Proteomics and Lipidomics of Black Soldier Fly (Diptera: Stratiomyidae) and Blow Fly (Diptera: Calliphoridae) Larvae

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Abstract

Farming insects has recently emerged as a new source of protein and lipid production. To date, research has mostly focused on food applications of insects. Focusing on nonfood potential of oil and proteins of insects, high-throughput studies of insect lipids and proteins are needed. We performed proteomics and lipidomics investigation on black soldier fly (Hermetia illucens) and blow fly (Lucilia sericata) larvae to investigate new potential and applications. We used mass spectrometry for proteomics and lipidomics analysis of control and treated larvae. Treatment was performed by incubation with a biological decomposer. We provide the list of all fatty acids with their concentration in control and treated larvae. This result showed high levels of lauric acid in black soldier fly, which could even increase after biological decomposition. Proteomics analysis showed the presence of proteins like collagen of cosmetic interest, and proteins with antimicrobial properties such as phenoloxidases and enzymatic activities, such as amylase and trypsin. Insects harbor high potential for nonfood usage as additives, antimicrobial effects, and even pharmaceuticals and cosmetics. These data open avenues for future research in pharmacological and cosmetic approaches to find new molecules of interests.

Key words: black soldier fly larvae, blow fly larvae, proteomics, lipidomics, nonfood application

The world population is expected to reach 9 billion people in 2050 and this increased demand for feed and food make the search for new and secure resources a top priority in the global bioeconomy (van Huis 2013, Müller et al. 2017, Purschke et al. 2018). Over the last decade, investigations into new sources of protein and oil have highlighted the potential of insects in this area (Dobermann et al. 2017). It is known that insects are an important source of protein and other nutrients, and their use as food has ecological advantages over conventional meat and, in the long run, economic benefits (Belluco et al. 2013). Therefore, insect farming has emerged as a new industry, based on its agricultural advantage as planet-friendly farming with high yield (Oonincx et al. 2015).

Among farmed insects, the black soldier fly (Hermetia illucens) has garnered particular interest thanks to its high rate of conversion of biomass to protein and lipid, and its potential role in waste management (Wang and Shelomi 2017).

Up to the present day, the main goal of insect farming has been to integrate the human food chain, either directly or indirectly (as feed for animals). From a legal point of view, the suitability of insects for human consumption is a continuous challenge (Belluco et al. 2013). However, processing of insect lipids and proteins may facilitate this matter, but investigations are still ongoing to identify the optimum conditions for protein and oil separation (Choi et al. 2017).

Farmed insects have been garnering increasing research interest recently, but there remains a gap in our knowledge of the potential of their lipids and proteins. These materials could be of substantial benefit in other industries desirous of new resources in terms of lipids and proteins, such as the cosmetics or pharmaceutical industries.

The oil of insects is a promising potential replacement for fossil oil and plant oils in the oleochemical industry (Verheyen et al. 2018). In the cosmetic industry, there is a need to find an alternative for mink oil and macadamia nut oil in particular, which have become prohibitively expensive (Verheyen et al. 2018). In the agricultural industry, oil from black soldier fly holds promise for its possible antimicrobial effects in the feed of monogastric farm animals (Spranghers et al. 2018).

The protein content and amino acid levels of farmed insects have previously been studied (Yi et al. 2013, Yi, Van Boekel, and Lakemond 2016, Yi, Van Boekel, Boeren, et al. 2016, Zhao et al. 2017).
2016, Janssen et al. 2017). These studies aimed to understand the nutritional value of insect proteins, but there is a gap in our knowledge of proteomes of farmed insects. There are some studies in this area but mostly focused on their antimicrobial peptides (AMPs; Vogel et al. 2018). This idea stems from the ability of insects to feed on nutrition that could be contaminated with high loads of bacteria, fungi, or viruses and yet they survive. Therefore, the antimicrobial proteins in the immune system of farmed insects have been at the center of attention in nutritional immunology (Vogel et al. 2018). These potential antimicrobial proteins could be considered as natural additives to human and animal foods, to act as natural biopreservatives (Rai et al. 2016). Nonetheless, the possibility of finding new antibiotics has been reserved for insect proteins in pharmaceutical researches (Chernysh et al. 2015).

