bacteria especially mammalian intestinal commensals.

In contrast to pathogens, commensals challenge the host and trigger immune responses but the host immune system is able to maintain immune homeostasis. *G. mellonella* is able to clear the initial force-fed bacterial load until finally no bacteria were detectable anymore (**Figure 2**)⁸. The 16s gene copy numbers of both *B. vulgatus* and *E. coli* substantially decreased within 24 h.

We demonstrated that commensal-administered *G. mellonella* larvae induce RNA gene expression of different innate immunity marker genes: LPS-recognition molecules – apolipoprotein (ApolIII) and hemolin (**Figure 3A,B**) were shown to be generally higher expressed in *E. coli*-administered larvae compared to *B. vulgatus*-administered larvae⁸. Further, marker gene expression of two kinds of antimicrobial molecules can be monitored. The production of reactive oxygen and nitrogen species (ROS/RNS) can be estimated by the measurement of *Nos* and *Nox-4* gene expression which were demonstrated to be strongly upregulated upon *E. coli* force-feeding compared to *B. vulgatus* (**Figure 4A,B**)⁸. Furthermore, gene expression of antioxidative *Gst* could be observed (**Figure 4C**)⁸.

In addition we showed that different antimicrobial peptide expression was induced stronger after *E. coli* administration than in response to *B. vulgatus* force-feeding. We observed upregulation of defensin-like gallerimycin peptide, LPS-interacting gloverin peptide, cecropin and moricin (**Figure 5A,B,C,D**)⁸.

FIGURES AND TABLES

Figure 1: Force-feeding setup using a microsyringe pump. A blunt-ended needle is adjusted into microsyringe pump which allows precise injection of bacteria.

Figure 2: Persistence of bacterial load in *Galleria mellonella* larvae after force-feeding. Copy numbers of *B. vulgatus*- and *E. coli*-specific 16s rDNA genes were determined from 5 ng of cDNA at different time points using RT-PCR. Data points are shown with indication of the median. Modified from reference 8.

Figure 3: Differential pattern recognition of bacteria by *G. mellonella*. The larvae were administrated with two different intestinal commensals, RNA was isolated after 1-6 h, and mRNA expression of LPS recognition molecule apolipoprotein (ApolIII) (**A**) and hemolin (**B**) was

determined. Data points represent geometric means with standard error of the mean (SEM) ($p > 0.05$; *, $p < 0.05$; **, $p < 0.01$; ***, $p < 0.001$).⁸

Figure 4: ROS marker gene expression after bacterial challenge. *E. coli* and *B. vulgatus* were force-fed and ROS defense marker gene expression was analyzed over time. *Nos* (A), *Nox-4* (B) and *Gst* (C) mRNA expression was measured in isolated larval RNA. Data points represent geometric means with standard error of the mean (SEM) ($p > 0.05$; *, $p < 0.05$; **, $p < 0.01$; ***, $p < 0.001$). Modified from reference 8.

Figure 5: Commensal-induced defensin-like antimicrobial peptide expression in *G. mellonella* larvae and human epithelial cells. Larvae were orally administered with *B. vulgatus* or *E. coli*, immune responses were observed over time and RNA was isolated from larval individuals. gallerimycin (A), cecropin (B), gloverin (C), moricin (D) mRNA expression was determined. Data points represent geometric means with standard error of the mean (SEM) ($p > 0.05$; *, $p < 0.05$; **, $p < 0.01$; ***, $p < 0.001$). Modified from reference 8.

DISCUSSION

The *G. mellonella* model is a frequently used model to assess bacterial virulence factors in a systemic infection approach²¹. Since many pathogens and bacteria enter the host via the oral colonization or infection route, new insights need to be found to evaluate *G. mellonella* as a model for oral colonization and infection.

The possibility to rear *G. mellonella* between 15-37 °C is a great advantage since most mammalian models maintain body temperatures of 37 °C⁵. *G. mellonella* larvae can be purchased from different suppliers but the establishment of an own breeding population provides many advantages such as the absence of antibiotics that interfere with the assays, better estimation when to start experiments since the suppliers do not always provide larvae in a ready-to-use stage and stress responses are avoided due to transportation or temperature changes. Due to the temperature tolerance of *G. mellonella* the temperature range at which breeding can be performed is high. Higher temperatures lead to faster development of the larvae and according to the breeding temperature, we can estimate the lifecycle from egg to last instar larva. When larvae were selected for experiments, only pale and fast-moving individuals were chosen to avoid any stress and immune reactions to interfere with the experiments.

