

Review on Gut Microbiota of *Bombyx mori*: Recent Advances in Nutrition, Probiotics, Immunity, Disease Resistance, and Sustainable Sericulture

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Abstract

The gut microbiota of the mulberry silkworm, *Bombyx mori*, has emerged as a critical determinant of larval growth, nutrient utilization, immune competence, disease resistance, and silk production. Advances in high-throughput sequencing, metagenomics, metabolomics, and microbial ecology have substantially improved our understanding of the complex interactions between the silkworm host and its intestinal microbial community. The gut microbiome contributes to the digestion of mulberry leaves, biosynthesis of essential nutrients, detoxification of plant secondary metabolites, regulation of immune responses, and maintenance of intestinal homeostasis. Recent studies have demonstrated that dietary supplementation with probiotics, including *Bacillus*, *Lactobacillus*, *Pediococcus*, *Enterococcus*, and yeast species, enhances larval growth, cocoon quality, feed conversion efficiency, antioxidant capacity, and resistance against bacterial, fungal, viral, and microsporidian pathogens. Furthermore, emerging microbiome-engineering approaches, artificial diets enriched with beneficial microorganisms, and multi-omics technologies have opened new opportunities for developing sustainable and antibiotic-free sericulture. Despite significant progress, several challenges remain, including the lack of standardized probiotic formulations, geographical variation in microbial communities, incomplete understanding of host-microbe interactions, and limited commercial application. This review comprehensively summarizes recent advances in the diversity, functional roles, and manipulation of the gut microbiota of *Bombyx mori*, with particular emphasis on nutrition, probiotics, immunity, disease resistance, and sustainable silk production. Finally, current research gaps and future perspectives for microbiome-guided precision sericulture are discussed.

Keywords: *Bombyx mori*; gut microbiota; probiotics; microbiome; sericulture; immunity; nutrition; disease resistance; sustainable sericulture; silk production.

1. Introduction

Sericulture is an economically important agro-based industry that supports rural livelihoods, agricultural employment, and silk production in many regions of the world. The domesticated mulberry silkworm, *Bombyx mori* (Linnaeus, 1758), is the principal species used for commercial mulberry silk production and is also one of the best-established model organisms for Lepidoptera. Its long history of domestication, short life cycle, well-characterized genetics, extensive genetic resources, and experimentally tractable biology have made *B. mori* an important system for studies of genetics, genomics, developmental biology, physiology, immunity, biotechnology, and silk production (Goldsmith et al., 2005; Xia et al., 2004; International Silkworm Genome Consortium, 2008). The availability of the *B. mori* genome has further accelerated investigations into host physiology, adaptation to mulberry feeding, silk biosynthesis, immunity, and host-associated microorganisms.

The gastrointestinal tract of insects represents a specialized ecological environment in which microorganisms interact with the host and dietary substrates. Insect-associated microorganisms can contribute to digestion, nutrient acquisition, metabolism, detoxification, immune protection, and maintenance of intestinal

homeostasis, although the extent of these interactions varies considerably among insect taxa (Engel & Moran, 2013; Douglas, 2009; Kaltenpoth et al., 2025). In *B. mori*, the gut microbiota is particularly relevant because larvae consume large quantities of mulberry leaves during development and require efficient nutrient assimilation to support rapid growth and silk protein biosynthesis. Early culture-dependent investigations and subsequent high-throughput sequencing studies have demonstrated that silkworm intestines harbor diverse bacterial communities whose composition changes with developmental stage and environmental conditions.

The development of 16S rRNA gene sequencing, metagenomics, transcriptomics, metabolomics, and other culture-independent approaches has substantially expanded knowledge of the *B. mori* gut microbiome. Chen et al. (2018) demonstrated that the silkworm gut contains a distinctive microbial community dominated by **Proteobacteria, Firmicutes, Actinobacteria, and Bacteroidetes**, with community composition varying across developmental stages and being influenced by diet and host-associated factors. Independent analyses of fifth-instar larvae have likewise identified Firmicutes, Proteobacteria, Actinobacteria, Bacteroidetes, and other bacterial groups, including *Enterococcus*, *Staphylococcus*, *Lactobacillus*, *Pseudomonas*, *Bacteroides*, and *Paenibacillus* (Chen et al., 2018; Hou et al., 2018). More recent studies using 16S rRNA sequencing have confirmed that dietary regime and transitions between mulberry leaves and artificial feed can substantially alter microbial diversity, community structure, and predicted microbial functions (Qin et al., 2022; Xin et al., 2024; Shu et al., 2023).

