Insect Symbionts and Their Potential Applications in Pest and Disease Control: Postprint

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Abstract

Insects are characterized by rich species diversity and harbor a vast array of microorganisms within their bodies. Through long-term coevolution, these microorganisms have established interdependent symbiotic relationships with their host insects. Symbiotic bacteria play pivotal roles in numerous physiological functions of insects, including nutrition, metabolism, immunity, and reproduction. Consequently, insect symbiotic bacteria represent an integral component of the insect organism, and a comprehensive understanding of insect life activities necessitates consideration of the roles and impacts of these bacteria. Furthermore, insect symbiotic bacteria hold significant promise for applications in developing novel biological control strategies for pests, biodegradation of waste, and blocking and control interventions for vector-borne diseases. This review synthesizes the diversity, biological functions, and host interaction mechanisms of insect symbiotic bacteria, along with their applications in pest and disease management and vector-borne disease control, and offers perspectives for future research.

Full Text

Preamble

Special Topic: Targeted Management of Crop Pests and Diseases
Decoding the Mechanisms of Bio-interactions for Targeted Management of Agricultural Pests
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Insect Symbionts and Their Prospects in Pest and Vector-borne Disease Control

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Insects represent one of the most diverse and abundant animal groups on Earth, harboring a vast array of microorganisms within their bodies. Through long-term coevolution, these microbes have formed interdependent symbiotic relationships with their insect hosts. Symbionts play crucial roles in numerous physiological functions, including nutrition, metabolism, immunity, and reproduction, making them integral components of the insect organism. Consequently, a comprehensive understanding of insect life activities must account for the influence and impact of these symbiotic microorganisms. Moreover, insect symbionts hold significant promise for developing novel biological control strategies against pests, biodegradation of waste materials, and blocking the transmission of vector-borne diseases. This article reviews the diversity of insect symbionts, their biological functions, mechanisms of interaction with hosts, and their applications in pest and vector-borne disease management, while offering perspectives on future research directions.

Keywords: coevolution, gut microbiota, symbionts, insect-microbe interaction, symbiotic control
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Insects are the most species-rich animal group on Earth, exhibiting diverse ecological habits and wide distribution, with significant impacts on agricultural production and human health [1]. Like all animals, insects host a wide variety of microorganisms that directly or indirectly affect insect physiology and health, playing irreplaceable roles in insect evolution and the formation of species diversity. These microorganisms primarily colonize the digestive tract as gut microbiota, participating in most life activities of insects [2] and performing vital functions in nutrition, metabolism, immunity, and other physiological processes. These functions include regulating intestinal physiology and homeostasis, extracting energy from food, assisting in digestion, synthesizing important metabolites, promoting immune system development and maturation, defending against parasites and pathogens, facilitating inter- and intra-specific communication, and influencing mating and reproduction. Conversely, the community structure and metabolic activities of insect gut microorganisms are also influenced by host genetic factors and the intestinal microenvironment, resulting in gut microbiota with both diversity and host specificity. Given the important functions and application value of insect gut microorganisms, research in this area has attracted considerable attention from scholars worldwide. Foreign researchers have begun to regard gut microbiota as a special "multifunctional organ" of insects and an integral component of the insect organism. Therefore, to fully understand insect life activities, the influence of microorganisms within the insect body must be considered.

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Insect Symbiont Diversity

Symbionts are widely distributed throughout various parts of insects, with their location and form varying according to insect species and microbial type. Insect symbionts are mainly divided into two categories: ectosymbionts and endosymbionts. Ectosymbionts are microorganisms that live outside insect cells, including bacteria attached to intestinal wall cells and free bacteria in the intestinal lumen. Endosymbionts are microorganisms that live within insect tissue cells, among which *Wolbachia* is the most widespread Gram-negative intracellular symbiont known in nature, naturally carried by approximately 65% of insect species [3]. Ectosymbionts primarily aggregate in the digestive tract as gut microbiota, forming a complex ecosystem that includes bacteria, fungi, viruses, and protozoa, with bacteria being the most diverse and abundant group in insect gut microorganisms.