In order to establish the force-feeding model, it needs to be assured that the oral application was successful. Therefore, it was helpful to set up several trials for which a strong bromophenol dye was added to the solution intended for force-feeding. This helps to exclude any injured larvae and select for the larvae that have the blue dye only within their gut²².

Using this model, we found that *G. mellonella* larvae are useful to investigate innate immune response kinetics of certain marker genes. During the establishment of the oral administration model and the study of immune response kinetics we found gene expression to be not locally expressed in the midgut. First experimental trials to extract midgut RNA after oral

administration of commensal bacteria did not provide conclusive results. Therefore, the immune responses were determined “globally” in whole individuals. These findings support the hypothesis of global recognition via intestinal receptors, transmission of the signal and triggering extraintestinal gene expression. Generally, *G. mellonella* is able to induce AMPs mainly in the fat body, but further in hemocytes and the intestinal system⁹. Since there is no precise information available about tissue-specific production of antimicrobial molecules in *G. mellonella* larvae after infection, the whole larval RNA was extracted from complete individuals and used for assaying RNA gene expression. A further advantage of whole larval RNA extraction is the complete containment of the living bacteria inside the gut and the possibility to quantify the bacterial load. The dissection of the gut could lead to the loss of bacteria due to preparation.

Since most *G. mellonella* research is performed on bacterial virulence traits we were especially interested if and how the larvae trigger immune responses towards non-pathogenic bacteria which are part of the mammalian microbiota. Recently, we showed that both *G. mellonella* and mammals share similar components of the innate immune response, which are homologous and evolutionary conserved. The nitric oxid synthase (*Nos*) and NADPH oxidase (*Nox*) genes share a high degree of similarity⁸. *G. mellonella* harbors further a defensin-like antimicrobial peptide gallerimycin which shares structural similarities with mammalian β -defensin 2⁸.

Using the oral administration model it was possible to demonstrate differential bacterial recognition of either anti-inflammatory symbiotic *B. vulgatus* or pro-inflammatory pathobiotic *E. coli*. In addition downstream oxidative stress responses and antimicrobial peptide production were higher induced after *E. coli* administration compared to *B. vulgatus* administration⁸.

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DISCLOSURES:

The authors have nothing to disclose.

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Figure 1

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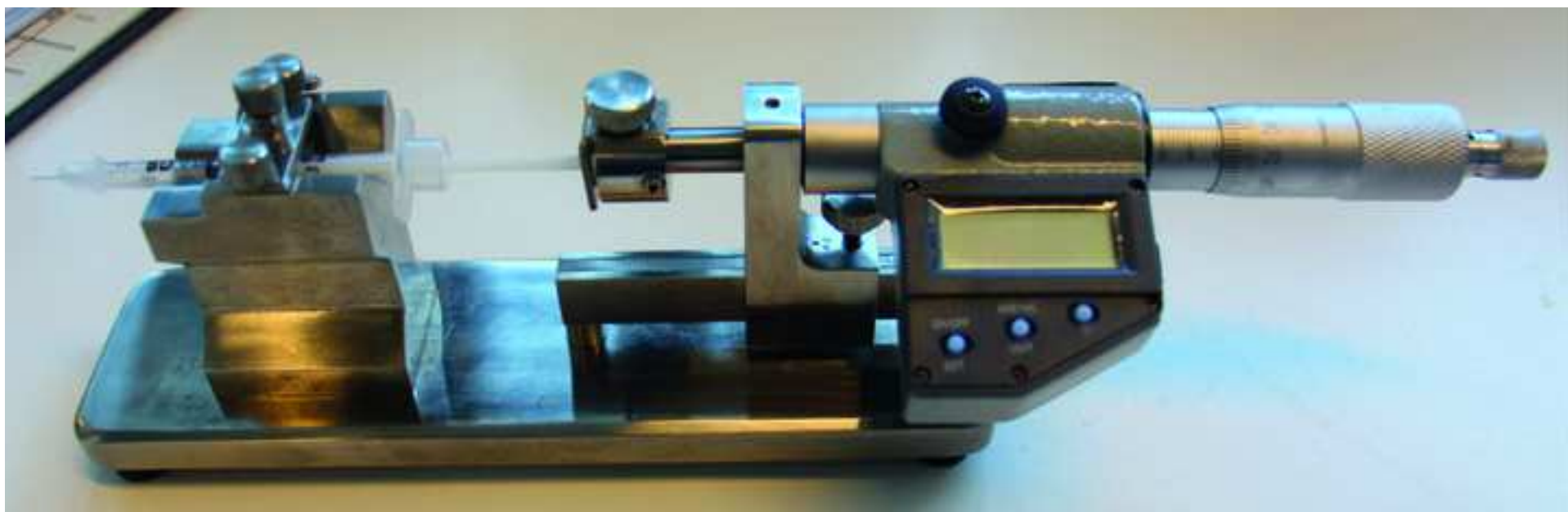


