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INSECTS-MICROBES SYMBIOSIS: A REVIEW ON THE BIOLOGICAL SIGNIFICANCE OF INSECTS' SYMBIONTS ON THEIR HOSTS

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Abstract

Insects are an ancient group of Earthly creatures that belong to the “phylum Arthropoda”. They are the only invertebrates that have wings, and their body is divided into three parts: head, thorax, and abdomen. A chitinous exoskeleton covers their body. On the geological timescale, their existence dates back to the Paleozoic era. Based on the order, Orthopterans and Hemipterans are the first insects to have appeared on Earth (Misof et al., 2014). Though we are often concerned about the symbiotic association between humans and different microbes, we have a very limited understanding of the insect–microbial symbiosis. Different researchers have discovered that insects harbour some beneficial microbes that have immense physiological effects on their host. Those microbes help their host in different ways, like food digestion, degradation of plant phytotoxin, insecticide resistance, protection against different pathogen-predators, parasitoids, etc. Some microbes are also used as bio-pesticides to control different insect pest populations in agricultural fields. For example, *Bacillus thuringiensis* is used to control brinjal shoot and fruit borer *Leucinodes orbonalis*. Through this review, we will gain a detailed idea about the different symbiotic associations between insects and microbes and their roles in their hosts’ lives.

INTRODUCTION

Insects are the world’s most diverse and ancient organisms, which belong to the phylum Arthropoda. They are the most abundant animals in terms of species diversity, and they can reside in all ecological habitats (Nagarajan et al., 2022). On the geological time scale, their existence dates back to the Palaeozoic era when Orthopterans and Hemipterans first emerged on Earth (Misof et al., 2014). Genealogy has shown that there are an estimated 5.5 million insect species, and among them, approximately one million species have been named and compiled in the “Catalog of Life”. They inhabit different ecological habitats and can combat adverse environmental conditions due to their large population size, short reproductive cycles, and high reproductive rates. Another specific reason for their diversification and evolutionary success, which has been identified, is the presence of certain symbiotic bacteria in their gut (Janson et al., 2008). For a while, scientists were only aware of harmful bacteria, but then they noticed that insects harbour some bacteria that help them adapt and grow in different environments. Symbiotic association in herbivorous insects depends on different factors, such as where the bacteria are located on the host body (Pan et al.,2020). The degree of dependency between symbiotic partners and the mode of transmission of the symbionts through the generations also differentiates their symbiotic association. These mutualistic relations significantly influence insect physiology, behaviour, and interactions with other organisms. Many insects, mostly herbivores, depend on their gut symbionts for the breakdown of complex plant materials and extract essential nutrients (Giron et al., 2017). The microbiome also plays a crucial role in synthesizing vitamins and other compounds that the insect host cannot produce on its own (Klepzig et al., 2009). Additionally, plants have different allelochemicals to protect themselves from sap-feeding insects. Due to the presence of symbionts, insects can feed on a wider range of plant species. (Douglas, 2015). According to a scientific study, there are different types of symbiotic associations present between insects and microbes, such as commensalism, mutualism, or parasitism, based on the fitness impacts of the interaction on its members (Moya et al.,2008). Most of the scientists emphasized primary or obligate and secondary or facultative symbiosis. These types are classified based on the extent to which bacteria depend on each other. If this symbiotic association is essential for host survival and fertility and shares a strong evolutionary relationship, then it is known as primary symbiosis. These symbionts show vertical transmission from mother to egg and are confined in a very specialized cell, bacteriocytes. On the contrary, secondary symbionts are necessary for other essential physiological functions, and they can revert to their free-living state (Ramadhar et al.,2014). The pea aphid harbors bacteria *Buchnera aphidocola* in specialized bacteriocytes cell which play important roles in providing essential amino acids and vitamins to its host (Baumann et al., 1995). S-symbionts affect their hosts in different ways. For example, *Rickettsia sp*. boosts host resistance to *P. syringae*, an

entomopathogen prevalent in whiteflies, and generally improves host fitness (Himler A.G.et al.,2011; Hendry T.A., et al., 2014). Another example of an S-symbiont is the uncommon endosymbiont of sap-sucking insects, *Hamiltonella defensa* (Enterobacterales: Enterobacteriaceae), which defends hosts against parasitic wasp assaults (Cho Y.L.et al.,2013). The primary objective of this review is to examine various types of insect-microbe symbiosis, as well as their impact on both the host and the environment. Through this review, researchers can design their experiments more effectively and interpret the results for the betterment of humans as well as the host.