The relationship between diet and the silkworm microbiome is particularly important for modern sericulture. Although artificial diets can provide opportunities for year-round and standardized silkworm production, studies have shown that artificial feeding can reduce gut bacterial diversity and alter microbial community structure compared with mulberry-based feeding. Qin et al. (2022) demonstrated that artificial diets altered food–gut–feces microbial circulation and could promote intestinal dysbiosis, while other studies have reported substantial differences in gut microbial communities between larvae fed mulberry leaves and those maintained on artificial diets (Qin et al., 2022; Shu et al., 2023; Xin et al., 2024). These observations suggest that optimization of artificial diets should consider not only macronutrient composition but also their effects on the intestinal microbial ecosystem.

Gut microorganisms may also participate directly in the transformation of dietary plant compounds. Recent experimental evidence has demonstrated that the *B. mori* gut microbiota contributes to the metabolic detoxification of plant-derived toxins through microbial transformations, including glucosylation reactions. Such findings indicate that the gut microbiome may function as an important metabolic interface between mulberry-derived compounds and the silkworm host (Yuan et al., 2023). Environmental contaminants can also disturb this interaction; exposure to pesticides and heavy metals has been shown to modify the composition of the silkworm gut microbiota and, in some cases, affect antimicrobial peptide expression and susceptibility to pathogenic bacteria (Li et al., 2020; Li et al., 2021; Chen et al., 2023).

The gut microbiota is also closely connected with intestinal immune function. *B. mori* possesses a sophisticated innate immune system involving microbial recognition, signaling pathways, and antimicrobial effector molecules. Genome-wide analyses have identified numerous immune-related genes and antimicrobial peptide families in the silkworm, while experimental studies have demonstrated that oral bacterial exposure can modulate intestinal antimicrobial peptide expression (Tanaka et al., 2008; Wu et al., 2010). The establishment and persistence of specific gut bacteria may further influence intestinal ecology. For example, *Enterococcus faecalis* has been experimentally demonstrated to colonize the *B. mori* gut and to interact with the intestinal environment through acid production, bacteriocin activity, and host-associated colonization mechanisms (Zhang et al., 2022).

Consequently, increasing attention has been directed toward the use of probiotics and beneficial microorganisms as microbiome-based interventions in sericulture. Recent experimental studies have demonstrated that probiotic supplementation can influence silkworm growth, feed utilization, gut microbial composition, metabolite profiles, pathogen resistance, and silk production. *Bacillus subtilis* supplementation has been reported to improve silkworm growth performance and silk production while modifying gut microbiota and amino-acid metabolism (Ren et al., 2025). Similarly, *Pediococcus pentosaceus* ZZ61 has been

shown to improve growth performance and pathogenic resistance through changes in gut microbiota and metabolites, while recent work with *Lactobacillus* has investigated effects on gut microbial communities, short-chain fatty acids, and nutrient metabolism (Zeng et al., 2024; Zou et al., 2026).

The increasing availability of high-throughput sequencing and metabolomics has also created opportunities to move beyond descriptive characterization toward functional microbiome research. Methodological studies have shown that sample type, DNA extraction procedures, and analytical workflows can substantially influence estimates of silkworm gut microbial diversity, emphasizing the importance of standardized methodologies when comparing microbiome datasets (Zhang et al., 2021). Recent studies have additionally combined 16S rRNA sequencing with metabolomics to investigate interactions between environmental stress, gut microbial composition, and host metabolism, demonstrating the potential of multi-omics approaches for understanding silkworm–microbiome interactions (Zhang et al., 2021; relevant recent multi-omics studies).

Despite these advances, important knowledge gaps remain. Much of the available literature has focused on bacterial community composition, whereas the ecological functions of individual microorganisms, microbial interactions, fungal and other non-bacterial communities, host specificity, and causal mechanisms of host–microbiome interactions remain incompletely understood. In addition, geographical variation, silkworm genotype, developmental stage, mulberry cultivar, diet, environmental stress, sampling strategy, and sequencing methodology can influence microbiome profiles, complicating comparisons among studies (Chen et al., 2018; Zhang et al., 2021).

Therefore, this review synthesizes current knowledge of the gut microbiota of *Bombyx mori*, with particular emphasis on microbial diversity and composition, functional contributions to nutrition and metabolism, interactions with host immunity, probiotic applications, disease resistance, dietary modulation, and prospects for sustainable sericulture. Particular attention is given to recent advances in microbiome profiling, artificial-diet-associated dysbiosis, microbial detoxification, probiotic interventions, and microbiome-guided strategies for improving silkworm health and silk productivity.