Figure 2

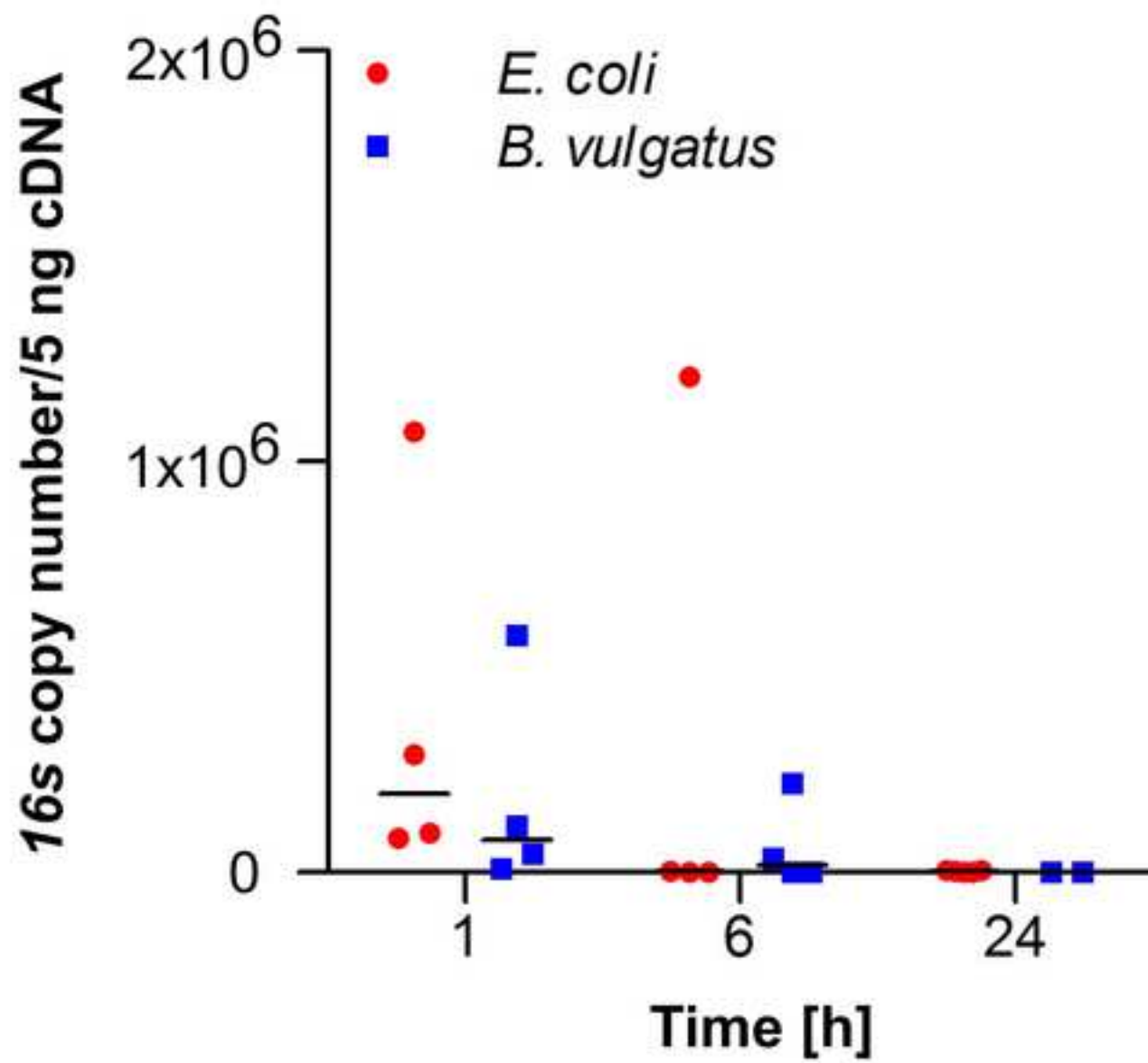