Focusing on medicinal applications of insects, another interesting candidate is the blow fly *Lucilia sp*. These flies are famous for their success in wound healing throughout history. Today, maggot debridement therapy (MDT) is approved by the FDA (Choudhary et al. 2016). It has been shown that besides removal of necrotic tissue and pathogens, maggots help healing by their antimicrobial activity (Andersen et al. 2010). Furthermore, it has also been demonstration that the secretions of maggots increase human fibroblasts in vitro (Gołębiewski et al. 2012). However, the proteome of these larvae has also not been completely studied.

In terms of the nonfood potential of oil and proteins of insects, high-throughput studies of the lipids and proteins of these two flies are lacking. In the present study, we performed proteomics and lipidomics investigations on these two fly species to prepare datasets that would advance our knowledge of their properties, and identify new potential and new applications for them, with a particular focus on proteins with antimicrobial or enzymatic properties. To address this question, we used an easy-to-conduct, rapid, eco-friendly, and inexpensive biodecomposition procedure that mimics natural biodegradation of insects, and seems compatible with downstream nonfood applications.

### Material and Methods

#### Sample Preparation

Two insect species were chosen based on their scientific relevance, their commercial availability and their importance for the insect market. The insect species studies were as follows: *Hermetia illucens* (black soldier fly) and *Lucilia sericata* (blow fly), hereafter termed *Hermetia* and *Lucilia*.

AmiRoy Company provided larvae of *Hermetia* and *Lucilia*. The solution for a biological decomposer (sealed envelope n°28497 registered with the national institute for intellectual property [INPI, Institut National de la Propriété Industrielle]) to separate insect lipids without pressing or warming was also provided by AmiRoy company.

All live insects were fasting for about 24 h. After this period, the insects were stored for 24 h at −80°C. One hundred grams of frozen larvae were ground for at least 5 min. Ground insect was divided into control and biodecomposed groups.

The control group was not subjected to any treatments. The biodecomposed group was solubilized in 50 ml of water containing 1 ml of biological decomposer. The pH was adjusted to 6 with acetic acid 5%. Solutions were incubated for 24 h at 39.5°C with gentle stirring (150 RPM) using a magnet stirrer and 12 h in 41°C without stirring. We obtained a three-phasic solution at the end of incubation (Fig. 1). The three phases were collected from the top to the bottom of the container, vortexed, and stored at −80°C before lipid and protein analysis.

For lipidomics analysis, control, and upper phase after biodecomposition were analyzed for each species. For proteomics analysis, control, middle, and bottom phase after biodecomposition were analyzed for each species.

#### Lipidomics Analysis

Control larvae and the first lipid phase after biodecomposition were subjected to lipidomics analysis for total fatty acids. Total fatty acids...
were analyzed based on Blondelle et al. (2017). Briefly, a mixture of internal deuterated fatty acid standards was prepared. This mixture contained 1300 ng of myristic acid-d3, 5640 ng of palmitic acid-d3, 4200 ng of stearic acid-d3, 3521 ng of linoleic acid-d4, 5.2 ng of arachidic acid-d3, 2160 ng of arachidonic acid-d8, 54 ng of behenic acid-d3, 540 ng of DHA-d5, 26 ng of Lignoceric acid-d4, and 20 ng of cettic acid-d4.

The samples were analyzed by an Agilent 7890A Gas Chromatograph equipped with a 7683 injector and a 5975C Mass Selective Detector (Agilent Technologies, Santa Clara, CA) with chemical ionization in negative mode.