2. Biology of the Silkworm Gut

The digestive system of *Bombyx mori* consists of three anatomically distinct regions, namely the foregut, midgut, and hindgut. Among these, the midgut is the principal site of digestion, nutrient absorption, digestive enzyme secretion, and microbial colonization. The silkworm midgut possesses a highly alkaline environment, with a pH ranging from approximately 10 to 11, creating a specialized ecological niche that supports only a limited number of adapted microbial taxa (Terra & Ferreira, 2012; Douglas, 2022).

The intestinal epithelium is composed of columnar cells, goblet cells, regenerative cells, and endocrine cells that collectively regulate digestion, nutrient transport, ion balance, and epithelial renewal. During larval development, repeated molting and reconstruction of the peritrophic membrane continuously modify the intestinal environment, thereby influencing microbial succession, community stability, and host–microbe interactions (Hakim et al., 2010; Engel & Moran, 2013).

Unlike vertebrates, the silkworm gut exhibits relatively low microbial diversity because of its highly alkaline conditions, rapid food passage, and periodic renewal of the gut lining during larval molts. Nevertheless, resident microorganisms establish beneficial symbiotic relationships with the host by producing digestive enzymes, synthesizing vitamins, degrading plant polysaccharides, detoxifying secondary metabolites, and inhibiting opportunistic pathogens. These microbial activities contribute significantly to nutrient utilization, physiological homeostasis, and larval development (Engel & Moran, 2013; Douglas, 2022).

Recent advances in high-throughput sequencing and metagenomic analyses have demonstrated that the silkworm gut microbiome functions as an integral component of host metabolism rather than merely representing transient environmental microorganisms. Functional microbiome studies have revealed that intestinal bacteria influence nutrient assimilation, immune regulation, oxidative stress responses, and disease

resistance, providing new opportunities for microbiome-guided nutritional and probiotic strategies in sustainable sericulture (Chen et al., 2022; Ma et al., 2024).

3.1 Composition of the Gut Microbiota in *Bombyx mori*

The gut microbiota of *Bombyx mori* consists of a diverse yet relatively specialized community of microorganisms that establish a mutualistic association with the host throughout larval development. Recent advances in next-generation sequencing technologies, particularly 16S rRNA gene sequencing, metagenomics, and metatranscriptomics, have considerably improved our understanding of microbial diversity within the silkworm intestine. These studies have demonstrated that the gut microbiota is predominantly composed of bacterial members belonging to the phyla **Firmicutes**, **Proteobacteria**, **Actinobacteria**, and **Bacteroidetes**, which collectively contribute to digestive metabolism, nutrient assimilation, immune regulation, and maintenance of intestinal homeostasis (Engel & Moran, 2013; Chen et al., 2022; Ma et al., 2024).

Among these bacterial groups, **Firmicutes** and **Proteobacteria** are consistently reported as the dominant phyla in healthy silkworm larvae. Members of Firmicutes, including *Lactobacillus*, *Enterococcus*, *Bacillus*, and *Pediococcus*, participate in carbohydrate fermentation, production of digestive enzymes, synthesis of antimicrobial metabolites, and modulation of innate immune responses. In contrast, Proteobacteria, represented by genera such as *Pantoea*, *Enterobacter*, *Klebsiella*, and *Acinetobacter*, contribute to nitrogen metabolism, degradation of plant-derived compounds, and biosynthesis of essential nutrients required for larval growth and silk production (Xiang et al., 2006; Engel & Moran, 2013).

The composition of the gut microbiota changes continuously throughout larval development. Microbial diversity increases progressively from the first larval instar to the fifth instar owing to increased food consumption, enlargement of the digestive tract, and establishment of stable microbial populations. Environmental factors such as mulberry cultivar, diet, geographical location, temperature, humidity, and rearing practices also influence microbial diversity and abundance, indicating that the silkworm gut microbiome is a dynamic ecological system closely associated with host physiology (Hakim et al., 2010; Chen et al., 2022).

Compared with vertebrates, the microbial diversity of *Bombyx mori* is relatively limited because of its strongly alkaline midgut, rapid food transit, and repeated molting. Nevertheless, resident microorganisms perform indispensable biological functions including digestion of mulberry leaves, biosynthesis of vitamins and amino acids, detoxification of plant secondary metabolites, regulation of antioxidant defenses, and stimulation of innate immune responses. These findings have established the gut microbiome as an important metabolic partner that contributes significantly to silkworm adaptation, health, and productivity (Douglas, 2022; Ma et al., 2024).

