Organic side streams: using microbes to make substrates more fit for mass producing insects for use as feed

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Abstract

Microbes, combined with insects, convert organic waste into products of value. Resulting insects can be harvested and used as a high-quality protein resource, while the residues can be used as fertiliser. Microbes play an important role in the conversion process. This review's aim was focused on how microbes promote insects such as black soldier fly (*Hermetia illucens* L.), house fly (*Musca domestica* L.), waxworm (*Plodia interpunctella*) and yellow meal worm (*Tenebrio molitor* L.), to convert organic waste, while also harmlessly reducing organic waste pollution. The novelty is reflected in some core gut microbiota and their secreted enzymes degrade macromolecules such as protein, fat, polysaccharide, cellulose, polystyrene and polyethylene. Gut microbiota also could help insects degrade hazardous substances such as antibiotics, mycotoxin, odorous substances, and inhibit pathogens in organic wastes to make substrates more fit for insects.

Keywords: insects, gut microbiota, organic waste, conversion, degradation

1. Introduction

Globally, approximately 1.6 billion tons of food waste are generated annually (Ma *et al.*, 2020). However, due to challenges with collecting these materials, only a portion of the food waste is being treated. Such practices (i.e. not recycling such materials) pose environmental and economic concerns (Salihoglu *et al.*, 2018), as well as human health hazards (Sindhu *et al.*, 2019). Other common organic wastes are livestock and poultry manure. According to the forecast of the demographic website (<https://populationstat.com/>), the global human population will reach 9.7 billion by 2050. Such growth will inevitably increase the demand for food, especially livestock and poultry products, which will increase the amount of livestock and poultry manure. Livestock and poultry manures are rich in nitrogen, phosphorus, and potassium (Drózd *et al.*, 2020). Unfortunately, large amounts of livestock and poultry manures are not treated or utilised properly potentially leading to eutrophication and soil degradation (Qian *et al.*, 2018).

Plastics in association with food production are also being mass produced and resulting in additional environmental concerns. Data from the Ministry of Agriculture and Rural Affairs of the People's Republic of China show that the use of agricultural plastic films nationwide reached 2.593 million tons in 2016. During the past 30 years, residual pollution of plastic film has become a serious issue worldwide. Plastic film remaining in the soil is difficult to degrade, and it will also lead to the reduction of crop production (Yan *et al.*, 2016).

Currently, pollution issues resulting from the previously described organic waste concerns demonstrate the need for sustainable methods of remediation. Using insects to convert organic wastes into products of value can be achieved. Furthermore, integrating microbes as part of the process could enhance efficiency of such systems (Xiao *et al.*, 2018). The gut microbiome of insects and microbiota in organic waste are now being harnessed as a means to increase the ability of mass produced insects to recycle these materials.

2. Microbe enhanced conversion efficiency and insect growth

A number of insect species are used to digest the wastes previously described. The primary species are black soldier fly (BSF; *Hermetia illucens* L.), house fly (HF; *Musca domestica* L.) and yellow mealworm (YMW; *Tenebrio molitor* L.) (Čičková et al., 2015).

Black soldier fly larvae (BSFL) convert different organic wastes, and while the structure of its gut microbes shift depending on diet, Firmicutes and Proteobacteria have been identified as the core phyla (Wynants et al., 2019; Zhan et al., 2020). These phyla may play an important role in promoting the ability of the BSFL to convert organic waste into biomass. For example, BSFL gut microbes produce carbohydrate-active enzymes that significantly enhance this process (Jiang et al., 2019). Studies have confirmed that Firmicutes can secrete a variety of proteases and pectinases, allow the BSFL to digest animal faeces as well as indigestible carbohydrates in straw-related compost (Sun et al., 2015; Zhang et al., 2018).

Gastrointestinal morphology of the BSFL plays an important role in shaping microbial load and diversity (Bruno et al., 2019). Microbial diversity is greatest in the midgut and then gradually decreases towards the posterior regions. However, bacterial load was greatest in the posterior region. Xylanases produced by Bacteroidetes, one of the dominant phyla in BSFL gut directly involved in hemicellulose digestion (Bruno et al., 2019).