Proteomics and Proteins Analysis
Ground control larvae, and the middle and bottom phase after biological decomposition of both species were subjected to protein extraction by the TCA and Acetone method to obtain pellets of extracted proteins. These pellets were assayed for their protein concentrations using the BCA Protein Assay Kit (Pierce, Rockford, IL). Pellets were resuspended in Dulbecco’s phosphate buffered saline (PBS) (Dominique Dutcher, Brumath, France) pH 7.4 containing 0.25% Triton X100 (Fluka, Sigma–Aldrich, Lyon, France). Samples and standards were mixed with reagent and incubated 2 h at +37°C. Absorbances were measured at 560 nm.

Proteomics Analysis
Pellets of extracted proteins of ground control larvae, and the middle and bottom phase after biological decomposition of both species were subjected to proteomics analysis.

Protein pellets were resuspended in buffer (Urea 6 M, Thiorourea 2 M, DTT, 10 mM, TrisHcl 30 mM).

After second quantification of proteins, samples were subjected to digestion by trypsin overnight. Digested samples were analyzed by NanoLC-Ultra (Eksigent, United Kingdom), Version Eksigent 4.1 and Q exactive (Thermo Scientific, France).

Peptides were identified based on their spectra, and by using X! Tandem Alanine (2017.2.1.4) software and NCB! (https://www.ncbi.nlm.nih.gov/protein/?term=txid7203%5bOrganism:exp%5d) and Uniprot as sources, then protein profiles were constructed. Protein identification was done by coverage of minimum two peptides.

Gene annotation was done by ‘Quick Go’ (https://www.ebi.ac.uk/QuickGO/).

Immunoblot Analysis
Sodium dodecyl sulfate polyacrylamide gel electrophoresis (SDS-PAGE) was used to visualize distribution of the insect protein fractions. The samples were dissolved in Laemmli buffer and were heated at 95°C for 5 min, then applied to 12% acrylamide gels (2 kDa to 250 kDa). Gel was stained by Coomassie blue R-250 to visualize protein bands. Photographs of gel were taken using the ChemiDoc system (Bio-Rad, Hercules, CA).

Results
Lipidomics
The global fatty acids profile of the four experimental groups, namely 1) Hermetia control, 2) Hermetia biodecomposed, 3) Lucilia control, and 4) Lucilia biodecomposed, were determined by GC-MS. Overall, 36 species of fatty acids were found in the four experimental groups, of which 16 were saturated and 20 unsaturated fatty acids (Table 1). Extracted lipids are presented as a percentage of each fatty acid in the total of fatty acids in each experimental group. The most abundant fatty acid in Lucilia was C18:1 n-9, and C12:0 in Hermetia. Based on the type of fatty acids, long-chain fatty acids were the most abundant. The number of each type of fatty acids in all experimental groups is presented in Fig. 2.

In control Lucilia, C18:1 n-9 (oleic acid), C16:0 (palmitic acid), and C16:1 n-7 (palmitoleic acid) were found to be major fatty acids. After biological decomposition, they remained dominant, but their percentages changed. Unsaturated C18:1 n-9 and C16:1 n-7 decreased to 34 and 9%, respectively, whereas saturated C16:0 increased to 27% and C12:0 (lauric acid) showed up to 8%, as well as C18:0 (stearic acid) (Table 1).

In control Hermetia, major fatty acids were C12:0 (lauric acid) 3, C18:1 n-9 (oleic acid), C16:0 (palmitic acid), and C18:2 n-6 (linoleic acid). After biological decomposition, the major fatty acids remained the same, but C18:1 n-9 and C18:2 n-6 decreased to 18% and 16% respectively, whereas C12:0 and C16:0 increased to 41% and 16%, respectively (Table 1).

Comparison of Lucilia (control and biodecomposed) and Hermetia (control and biodecomposed) showed that Hermetia contained more mid-chain fatty acids (MCFAs) (C12:0 and C14:0) (Fig. 2).