TYPES OF ASSOCIATION

The association between insects and microorganisms can either be symbiotic or detrimental. A symbiotic relationship signifies the strong connection of two distinct species (Moya et al.,2008). Different types of factors, such as the dietary habits, the nature of host plants, seasonal changes, population density, and geographic location, can affect gut bacterial diversity (Priya et al.,2012). The endosymbionts harbored by insects are categorized as obligate symbionts, facultative symbionts, and phytopathogenic symbionts. This association might be mutualistic, commensalistic, or parasitic. The most evident illustration of commensalism is exhibited in the bark beetle galleries, which provide both nutrients and shelter for a range of insects and microbial commensals, most of which have minimal or no impact on the bark beetle (Stephen et al.,1993). In mutualism, for instance, numerous essential elements are needed for the survival and reproduction of certain insects, such as termites and their protozoan and bacterial companions (Bayen et al,2021). Additionally, when one species enhances its own fitness at the expense of the others, it is said to be parasitic (Dillon et al.,2004). These microbial symbionts can be categorized into endosymbionts and ectosymbionts based on the location where they live, within the tissue cells of insects or where they colonize the lumen or lining of the cavity walls on the insect's body surface (Pan et al.,2020). Based on dependency, symbiosis may be primary or facultative. When this interaction is essential or crucial for insects' survival, it is called primary symbiosis. However, when this interaction builds due to some beneficial or advantageous purpose, this interaction is known as facultative symbiosis. Microbes can either be obtained via horizontal or vertical transmission. Obligate symbionts are transferred vertically from the mother to her offspring before or during birth, either through the egg surfaces or specific behaviors that facilitate the transfer of essential microbes. Bacteriocytes are primarily located near the digestive system (specifically the midgut epithelium). Upon entering the insect's body, primary symbionts localize within bacteriocytes, which are sometimes aggregated into organ-like structures called bacteriomes (or mycetomes), provide benefits and fitness advantage to the host, and are transmitted maternally across generations. They establish a highly stable mutualistic relationship with their host. They provide essential amino acids and rare vitamins to their host, especially for the hemimetabolous sap-sucking insects that feed on nutrient-deficient diets. For example, in *Buchnera aphidicola*, an obligate symbiont of aphids, and probably the most extensively researched model, it has been shown that the bacteria fulfill the nutritional requirement of the insect host to a degree that their absence dramatically affects aphid survival and reproductive success (Feng et al., 2019). Similarly, symbiosis between the sap-feeding insect *Megacopta cribraria* and its primary bacterial symbiont, *Candidatus Ishikawaella capsulata*, is crucial for the survival of the host into adulthood (Couret et al., 2019). Not only is the insect dependent upon these obligate symbionts, but many obligate symbionts over time have become highly dependent in the long term on their insect host. For instance, *Buchnera*, which lives in a metabolic collaboration within the pea aphid (*Acyrthosiphon pisum*), has lost its genes for the synthesis of various branched-chain amino acids (such as isoleucine, valine, and leucine). *Buchnera* is, therefore, entirely reliant on its insect host for the supply of these amino acids, which are essential in vitamin biosynthesis pathways (Wilson et al., 2010; Hansen et al., 2011; Russell et al., 2013). Insects like aphids, tsetse flies, and psyllids depend on a primary symbiont for their protection and to gain vital nutrients (Crotti et al.,2012). Whiteflies, specifically *Bemisia tabaci* Gennadius (Hemiptera: Aleyrodidae), primarily harbor *Candidatus Portieraaley rodidarum Costa* (referred to as *Portiera sp.*) as their key symbiont. Like the *Portiera* sp., some other significant symbionts of phloem-feeding insects supply essential carotenoids and amino acids for their whitefly hosts (Sloan et al.,2012). Another example of a major symbiont is *Buchnera aphidicola* (Enterobacterales: Erwiniaceae), which resides within bacteriocytes in the abdominal body cavity of almost all aphids and provides necessary amino acids that are absent from the insects' phloem sap diet (Shigenobu et al., 2000). These symbionts maintain a highly stable accommodation in hemipteran sap sucking insects, where the diet is devoid of essential nutrients. In aphids, the obligate symbiont *Buchnera* *aphidicola* accomplishes the nutritional requirements by synthesizing rare vitamins and essential amino acids (Feng et al., 2019). Transmission of facultative microbes is different from primary microbes. Sometimes, facultative microbes are transmitted vertically. It has been demonstrated that the community structure of various facultative microbes is highly affected by the host's developmental stage and diet (Ojha et al., 2017). They are known to inhabit various parts of an insect's body, and some are localized to the hemocoel in a scattered distribution. Others are restricted to the bacteriocytes (confined pattern) (Marubayashi et al., 2014). The facultative symbionts have evolved various fascinating mechanisms to ensure their transmission and propagation inside an insect's body. Although having a beneficial role in the insect body, facultative symbionts can become commensals or pathogenic under certain circumstances (Marubayashi et al., 2014). Secondary symbionts are generally diverse and exhibit less host-specific commitments (Himler et al.,2011). For instance, *Wolbachia*, *Spiroplasma*, and *Cardinium* are retained, while others like *Burkholderia* and *Serratia* are newly acquired with each generation. For example, *Sodalis glossinidius*, a facultative symbiont of the tsetse fly, has developed the capacity to be transmitted through transovarial transmission via haemolymph (Cheng and Aksoy, 1999) or vertically to the intrauterine larvae through milk gland secretions, and in certain cases, horizontal transmission occurs during mating (De Vooght et al., 2015). Apart from this, there are substantial number of interesting studies indicating the nature of various bacterial symbionts across different insect orders. The cytoplasm of the bacteriocyte houses an Enterobacteriaceae family bacterium, whose expression is partially controlled by the host. This bacterium serves as the insect's source of a number of essential vitamins, including biotin, pantothenic acid, and riboflavin (Simpson et al.,2015). Additionally, the facultative symbionts primarily assist their insect hosts in digestion and xenobiotic detoxification. For example, certain species of *Pseudomonas*, which are gram-negative Gammaproteobacteria found in *Spodoptera frugiperda*, play a vital role in pesticide resistance to their hosts (de Almeida et al., 2017). *Serratia grimesii*, found in nematodes, possesses genes involved in the degradation of phytotoxins such as terpenes, and *Candidatus Ishikawaella* capsulate is recognized for its capacity to metabolize alkaloids in stinkbugs (Itoh et al., 2018). Additionally, various groups of vertically transmitted facultative endosymbionts such as *Wolbachia, Rickettsia, Arsenophonus, Spiroplasma*, and *Cardinium* are involved in sex determination and are known to induce sexual aberrations in different insect orders (Kageyama et al., 2012). Facultative symbionts help host insects in pesticide detoxification, e.g., the symbiont *Pseudomonas* assists the host insect to eliminate ingested pesticides (Almeida et al., 2017). Facultative symbionts, which facilitate favorable nonessential tasks for their host, are usually obtained from the environment through feeding or contact, leading to horizontal transmission (Kikuchi et al. 2011, Caspi-Fluger et al. 2012, Hannula et al. 2019). There are also mixed modes of transmission in which symbionts can be obtained both vertically and horizontally, called pseudo-vertical transmission (Bright and Bulgheresi 2010). Facultative symbionts serve a variety of important functions for their hosts, including high-temperature tolerance, influencing sex determination, and affecting body coloration (Montllor et al. 2002, Dillon and Dillon 2004, Werren et al. 2008, Tsuchida et al. 2010). For example, red pea aphids, that are infected with a *Rickettsiella* facultative endosymbiont, change to green as a result of producing blue-green polycyclic quinones (Tsuchida et al. 2010). An endosymbiont found in *Sitophilus oryzae L.* (Coleoptera: Curculionidae) (rice weevil) (2 × 103 bacteria per host cell) is commonly known as the SOPE or S. oryzae primary endosymbiont (Simpson et al.,2015). In addition to obligate and facultative symbionts, several phytopathogenic microbes are also found in insect bodies. The phytopathogenic symbionts inhabit in insect body, and they rely on the insect vector for their transmission to plants. These symbionts are actively involved in interaction with insect hosts and facilitate insects in feeding. However, the immobility of plants becomes a major obstacle in the transmission of these phytopathogenic bacteria. This led to the dependency of these microbes on vectors, which are usually insects, for their dispersal and propagation. These bacteria not only engage actively with their insect host but also modify it for their own benefit. Some microbes are capable of reproducing within their insect vector (propagative), whereas others are not (nonpropagative). This implies that in addition to serving as the vector, the insect also serves as an alternate host for these bacteria (Nadarasah and Stavrinides, 2011). Some microbes, once acquired by the vector, are readily transmitted to the host plant (semipersistent, non-circulative) while others move through the insect's body and are transmitted only after a period of latency (persistent, circulative transmission (Perilla-Henao and Casteel, 2016). Upon entering the insect's body, they move to the midgut or hindgut epithelium and are subsequently released into the haemolymph. From the haemolymph, they enter the salivary gland and are passed on to the plant during the feeding process (Kwon et al., 1999). *Xylella fastidiosa* is the phytopathogenic symbiont that lives in the foregut of leafhoppers and spittlebugs (Chatterjee et al., 2008). Certain phytopathogenic bacteria particularly

belong to the Enterobacteriaceae family. Instances of phytopathogenic insect symbionts include *Phytoplasma*, which represent a highly diverse category of Gram-positive, pleomorphic-shaped phytopathogenic bacteria that inhabit both insects and plants at the intracellular level (Sugio et al. 2011). Because they colonize host cells, they benefit from the cellular processes of the host and do not require complex genomes. Phytoplasma possess the smallest genomes among all known phytopathogenic bacteria, averaging approximately ~0.7 Mb with a low G+C content (Kube et al. 2012). They have a broad host range, infecting more than 800 distinct plant species and causing more than 1000 plant diseases (Mitchell 2004, Weintraub and Beanland 2006, Hogenhout et al. 2008). Hemipteran insects are most successful in transmitting phytoplasma. Spiroplasma are Gram-positive helical-shaped intracellular bacteria that share a distant relationship with Phytoplasma, of which only some are phytopathogens (Ammar et al. 2004, Sugio et al. 2011). Hemipteran insects, particularly leafhoppers and planthoppers, are known to transmit phytoplasmas. *Spiroplasma kunkelii* is responsible for corn stunting disease, i.e., transmitted by leafhoppers and in severe cases leads to the complete loss of corn seed production (Özbek et al. 2003, CABI 2020). *Spiroplasma citri* causes citrus stubborn disease and is transmitted by leafhoppers to other plant species such as carrot and periwinkle, leading to leaf discoloration (Mello et al. 2009). Rickettsia-like organisms (RLOs) are intracellular Gram-negative bacteria found in insects, playing significant roles in primary nutrition. They can manipulate insect reproduction and are transmitted to plants, where they become pathogenic. Insects transmitting RLOs are white flies, cicadas, leafhoppers, and psyllids (Caspi-Fluger et al. 2012, Constable and Bertaccini 2017). In plants, RLOs are responsible for lethal yellows, grape vine yellows, strawberry green petal, Papaya bunchy top disease, and a couple of other diseases (Streten et al. 2005).