Insect gut structure varies considerably among species, likely resulting from long-term evolution to adapt to various specialized ecological niches and feeding habits. This coevolution has gradually led to the phenomenon of specific gut microorganisms colonizing specific gut regions in insects [4]. The microbial groups in insect guts are extremely rich, including Proteobacteria, Bacteroidetes, Firmicutes, Clostridia, Actinomycetes, Spirochetes, and Verrucomicrobia [5]. However, different types of insects show significant differences in gut microbiota composition. In isopteran termites, the dominant gut microorganisms include Bacteroidetes, Firmicutes, Spirochetes, and Proteobacteria. In lepidopteran insects, the dominant bacteria are Enterococcus from Firmicutes and Proteobacteria. In orthopteran insects, such as the desert locust, the dominant gut flora belongs to the Enterobacteriaceae family of Proteobacteria. In dipteran mosquitoes, the adult gut is dominated by bacteria from the Enterobacteriaceae family of Proteobacteria.

There are also substantial quantitative differences in gut microbiota among different insects. The gut of an adult *Drosophila melanogaster* contains approximately 10 bacteria, an adult locust about 10 bacteria, while an adult honeybee harbors as many as 10 bacterial cells. Although most insects feeding on plant sap have few bacteria in their guts, they are rich in intracellular endosymbionts. Insects feeding on humus or wood debris, such as termites, crickets, cockroaches, and beetles, have the highest proportion of gut microorganisms relative to total bacterial biomass in the host [6]. Insects with relatively low gut microbial content, such as fruit flies, mosquitoes, and aphids, have long, narrow guts that may facilitate better nutrient absorption by the host.

Early research on insect gut microorganisms primarily relied on traditional microbial isolation and culture techniques, as well as methods based on 16S rRNA gene analysis including PCR-DGGE, RFLP, 16S rRNA probes, and 16S rRNA clone library sequencing. However, some insect gut microorganisms are difficult to culture in vitro, limiting the discovery of these unculturable microbes. With the rapid development of biotechnology and high-throughput sequencing technologies, new techniques and methods for studying genomics, transcriptomics, proteomics, and metabolomics have begun to be applied to investigate gut microbiota structure, functional protein composition, metabolic activity, and metabolic pathways. These technological advances facilitate a better understanding of insect gut microbial diversity and function.

Main Functions of Insect Symbionts

Nutritional and Metabolic Functions

Through long-term coevolution, insects and gut microorganisms have formed interdependent symbiotic relationships. Gut microbiota plays a crucial role in maintaining normal insect growth, development, and physiological balance. Insects provide stable living environments and necessary nutrients for gut microorganisms, while gut microbes participate in various metabolic processes, providing insects with certain nutrients and assisting in digesting complex carbohydrates. Some insects can adapt to various ecological niches and reproduce under conditions of nutrient scarcity or poorly digestible food, where nutritional symbiosis between insects and microorganisms likely plays an indispensable role.

Gut symbionts provide specific nutrients for some insects, such as B vitamins, sterols, and amino acids. For example, the gut symbiont *Rhodococcus rhodnii* provides vitamin B for its host *Rhodnius prolixus* [7]. In herbivorous animals, nitrogen is often a limiting factor, and many insects rely on probiotic bacteria with nitrogen-fixing systems to compensate for nitrogen deficiency. Symbionts in termite guts can not only recycle nitrogenous waste secreted by the host into high-value nutrients but also directly absorb atmospheric nitrogen for nitrogen fixation [8]. Cockroaches and some herbivorous ants harbor endosymbionts capable of nitrogen cycling to synthesize essential amino acids. Cockroaches can utilize their stored nitrogenous waste uric acid with the help of endosymbionts (*Blattabacterium*) under nitrogen-limiting conditions, although *Blattabacterium* lacks the gene encoding uricase necessary for uric acid degradation, suggesting that uricase may originate from other gut symbionts or the host itself [9]. Additionally, the aphid symbiont *Buchnera* can produce various essential amino acids to compensate for nutritional deficiencies caused by the aphid' s monotonous diet of plant sap [10].