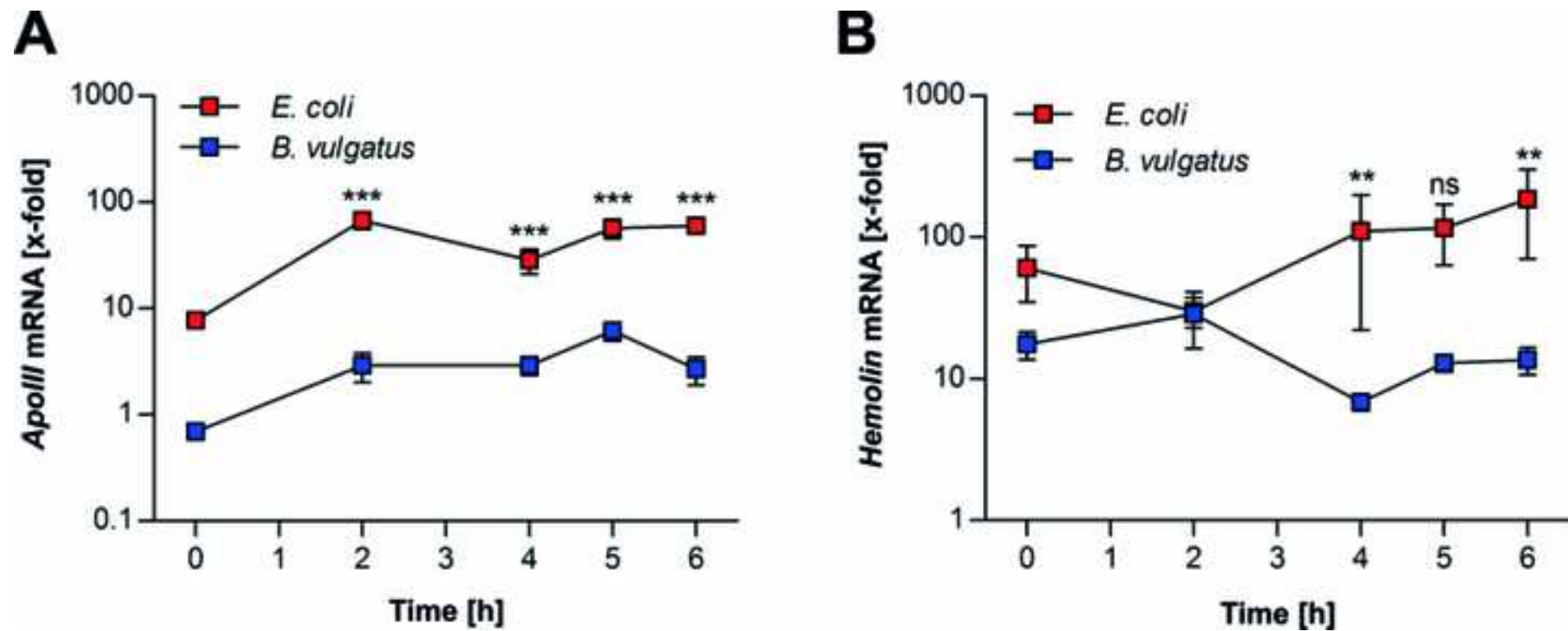