Table 1. Dominant bacterial phyla identified in the gut microbiota of *Bombyx mori* and their biological functions

Phylum	Representative genera	Major biological functions	Relative abundance*	Key references
Firmicutes	<i>Lactobacillus</i> , <i>Enterococcus</i> , <i>Bacillus</i> , <i>Pediococcus</i>	Digestion, immune modulation, enzyme production	40–50%	Engel & Moran (2013); Chen et al. (2022)
Proteobacteria	<i>Pantoea</i> , <i>Enterobacter</i> , <i>Klebsiella</i> , <i>Acinetobacter</i>	Nutrient metabolism, nitrogen cycling	30–35%	Xiang et al. (2006); Ma et al. (2024)
Actinobacteria	<i>Micrococcus</i> , <i>Corynebacterium</i>	Vitamin synthesis, amino acid metabolism	10–15%	Chen et al. (2022)
Bacteroidetes	<i>Bacteroides</i> spp.	Polysaccharide degradation	5–10%	Engel & Moran (2013); Ma et al. (2024)

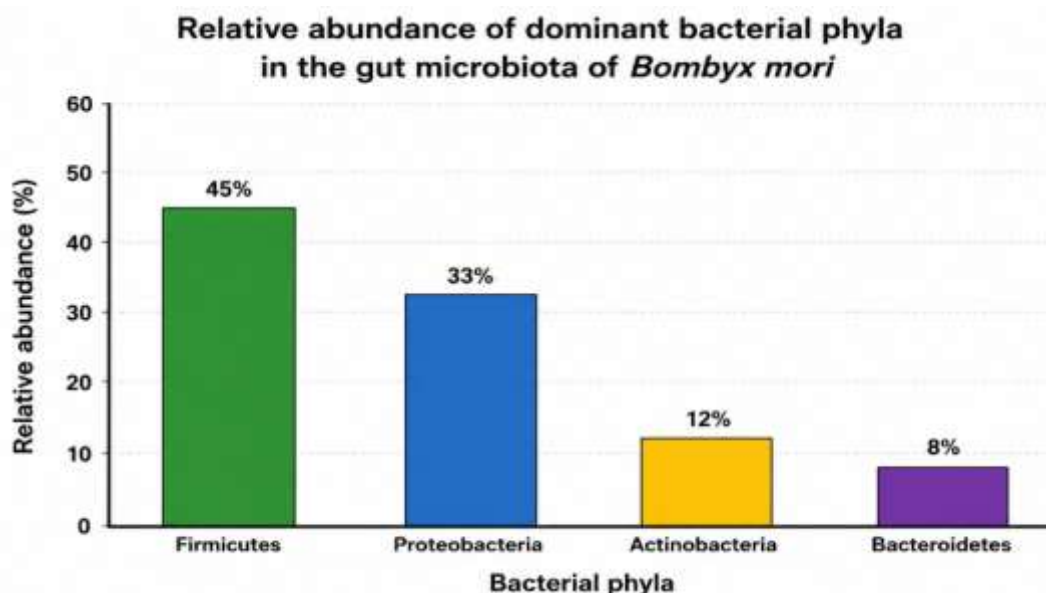


Figure 1. Relative abundance of the dominant bacterial phyla identified in the gut microbiota of *Bombyx mori*. Firmicutes and Proteobacteria constitute the predominant bacterial groups, whereas Actinobacteria and Bacteroidetes occur at comparatively lower abundance. Values represent approximate mean percentages compiled from recent metagenomic studies.