Some insect genomes lack genes encoding metabolic enzymes for degrading complex carbohydrates, and gut microorganisms can help insects break down these difficult-to-digest macromolecules, promoting carbon and nitrogen absorption and utilization, enabling insects to survive in nutritionally imbalanced environments [11]. This is particularly important for insects feeding on plant xylem and phloem, which typically harbor abundant microbial groups associated with cellulose degradation [12]. Cellulose is a rich carbon source but exists mostly as crystalline or amorphous microfibrils in plant cell walls, making it difficult for insects to utilize. Symbiotic microorganisms are needed to degrade cellulose into simpler sugar residues. For example, bacteria colonizing the termite hindgut can produce various glucanases to help the host break down cellulose into glucose. Additionally, common mosquito symbionts *Serratia* and *Enterobacter* can secrete hemolytic enzymes that facilitate blood digestion after feeding [13]. Symbionts *Acinetobacter baumannii* and *Acinetobacter johnsonii* isolated from *Aedes albopictus* guts not only participate in blood digestion and absorption but also in nectar digestion [14]. Thus, insects represent "superorganisms" comprising metabolism jointly participated by both insect genes and microbial genes.

Insect gut microorganisms also play important roles in detoxification. Symbiotic yeasts in the cigarette beetle (*Lasioderma serricorne*) gut can break down toxins in the host' s food, enhancing the beetle' s resistance to toxins. During detoxification of insecticides, gut microorganisms can be induced to synthesize detoxification enzymes and degrade insecticides through mineralization or cometabolism into one or several metabolites that can be absorbed and utilized by insects. When the stinkbug *Riptortus pedestris* is exposed to the chemical pesticide fenitrothion, the gut symbiont *Burkholderia* can help degrade it, thereby increasing host resistance to chemical insecticides [15].

Effects on Insect Growth and Development

Some insect symbionts exist across insect generations through vertical transmission or environmental acquisition, playing essential roles in host development and reproduction. For example, midgut *Burkholderia* is important for the growth and reproduction of *Riptortus pedestris* [16]. Additionally, although germ-free fruit flies can survive, their growth and development show certain defects, primarily manifested as slower larval growth rates or relatively smaller adult body size, indicating that fruit fly gut symbionts play important roles in fly development. Under natural conditions, fruit flies mainly feed on decaying fruits and harbor abundant fermentative microorganisms in their guts, most notably *Acetobacter* and *Lactobacillus*. Studies have confirmed that *Acetobacter* participates in regulating the host insulin signaling pathway through pyrroloquinoline quinone-dependent alcohol dehydrogenase (PQQ-ADH) to promote fruit fly development [17].

Wolbachia is a common intracellular symbiont in insects that can colonize mosquito reproductive organs and affect mosquito reproductive capacity through cytoplasmic incompatibility mechanisms. Mating between infected males and uninfected females or females infected with different *Wolbachia* strains or species cannot produce viable fertilized eggs. Therefore, releasing large numbers of *Wolbachia*-infected males can suppress mosquito populations [18]. Besides *Wolbachia*, other bacteria such as *Bacillus* and *Staphylococcus* can also affect the oviposition rate of *Culex pipiens* [19].

Influence on Insect Behavior

Recent studies have found that insect gut microorganisms also participate in regulating insect behavior. Symbionts can synthesize or decompose metabolites within insects, some of which are used by the host to synthesize pheromones or kairomones, thereby influencing insect behavior. For example, the desert locust gut symbiont *Pantoea agglomerans* can utilize lignin-derived vanillic acid from locust digestive waste products to synthesize guaiacol, a precursor of locust aggregation pheromone that attracts more locusts to swarm through fecal volatilization [20]. Conversely, locust microsporidia can alter locust aggregation chemical signals, thereby preventing locust swarming behavior. Normally, locust swarms may be triggered and maintained by a set of aggregation pheromones that cause solitary locusts to aggregate into migratory swarms. Microsporidia disrupt locust nervous systems by altering the locust immune system and gut chemistry, killing large numbers of gut microorganisms involved in synthesizing locust aggregation pheromones, thereby reducing levels of neurotransmitters (serotonin and dopamine) that induce and maintain gregarious behavior, causing gregarious locusts to revert to solitary behavior [21].