Figure 3

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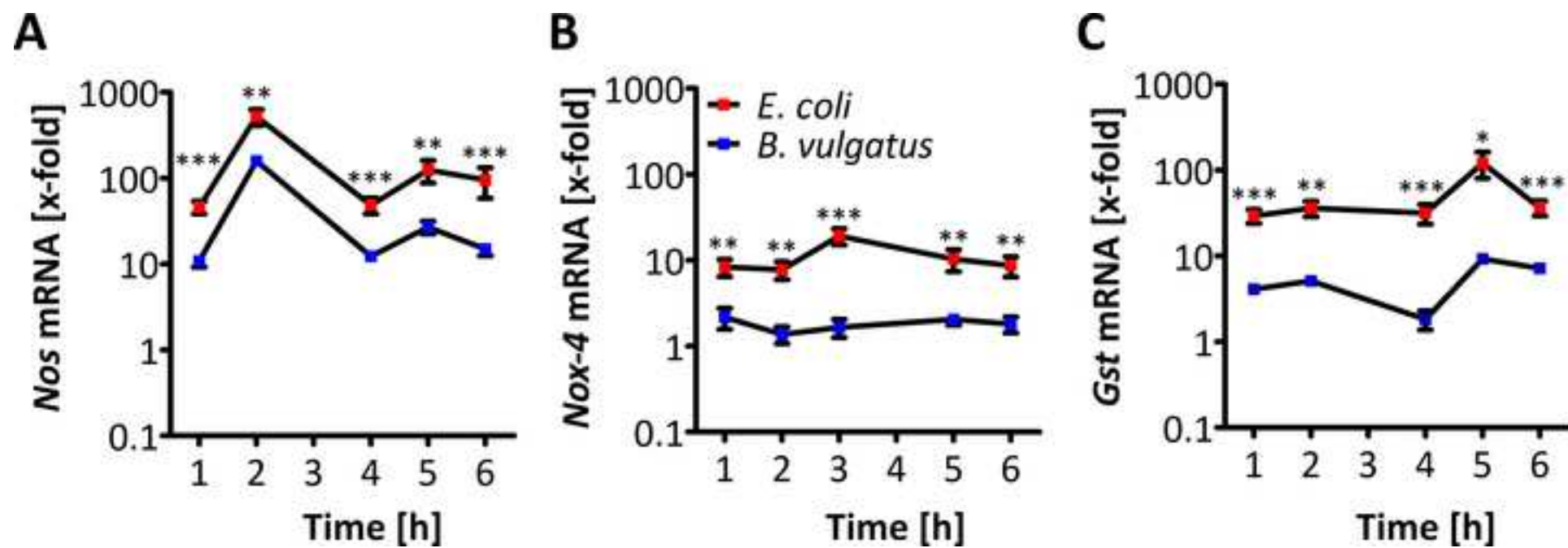
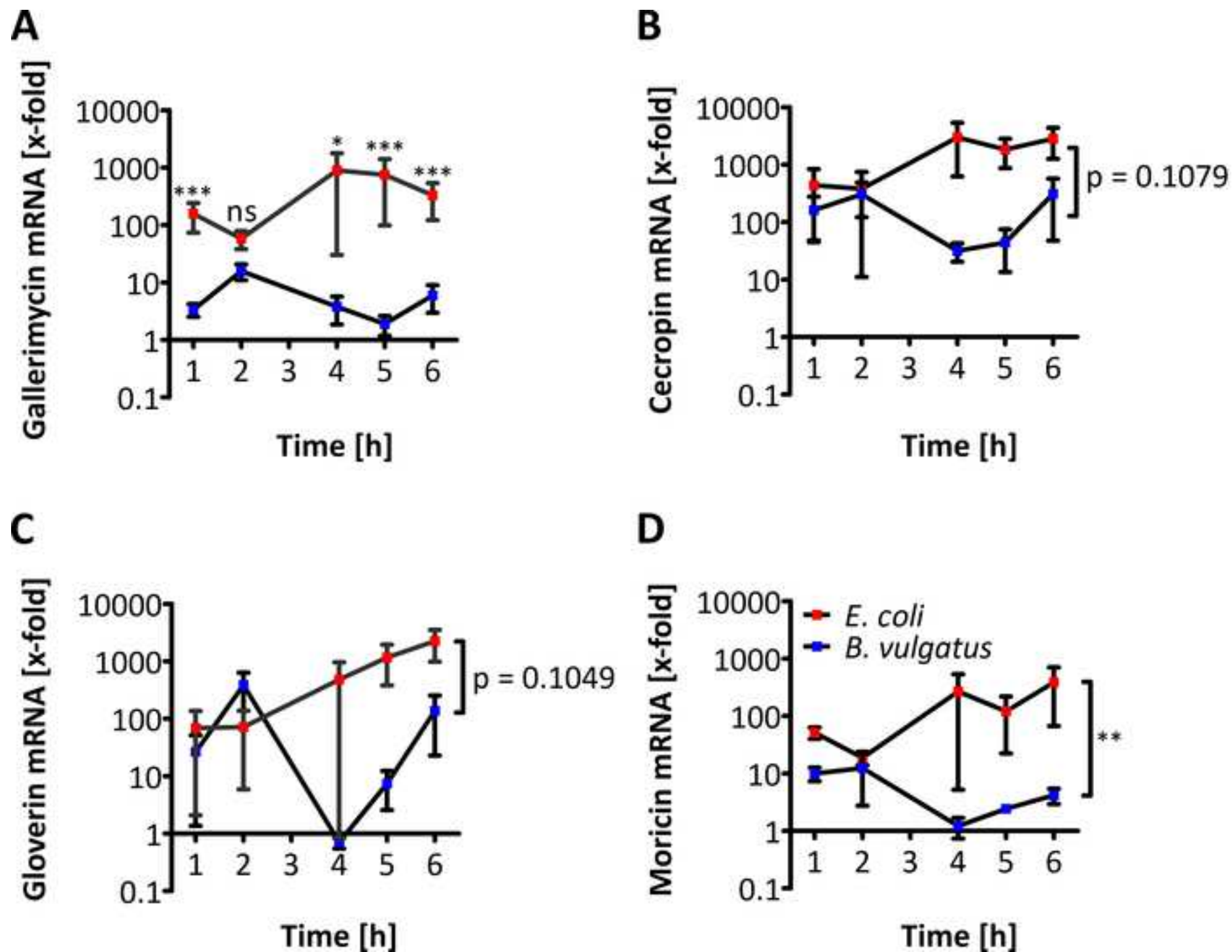