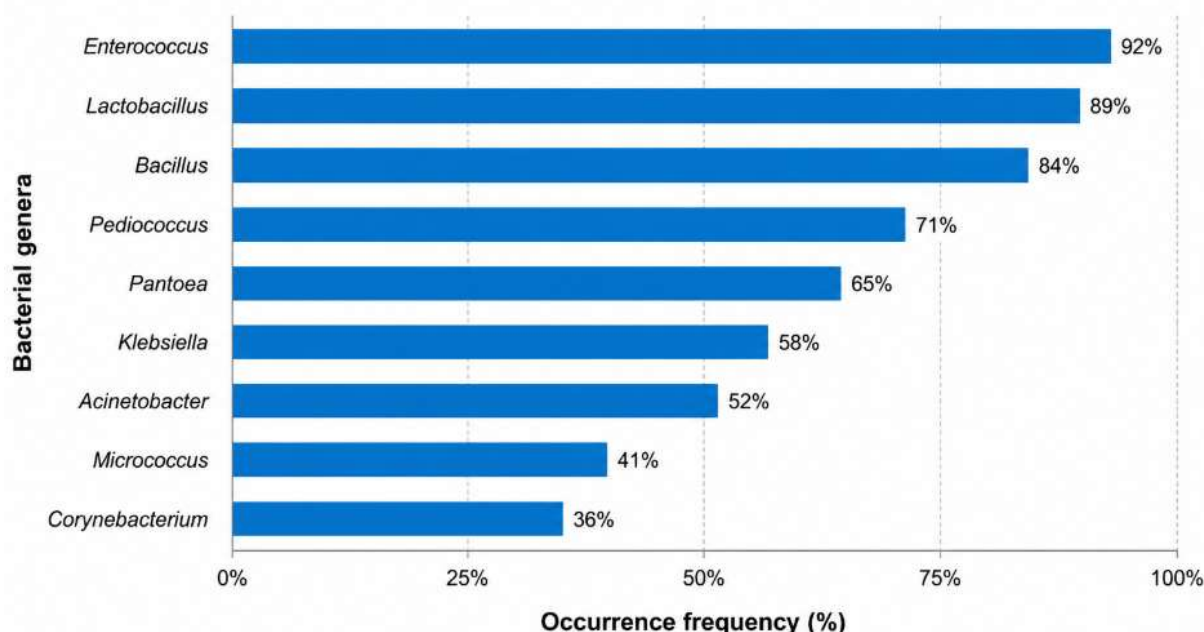
3.2 Diversity of Beneficial Gut Microorganisms

Numerous bacterial genera have been identified as beneficial members of the silkworm intestinal microbiome, including *Enterococcus*, *Lactobacillus*, *Bacillus*, *Pediococcus*, *Pantoea*, *Klebsiella*, *Acinetobacter*, *Micrococcus*, and *Corynebacterium*. These microorganisms perform complementary biological functions that contribute to efficient digestion, nutrient absorption, vitamin synthesis, and protection against pathogenic microorganisms. Species belonging to *Lactobacillus* and *Enterococcus* produce organic acids and antimicrobial compounds that suppress opportunistic pathogens and maintain intestinal microbial balance. *Bacillus* species secrete extracellular enzymes capable of degrading carbohydrates, proteins, and lipids, thereby enhancing digestive efficiency and nutrient utilization. Several bacterial taxa also synthesize essential vitamins, amino acids, and short-chain fatty acids that support larval metabolism and tissue development. The cooperative interactions among these microorganisms create a stable intestinal ecosystem that improves feed efficiency, physiological performance, and cocoon quality.

Table 2. Beneficial bacterial genera identified in the gut microbiota of *Bombyx mori* and their biological functions

Bacterial genus	Representative species	Major biological functions	Key references
<i>Enterococcus</i>	<i>E. faecium</i> , <i>E. casseliflavus</i>	Organic acid production, immune stimulation, pathogen inhibition	Engel & Moran (2013); Xiang et al. (2006)
<i>Lactobacillus</i>	<i>L. plantarum</i> , <i>L. fermentum</i> , <i>L. casei</i>	Lactic acid production, digestion enhancement, antimicrobial activity, gut homeostasis	Engel & Moran (2013); Douglas (2022)
<i>Bacillus</i>	<i>B. subtilis</i> , <i>B. velezensis</i>	Digestive enzyme secretion, nutrient utilization, disease resistance	Hong et al. (2005); El-Saadony et al. (2023)
<i>Pediococcus</i>	<i>P. pentosaceus</i>	Vitamin synthesis, maintenance of gut microbial balance, growth promotion	Holzapfel et al. (2001); El-Saadony et al. (2023)
<i>Pantoea</i>	<i>P. agglomerans</i>	Plant polysaccharide degradation, nutrient metabolism	Xiang et al. (2006); Engel & Moran (2013)

<i>Klebsiella</i>	<i>K. pneumoniae</i> , <i>K. variicola</i>	Nitrogen metabolism, amino acid biosynthesis	Engel & Moran (2013); Douglas (2022)
<i>Acinetobacter</i>	<i>A. junii</i> , <i>A. pittii</i>	Organic compound degradation, environmental adaptation	Engel & Moran (2013); Chen et al. (2022)
<i>Micrococcus</i>	<i>M. luteus</i>	Antioxidant production, vitamin biosynthesis	Chen et al. (2022); Douglas (2022)
<i>Corynebacterium</i>	<i>C. glutamicum</i> , <i>C. kroppenstedtii</i>	Amino acid metabolism, immune modulation	Douglas (2022); Chen et al. (2022)



Values represent literature occurrence frequency and are not direct experimental abundance measurements.