In recent years, the close relationship between gut microorganisms and insect behavior has been increasingly discovered and elucidated, which is of great significance for developing novel pest control strategies. Gut microorganisms can not only affect insect behavior by synthesizing pheromones but also influence insect mating orientation or preferences. Studies on *Drosophila melanogaster* have found that gut symbionts can affect mating orientation [22], with fruit flies tending to mate with individuals having similar gut microbiota compositions. This mating preference could ultimately lead to new species formation [22]. A study on jewel wasps confirmed that gut symbionts can influence speciation. Researchers attempted to pair two jewel wasp species that had undergone population separation 1 million years ago, finding that their offspring could not survive. However, after removing the gut microbiota, the reproductive offspring of these two species could almost all survive [23].

Protective Functions of Symbionts

Insects face various survival pressures in natural environments, including attacks from natural enemies, infections from pathogens and parasites, and stress from adverse conditions such as high and low temperatures. Numerous studies have shown that besides providing scarce nutritional resources, symbionts can protect hosts against pathogenic microorganisms and predators, and assist hosts in tolerating certain adverse environments.

Body color typically serves as an important recognition characteristic, significantly influencing various life activities such as species recognition, mate selection, camouflage, and warning. Recent studies have shown that insect symbionts can control insect body color to protect them from predation. In pea aphids (*Acyrthosiphon pisum*), a facultative endosymbiont—*Rickettsiella*—was found to induce aphids to synthesize green pigment, changing their body color from red to green, which helps aphids avoid predation by natural enemies that prefer red aphids. Meanwhile, these color-changed aphids also harbor endosymbiotic bacteria *Hamiltonella* and *Serratia* that help pea aphids escape parasitism by parasitoid wasps. *Rickettsiella* often coexists with these two symbionts in pea aphids, enabling green aphids to simultaneously avoid predation by natural enemies and invasion by parasitoid wasps [17].

In the battle between insects and pathogenic bacteria, symbionts play important protective roles. Germ-free insects are more susceptible to pathogen and parasite infections than untreated insects. This phenomenon where symbionts inhibit colonization or proliferation of other foreign microorganisms is called colonization resistance. Studies have found that termite symbionts have redox capabilities that can inhibit invasion by foreign pathogenic microorganisms [24]. *Drosophila* C virus (DCV) is a non-enveloped RNA virus that shows high pathogenicity and lethality to *Drosophila melanogaster*. However, infection with the intracellular symbiont *Wolbachia* can significantly reduce mortality caused by DCV, and *Wolbachia*-free fruit flies are more susceptible to DCV [25]. The colonization resistance of insect symbionts is also effective against pathogenic fungi. *Erynia* fungi are major natural enemies of pea aphids. When the endosymbiotic bacterium *Regiella insecticola* is present, the pea aphid' s resistance to *Erynia* infection can be increased at least fivefold. Even if the fungus infects and kills the aphid, the number of spores produced is severely affected, reaching only 1/10 of normal levels [26]. Therefore, the endosymbiotic bacterium *R. insecticola* provides certain protection to the entire aphid population. Additionally, gut microorganisms are indispensable in promoting insect immune system development and maintaining normal immune function. Gut microbiota can help bees resist *Bacillus* infection by inducing the host to produce antimicrobial peptides and maintaining normal immune capacity [27,28].

Symbionts can also protect host insects from predation by producing toxic metabolites. The sensitivity of pea aphids to the parasitoid wasp *Aphidius ervi* is directly related to the presence of certain symbionts. The toxin produced by symbiont *Hamiltonella defensa* can directly kill larvae of *A. ervi* [29]. Additionally, symbionts in termites can produce methane gas to prevent predation by ants and other natural enemies. The symbionts in rove beetles (*Paederus*) synthesize a polyketide toxic substance called pederin to resist predation by wolf spiders [30]. Female European beewolves (*Philanthus triangulum*) rely on antibiotics synthesized by symbiotic actinomycetes *Streptomyces* in their antennae to resist infection by pathogenic fungi [31].