Among the four experimental groups, Lucilia control contained more mono-unsaturated fatty acids (MUFA) while polyunsaturated fatty acids (PUFA) were more abundant in Hermetia control (Table 1).

Table 1. Overall fatty acid (FA) profiles are presented as a percentage of concentration each FA out of the sum of all FAs in each experimental group.

| Lipid     | Lucilia control | Lucilia biodecomposed | Hermetia control | Hermetia biodecomposed |
|-----------|-----------------|-----------------------|------------------|------------------------|
| C10:0     | 0.0             | 1.09                  | 0.0              | 0.86                   |
| C12:0     | 0.30            | 8.08                  | 36.40            | 40.79                  |
| C13:0     | 0.03            | 0.17                  | 0.02             | 0.02                   |
| C14:1     | 0.38            | 0.33                  | 0.18             | 0.13                   |
| C14:0     | 2.59            | 2.77                  | 6.89             | 6.56                   |
| C15:0     | 0.60            | 0.66                  | 0.13             | 0.13                   |
| C16:1 n-7 | 13.93           | 8.82                  | 2.39             | 2.36                   |
| C16:1 n-9 | 4.83            | 0.32                  | 0.72             | 0.45                   |
| C16:0     | 25.53           | 27.33                 | 15.317           | 16.27                  |
| C17:0     | 0.65            | 0.65                  | 0.08             | 0.12                   |
| C18:1 n-9 | 40.66           | 33.40                 | 21.10            | 18.24                  |
| C18:1 n-7 | 0.96            | 1.87                  | 0.58             | 0.67                   |
| C18:0     | 3.35            | 7.34                  | 1.404            | 1.43                   |
| C18:2 n-6 | 3.53            | 3.37                  | 11.01            | 10.07                  |
| C18:3 n-6 | 0.09            | 0.0                   | 0.0              | 0.0                    |
| C18:3 n-3 | 1.12            | 0.68                  | 2.50             | 1.60                   |
| C19:0     | 0.02            | 0.01                  | 0.01             | 0.01                   |
| C20:0     | 0.03            | 0.09                  | 0.05             | 0.08                   |
| C20:1 n-9 | 0.03            | 0.11                  | 0.0              | 0.0                    |
| C20:1 n-7 | 0.04            | 0.14                  | 0.09             | 0.10                   |
| C20:2 n-6 | 0.01            | 0.0                   | 0.0              | 0.0                    |
| C20:3 n-6 | 0.06            | 0.05                  | 0.0              | 0.0                    |
| C20:3 n-9 | 0.02            | 0.0                   | 0.0              | 0.0                    |
| C20:4 n-6 | 0.50            | 0.32                  | 0.02             | 0.02                   |
| C20:5 n-3 | 0.65            | 0.40                  | 0.04             | 0.02                   |
| C21:0     | 0.0             | 0.01                  | 0.0              | 0.01                   |
| C22:0     | 0.0             | 0.01                  | 0.0              | 0.01                   |
| C22:1 n-9 | 0.0             | 0.02                  | 0.0              | 0.0                    |
| C22:4 n-6 | 0.01            | 0.0                   | 0.0              | 0.0                    |
| C22:5 n-3 | 0.03            | 0.04                  | 0.0              | 0.0                    |
| C22:6 n-3 | 0.01            | 0.011                 | 0.0              | 0.0                    |
| C24:0     | 0.0             | 0.02                  | 0.0              | 0.0                    |
| C26:0     | 0.0             | 0.02                  | 0.01             | 0.01                   |

FAs comprising >10% in each experimental group are in bold.
fatty acids (PUFA) were more pronounced in *Hermetia* control and biodecomposed. ω-6 was found more frequently in *Hermetia* (both control and biodecomposed; Fig. 3).

**Protein Analysis of Control, Middle, and Bottom Phase of Biodecomposed Groups**

The biodecomposition procedure used in this study enabled us to separate different kinds of proteins in different water phases (middle and bottom). SDS–PAGE analysis and proteomics were applied to elucidate the different kinds of proteins existing in each of these two parts.