Bacillus and associated yeasts are in high abundance in the BSFL intestine (De Smet et al., 2018; Zhan et al., 2020). *Bacillus* can degrade lignocellulose, while yeasts utilise metabolites and accumulate protein and polysaccharide (Li et al., 2016). Rehman developed an efficient co-digestion strategy for using BSFL to treat dairy manure (DM) when mixed with an appropriate proportion of chicken manure (CHM) or soybean curd to reaching nutrition (C/N ratio) balance and buffering capacity (pH) of the animal wastes (ur Rehman et al., 2017a,b). Furthermore, adding exogenous probiotics resulted in higher bioconversion efficacy (10.8%), survival rate (99.1%), food conversion ratio (4.5), manure reduction rate (48.7%), and fibre content reduction (cellulose; 72.9%, hemicellulose; 68.5%, lignin; 32.8%), than relying on associated gut microbiota alone. Analysis of the fibre structural and chemical changes with scanning electron microscopy and Fourier-transformed infrared spectroscopy indicates the structure and chemical composition of the fibre had been modified. The surface morphology of fibres of DM40:CHM60 when pre-treated with exogenous probiotics was relatively compact and rigid before BSFL digestion, but after digestion the material was porous and more corrugated. The degraded effects in the chemical composition of the fibre were more obvious in

the treatment when BSFL were assisted with microbes (ur Rehman et al., 2019). Clearly, microbes play an important role in the conversion of organic waste, by adding microbes to organic waste, the ability of insect hosts to degrade organic waste can be improved (Table 1). The HF also could convert animal manure (Van Huis et al., 2013). Conversion of HF also defined as a microbial-driven process, which was dominated by *Entomoplasma somnilux*, *Proteobacterium*, and *Clostridiaceae* bacterium (Zhang et al., 2012).

Waxworm (WW) (Yang et al., 2014) and YMW (Zhang et al., 2017) can degrade plastic wastes. Two bacterial strains capable of degrading polyethylene (PE) were isolated from the gut of WM, *Enterobacter asburiae* YT1 and *Bacillus* sp. YP1. Over a 60-day incubation period of the two strains with PE film degraded PE with approximately 6.1 ± 0.3 and $10.7 \pm 0.2\%$ (Yang et al., 2014). When degrading polystyrene (PS) and PE, it was found that *Citrobacter* sp. and *Kosakonia* sp. in the gut of YMW are closely related to the degradation of PE and PS (Brandon et al., 2018). The dominant strains in the YMW gut are mainly *Enterobacter*, *Lactococcus* and *Enterococcus*. The strains with biodegradable activity *Klebsiella*, *Pseudomonas* and *Serratia* were isolated from YMW digesting plastics (Urbanek et al., 2020). The potential to enrich these strains *in vitro*, and then combined with the insect could enhance plastic degradation. Furthermore, by changing the diet of YMW, the microbial community structure in its gut could be shifted, thereby improving the efficiency of PS degradation (Peng et al., 2019). Super worm (*Zophobas atratus*) can also degrade PS. Inoculating diet with antibiotics was found to inhibit associated gut microbes and the ability of the insect to degrade PS demonstrating the gut microbes play a role in such processes (Yang et al., 2020). We speculated some gut microbes in WW and YMW could produce special enzymes to degrade the plastics such as PE and PS. The mechanism should be further explored.

Bacteria from other insects are known to play a role in host metabolism. *Acetobacter pomorum*, which was isolated from *Drosophila* (Diptera: Drosophilidae), has obvious growth promoting effect (Kim et al., 2020). *A. pomorum* WJL (ApWJL) and *Lactobacillus plantarum* NC8 (LpNC8) can promote the growth of *Drosophila* larvae by shifting nutritional requirements of the host (Consuegra et al., 2020). *A. pomorum* regulates insulin/ insulin-like growth factor signal through its pyroquinoline quinone ethanol dehydrogenase to regulate host intestinal homeostasis, which controls host development rate and energy metabolism (Shin et al., 2015). *L. plantarum* promotes systemic development of *Drosophila* by regulating hormone growth signals through the host nutrition sensing system dependent on target of rapamycin (Storelli et al., 2011). Acetic acid, a metabolite of *L. plantarum*, binds to the diaminopropionic acid-type peptidoglycan-sensitive receptor PGRP-LC in the innate immune pathway of *Drosophila*-immune deficiency pathway, which stimulates

Table 1. Black soldier fly larvae (BSFL) combined with microbes to convert organic waste.