INSECTS GUT STRUCTURE

Due to favorable physiological conditions in the gut, most of these symbionts are retained on the gut epithelium. To understand the functional role of these gut symbionts, it is necessary to study their distribution. This mutually beneficial interaction between microbes and insects can cause the reestablishment of epidermal cells and the induction of intestinal stem cell proliferation. In the digestive tracts, insects have developed several specialized structures and cells, such as midgut crypts, mycangia, and microbiomes for retaining certain obligatory bacteria (Siddiqui et al., 2022). Insects' guts contain several microbes that help them adapt to various ecological niches. Various bacterial phyla, such as Betaproteobacteria, Bacteroidetes, Firmicutes, including *Lactobacillus* and *Bacillus* species, *Gammaproteobacteria, Alphaproteobacteria, Clostridia, Actinomycetes, Spirochetes, Verrucomicrobia,* and others, are frequently found in the insect gut. The insect gut is divided into three primary regions: the anterior midgut or foregut, the posterior midgut, and the hindgut (Wang G.-H. et al., 2020). The embryonic epithelium gives rise to the anterior midgut and hindgut. An exoskeleton of chitin and integument glycoproteins protects them from pathogens, while the posterior midgut is mainly utilized for absorption and digestion (He et al., 2018). In addition, the hindgut of insects serves as an extension of the body cavity and is used to collect dietary waste (Siddiqui et al., 2022). However, it provides a suitable environment that promotes the proliferation and diversification of insect gut microbiomes (Bruno et al., 2019). In insects, the exoskeleton is made up of cuticular glycoproteins and chitin, which lines the foregut and hindgut, are both derived from embryonic ectoderm (Chapman et al.,1998). This exoskeleton, which separates the intestinal lumen from the epidermal cells, is shed at each ecdysis (Siddiqui et al.,2022). Insect foreguts frequently have distinct crops or diverticula for short-term food storage, and their hindguts contain separate sections, such as fermentation chambers and recta, which are used to store feces before defecation (Siddiqui et al.,2022). The foregut of many lepidopteran insects comprises the crop and oesophagus, where food fragments are stored. *Buchnera* is an endosymbiont, whereas *Ishikawaella* lives in the extracellular tissue of the adult stingbug's posterior midgut (enlarged portion) (Nikoh et al., 2011). The midgut of many insects, which is made of endodermal cells and lacks cuticle, is the primary site of digestion and absorption. The midgut epithelial cells of numerous insects develop a covering known as the peritrophic matrix, also referred to as the peritrophic membrane or PM. The peritrophic matrix separates the midgut into two different spaces: the endoperitrophic and the ectoperitrophic space. In order to avoid direct contact with the midgut epithelium, the microbes are frequently restricted to the former (Engel, P et al.,2013). The two basic types of peritrophic matrix are type I peritrophic matrix and type II peritrophic matrix (Engel, P. 2013). Certain lepidopterans, several coleopterans, dictyopterans, and orthopterans, as well as some hymenopterans, are examples of insects with a type I peritrophic matrix. A small number of lepidopteran and some dipteran insects contain type II PM (Klowden, M.J.2013).

Several distinct roles are performed by the peritrophic membrane. Not only does this membrane concentrate food and digestive enzymes, but it also acts as a barrier to prevent the epithelium from being exposed to large toxin molecules. These toxins are found in food from food particles being infected with mechanical injury to microbial invasion (Shao et al.,2001). For example, different phytophagous stinkbugs have obligatory symbionts in a specialized midgut region that comprises multiple crypts (Siddiqui et al.,2022). According to recent studies, it has been revealed that the midgut crypts of the Largidae family of the superfamily Pyrrhocoroidea harbor a *Burkholderia cepacia* Yabuuchi (Burkholderiales: Burkholderiaceae) symbiont (Takeshita, K et al, 2015). In fact, midgut stem cell-mediated response to bacterially induced tissue damage has been studied in *Drosophila melanogaster* Meigen (Nászai et al., 2015; Bonfini, A et al.,2016; Jiang et al.,2016). Pine beetle and their mycangium have been found to harbor several different antibiotic-producing actinomycete symbionts (Jang, S et al.,2020). For most lepidopteran larvae, including silkworms, the midgut is observably larger than the foregut and hindgut, secreting the vast majority of enzymes and small molecules for food digestion, such as proteases and carbohydrases. Therefore, the midgut is the primary site for digestion and absorption. In addition, the midgut lines the peritrophic matrix, which is made up of three different cell types: goblet cells, columnar cells, and stem cells (Edwards, M.J. et al.,2000; Egert, M. et al.,2003; Engel, P. et al.,2013).Lepidopteran insect goblet cells have a critical role in the gut immune defence, and goblet cells are considered to be different from stem cells (Genta, F.A. et al.,2006; Johnson, K.S. et al.,2000; Emery, H. et al., 2019). The midgut is divided into two spaces: endo-peritrophic and ecto-peritrophic areas by the peritrophic matrix. Normally, gut microorganisms are unable to cross the endo-peritrophic space, which prevents them from coming in direct contact with midgut epithelial cells (Hongoh, Y.2010; Hongoh, Y.J. 2011; Liu, X. et al.,2019). Another great example of such an obligatory symbiotic relationship is *Ishikawaella capsulata* and the plataspid stinkbug *Megacopta punctatissima*. *Ishikawaella capsulata* shares striking similarities with *Buchnera*. Both the stinkbug species *Murgantia cribraria* Fab. and the bean bug species *Riptortus pedestris* Fab can generate several sac-like structures towards the posterior part of the midgut. These symbiotic bacteria are contained in this sac (Kikuchi, Y.2008). In the plataspid stinkbug, the bacteria are found in crypts of the midgut (Hosokawa, T. et al., 2012). The lepidopteran larva’s alimentary canal is divided into three primary regions: The foregut and hindgut, which arise from the embryonic ectoderm and are lined with the chitin exoskeleton, and the midgut originates from the ectoderm (Engel, P.et al.,2013; Gomes, F.M. et al.,2013; Guarner, F. et al.,2003). The demarcations of each part are distinguished by the cardiac valve (between the foregut and midgut) and pylorus (between the midgut and hindgut). Insect hindguts serve as an extension of their body cavities and are essential for collecting nutritional waste (Siddiqui et al.,2022). Consequently, they provide the gut microbiota with a perfect feeding environment, promoting their diversity and growth (Bruno et al.,2019). The hindgut of lepidopteran insects consists of three sections: the ileum, the rectum, and the posterior rectum. They mediate the uptake of uric acid, water, and salts from Malpighian tubules, which are part of the excretory system of insects (Johnson, K.S. et al., 2000; Thong-On, A. et al.,2012). The caterpillar benefited from all these structures, leading to very high feeding and food digestion rates (Mason, C.J. et al.,2019; Chen, B. et al.,2020). For instance, *Cyclocephalla signaticollis* Burmeister (Coleoptera: Scarabaeidae) has a typical alimentary tract with a modified extended part of the hindgut known as the fermentation chamber (Huang, S.W.; Zhang, H.Y.; Marshall, S.; Jackson, T.A.2010). The majority of scarab larvae are concentrated in a fermentation chamber of the hindgut and are crucial for the digestion of plant material (Huang, S.W. et al, 2010).