**Protein Analysis by SDS–PAGE**

Due to the different distribution of protein bands, SDS–PAGE analysis of all the extracted fractions was also performed (Fig. 4). It is apparent that both intensity and the band pattern tended to be quite different in all experimental groups (*Hermetia* and *Lucilia*—control or biodecomposed). Comparing control to middle and bottom phases of biodecomposed *Lucilia*, we observed more protein bands in the bottom phase after biodecomposition. In *Hermetia*, we also observed depletion of protein bands after biodecomposition (Fig. 4). There are some bands that presented in all four groups as a 75 kDa protein band.

**Proteomics**

Quantification of proteins by BCA assay showed that middle and bottom phase of *Lucilia* contained higher levels of protein than control, middle, and bottom phases of *Hermetia* and *Lucilia* control (Fig. 5).

Proteomics analysis by Tandem X! identified about 900 proteins overall in *Lucilia*, and 531 proteins in *Hermetia* control and biodecomposed.

Venn diagrams of *Lucilia* control and middle and bottom phase after biological decomposition, showed that 47 of proteins were found only in control larvae. After biodecomposition, 60 proteins appeared (Fig. 6). Venn diagrams of *Hermetia* control and middle and bottom phase after biodecomposition showed that 28 proteins were found only in control *Hermetia*, and after decomposition, 21 proteins appeared (Fig. 6).

Important proteins in these two groups are listed in Supp Tables 1S and 2S (online only).

**Gene Ontology and Annotation**

Based on gaps in genomics data in the selected species, we had great difficulty performing gene ontology (GO) and gene annotation. Our gene ontology and gene annotation analysis relied on the Uniprot site and ‘Quick Go’ (https://www.ebi.ac.uk/QuickGO/) (Supp Data and Table 3S [online only]).

Calmodulin, in *Hermetia* control and middle phase after biodecomposition and Drab 5, in the bottom phase, were the most annotated proteins.

‘Oxidation–reduction process’ as a molecular function, and ‘Cytoplasm’ as a cellular component were the most ontologized terms in all three *Hermetia* groups (control, middle, and bottom phases after biodecomposition).

In all three groups of *Lucilia* (control, middle, and bottom phases after biodecomposition), 1,2-dihydroxy-3-keto-5-methylthiopentene dioxygenase was the most annotated protein and ‘oxidation–reduction process’ as a molecular function as well as ‘membrane’ as a cellular component, were the most ontologized terms.
Fig. 3. Saturation profile of fatty acids in experimental groups.

Fig. 4. The isolated protein fraction from experimental groups resolved by SDS–PAGE and visualized by Coomassie blue.
The top 10 proteins with the most annotations and the GOs with more than 40 proteins in their ontologized category for each experimental group are presented in Supp Tables 4S–15S (online only).

**Antimicrobial and Enzymatic Properties**

To investigate proteins with antimicrobial or enzymatic activity, we searched for matches to selected key words.

For Antimicrobial activity, key words of Bacterium, defense, fungus, and virus were searched through the GOs ID from the Uniprot site. The family and domain of proteins thus identified were studied through the 'InterPro' site (https://www.ebi.ac.uk/interpro/protein/B3M187).

In *Hermetia*, we found proteins from Hemocyanin, peroxiredoxin, peptidase, and ferritin families.
These proteins are presented extensively in Supp Table 16S (online only). All proteins were found in control and middle and bottom phases of biodecomposed Hermetia, except Fl02842p, which was not found in the middle phase.

AOA0L0C17 was found in control and middle and bottom phases of biodecomposed Lucilia. However, AOA0L0BZ83 was found only in the middle and bottom phases of biodecomposed Lucilia. AOA0L0BZ83 had a high similarity to Rab14, isoform B. These proteins belonged to dehydrogenase and small GTPase families. These proteins are described in Supp Table 17S (online only).