Figure 5

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Name of Material/ Equipment	Company	Catalog Number	Comments/Description
1.5 mL tubes	Eppendorf	0030120086	
100 bp DNA ladder	Thermo Fisher Scientific	15628019	
1-Bromo-3-Chloropropane (BCP)	Sigma-Aldrich	B9673	
2 mL tubes	Eppendorf	0030120094	
2x Mangomix	Bioline	BIO-25033	Colony PCR
50 mL tubes	Greiner Bio-One	210 261	
Agarose	Biozym	840004	
Beeswax	Mixed-Store.de	-	
Brain heart infusion broth	Thermo Fisher Scientific	CM1135	
CloneJET PCR Cloning Kit	Thermo Fisher Scientific	K1232	Cloning vector for 16S fragments
Corn grits	Ostermühle Naturkost GmbH	306	Organic cultivation
Difco LB Agar, Miller (Luria-Bertani)	Becton Dickinson	BD	
Difoco LB Broth, Miller (Luria-Bertani)	Becton Dickinson	244610	
DNA-free DNA Removal Kit	Thermo Fisher Scientific	244510	Dnase digestion
Dried yeast	Rapunzel	-	Organic cultivation
Dulbecco's Phosphate-Buffered Saline	Thermo Fisher Scientific	14040	
Ethanol	VWR	20821.330	
Glycerol	Sigma-Aldrich	W252506	
Honey	Ostermühle Naturkost GmbH	487	
Isopropanol	VWR	20842.330	
Lightcycler 480 Instrument II	Roche Molecular Systems	5015278001	
LightCycler 480 Multiwell Plate 96, white	Roche Molecular Systems	4729692001	
Manual Microsyringe Pump with Disposable Syringes	World Precision Instruments	DMP	
Micro-Fine+ U-100 insulin syringe 0.3 mL	Becton Dickinson	324826	Oral administration
Mortar, unglazed	VWR	410-9327	
Nanodrop	Thermo Fisher Scientific	13-400-518	
Nuclease-free water	Thermo Fisher Scientific	10977035	
Oxid AnaeroGen sachets	Thermo Fisher Scientific	AN0025A	Quality and quantity of RNA
PCR stripes	Biozym	710970	

Pestle, unglazed grinding surface	VWR	410-9324	
Phusion proof-reading enzyme	Thermo Fisher Scientific	F553S	
Primers	Biomers	-	
PureYield Plasmid Miniprep System	Promega	A1222	
QuantiFast SYBR Green PCR kit	Qiagen	204056	qPCR for bacterial copy number measurment
QuantiFast SYBR Green RT-PCR Kit	Qiagen	204156	qRT-PCR for gene expression measurements
QuantiTect Reverse Transcription K	Qiagen	205311	cDNA synthesis
Qubit Assay Tubes	Thermo Fisher Scientific	Q32856	
Qubit dsHS DNA kit	Thermo Fisher Scientific	Q32851	Quantification of plasmid and cDNA samples
Qubit fluorometer	Thermo Fisher Scientific	Q33226	Quantification of plasmid and cDNA samples
RNase-ExitusPlus	AppliChem	A7153	
Rnasin Ribonuclease Inhibitor	Promega	N2511	
Skimmed milk powder	Sucofin	-	
SYBR safe DNA Gel Stain	Thermo Fisher Scientific	S33102	
TRI reagent	Sigma-Aldrich	T9424	
Weighing boat	VWR	10803-148	
Wheat meal	Ostermühle Naturkost GmbH	6462	Organic cultivation



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Author's response Letter to the editor and reviewers

We want to thank you sincerely for your detailed comments and suggestion which we included in our work. We feel that it significantly improved our manuscript.

Editorial comments:

1. Please take this opportunity to thoroughly proofread the manuscript to ensure that there are no spelling or grammar issues.