FACTORS AFFECTING GUT SYMBIONTS

Acquisition of bacteria by insects via the environment is the initial step to establish the microbial symbiosis. After entering the insect's body, these bacteria change their free-living status to symbionts. Such intracellular bacteria acquired by insects are rather prevalent in nature, and it is predicted that almost 15% of insects possess such mutualistic microbes (Douglas, 1989). Insects provide a special niche and a slot for these microbes, and their existence strongly depends on the physiological circumstances and life cycle of the host (Engel and Moran, 2013). Different types of factors influence the composition of gut microbiota, including insect developmental stage, biochemical changes in distinct intestinal locations, and the insect’s ability to access available nutrients (Crotti, E et al., 2013). Gut microbial metabolic activity can be controlled by different gut physicochemical conditions, including pH, oxygen availability, redox conditions, ion concentrations, and digestive enzymes.

1. EFFECT OF FEEDING ON MICROBIOME

Feeding can change the gut microbial community in an insect's gut. It has been noted that the lepidopteran insect gut microbial community is altered by feeding (Tang, X.et al.,2012; Hu, L.et al.,2022). For example, when the 5th-instar larvae of *B. mori* feed on mulberry leaves (the conventional rearing method), the gut microbiota is dominated by *Rhodococcus, Escherichia*, and *Enterococcus* (Zhang, X.et al.,2021; Prem Anand, A.A.et al.,2012). *Bacteroides* and *Acinetobacter* were the predominant species when the diet was switched to lettuce leaves (Liang, X.et al.,2014). The study finds that the insects' microbial diversity is impacted by temperature, food, and antibiotics (Russell, J.A.et al.,2009; Raza, M.F.et al.,2020). One scientific study using high-throughput sequencing technology was conducted on *Spodoptera frugiperda* to investigate how microbial diversity in the gut was changed depending on different foods. They feed on maize, wild oats, oilseed rape, and pepper. This finding showed that the rapeseed-fed insects showed the highest microbial diversity, and the wild oats-fed gut microbial diversity of insects was the lowest, while the gut microbial diversity of insects fed maize without a seed coating agent was significantly higher than that with such an agent (Lv, D.et al.,2021). Liang et al. found that the midgut microbes of the 5th instar *Helicoverpa armigera* larvae feeding on lettuce leaves were significantly different from those of common silkworms at the genus level. The bacteria of the genera *Acinetobacter* and *Anaerofilum* are the main bacteria, while *Bacillus* and *Arcobacter* are the main bacteria in the normally fed *H. armigera* (Liang, X.et al.,2014). According to Priya et al, it was found that bacterial diversity in *H. armigera* not only varies depending on different host plants, but also due to the different locations of the same host plant. Insects that consume artificial diets have less microbial diversity than that of insects fed on crops (Priya, N.G.et al.,2012). Thakur et al. 2016 examined the effects of adding *streptomycin* to artificial diets on the survival and fitness of *Spodoptera litura* (Lepidoptera: Spodoptera) and its gut microbial diversity.

2. TEMPERATURE, pH, and SEX EFFECT

Furthermore, *Nezara viridula* depends on intestinal symbiotic bacteria for survival. The degree of host survival and microbial diversity may decrease with increasing temperature. The same effects were seen in the animal treated with antibiotics (Kikuchi, Y.et al.,2016). Hence, it can be beneficial to study the influence of the external environment on the diversity of beneficial microbes in the insect intestinal tract. This environmental effect on microbes helps the scientist to manage the rise and fall of pest populations (Gupta, A. and Nair, S.2020). Microbial colonization is heavily affected by the gut pH and other physicochemical conditions. Insects house a large number of microbial communities with optimal pH within the gut, creating a beneficial environment for them (Engel and Moran, 2013). There have been reports of several different types of bacterial endosymbionts present within the insect body, each with unique characteristics. Gut physicochemical conditions such as pH, oxygen availability, redox conditions, ion concentration, and digestive enzymes can influence the metabolic activity of gut microbes (Johnson, K.S.et al.,2000; Maslowski, K.M.et al.,2009+; Peri´c-Mataruga, et al,2019). The pH of the digestive tract is energetically controlled and frequently deviates from the haemolymph, which is typically around 7 (Liu, H.et al.,2016; Lu, X.et al.,2014; Darvishzadeh, A.et al.,2008). The gut of lepidopteran larvae generally exhibits extreme alkalinity, with a midgut pH as high as 7–12 (Fukatsu, T.2017). The alkalinity of the foregut and hindgut is comparatively low compared to the midgut. As a result, digestive enzymes in the lepidopteran gut are accustomed to alkaline conditions (Holtof, M.et al.,2019; Gao, X.et al.,2019). The diversity and proportion of insect gut microbes differ as per their sexes. The intestinal tract of male and female larvae of the 5th instar of *B. mori* was dominated by *Enterococcus, Delftia, Pelomonas, Ralstonia*, and *Staphylococcus*. The abundance of Enterococcus was significantly lower in female larvae than in male larvae, while the abundances of *Delftia, Aurantimonas*, and *Staphylococcus* were significantly increased (Sun, Z.et al.,2016).

3. DEVELOPMENTAL STAGE EFFECT

Insects provide a special niche for these microbes, and their survival strongly depends on the host's physiological conditions and life cycle (Engel and Moran, 2013). Chen et al. discovered that the 4 phyla Proteobacteria, Firmicutes, Actinobacteria, and Bacteroidetes were detected throughout the life history of silkworms and found that all these phyla were also present in the mulberry-eating larvae of *Acronicta major* and *Diaphania pyloalis*. In line with host developmental changes, the

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microbial community of *B. mori* varies considerably between its early and late age larvae (Chen, B.et al.,2018). *Enterococcus, Pseudomonas*, and *Asaia* are abundant in the eggs of *Spodoptera exigua*, but *Methylobacter* and *Halomonas* are predominant in freshly hatched larvae, and *Enterococcus* dominates in 3rd and 5th-instar larvae. The greatest diversity of microorganisms is found in the pupal stage. There were no significant microbial differences between newly hatched male and female *S. exigua* larvae (Gao, X.et al.,2019). Francisco et al. demonstrated that the bacterial composition of *Brithys crini* was stage-specific, and *Rosenbergiella* and *Serratia* were highly prevalent in the eggs. Twenty-seven genera (Empedobacter, 23%; Enterococcus, 10%) were statistically more abundant in larvae, while only one genus (Serratia, 75%) was significantly more abundant in adults (Gonzalez-Serrano et al.,2020). The introduction of modern technologies such as high-throughput sequencing, various functional omics, gene editing, etc., has fuelled the discovery of novel bacteria in a rapid and accelerated manner. The above results reveal that there are different dominant flora in different developmental stages and sexes of insects, which may play an important role in different developmental stages and sexes. However, additional experimental research evidence is required to identify the strains with specific functions.