Proteins With Enzymatic Activity
In datasets of proteins of both Hermetia and Lucilia, we searched for proteins with enzyme activity as a key word. Caspase, peroxidase, amylase, Thioredoxin reductase, Phenoxidase, and enolase are some of the most known. Comprehensive lists of these enzymes are presented in Supp Table 17S (online only).

Discussion
In this study, we performed lipidomic and proteomics analysis of Hermetia and Lucilia control and biodecomposed larvae.

Properties of the fats depend on the fatty acid profile. Therefore, in the first step, we investigated the fatty acid profile of larvae before studying other lipid species.

Gołębiowski et al. (2012) showed that major fatty acids (cyclic and internal) in Lucilia sericata are 16:0 and 18:1 n-9. Our results are in line with their findings as regards control Lucilia larvae.

However, in Lucilia, after biodecomposition, we found lauric acid present as 8% of total fatty acids, compared to control Lucilia, where this fatty acid only represented about 0.3% of total fatty acids (26-fold increase). After biodecomposition, the percentage of C16:0 and C18:1 n-9 was decreased in Lucilia. Considering these findings, we can hypothesize that the biological decomposer has an impact on the breaking down and saturation of lipids. We observed this saturation effect on both biodecomposed Hermetia and Lucilia, because the lipid profile of biodecomposed larvae contained more saturated and shorter chains, compared to control larvae. However, we did not perform any statistical analysis since the present work was a pilot study.

Hermetia oil is a good candidate source of lauric acid. Indeed, lauric acid (C12: 0) is the most potent antimicrobial saturated fatty acid in the control of Gram-positive bacteria (Wille and Kydonieus 2003, Skrivanová et al. 2005). It has even been proposed as a natural antibiotic against some dermal infections, such as acne (Nakatsuji et al. 2009). In addition, it has been shown that lauric acid is safe based on the lack of toxicity on human sebocytes (Nakatsuji et al. 2009). Furthermore, both intradermal injection and epicutaneous application of lauric acid decreased the number of Propionibacterium acnes colonies, thereby relieving P. acnes-induced swelling and granulomatous inflammation (Nakatsuji et al. 2009). Consequently, lauric acid could be a strong alternative treatment for antibiotic therapy of acne (Nakatsuji et al. 2009, Yang et al. 2009).

On the other hand, because of its antibacterial properties, lauric acid could be used as a natural additive in animal food, especially for pigs (Roth and Kirchgessner 1998). Normally, animal feeds have been widely supplemented with antibiotics at subtherapeutic concentrations to prevent post-weaning diarrhea and to increase the overall productivity of pigs (Omonijo et al. 2018). Although the use of antibiotics in animal feed has been banned in Europe, and other countries have also started to minimize their use in animal production, this practice still exists in large parts of the world (Hassan et al. 2018). Therefore, replacing antibiotics with cost-effective alternatives remains crucial to ensure sustainable animal-food production. Other experiments have shown that lauric acid could be used in this way (Zentek et al. 2013, Spranghers et al. 2018). Therefore, based on our results, which suggest that Hermetia oil is rich in lauric acid, the oil from Hermetia could be a good choice as an additive for animal feed. If there is a need for lauric acid, biological decomposition could be an alternative. Besides its antimicrobial effects for dermal applications, Verheyen et al. showed that Hermetia fat is a suitable choice for hand cream that served as a model system for a typical oil-in-water emulsion (Verheyen et al. 2018). Hermetia has a fatty acid profile similar to that of coconut oil and palm kernel oil (Dubois et al. 2007). These oils are frequently used in cosmetics, mostly as starting material for the preparation of surfactants (e.g., Amillite GCS-11). Therefore, Hermetia oil could be used in the same manner and this could be a novel application for insect fats (Verheyen et al. 2018). It is noteworthy that the quality of lipids from Hermetia larvae is high, and matches the quality of products from other animal and herbal sources oil (Müller et al. 2017). The mechanism of lauric acid antimicrobial effects could be related to a reduction in pH (Roth and Kirchgessner 1998). An alternative proposition is that lauric acid is converted into monolaurin, which is an antiviral, antibacterial antiprotozoal glyceride (Ushakova et al. 2016).