Some studies have found that symbionts can indirectly protect insect hosts by protecting "important third parties." The relationship between leaf-cutter ants and fungi in the family Lepiotaceae is a classic case in symbiosis research. Leaf-cutter ants have the unique ability to select and cultivate Lepiotaceae fungi as a food source, but these fungi lack competitive ability. When other fungi invade and compete with Lepiotaceae fungi, a *Streptomyces* symbiont on the ant' s body surface can produce antifungal substances that kill non-Lepiotaceae fungi, thereby protecting the symbiotic relationship between leaf-cutter ants and Lepiotaceae fungi from destruction [32].

In addition to facing various threats from natural enemies, insects also face survival pressures from human activities such as the extensive use of pesticides. Recent studies have found that symbionts are also involved in insect resistance to insecticides. Japanese scientists discovered that a *Burkholderia* strain capable of degrading insecticides exists in small quantities in farm soils. Legume pests such as *Riptortus pedestris* and related stinkbugs can acquire this symbiont from soil during the larval stage. Applying fenitrothion to farms can enrich this bacterium in soil, forming a symbiotic relationship with *R. pedestris* and conferring insecticide resistance [15]. Additionally, adverse natural environments such as high temperatures threaten normal insect survival. Studies have confirmed that symbionts contribute to insect temperature tolerance. For example, the aphid endosymbiont *Buchnera* can enhance aphid tolerance to high temperatures—during high-temperature periods, the infection rate of *Buchnera* in aphids significantly increases, while the bacterial molecular chaperone GroEL is continuously expressed, helping insect host proteins maintain stability under high-temperature conditions [33]. Symbiont-mediated protection is a phenomenon predicted by ecological models and increasingly observed in practice. The protection provided by symbionts to host insects gives the symbiotic combination greater competitive advantages, conducive to the stable maintenance of the symbiotic relationship.

Mechanisms for Recognizing Beneficial Bacteria and Resisting Pathogens

The insect digestive system possesses multi-layered defense systems that are crucial for shaping the gut microbiota. This defense system enables insects to recognize beneficial bacteria while resisting pathogens. Current immunological research has focused primarily on how insects resist foreign pathogens, while much less is known about how insects recognize beneficial symbionts. It is well known that most insect midguts have a peritrophic matrix, a non-cellular thin membrane structure secreted by midgut epithelial cells, mainly composed of chitin, proteins, and polysaccharides [34]. The peritrophic matrix is semi-permeable, allowing nutrients, digestive enzymes, and effector molecules to pass through while protecting the insect' s epithelial cell layer from direct exposure to microorganisms or toxins. Mucosal layers on foregut and hindgut epithelial cells may also have protective functions similar to the peritrophic matrix. These physical barriers between epithelial cells and the lumen reduce the impact of microorganisms on the host to some extent. In addition, the insect' s own immune system is an important line of defense, with insect innate immunity being remarkably similar to mammalian immune mechanisms [35]. Using *Drosophila* as an example, symbionts mainly enhance immune responses in gut epithelial cells by inducing the production of antimicrobial peptides (AMPs) and reactive oxygen species (ROS). Both induced responses are typical resistance mechanisms that precisely regulate the insect immune system through negative feedback regulatory mechanisms and other regulatory elements [27].

How does the insect gut, with its large microbial population, distinguish between beneficial symbionts and pathogens, and how does it cope with continuous immune system activation? Using fruit flies as an example, insects mainly acquire immune tolerance to beneficial gut microbial groups by regulating the expression levels of the IMD signaling pathway and the DUOX system. The IMD (immune deficiency) pathway suppresses transcription of AMP genes in the gut through the transcriptional repressor Caudal [28]. Meanwhile, amidases secreted by midgut epithelial cells can decompose peptidoglycan (PGN), which triggers inflammation, maintaining PGN secreted by symbionts at low levels [36]. Additionally, the Pirk protein can sequester specific PGN-binding receptors in the cytoplasm, thereby reducing receptors localized to the cell surface and delaying IMD pathway signal transduction [37]. Another PGN-binding protein, PGRP-LE, may also play an important role in immune regulation in the *Drosophila* gut: on the one hand, for invasion by pathogenic bacteria, PGRP-LE can induce Relish-dependent immune responses; on the other hand, it can ensure immune tolerance to beneficial bacteria by regulating amidase and Pirk protein expression levels [38].