4. PESTICIDES EFFECT

It has been noted that extensive use of pesticides can affect insects' food digestion, nutrient absorption, metabolism, immune response, defense against the invasion of harmful microorganisms, and microbial homeostasis (Sun, Z.et al.,2016; Wei, G.et al.,2017; Gu, Z.et al., 2017). Li et al. found that following phoxim consumption, the growth of *B.mori* was slowed down and the activity and expression of enzymes linked to food metabolism in the midgut were out of control (Li, F.et al.,2016). Sun et al. studied the impact of microbial pesticides and camptothecin on the mortality of two lepidopteran insects, *Trichoplusia ni* and *S. exigua*.Camptothecin significantly increased the toxicity of *B. thuringiensis* to *S. exigua* and *T. ni*, as well as Autographa californica nucleopolyhedrovirus (AcMNPV) and *S. exigua* nuclear polyhedrosis virus (SeMNPV). It is hypothesized that camptothecin can affect the permeability of the peritrophic membrane to increase its toxicity (Sun, S.et al.,2012). Motta et al. discovered that glyphosate consumption by honeybees under laboratory or field conditions can disrupt the host gut microbiota and has negative health effects (Motta, E.et al.,2020). Dai et al. examined in the laboratory how glyphosate affected the variety of bacteria in the midgut of Italian honeybees. Following administration of 20 mg/L glyphosate, the species diversity and richness in the intestinal tract of honeybees changed significantly, and their survival rate dropped (Dai, P.et al.,2018). Zhu et al. discovered that metabolic activity, detoxification, and immune-related genes were significantly changed after the consumption of neonicotinoid insecticide nitenpyram by *Apis mellifera* L. This ingestion can lead to an imbalance in intestinal flora, which further reduces food consumption and the survival of honey bees (Zhu, L.et al.,2020).

ROLE OF INSECT GUT BACTERIA ON ITS HOST INSECTS

The insect gut harbored a large number of bacterial communities. Not only do these microbes play an important role in food digestion, essential amino acid synthesis, and the production of vitamins, but they also protect their host from various pathogens by enhancing the insect's immune responses. These microorganisms detoxify plant allelochemicals, degrade plant phytotoxins and pesticides. This detoxification is achieved by breaking down the toxic chemicals or by controlling the expression of host genes. Insect gut microbiota has shown great application potential in the fields of pest management and control. It has been discovered that *B. thuringiensis kurstaki* can induce the mortality of *Lymantria dispar*, which depends on the intestinal bacteria of the host. Paramasiva et al. found that the exclusion of gut microbes in H. armigera affected the susceptibility of *B. thuringiensis* to *H. armigera*. However, it has been reported that the insecticidal activity of the *B. thuringiensis* HD-73 strains against *Manduca sexta* and the *B. Thuringiensis* HD-1 and HD-73 strains against *P. xylostella* larvae demonstrates that gut microbes are not essential for their insecticidal activity. Insect intestinal flora has been isolated and purified from different insects, and the role of a few microbes has been reported. Further study is necessary to understand the role of different microbes in their host's life. This review focuses on different functional roles of microbes in insect hosts, such as food digestion, protection against plant defense systems, pest management, pesticide degradation, protection against pathogens, predators, and parasitoids, etc.

1. FOOD DIGESTION, VITAMIN SUPPLY, AND NITROGEN FIXATION

Insects provide stable environments and nutrition for gut symbionts, and in return, microbes produce nutrients that are lacking in natural food but are essential for the development of the host organism. Insects that harbor the bacterial symbionts feed exclusively on plant sap from xylem and phloem, which are rich in sugar but lack vitamins and essential amino acids. They are unable to produce essential amino acids, vitamins, and sterols. Their symbionts help them synthesize those essential substances, thereby expanding host diet options and even changing eating habits. Vitamins are fundamental micronutrients normally found as precursors of various enzymes that are essential for various biochemical reactions during the growth and development of insects. Hassan et al. tested the hypothesis that two actinobacterial symbionts provide *Dysdercus fasciatus* with B-vitamins. The gut symbionts of ants utilize reclaimed recycled N to recycle urea or uric acids required by the host in large quantities (Hu et al.,2018). Blow et al. confirmed that symbiotic bacteria *Buchnera aphidicola* provide vitamin B2 and B5 to its host *Acyrthosiphon*. The intestinal microbiota of insects can secrete various enzymes, which can digest carbohydrates, protein, and lipid. For example, *Pseudomonas, Clostridium,* and *Klebsiella pneumonia* microbes of *B.mori* can digest cellulose by secreting cellulase (Anand et al., 2010). *Locusta migratoria manilensis* can degrade grass, which converts into carbohydrates, amino acids, and sugars in the presence of its gut microbes, *Klebsiella pneumonia* (Su et al.,2014). It has been reported that 118 culturable bacterial strains are present in the intestine of *Diatraea saccharalis* larvae. Among them, *Bacillus, Microbacterium, Stenotrophomonas, Klebsiella, and Enterococcus* were found to possess the enzyme that has cellolytic activity. *Bacillus* and *Klebsiella* showed the highest degradation activity of cellulose (Dantur et al.,2015). Microbes of termites can digest cellulose by cellobiohydrolase activity (Tokuda et al.,2005). Lepidopteran insects harbored the Gram-positive and Gram-negative strains. Among the *Proteus vulgaris*, *Serratia liquifaciens*, and *Erwinia sp*., can utilize pectinolytic, xylanolytic, and polysaccharides, respectively, whereas *Klebsiella* can hydrolyse starch (Bridges 1981). Different gut symbionts of insects help their host fix nitrogen. It has been reported that the bacterial genus is primarily responsible for nitrogen fixation in the bark beetle, *Dendrotonus ponderosae* Hopkins (Coleoptera)(Bridges 1981). Termites mostly feed on wood and have a great capacity for nitrogen fixation due to their gut symbionts, *C.freundii* and *Enterobacter agglomerans* Beijerinck(Breznak et al.,1994). Gut microbes have a significant role in lipid metabolism. Microbes can generate triglyceride metabolites for their host insects, which are utilized as a carbon and energy storage source. Polyhydroxyalkanoates (PHAs), a group of crucial lipid compounds, are generated by gut microorganisms (Ong et al.,2018).

2. FIGHT AGAINST PLANT DEFENSE SYSTEM

Insects and plants have evolved simultaneously and the cohabited for more than 350 million years. Their association helps balance their survival. However, they can also develop and acquire unique traits that can adversely impact each other. Plant phloem serves as an essential source for insects. When insects feed on phloem sap, it leads to the initiation of the plant defense system by inviting natural enemies of the insect pest or by secreting some toxic material (Casteel et al., 2012; Su et al.,2015). Plants can develop different morphological structures such as spines, hair, thorns, trichomes, and also secrete some secondary metabolites like phenol, alkaloids, terpenoids, etc, which can cease the development of insect pests (Dudareva et al.,2006; Howe and Jander,2008; Arimura et al.,2009; Rani et al.,2009; Verhage et al.,2010; Hare,2011; War et al.,2011). The constitutive defense system of plants secretes various volatile secondary metabolites to get rid of their insect pests. Different phytohormones, such as salicylic acid and jasmonic acid, are secreted by plants in response to herbivore insect attack. The jasmonic acid pathway is activated upon attack of insects having chewing and biting mouthparts, whereas the salicylic acid pathway gets promoted by the attack of piercing-sucking herbivores (Glazebrook, 2005; Schoonhoven et al., 2005; Kawazu et al., 2012). To withstand these plant defense systems, insect gut symbionts play a crucial role in detoxifying such toxic plant material and sometimes suppress the gene responsible for the plant defense pathway. These suppressions result in the production of altered primary and secondary metabolites (Body et al., 2013; Giron et al., 2013; Zhu et al., 2014; Sugio et al., 2015). Along with the modulation of the JA and SA pathway, insect gut microbes can also hijack other pathways, which benefits their host insects (Panteleev et al., 2007). *Phyllonorycter blancardella*, the apple tree leaf minor harbored *Wolbachia* symbionts that can modulate phytohormone profile in mined leaves, and can