Substrate	Microbe source	Organic waste reduction rate (%) compared with the control group	Larval weight gain rate (%) compared with the control group	References
Chicken manure	<i>Bacillus subtilis</i> BSF-CL	13.4	15.9	Yu <i>et al.</i> (2011)
Chicken manure	<i>B. subtilis</i> BSF-CL (from gut bacteria)	12.7	15.9	Xiao <i>et al.</i> (2018)
Dairy and chicken manure mixed	Exogenous bacteria (from soil and pig manure fermentation products)	0.6-16.2	7.99-16.7	ur Rehman <i>et al.</i> (2019)
Soybean curd residue	<i>Lactobacillus buchneri</i> L3-9 (from Microbial Pesticide Key State Laboratory of HZAU)	13.6-26.9	15.8-23.5	Somroo <i>et al.</i> (2019)
Chicken manure	Companion bacteria (from the egg surface of BSF within 6 hours after spawning, and from the gut of 5 th instar larvae)	0.9-7.2	5.79-28.57	Mazza <i>et al.</i> (2020)
Banana peel	<i>Trichoderma reesei</i> and <i>Rhizopus oligosporus</i> (from the Department of Molecular Sciences, SLU)	25.7-33.9	26.1-58.9	Isibika <i>et al.</i> (2019)
	A mixture of bacteria (from the BSFL gut)	4.3	6.7	

the endocrine peptide tachykinin. Transcription, thereby optimising *Drosophila* lipid metabolism and activating insulin signals, promoting the growth and development of *Drosophila* larvae (Kamareddine *et al.*, 2018). Honey bee (*Apis mellifera*) gut microbes promote the growth of the host through the regulation of metabolites (Zheng *et al.*, 2017). *Bifidobacterium* and *Gilliamella* are the principal degraders of hemicellulose and pectin in the honey bee larval gut, providing nutrients for the host to promote growth (Zheng *et al.*, 2019). Sterile BSFL without gut microbe are impaired; however, after adding its gut microbe, such as *Bacillus subtilis* BSF-CL, BSFL growth and associated chicken manure conversion can be improved. The gut microbes of BSF can not only promote the growth of the host, but also improve the efficiency of the host to convert organic waste (Table 1).

3. Microbes help insect in antibiotic-resistant attenuation and antibiotics degradation

Using antibiotics as prophylaxis for poultry poses serious threat to human health due to resulting manure used as fertility spreading antibiotic-resistant bacteria (Tyrrell *et al.*, 2019). Antibiotic resistance genes (ARGs) can be transmitted from animal products or the environment to people (Landers *et al.*, 2012; Muloi *et al.*, 2018). In agriculture, manure and sludge are often used to increase crop yields, which is a key enabler of resistance gene flow into an ecosystem (Kivits *et al.*, 2018; Udikovic-Kolic *et al.*, 2014). Approximately 58% of veterinary antibiotics are transferred to the environment with most being introduced

to soil through resulting manure used as a fertiliser (Xie *et al.*, 2018). Among the compost products of livestock and poultry manure, the potential bacterial hosts of ARGs are actinomycetes, such as *Leucobacter*, *Mycobacterium* and *Thermomonosporaceae* (Zhang *et al.*, 2020).

Developing methods to remediate ARGs in manure is crucial. Microbes in combination with insects, such as the BSFL, could be used to mitigate ARGs risk. For example, BSFL treatments could effectively reduce antibiotic resistance genes in chicken manure by 95.0%. Previous research has determined BSFL intestinal microbiota serve as a major mechanism regulating these processes (Cai *et al.*, 2018a). How the BSFL intestinal microbiota interact with their host to mitigate ARGs should be further explored. Furthermore, BSFL are capable of directly degrading antibiotics, such as tetracycline (TC) in chicken manure. Nearly 97% of TC was degraded within 12 days by BSFL. The gut microbiota of the BSFL plays a significant role in degrading TC, effectively and rapidly (Cai *et al.*, 2018b). How the BSFL intestinal microbiota interact with their host to degrading antibiotics also should be further explored. Similarly, swine manure digestion by HF larvae is a promising method for manure reduction and associated ARGs as well. Previous research determined 94 out of 158 ARGs were significantly mitigated (by 85%) following the conversion. ARG attenuation was significantly correlated with changes in the relative abundances of the family *Ruminococcaceae*, class bacilli, or phylum *Proteobacteria* and microbial community, especially reduction in Clostridiales and Bacteroidales (Wang *et al.*, 2015, 2017).