The *Drosophila* DUOX system has similar regulatory mechanisms. Bacterial PGN alone cannot activate the DUOX pathway; it requires microbially produced ROS to activate the DUOX pathway. When commensal symbionts are present in the gut, DUOX gene expression is inhibited by MKP3, thereby suppressing ROS molecule synthesis. However, fruit flies can induce DUOX enzyme activity through intracellular calcium ions, so ROS content remains at baseline levels. Recent studies have found that uracil produced by pathogenic bacteria can activate the DUOX pathway in the fruit fly gut [39]. Gut symbionts may have evolved mechanisms to generally not synthesize uracil in the insect gut, thus distinguishing themselves from pathogenic bacteria and allowing stable colonization in the insect gut without excessively activating immune responses. In summary, by regulating these two immune pathways—IMD and DUOX—insects can effectively recognize beneficial symbionts and resist harmful pathogens, maintaining the gut in a normal physiological state.

Applications of Insect Symbionts in Pest and Disease Control

Insects are closely related to human activities, with some causing serious damage to agricultural production, human health, and ecological environments. With deepening research on insect symbionts, strategies utilizing symbionts to control pests have received widespread attention in recent years. Many theories based on symbiont-mediated pest control have been proposed, some of which have been successfully applied. *Wolbachia* is a cytoplasmically inherited symbiotic microorganism widely present in arthropods, with reproductive regulatory effects in many insects, including inducing cytoplasmic incompatibility, parthenogenesis, feminization, and male killing. It can also inhibit infection by mosquito-borne viruses and shorten mosquito lifespan, showing great potential for pest biological control and blocking transmission of vector-borne diseases.

Using *Wolbachia* with bidirectional cytoplasmic incompatibility can achieve population suppression, similar to the sterile male release method to reduce pest populations. Additionally, *Wolbachia* can be used to induce parthenogenesis in natural enemies of pests, achieving pest control by manipulating pest reproduction. In natural mosquito populations, *Wolbachia* is only found in *Culex pipiens* and a few *Aedes* species. Scientists introduced *Wolbachia* into *Aedes aegypti*, which can effectively inhibit dengue virus infection and shorten female mosquito lifespan, significantly reducing the vectorial capacity of *Ae. aegypti* for dengue transmission. Through microinjection technology, *Wolbachia* has also been successfully introduced into *Anopheles stephensi*, and it was confirmed that *Wolbachia* can inhibit *Plasmodium* development [40]. Additionally, when *Serratia* and *Enterobacter* are present in mosquito midguts, they can significantly inhibit *Plasmodium* development in the mosquito midgut [41].

Bacillus thuringiensis (Bt) is an important microbial insecticide. Studies have shown that insect gut microorganisms play important roles in the insecticidal process of Bt. When Bt infects insects, it typically causes damage to host gut epithelial cells. Certain gut symbionts, particularly *Serratia* and *Clostridium*, can enter the hemocoel through damaged areas of the host gut, proliferate extensively, weaken host immune responses, and accelerate host death [42]. The pine wood nematode is a highly destructive forest pest that relies on its host *Monochamus alternatus* for dispersal, causing pine wilt disease—one of the most harmful forest diseases. The harm caused by pine wood nematodes is inseparable from their associated bacteria, whose metabolites—phenylacetic acid, benzoic acid, phenol, phenylconiferyl alcohol, and 10-hydroxyverbenone—are toxins that cause pine wilting. Recent studies have found that an associated fungus of pine wood nematodes can promote nematode reproduction and significantly increase the proportion of female individuals in their offspring [43]. Therefore, further elucidating the interaction mechanisms between pine wood nematodes and their associated bacteria is important for controlling pine wilt disease.