deliver cytokines which are synthesized in the insect's body (Kaiser et al., 2010; Body et al., 2013). It has been noticed that the removal of *Wolbachia* from its host resulted in the loss of cytokine-induced green islands on apple tree leaves and also reduced cytokinin levels in larvae (Kaiser et al., 2010; Body et al., 2013). Sometimes, instead of modulating plant physiological conditions, gut microbes can also inhibit the plant defense system. Such instances have been observed in gut symbionts of the cigarette beetle (Dowd and Shen, 1990). These symbionts produce an enzyme that neutralizes plant defense compounds. The gut microbes of the mountain pine beetle, *Dendroctonus ponderosae*, can degrade plant defense product terpenoids (Boone et al., 2013). Along with those microbes' activity against the plant defense system, the insect's genome can also resist the toxic material from the plant. Repeated use of insecticides and repeated encounters with plant chemicals enhance the resistance of insects through the rearrangement or mutation of their genome. Insects contain different gene families, such as CYP450 and GST, that are responsible for the detoxification of plant chemicals. (reference). Gene from insect gut microbes can also code some enzymes that are capable of degrading phytotoxin (Nagata et al., 2010). For instance, *Myzus percicae* Sulzer (Hemiptera: Plataspidae) harbors the bacterium *Achromobacter xylosoxidans* Yabuuchi and Yano (Burkholderiales: Alcaligenaceae), which carries the gene carboxylesterase for the enzyme N-methylcarbamate hydrolase, responsible for phytotoxin degradation (Tomasek et al., 1989). Caffeine, an alkaloid allelochemical, serves as a defensive chemical to ward off the attack of herbivorous insects. It has been noted that *Hypothenemus hamper* (Coleoptera: Curculionidae) harbor bacteria that can degrade caffeine. (Ceja-Navarro et al.,2015). The gut microbe of coffee borer *P.fulva* carries the ndmA gene, which encodes an enzyme called methylxanthine N1-demethylase that catalyzes the initial step in caffeine breakdown (Summers et al., 2012)

3.DEGRADATION AND RESISTANCE AGAINST PESTICIDES

Pesticides have been applied to control the pest population to increase crop production. However, the uncontrolled use of pesticides accumulates in the ecosystems and gets contaminated with plants, air, soil, and water (Lewis et al.,2016). Different studies have shown that insects can develop resistance to those insecticides due to a wrong selection and overuse of pesticides, as well as target site mutation, environmental changes, and the degradation of insecticides by gut microbes of insects (Naik et al., 2018; Hawkins et al., 2019., Matsuda et al.,2020). Insects' digestive systems have a robust defensive system due to the presence of various microbial species such as bacteria, archaea, fungi, and protozoa (Chen et al.,2021). It has been reported that insect gut bacteria can degrade organic insecticides such as dimethoate, chlorpyrifos, and ethoprophos. Different gut symbionts of insects show esterase activity, which is essential for the degradation of insecticides. After the degradation, they extract carbon, nitrogen, and phosphorus from insecticides as an energy source (Li et al.,2017). Gut symbionts of bean bug *Riptortus pedestris*, some soil *Burkholderia* strains can enhance host resistance to fenitrothion by degrading this insecticide (Kikuchin et al.,2013; Kim and Lee,2017). *B.cereus* microbes from *P.xylostella*(Linnaeus) can degrade indoxacarb, capable of extracting carbon from this insecticide, for the growth and metabolism (Ramaya et al.,2016). *B.mori* with gut mirobes, *Stenotrophomonas*, enhanced host resistance to organophosphate, chlorpyrifos. Organophosphate fenitrothion is also degraded by *Burkholderi*a, a symbiont of the serious rice pest Cletus punctiger (Ishigami et al.,2021). Major stored grain pests (*Tribolium castaneum*, *Rhizopertha dominica, Sitophilus granaries*, and *Trichoderma granarium*) developed resistance against phosphine fumigant (Wakil et al.,2021). Different symbionts like *Klebsiella, Wolbachia, Lactobacillus, Arsenophonus* and *Acinetobacter* from *Nilaparvata lugens* can develop resistance to tetracycline and ciprofloxacin. Antibiotic treatment of *N.lugens* shows more susceptibility towards this antibiotic due to the death of such microbes. Studies have proved that those bacteria help *N.lugens* develop resistance to insecticides by increasing the overexpression of insecticide-degrading enzymes cytochrome P450 and glutathione S-transferase (GST) (Vontas et al, 2002; Zhang et al, 2016).

4. PEST CONTROL AND MANAGEMENT

According to the WRI (2019) report, an exponentially increasing human population by 2050 can increase the food demand anywhere between 60-90%. It is one of the major global challenges to increase this amount of food production for such a rapidly growing population. Numerous biotic and abiotic factors adversely affect the food production rate. Among those are

the insect pests that can cause significant damage to crop production. Insects like lepidopteran worms, wasps, hornets, and bees are known to cause several damages to crops. According to FAO, the loss of 40% crops is reported each year. To control the insect pest, several insecticides have been invented. However, due to the improper use of insecticides, insects develop resistance to these pesticides. Therefore, devising a pest management strategy without compromising the sustainability of agro-ecosystems is a major challenge. So, there is an urgent need to develop eco-friendly alternatives for controlling the pest population in the long term. Different scientific studies prove that the gut microbiota of insects has emerged as an extremely beneficial tool for introducing biocontrol strategies. According to Fisher et al. (2017), it has been reported that vertically transmitted microbes of insects have a greater fitness effect on their host than horizontally transmitted symbionts (Ferreira et al., 2019). Different lepidopteran pests, such as *P.xylostella, S.littoralis*, and *C.funiferana*, can be controlled by microbial control agents (MCAs) (Xia et. al, 2013). *Bacillus thuringiensis* (*Bt*) strains have been developed as commercial biopesticides for more than a decade. It has also been shown that, when the wMel strain of *Wolbachia* was introduced into *Aedes aegypti*, its ability to act as a dengue vector was negatively impacted (Kien et al.,2023). Cytoplasmic incompatibility is one of the most common phenotypes of *Wolbachia*. Through this cytoplasmic incompatibility, they can control *Homona magnanima* by increasing the *H. magnanima* pupal weight and shortening the host development time (Arai et al.,2019). African migratory locust, *Locusta migratoria migratorioides,* can be controlled by *Photorhabdus luminescens*, entomopathogenic bacterium (Jihan et al., 2025)). Brinjal shoots and fruit borer, *Leucinodes orbonalis* Guenee, is controlled by the indigenous *Bacillus* strain VKK-BB2 9 (Pola et al., 2022).*B.thuringiensis* can generate cry toxin protein, which, combined with cry protein receptors on intestinal epithelial cells, causes hole formation in epithelial cells (Lucena et al., 2014). High mortality rate has been observed in the oriental fruitfly, *Bactrocera dorsalis*, when they are fed genetically modified *E. coli* (Mohanpuria et al., 2021). Interaction between *B.bassiana* and mosquitoes' gut bacteria accelerates the death of mosquitoes (Wei et al.). Mason et al. discovered that when the larvae of the *M.sexta* were infected with *Enterococcus faecalis* and *B. thuringiensis*, *Enterococcus faecalis* would translocate to the blood cavity and induce sepsis, increasing the sensitivity of the *M. sexta* to *B. thuringiensis* (Mason et al., 2011).