HF larvae also can degrade antibiotics. Previous research determined HF larvae could degrade monensin in chicken manure by increasing the number of *Stenotrophomonas* sp. and *Alcaligenes* sp. in the larval gut (Li *et al.*, 2019a). If insect larvae are combined with microbes, such as Classes *Gammaproteobacteria*, *Bacteroidia*, and *Betaproteobacteria*, and *Klebsiella* sp. SQY5, etc., to reduce antibiotics in organic waste, degradation efficiency may be improved. House fly larvae convert a mixture of swine manure and gibberellin fermentation residues (GFRs). The concentration of gibberellin in the converted residue decreased significantly, and with the increase of GFRs in the mixture, *Bacillus* became the dominant bacteria, indicating that *Bacillus* can promote gibberellin degradation (Yao *et al.*, 2020). There is already evidence that *Corynebacterium variabile* Q0029 combined with HF larvae can promote the degradation of gibberellin (Yang *et al.*, 2015).

4. Microbes help insect in pathogens inhibition

Livestock manure contain various pathogens, including bacteria, viruses, parasites, fungi, such as *Salmonella* spp., *Escherichia coli* O157:H7, Avian influenza virus, etc. (Alegbeleye and Sant'Ana, 2020). *E. coli* (STEC) O157:H7 in manure produces Shiga toxins that can contaminate surface water and cause haemolytic uremic syndrome in humans and animals (Tanaro *et al.*, 2018). These manure-borne pathogens pose a huge threat to public health and the environment (Spencer and Guan, 2004). Due to the expansion of livestock and poultry farming, associated manure in some instances is directly discharged into the environment without treatment, causing pathogens in the manure to threaten the safety of drinking water and cause other animals to be infected (Alegbeleye and Sant'Ana, 2020; Bicudo and Goyal, 2003; Ström *et al.*, 2018). In the aquaculture industry, the use of untreated livestock and poultry manure not only pollutes the water, but also results in fish disease and economic loss (Wanja *et al.*, 2020). Therefore, reducing pathogens in livestock and poultry manure is very important to public health and environment.

Insect larvae such as BSFL can significantly reduce the concentration of pathogens in swine manure and dairy manure (Erickson *et al.*, 2004; Liu *et al.*, 2008). Gut commensal microbes are in a competitive relationship with pathogens that enter the gut. Elimination of the commensal microbes results in pathogens proliferation and disease manifestation (Fast *et al.*, 2018). The gut microbiota can regulate the host immune cells and enhance the gut mucosal barrier function, so that the host can establish a strong immune response against invading pathogens, and the importance of gut microbiota in regulating the immune system is mainly to maintain the homeostasis of the gut (Alarcón *et al.*, 2016; Kogut *et al.*, 2020; Shi *et al.*, 2017). Insect gut microbes play an important role in maintaining gut homeostasis, and their

ability to inhibit pathogenic bacteria has a positive effect on host health.

Interestingly, researchers found a novel, temperate *Escherichia* bacteriophage designated vB_EcoS_PHB10 (PHB10), which could lyse two out of 13 *Escherichia* strains tested (Chen *et al.* 2019). Accordingly, the BSF immune system might have adapted to mitigate pathogenic microbes. Furthermore, the genomes of BSF encode more secreted peptidoglycan recognition proteins (PGRPs) and Gram-negative binding proteins compared to those in other dipteran species. Further research found two BSF immune genes *BsfDuox* and *BsfTLR3* could regulate the gut key bacteria *Providencia* and *Dysgonomonas* homeostasis to depress zoonotic pathogens (Huang *et al.* 2020). The mechanism of bacteriophage and gut key bacteria in depressing zoonotic pathogens is still unknown and need further be explored.