Comment: Thank you for the advice to thoroughly proofread our manuscript to avoid spelling or grammar problems.

2. Please rephrase the Summary to clearly describe the protocol and its applications in complete sentences between 10-50 words: "Here, we present a protocol to ..."

Comment: Thank you for this suggestion we rephrased the Summary to describe the protocol and the method applications.

3. Please convert centrifuge speeds to centrifugal force (x g) instead of revolutions per minute (rpm).

Comment: Thanks for the comment. We exchanged centrifuge speeds from rpm to xg.

4. Please revise the protocol text to avoid the use of any personal pronouns (e.g., "we", "you", "our" etc.).

Comment: Thank you for this suggestion we rephrased the protocol to avoid any personal pronouns.

5. Please revise the protocol to contain only action items that direct the reader to do something (e.g., "Do this," "Ensure that," etc.). The actions should be described in the imperative tense in complete sentences wherever possible. Avoid usage of phrases such as "could be," "should be," and "would be" throughout the Protocol. Any text that cannot be written in the imperative tense may be added as a "Note." Please include all safety procedures and use of hoods, etc. However, notes should be used sparingly and actions should be described in the imperative tense wherever possible. Please move the discussion about the protocol to the Discussion.

Comment: Thank you for this advice. We revised the protocol and used the imperative tense throughout the protocol. In rare cases we included a "note" when the imperative tense could not be used. Further we moved discussion into the discussion section.

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Comment: Thank you for this comment since we have not been aware of the commercial language. We revised the protocol and used generic terms instead. Sometimes we mentioned as advised "see table of materials".

7. Please add more details to your protocol steps. There should be enough detail in each step to supplement the actions seen in the video so that viewers can easily replicate the protocol. Please ensure you answer the “how” question, i.e., how is the step performed? Alternatively, add references to published material specifying how to perform the protocol action. See examples below.

Comment: We agree to add more details to the protocol steps. (see point 8-13.)

8. 4.1: Please describe how to homogenize the larvae and specify the incubation temperature.

Comment: We added more details to this essential step of the protocol. We provided more details for how the homogenization needs to be performed and mentioned the incubation time.

9. 4.3: Is the pellet discarded? Is 500 µL isopropanol added to the new tube containing the upper layer? Please specify.

Comment: Yes, the pellet is discarded and the isopropanol is added to the upper layer. We modified the step to contain more details.

10. 5.1: Please specify PCR conditions.

Comment: We specified the PCR recipe and the program. Further we changed 5.1 into 5.1.1 since there were more details and we still want the protocol to be clearly structured.

11. 5.2, 5.3, 5.5, 5.7, 6.2, 6.3: Please add more details to these steps. This step does not have enough detail to replicate as currently written. Alternatively, add references to published material specifying how to perform the protocol action.

Comment: We added more details to these steps and changed 5.2 into 5.1.2-5.1.5, 5.3 into 5.1.6-5.1.7, 5.5 into 5.2.1, 5.7 into 5.3 (5.3.1 and 5.3.2), and 6.2 into 4.9, 6.3 was left without renaming it. The renaming of the points should help to keep the clearly structure of the protocol.

12. Please ensure that conditions and primers are listed all PCR procedures.

Comment: We added more details and described the PCR recipe and the program.

13. 6.1: Please describe how to assess the primer efficiency.

Comment: We added more details to the primer efficiency assessment and divided 6.1 into 6.1 and 6.2. We provided essential information to calculate the primer efficiency.

14. After you have made all the recommended changes to your protocol (listed above), please highlight 2.75 pages or less of the Protocol (including headings and spacing) that identifies the essential steps of the protocol for the video, i.e., the steps that should be visualized to tell the most cohesive story of the Protocol.

Comment: After having introduced all the suggested and advised changes to the protocol we highlighted the essential steps of the protocol for the video. The highlights include almost 2 pages.

15. Please highlight complete sentences (not parts of sentences). Please ensure that the highlighted part of the step includes at least one action that is written in imperative tense.

Comment: We assured to highlight the complete sentences.

16. Please include all relevant details that are required to perform the step in the highlighting. For example: If step 2.5 is highlighted for filming and the details of how to perform the step are given in steps 2.5.1 and 2.5.2, then the sub-steps where the details are provided must be highlighted.

Comment: We followed this advice and highlighted the details to perform the highlighted steps.

17. Figure 2: Please change “100 6” to “106” (i.e., delete 0 and the space between).

Comment: We followed this advice and performed the suggested changes.