5. PROTECTION AGAINST PATHOGENS, PREDATORS, AND PARASITOIDS

Besides nutritional, defensive, and resistant benefits, symbionts also play a crucial role in shaping the interaction between insects and natural enemies. Like other organisms, insects are also susceptible to a wide range of microbial pathogens such as bacteria, viruses, protozoans, and fungi. Insects themselves possess different defence mechanisms such as physiological barriers, cellular and humoral responses involving the production of antimicrobial peptides as a mode of protection against pathogens (Lemaitre and Hoffmann,2007; Sheehan et al.,2018). Insect microbial symbionts play an important role in getting rid of these harmful microbes. These microbes can synthesize different harmful toxins that can diminish the pathogen by destroying the cellular components and modifying the signaling pathways (Caragata et al.,2013; Paredes et al.,2016). The female solitary hunting wasp *Philanthus triangulum* harbors *Streptomyces* bacteria in its specialized antennal glands. Before the oviposition, these bacteria are transferred to the brood cells. After emerging from the egg, larva also acquires these bacteria deposited in the brood cells. These bacteria enhance the survival rate and protect the bacteria from fungal infection. Microbe-mediated protection against protozoan infection is observed in the cardia of the *Anopheles gambiae* gut (Warr et al.,2007). Different types of anti-plasmodium factors, synthesized from the gut of mosquitoes, affect the parasite development in the gut (Dimopoulos et al.,2007).

Some mutualistic symbionts of the insect can also protect their host from different predators. It has been seen that the *Paedeus* beetle gets protection from the wolf spiders through their endosymbionts. Pederin, synthesized by their endosymbionts, is harmful to their predators, the wolf spider (Kellner, 1999; Kellner, 2001; Kellner, 2002; Piel, 2002; Piel et al., 2004). Predator invasion is also expelled by the secretion of some toxic compounds by the symbionts.

Parasitoides affect insects by laying eggs outside their body. They affect the larval stage of the insects. Damage was caused by the piercing activity of parasitoid larvae, most commonly hymenopteran wasps. Peach potato aphid, *Myzus persicae*, is often attacked by hymenopteran parasitoids. The symbionts of aphids, *Hamiltonella defensa* and *Serratia* symbionts, play an important role in defending against the parasitoid wasp *Aphidius colemani*. These symbionts, interfering with the oogenesis of the parasitoid wasp *Myzus persicae*, were found to get protection from parasitoids *Ahidius colemani* due to the presence of *Regiella insecticola*, a facultative endosymbiont (Oliver et al., 2003, 2005; Moran et al., 2005b; Vorburger et al., 2009; Schmid et al., 2012; Brandt et al., 2017).

Pea aphid *Acyrthosiphon pisum* gets benefits from Rickettisial infection due to the presence of bacterial symbionts *Rickettsia.* Frequently, this aphid exists in nature in red color, and predators such as ladybird beetles mainly feed on red-colored pea aphids. As the population of ladybird beetles increases in the field, the Rickettisial infection of the aphid leads to increased blue–green quinone pigment synthesis in the host. This mechanism imparts the green color to the host. Eventually, amidst green crops, green aphids get camouflaged and protected from ladybird beetles. On the other hand, parasitoids such as wasps attack green-colored aphids. Whenever there is an attack by parasitoids, these symbionts turn the green host into the red host, and aphids get protected from parasitoids (Libbrecht et al., 2007; Tsuchida et al., 2014).

6. INSECT IMMUNITY

Insects lack adaptive immunity components, such as B and T cells, and completely depend on innate immune responses (Lemaitre et al.,2007). Insects' gut is the first line of defense because, by ingestion, most pathogens like bacteria, fungi, parasites, and viruses come in contact with insects. The peritrophic membrane is a semipermeable barrier that can prevent most pathogens from damaging the gut tissue (Daffre et al.,1994). Besides the peritrophic membrane, insects also rely on multiple innate immune defense mechanisms. For instance, Lepidopteran insect gut can generate ROS (Reactive oxygen species) to defend against harmful bacteria through cellular immune response (Konno et al,2018; Yang et al,2016; Konno et al,2016). The gut microbes of the Honey bee (*Apis mellifera*), *Snodgrassella alvi* and Gilliamella apicola, present in the form of dense biofilm, inhibit the entry of pathogens. *Apis mellifera* gets more infections from pathogens like *Serratia marcescens* when this bacterial colony has been disturbed (Kwong and Moran 2013). Gut symbionts enhance the immunity of insects (*Apis*) by modulating pH and oxygen level, producing short-chain fatty acids which suppress the virulence of the pathogen (Pickard et al,2017; Zhen et al,2017).

7. Plastic degradation

The improper use and disposal of plastic waste materials cause several environmental issues, as the polymer of PE (Polyethylene) is remarkably resistant to degradation. In addition to different biological significance, insect gut microbes might serve as a potential source for PE-degrading microorganisms. Due to their capacity to break down plastic, gut microbes of insects are receiving considerable interest in the field of bioremediation. Ren et al. isolated the *Enterrobacter* sp. D1 strain from the gut of *G. mellonella*, which can degrade PE films. (Ren et al., 2019) Two bacterial strains, *E. asburiae* and *Baccilus* sp., are isolated from the gut *of P. interpunctella* with the ability to degrade PE by forming biofilms that reduce the PE hydrophobicity (Yang et al.,2014). Recently, it has been discovered that *B.mori* has been applied in nanotoxicology to assess the potential effects of TiO_2 nanoparticles on intestinal microbes (Li et al.,2020). A potential fungal strain, *Aspergillus flavus*, was isolated from the gut contents of wax moth *G. mellonale* larvae that has the capacity to degrade microplastic particles due to the presence of extracellular enzymes. Yang et al. identified two plastic-degrading bacteria, *B. subtilis* and YP1 *Enterobacter,* from moth larvae. These two bacterial strains can convert PE long-chain skeleton C-C group into the –C=O (carbonyl group), which is a sign of PE breakdown (Albertsson et al.,1987). The larvae of *Tenebrio molitor* (yellow mealworm) can decompose Styroform, a polystyrene (PS), with their gut bacteria. Antibiotic treatment of their bacteria can diminish their ability to degrade the PS material (Yang et al., 2015).

Conclusion

Different beneficial microbes that reside in the insect's gut are crucial for the various physiological functions. These microbes provide benefits to their insect host in many ways, including food digestion, protection against the plant defence system, and insecticide degradation. The microbial community also helps its host to fight against pathogens, predators.

Negative effects of industrial pesticides on the ecosystem urge to an eco-friendly pest control strategy. By modulation these microbes, scientists can invent different pest control strategies. Insects' gut microbes also serve as a potential tool to integrate pest management for the improvement of agricultural practices and food safety. Though the detailed information about the interaction between the insect and their gut microbes is unknown. In the future, different relevant scientific discoveries will provide new opportunities to explore more gut microbial community and their industrial application in the agricultural field for the betterment of the environment as well as for the human population.