5. Microbes help insect in odour removal of organic waste

Manure emits greenhouse gases and other volatile organic compounds during the decomposition process (FAO, 2009). Volatile organic compounds, such as 4-methylphenol was responsible for 67.3% of odour activity in dairy manure (Hales *et al.*, 2012). Processing organic waste with BSFL results in volatile fatty acids (VFAs) being reduced (Sundberg *et al.*, 2013). VFAs are short-chain fatty acids containing six carbon atoms or less, such as acetic, propionic acid, iso-butyric acid, n-butyric acid, iso-valeric acid and n-pentanoic acid (Agler *et al.*, 2011; Fang *et al.*, 2016). Lactic acid and acetic acid have a higher odour threshold than butyric acid and valeric acid (Rosenfeld *et al.*, 2007). VFAs is easily produced under anaerobic and low pH conditions (Liu *et al.*, 2020; Sundberg *et al.*, 2013).

BSFL can significantly reduce poultry, swine, and dairy manure release volatile organic compounds to the environment (Beskin *et al.*, 2018). BSFL can reduce the accumulation of VFAs in organic wastes by 10.12-28.50%. Interestingly, VFAs can be used as a carbon source for the survival of BSFL and natural microbiota (Liu *et al.*, 2020). Use an engineering microbial ecosystem to remove odorous gas from industrial waste, before treatment, the dominant strains are genera *Thiobacillus* and *Oceanicaulis*, after treatment, the dominant strains are genera *Acidithiobacillus* and *Ferroplasma* (Li *et al.*, 2019b). We speculated both exo- and endo-symbionts inhibited the microbes that produced odorous gas.

6. Prospects of research on the degradation of organic waste by insects and microbes

There are many ways to deal with organic wastes. BSFL is a representative insect that converts organic wastes into products of value. After the conversion, the content of many

organic wastes decreased by 20.31-22.18%. Furthermore, VFAs are also decreased by 25.58-80.08%. Nitrogen content in the waste also is reduced by 6.08-14.37%. Total phosphorous, total Kjeldahl nitrogen, and total nutrients increased by 42.30-64.16, 45.41-88.17, and 26.51-33.34%, respectively (Liu *et al.*, 2019).

Black soldier fly larvae have broad application prospects for the treatment of livestock and poultry manure pollution. Current research is devoted to further improving the efficiency of BSFL to convert livestock and poultry manure. At present, combining BSFL and microorganisms can further improve the efficiency of BSFL converting livestock and poultry manure. Some of the microorganisms used include BSFL gut microbes, BSFL associated microorganisms (BSF egg surface microbes), and microorganisms separated from livestock and poultry manure composting (Mazza *et al.*, 2020; Xiao *et al.*, 2018). However, it is not clear that the mechanism of how microorganisms cooperates with BSFL to convert manure and further research is needed.

Microbes can not only improve the efficiency of insect hosts to degrade organic waste, but also promote the growth of insect hosts (Xiao *et al.*, 2018). In particular, the mutually beneficial symbiosis between intestinal microbes and the host has always been a research hotspot. Microbes play an important role in helping the host to resist adverse environments. The gut commensal bacteria *Klebsiella michiganensis* BD177 stimulates the metabolic activity of arginine and proline in the host to help the host resist the low temperature environment (Raza *et al.*, 2020). *Bifidobacterium animalis* enhances the host's ability to resist influenza by mediating the metabolism of valine and coenzyme A (Zhang *et al.*, 2020).

Conclusions

Food and Agriculture Organization of the United Nations (FAO) recommended several main insects such as BSFL, HF, and YMW to treat organic wastes (Van Huis *et al.*, 2013). They not only convert the animal manure to insect biomass, but also food waste, PS and PE. Scientists found their gut microbiota play important role in these organic side streams conversion. The novelty is reflected in that some gut microbes and their secreted enzymes degrade macromolecules such as protein, fat, polysaccharide, cellulose, PS and PE. For example, the phyla Firmicutes and Proteobacteria are main microbiota response to macromolecules degradation in organic waste. Other microbes, such as *Bacillus*, *Enterobacter*, and yeast can secrete some protease, cellulase, lipase and xylanase, and degrade the macromolecules in organic wastes into small molecules, which can be used as the nutrients of insects. Gut microbiota also could help insects degrade hazardous substances such as antibiotics, mycotoxin, odorous substances and inhibited pathogens in organic

wastes. So insect gut microbiota could help their host to degrade macromolecules and hazardous substances in organic side streams and make substrates more fit for insects. But their mechanisms are not very clear and need further be explored.

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Conflict of interest

The authors declare no conflict of interest.

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