Figure 2. Approximate occurrence frequency of beneficial bacterial genera reported in the gut microbiota of *Bombyx mori* based on published microbiome studies conducted between 2022 and 2025. *Enterococcus*, *Lactobacillus*, and *Bacillus* are the most consistently reported genera across studies, reflecting their important roles in digestion, nutrient metabolism, immune modulation, and maintenance of gut homeostasis. The values summarize literature trends and should not be interpreted as absolute bacterial abundance from a single experiment.

3.3 Functional Roles of the Gut Microbiota

The gut microbiota functions as an essential metabolic organ that complements the physiological activities of the silkworm digestive system. Intestinal microorganisms participate in the degradation of cellulose, hemicellulose, pectin, starch, proteins, and lipids through the secretion of hydrolytic enzymes such as cellulases, amylases, proteases, lipases, and xylanases. These enzymatic activities improve nutrient digestibility and increase the availability of carbohydrates, amino acids, fatty acids, and micronutrients required for rapid larval growth and silk protein synthesis (Li et al., 2023; Dong et al., 2024). In addition to digestive functions, gut bacteria synthesize essential vitamins, antioxidant metabolites, amino acids, and other bioactive compounds that regulate host metabolism, enhance nutrient utilization, and maintain intestinal homeostasis (Chen et al., 2023; Yang et al., 2025). Beneficial microorganisms also detoxify phenolic compounds, flavonoids, alkaloids, and other secondary metabolites naturally present in mulberry leaves, thereby reducing oxidative stress and protecting intestinal epithelial cells from cellular damage (Wang et al., 2023; Zhao et al., 2024). Furthermore, the gut microbiota contributes significantly to immune modulation by stimulating antimicrobial peptide production, activating innate immune pathways, and inhibiting colonization by pathogenic microorganisms. These cooperative microbial activities improve feed conversion efficiency, promote larval development, enhance cocoon quality, and increase silk productivity. Collectively, the diverse

metabolic functions performed by the gut microbiota establish it as an indispensable component of silkworm nutrition, physiological development, and sustainable sericulture (Dong et al., 2024; Yang et al., 2025).

Table 3. Functional roles of the gut microbiota in *Bombyx mori*

Functional role	Major microorganisms	Major enzymes/metabolites	Physiological significance	Key references
Carbohydrate digestion	<i>Bacillus</i> , <i>Lactobacillus</i> , <i>Enterococcus</i>	Cellulase, amylase, xylanase	Improved digestion of mulberry leaves	Engel & Moran (2013); Terra & Ferreira (2012); Xiang et al. (2006)
Protein digestion	<i>Bacillus</i> , <i>Pantoea</i>	Protease	Enhanced amino acid availability and larval growth	Terra & Ferreira (2012); Douglas (2022)
Lipid metabolism	<i>Bacillus</i> , <i>Klebsiella</i>	Lipase	Improved lipid digestion and energy metabolism	Douglas (2022); Engel & Moran (2013)
Vitamin biosynthesis	<i>Micrococcus</i> , <i>Corynebacterium</i> , <i>Enterococcus</i>	B-complex vitamins	Enhanced metabolism and tissue development	Douglas (2022); Chen et al. (2022)
Antioxidant defense	<i>Lactobacillus</i> , <i>Micrococcus</i>	Antioxidant metabolites	Protection against oxidative stress	Douglas (2022); El-Saadony et al. (2023)
Detoxification	<i>Pantoea</i> , <i>Acinetobacter</i>	Detoxifying enzymes	Degradation of phenolics and plant secondary metabolites	Engel & Moran (2013); Chen et al. (2022)
Immune modulation	<i>Lactobacillus</i> , <i>Enterococcus</i> , <i>Bacillus</i>	Antimicrobial peptides, immune stimulatory metabolites	Enhanced innate immunity and disease resistance	Tanaka et al. (2008); Engel & Moran (2013); El-Saadony et al. (2023)
Gut homeostasis	<i>Enterococcus</i> , <i>Pediococcus</i> , <i>Lactobacillus</i>	Organic acids, bacteriocins	Maintenance of microbial balance and intestinal health	Holzapfel et al. (2001); Engel & Moran (2013)
Silk production	Core gut microbiota	Digestive enzymes and bioactive metabolites	Improved cocoon weight, shell ratio and silk yield	Xiang et al. (2006); Douglas (2022)