The development of synthetic biology has merged with insect symbiont research to produce a new pest and disease control strategy—paratransgenesis, which involves genetic manipulation of insect symbionts to serve as gene expression vectors that produce transgenic effects in the host for pest and vector-borne disease control. This technology has emerged as a highly promising control method for blocking transmission of vector-borne diseases. Chagas disease is caused by the pathogenic microorganism *Trypanosoma cruzi* in triatomine bugs. Transferring anti-trypanosome effector genes into the triatomine bug midgut symbiont *Rhodococcus rhodnii* enables the symbiont to express anti-trypanosome effector proteins in the triatomine bug midgut, effectively inhibiting trypanosome development [44]. Our research team recently used the common *Anopheles* midgut symbiotic bacterium *Pantoea agglomerans* as a genetic modification target, utilizing the *Escherichia coli* hemolysin (HlyA) type I secretion system to secrete and express various anti-malarial effector molecules such as SM1, Scorpine, and (EPIP) in *P. agglomerans.* Feeding transgenic bacteria to *Anopheles* mosquitoes significantly inhibited *Plasmodium* development in the midgut. This new strategy provides novel approaches for controlling malaria and other mosquito-borne diseases as well as plant vector-borne diseases [45].

Future Perspectives

Thus far, research on insect gut microbial diversity and function has made some progress. However, given the diversity of insect species and life habits, the relationships between insect symbiotic microorganisms and host insects, as well as interactions among symbiotic microorganisms themselves, show diversity and complexity. While studies on gut bacteria are increasing, much less is known about other gut microbial groups. Since the vast majority of gut microorganisms are difficult to culture in vitro, this greatly limits the discovery and research of such symbionts. The development and application of metagenomic sequencing technology will effectively compensate for the limitations of traditional culture-based methods, facilitating deeper understanding of insect symbiont diversity and function.

During long-term coevolution, insects and their associated microorganisms have formed close symbiotic relationships, influencing, depending on, and coevolving with each other. Gut microorganisms play important roles in insect nutritional metabolism, immune regulation, defense against pathogens, and regulation of insect behavior and reproduction. Simultaneously, insects can recognize beneficial symbionts and foreign pathogens through their own immune systems to maintain healthy gut microbiota. With deepening gut microbiota research, greater understanding of how insects recognize non-pathogenic, beneficial, and pathogenic bacteria will facilitate better utilization of gut microorganisms to protect beneficial insects and control pests.

Currently, the complex interactions between insect symbiotic microorganisms and host insects, as well as the specific roles and molecular mechanisms of symbiotic microorganisms in various insect physiological activities, remain poorly understood—these areas represent important future research directions. In recent years, research on mammalian gut microorganisms has become increasingly mature, providing important references for studying insect gut microbiota-insect host interactions. The rapid development of multi-omics technologies including genomics, transcriptomics, proteomics, metabolomics, and microbiomics provides more effective tools for investigating the molecular mechanisms of insect symbiont-insect host interactions. Strengthening research on insect symbiotic microorganisms will not only facilitate understanding of insect-microbe relationships but also help obtain special functional microbial and genetic resources from the unique insect gut environment for use in pollution-free control of plant pests and diseases, biodegradation of waste, and control of vector-borne diseases.

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Insect Symbionts and Their Prospects in Pest and Vector-borne Disease Control

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Abstract

Insects are the most diverse and abundant group of organisms dominating terrestrial habitats in terms of species numbers. The evolutionary success of insects and their diversification into a wide range of ecological niches depends in part on beneficial members of their associated microbiome. Insects are colonized by complex populations of microorganisms in symbiotic relationships, varying from bacteria to viruses, yeasts, and protists. These diverse microbial communities provide important physiological functions for insect hosts in many ways, including provision of nutritional supplements, enhancement of digestive mechanisms, tolerance of environmental perturbations, modulation of host immune homeostasis, protection from parasites and pathogens, modulation of vector competence, contribution to inter- and intra-specific communication, and influence on insect mating and reproduction. Conversely, the insect host can affect the microbial community. Therefore, insect symbionts can no longer be ignored when studying insect biology and host-pathogen interactions. Insect symbionts have become promising tools for developing novel strategies for biological control of insect pests, biodegradation of wastes, and blocking the transmission of insect-borne diseases. Here, we provide an overview of insect symbiont diversity, the latest advances in understanding symbiotic relationships and interactions between insects and symbionts, and the development of novel strategies for controlling insect pests and vector-borne diseases. Finally, directions for future work are discussed.

Keywords: coevolution, gut microbiota, symbiosis, insect-microbe interaction, symbiotic control

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Special Topic: Targeted Management of Crop Pests and Diseases

Note: Figure translations are in progress. See original paper for figures.