18. Figure 3: Please describe the asterisk symbols in the figure legend.

Comment: We agree to explain the asterix symbol. Therefore we added the descriptions in the figure legends.

19. Discussion: As we are a methods journal, please also discuss critical steps within the protocol, any modifications and troubleshooting of the technique, and any limitations of the technique.

Comment: Thank you for this comment we discussed critical steps like rearing in the discussion section. Further we discussed limitation like the lack of gut-specific RNA expression analysis.

20. References: Please do not abbreviate journal titles.

Comment: We followed this advice and performed the suggested changes

21. Table of Materials: Please sort the items in alphabetical order according to the name of material/equipment.

Comment: Thanks for the comment. We sorted the items in alphabetical order and included more necessary material/equipment since we noticed that they were missing.

Reviewer 1:

Abstract: Improve and revise. Firstly, I advise to describe the focus of paper and the relation between invertebrate and vertebrate, link the importance of reduce of the number of vertebrate as the authors have already done. Finally, describe briefly the importance of intestinal microbiota and explain the validity of G. mellonella model in this contest and a final consideration about the obtained data.

Comment: Thank you for the advice to revise the abstract.

Protocol: line 119 : replace rpm with xg

Comment: Thanks for the comment. We changed rpm for xg.

Why the authors did not extract only the gut of the larvae? the procedure is quite simple.

Comment: We agree that the procedure of extracting the gut from the larvae is not difficult, and we performed this in a previous project but the expression analysis of midgut tissue was not conclusive. Since AMPs can be produced in several tissue types we chose to analyze “global” expression. That is why we use the RNA of whole larval individuals for RNA expression analysis. In our manuscript we mentioned this point already in the discussion section: “During the establishment of the oral administration model and the study of immune response kinetics we found gene expression to be not locally expressed in the midgut.”

Protocol/Representative results: line 132: Authors described that larvae were incubated between 1-6 hours; in line 229, authors suggested that 16s gene copy of both bacteria decreased within 24 hours. Is not clear if the incubation is between 1-6 hours or 1-24 hours? and if authors incubated larvae within 24 hours, are they sure that the administration of 10^7 bacteria not killed larvae in this interval?

Comment: We agree that these statements lead to confusion since we missed to mention the 24 h incubation in the protocol. That is why we corrected the incubation times in the protocol into “1-24 h”.

Further, we are sure that the larvae were still alive after 24 h since the RNA was only extracted from living *G. mellonella*. We added this information “living” in the protocol (4.1). After 24 h the oral-administered larvae were still light without any melanization symptoms. The administered bacteria are not pathogenic and lack any virulence factors.

Fig. 4 and 5: I advice to write one time the legend for these figures, the bacteria are only two. Define only one axis for "y", authors used different scale for the four graphs.

Comment: We followed this advice and included the legend of Figure 4 and 5 only once to each of the figures. Further, we changed the axis to have the same scale.

Caption of figure : "*" explain

Comment: We agree to explain the asterix. Therefore we added the explanations in the figure legends.

Reviewer 2:

I suggest to cite more pioneering original papers in which *Galleria mellonella* has been established as a powerful model for bacterial human pathogens to illustrate its importance as an alternative model host.

Comment: We followed this advice and cited more papers in the introduction to highlight the comparative character of *G. mellonella* and mice to support its alternative host model capabilities.

I would add more information on the selected antimicrobial peptides of *Galleria mellonella* (properties, activities). Gallerimycin is an antifungal peptide whereas cecropin has been demonstrated to display activity against human pathogen bacteria.

Comment: We thank for the advice to include more detailed information about the AMPs we selected, since this provide more helpful details for the reader. Therefore we introduced the following section into the introduction: “Generally, the AMPs have quite broad host specificity against Gram-positive and Gram-negative bacteria and fungi and have to provide a potent response since insects are lacking any adaptive response. Gloverins is an AMP which is active against bacteria and fungi and inhibits outer membrane formation. Moricins exhibit their antimicrobial function against Gram-positive and Gram-negative bacteria by penetrating the membrane and forming a pore. Cecropins provide activity against bacteria and fungi and permeabilize the membrane similarly like moricins. Gallerimycin is a defensin-like peptide with anti-fungal properties. Interestingly, it was found that the combination of cecropin and gallerimycin had a synergistic activity against *E. coli*.”

Lane 27: replace homologous by similar because this term implicates a common ancestral origin.

Comment: We followed this advice and changed “homologous” to “similar”.

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