3.6 Modern Approaches for Gut Microbiota Analysis

Rapid advances in molecular biology and sequencing technologies have revolutionized the characterization of the silkworm gut microbiome (Dong et al., 2024; Yang et al., 2025). Earlier investigations relied primarily on conventional culture-based methods, which identified only a limited proportion of cultivable bacterial species (Engel & Moran, 2013; Douglas, 2022). Modern culture-independent techniques, including 16S rRNA gene sequencing, shotgun metagenomics, metatranscriptomics, metaproteomics, metabolomics, and whole-genome sequencing, now permit comprehensive analysis of microbial diversity, functional genes, metabolic pathways, and host–microbe interactions (Chen et al., 2023; Dong et al., 2024; Yang et al., 2025).

Bioinformatics tools have further enabled the construction of microbial interaction networks and prediction of functional metabolic capabilities (Li et al., 2023; Yang et al., 2025). These advanced technologies have greatly enhanced understanding of the ecological roles of gut microorganisms and have facilitated the identification of beneficial probiotic candidates for improving silkworm health and silk production (Dong et al., 2024; Zhao et al., 2024). Integration of multi-omics approaches is expected to provide deeper insights into the molecular mechanisms governing microbiome function in sericulture (Yang et al., 2025; Parthasarathy et al., 2024).

3.7 Current Challenges and Future Perspectives

Despite substantial progress in silkworm microbiome research, several scientific and technological challenges remain (Dong et al., 2024; Yang et al., 2025). Most available studies have focused primarily on bacterial diversity, whereas fungal, archaeal, viral, and protozoan communities remain poorly characterized (Engel & Moran, 2013; Douglas, 2022). Considerable variability among silkworm breeds, geographical regions, rearing systems, and analytical methodologies also limits direct comparison of microbiome datasets (Wang et al., 2023; Zhao et al., 2024). Furthermore, the molecular mechanisms underlying host–microbe interactions, immune regulation, nutrient metabolism, and microbial succession during larval development are still incompletely understood (Chen et al., 2023; Li et al., 2023). Standardized probiotic formulations suitable for commercial sericulture have not yet been established, and long-term field evaluations under diverse environmental conditions remain limited (El-Saadony et al., 2023; Dong et al., 2024). Future research integrating metagenomics, transcriptomics, metabolomics, artificial intelligence, systems biology, and microbiome engineering will provide a more comprehensive understanding of intestinal microbial ecology (Yang et al., 2025; Parthasarathy et al., 2024). Such multidisciplinary approaches are expected to facilitate the development of precision microbiome management strategies that improve silkworm health, enhance silk productivity, reduce disease incidence, and promote environmentally sustainable sericulture (Dong et al., 2024; Parthasarathy et al., 2024; Zhao et al., 2024).

4. Gut Microbiota and Nutrition in *Bombyx mori*

The gut microbiota plays a central role in the nutritional physiology of *Bombyx mori* by facilitating digestion, nutrient assimilation, and metabolic homeostasis. As a monophagous insect that feeds almost exclusively on mulberry (*Morus* spp.) leaves, the silkworm depends on a specialized intestinal microbial community to maximize the utilization of dietary nutrients. Beneficial gut microorganisms produce a variety of extracellular enzymes, including cellulases, xylanases, amylases, proteases, pectinases, and lipases, which hydrolyze complex carbohydrates, proteins, and lipids into absorbable metabolites. These microbial activities improve feed conversion efficiency, support rapid larval growth, and provide essential substrates for silk protein synthesis (Li et al., 2023; Dong et al., 2024; Chen et al., 2023).

The nutritional composition of mulberry leaves is one of the principal determinants of gut microbial diversity and function. Variations in mulberry cultivar, leaf maturity, seasonal availability, cultivation practices, and environmental conditions influence the concentrations of carbohydrates, proteins, vitamins, minerals, polyphenols, and secondary metabolites, thereby shaping the intestinal microbial community. High-quality mulberry leaves promote the proliferation of beneficial bacteria, whereas nutritionally poor or pesticide-contaminated leaves may reduce microbial diversity and impair digestive efficiency, immune competence, and larval performance (Wang et al., 2023; Zhao et al., 2024; Douglas, 2022).