All biomass derived from insects (fat and proteins) needs to be capitalized upon in industrial applications in order to make the insect farming sector viable in a future circular economy. In this regard, we performed a proteomics analysis of Hermetia and Lucilia, and although our results suffer from a lack of genomics data, especially on Hermetia, we report here for the first time a dataset of all proteins identified in control and biodecomposed Hermetia and Lucilia larvae. These data underline the high potential of these insect proteins in food and nonfood applications. Our results showed that using the biodecomposer yielded two distinct phases of water solution (middle and bottom), which presented different protein profiles. Detailed profiling of the differences between these two phases will require further studies.

We found a large amount of structural and muscular proteins, in agreement with other findings, which proposed that insect protein could replace meat and soybean as an alternative protein source (Latunde-Dada et al. 2016, Altmann et al. 2018). Other interesting protein fractions of the flies studied here were enzymes and antimicrobial proteins. It has been suggested that Hermetia, due to its omnivorous mode of life, contains various degrading enzymes of scientific and industrial interest. Up to now, only trypsin and chymotrypsin activity has been published (Kim et al. 2011). We found this trypsin-like protein in Hermetia, mostly in the middle phase of biodecomposed Hermetia. We also identified many other enzymes, such as amylase, which could be of industrial interest. Applications with amylase first started in 1959 for the industrial production of dextrose powder and dextrose crystals from starch (The Amylase Research Society of Japan 1988).

We found phenoloxidases, which participate in the immune system (Vogel et al. 2018). Besides these enzymes, our gene ontology results (for proteins for which GOs were available) showed that there are proteins in both Hermetia and Lucilia that participate in the immune response to bacterium, fungi, and viruses. These proteins are mostly uncharacterized. There is no information on two proteins of Lucilia, which are reported to have a role in its immune system. However, we found some information about proteins found in Hermetia showing gene ontology of the immune system.
B3MI87 is an uncharacterized protein belonging to the Hexamerins family and found in the hemolymph of insects. It closely resembles phenoloxidase 2, which has a defense response to fungus and to Gram-positive bacterium (Binggeli et al. 2014). Ferritin has been found to be downregulated in fungusally challenged adults and unchanged after bacterial infections in adults. Conversely, ferritin was found to be up-regulated in LPS-induced larvae (Levy et al. 2004). Q3LBB1 belongs to the ‘odorant-binding proteins (OBPs)’, a class of small (14–20 Kd) water-soluble proteins. The product of a gene expressed in the olfactory system of Drosophila melanogaster (Fruit fly), OS-D, has a primary structure unlike OBPs (McKenna et al. 1994). Q9VVB7 plays a role in defending against Gram-positive bacteria in D. melanogaster, depending on the pathogenic activities of the infecting bacteria (Jin et al. 2008).

We have compared our protein data set to AMPs listed by Vogel et al. (2018), but we did not find any of them. This could be due to the different methods of protein investigation that we have chosen. AMPs are known as natural antibiotics, which are presumably protected from resistance development in bacteria (Laxminarayan et al. 2013). Finding AMPs in reared insects such as Hermetia (Elhag et al. 2017, Vogel et al. 2018) is a new and promising added value for insect farmers and for world health. Our findings regarding immune proteins could open avenues to further research in this area.

Conclusion

These data may not only be a helpful tool to underscore the added value of insect farming industries but may also shed light on future research opportunities in pharmacological and cosmetic approaches to find new molecules of interests. Our results highlight the compelling need for more basic researches on farmed insects.

Supplementary Data

Supplementary data are available at Journal of Insect Science online.

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