References

- Albertsson, A.; Andersson, S.O.; Karlsson, S. The Mechanism of Biodegradation of Polyethylene. Polym. *Degrad. Stab*. 1987, 18, 73–87.
- Ammar, El-D.; Fulton, D.; Bai, X.; Meulia, T.; Hogenhout, S. A. An attachment tip and pili-like structures in insect- and plant-pathogenic spiroplasmas of the class Mollicutes.*Arch. Microbiol.* 2004,181,97–105.
- Anand A.A.P.; Vennison S.J.; Sankar S.G.; Prabhu D.I.G.; Vasan P.T.; Raghuraman T.; Geoffrey C.J.; Vendan S.E. Isolation and characterization of bacteria from the gut of Bombyx mori that degrade cellulose, xylan, pectin and starch and their impact on digestion. *Insect Sci*. 2010,10,107.
- Arai, H.; Hirano, T.; Akizuki, N.; Abe, A.; Nakai, M.; Kunimi, Y. Multiple infection and reproductive manipulations of Wolbachia in Homona magnanima (Lepidoptera: Tortricidae). *Microb Ecol*. 2019,77,257–266.
- Arimura, G. I.; Matsui, K.;Takabayashi, J. Chemical and molecular ecology of herbivore-induced plant volatiles: proximate factors and their ultimate functions. *Plant Cell Physiol.*2009, 50, 911–923.
- Baumann, P; Baumann, L; Lai, C-Y; Rouhbakhsh, D; Moran, NA. Genetics, physiology, and evolutionary relationships of the genus *Buchnera*: intracellular symbionts of aphids.*Annu Rev Microbiol*. 1995,49,55–94.
- Bayen, S.; Roy, S.; Chakraborti, D.; Mukhopadhyay, A.; Kanta, L. Mutualistic relation of termites with associated microbes for their harmonious survival. *Symbiosis* 2021,85,145–161.
- Blow F.; Bueno E.; Clark N.; Zhu.T.D.; Chung.H.S.; Gullert S.; Schmitz.A.R.; Douglas.A.E.B-vitamin nutrition in the pea aphid-Buchnera symbiosis. *Insect Physiol*. 2020,126,104092.
- Body, M.; Kaiser, W.; Dubreuil, G.; Casas, J.; Giron, D. Leaf-miners co-opt microorganisms to enhance their nutritional environment.*J. Chem. Ecol*. 2013,39, 969–977.
- Chatterjee, S.; Almeida, R. P. P.; Lindow, S. Living in two worlds: the plant and insect lifestyles of *Xylella fastidiosa*.*Annu. Rev. Phytopathol*. 2008,46,243–271
- Chen, B.; Du, K.; Sun, C.; Vimalanathan, A.; Liang, X.; Li, Y.; Wang, B.; Lu, X.; Li, L.; Shao, Y. Gut bacterial and fungal communities of the domesticated silkworm (*Bombyx mori*) and wild mulberry-feeding relatives**.** *ISME J.*2018,9,2252–2262.
- Chen, B.; Xie, S.; Zhang, X.; Zhang, N.; Feng, H.; Sun, C.; Lu, X.; Shao, Y. Gut microbiota metabolic potential correlates with body size between mulberry-feeding lepidopteran pest species. *Pest. Manag. Sci.*2020*,*76, 1313–1323.
- Dantur, K.I.; Enrique, R.; Welin, B.; Castagnaro, A. Isolation of cellulolytic bacteria from the intestine of Diatraea saccharalis larvae and evaluation of their capacity to degrade sugarcane biomass. *AMB Express*. 2015, 5, 15.
- Darvishzadeh, A. Enzymatic activity of alpha-amylase in alimentary tract *Spodoptera littoralis* (Boisduval) (Lepidoptera: Noctuidae): Characterization and Compartmentalization.*Arthropods* 2014,3,138
- De Almeida, L. G.; De Moraes, L. A. B.;Trigo, J. R.; Omoto, C.; Cônsoli, F. L. The gut microbiota of insecticide-resistant insects houses insecticide-degrading bacteria: a potential source for biotechnological exploitation.*PLoS One* 2017,12, e0174754.
- Dillon, R.J.; Dillon, V.M. The Gut Bacteria of Insects: Nonpathogenic Interactions.Annu.Rev. *Entomol*. 2004,49,71–92.
- Dimopoulos, M. A.; Anagnostopoulos, A.; Kyrtsonis, M. C.; Zervas, K.; Tsatalas, C.; Kokkinis, G. Primary treatment of Waldenstrom macroglobulinemia with dexamethasone, rituximab, and cyclophosphamide. *J. Clin. Oncol*. 2007,25, 3344–3349.

- Gao, X.; Li, W.; Luo, J.; Zhang, L.; Ji, J.; Zhu, X.; Wang, L.; Zhang, S.; Cui, J. Biodiversity of the microbiota in *Spodoptera exigua* (Lepidoptera: Noctuidae).*Journal of Applied Microbiology*. 2019,126,1199–1208
- Gao,X.;Li, W.; Luo, J.; Zhang, L.; Ji, J.; Zhu, X.; Wang, L.; Zhang, S. Biodiversity of the microbiota in Spodoptera exigua (Lepidoptera: Noctuidae). Appl. Microbiol. 2019,126,1199–1208.
- Genta,F.A.; Dillon, R.J.; Terra, W.R.; Ferreira, C. Potential role for gut microbiota in cell wall digestion and glucoside detoxification in *Tenebrio molitor* larvae.*Insect Physiol*. 2006,52,593–601.
- Giron, D.; Frago, E.; Glevarec, G.; Pieterse, C. M.; Dicke, M. Cytokinins as key regulators in plant–microbe–insect interactions: connecting plant growth and defence.*Funct. Ecol.* 2013,27, 599–609.
- Glazebrook, J. Contrasting mechanisms of defense against biotrophic and necrotrophic pathogens.*Annu. Rev. Phytopathol*. 2005,43, 205–227
- Pickard, J. M.; Zeng, M. Y.; Caruso, R.; Núñez, G. Gut microbiota: role in pathogen colonization, immune responses, and inflammatory disease. *Immunol. Rev*.2017, 279, 70–89.
- Piel, J. A polyketide synthase-peptide synthetase gene cluster from an uncultured bacterial symbiont of Paederus beetles. *Proc. Natl. Acad. Sci. U. S. A*. 2002,99, 14002–14007.
- Piel, J.; Höfer, I.; Hui, D. Evidence for a symbiosis island involved in horizontal acquisition of pederin biosynthetic capabilities by the bacterial symbiont of Paederus fuscipes beetles. *J. Bacteriol*. 2004,186, 1280–1286.
- Pigott, C.R.; Ellar, D.J. Role of receptors in Bacillus thuringiensis crystal toxin activity. *Microbiol. Mol. Biol.* Rev. 2007, 71, 255–281.
- Pola, S.; Kesharwani, A. K.; Singh, J.; Singh, D.; Kalia, V. K. Endophytic
- Prem Anand, A. A.; Vennison, S.J.; Sankar, S.G.; Gilwax Prabhu, D.I.; Vasan, P.T.; Raghuraman, T.; Jerome Geoffrey, C.; Vendan, S.E. Isolation and characterization of bacteria from the gut of *Bombyx mori* that degrade cellulose, xylan, pectin and starch and their impact on digestion. *Insect Sci*. 2010,10,107.
- Siddiqui, J. A.; Khan, M. M.; Bamisile, B. S.; Hafeez, M.; Qasim, M.;Rasheed, M. T.Role of insect gut microbiota in pesticide degradation.*Front. Microbiol*. 2022,13,870462.
- Simpson, S.J.; Clissold, F.J.; Lihoreau, M.; Ponton, F.; Wilder, S.M.; Raubenheimer, D. Recent advances in the integrative nutrition of arthropods. Annu. Rev. *Entomol*. 2015,60,293–311.
- Sloan, D.B.; Moran, N.A. Genome reduction and co-evolution between the primary and secondary bacterial symbionts of psyllids.*Mol. Biol. Evol*.2012,29,3781–3792.
- Stephen, F.M.; Berisford, C.W.; Dahlsten, D.L.; Fenn, P.; Moser, J.C. Invertebrate and microbial associates. *In Beetle-Pathogen Interactions in Conifer Forests;* Schowalter, T.D., Filip, G.R., Eds.; Academic Press: San Diego, CA, USA, 1993; pp. 129–153.