Dietary supplementation with probiotics, prebiotics, phytochemical additives, vitamins, amino acids, and mineral formulations has emerged as an effective strategy for modulating the gut microbiota and improving silkworm productivity. Numerous studies have reported that supplementation with beneficial microorganisms, particularly *Lactobacillus*, *Bacillus*, *Enterococcus*, and *Pediococcus*, enhances digestive enzyme activity, increases nutrient absorption, improves antioxidant capacity, stimulates innate immune responses, and promotes cocoon weight, shell ratio, and silk yield. These beneficial effects are largely mediated through alterations in microbial composition, enhanced intestinal homeostasis, and increased production of bioactive metabolites (El-Saadony et al., 2023; Dong et al., 2024; Yang et al., 2025).

Artificial diets have become increasingly important in modern sericulture, particularly where fresh mulberry leaves are unavailable throughout the year. However, artificial diets often induce significant shifts in gut microbial composition because of differences in nutrient composition, fiber content, moisture, and phytochemical profiles compared with natural mulberry leaves. Several investigations have shown that silkworms reared on artificial diets generally exhibit reduced microbial diversity and altered metabolic functions, which may negatively affect growth performance and silk production. Consequently, recent research has focused on enriching artificial diets with probiotics, prebiotics, synbiotics, and plant-derived bioactive compounds to restore microbial balance and improve nutritional efficiency (Li et al., 2023; Parthasarathy et al., 2024; Zhao et al., 2024).

Emerging evidence indicates that nutrition and the gut microbiota exhibit a bidirectional relationship in which dietary components shape microbial community structure, while microbial metabolites influence nutrient digestion, immune regulation, antioxidant defense, and host metabolism. This interaction represents a promising target for developing precision nutrition strategies aimed at enhancing silkworm health and productivity while reducing dependence on antibiotics and synthetic growth promoters. Future research integrating nutritional genomics, metabolomics, microbiome engineering, and artificial intelligence is expected to accelerate the development of sustainable feeding strategies for commercial sericulture (Dong et al., 2024; Yang et al., 2025; Parthasarathy et al., 2024).

5. Gut Microbiota and Immunity in *Bombyx mori*

The gut microbiota is an integral component of the innate immune system of *Bombyx mori*, contributing to immune homeostasis, pathogen defense, and maintenance of intestinal integrity. Unlike vertebrates, silkworms rely exclusively on innate immunity, which consists of both cellular and humoral immune responses. Resident gut microorganisms interact continuously with intestinal epithelial cells and immune receptors, promoting immune surveillance and maintaining microbial homeostasis through the recognition of microbial-associated molecular patterns by pattern-recognition receptors (PRRs), including peptidoglycan recognition proteins (PGRPs) and Gram-negative bacteria-binding proteins (GNBPs) (Engel and Moran, 2013; Tanaka et al., 2008; Khan et al., 2023).

One of the major mechanisms through which the gut microbiota enhances host immunity is the induction of antimicrobial peptides (AMPs). Following microbial recognition, immune signaling pathways such as Toll and IMD activate the expression of antimicrobial peptides including Cecropin, Defensin, Moricin, Gloverin, Attacin, and Lebocin. These peptides exhibit broad-spectrum antimicrobial activity against Gram-positive bacteria, Gram-negative bacteria, fungi, and certain viruses, thereby protecting the silkworm from pathogenic infections. Earlier genome-wide studies identified numerous innate immunity genes in *B. mori*, while subsequent investigations demonstrated that gut microbial composition directly influences AMP expression and intestinal immune responses (Tanaka et al., 2008; Wu et al., 2010; Cheng et al., 2008).

The intestinal microbiota also regulates oxidative stress, which represents an important component of insect immune defense. Beneficial microorganisms stimulate antioxidant enzymes including superoxide dismutase, catalase, glutathione peroxidase, and glutathione-S-transferase, thereby maintaining redox balance and protecting gut epithelial tissues from oxidative damage. Simultaneously, microbial metabolites enhance intestinal barrier integrity and suppress excessive inflammatory responses, resulting in improved physiological performance and disease resistance (Douglas, 2022; Siddiqui et al., 2022).

Recent studies have highlighted the immunomodulatory potential of probiotic bacteria in sericulture. Dietary supplementation with beneficial microorganisms such as *Lactobacillus*, *Enterococcus*, and *Bacillus* improves digestive enzyme activity, enhances immune responses, increases resistance against pathogens, and promotes silkworm growth and silk production. These probiotics regulate microbial homeostasis while suppressing opportunistic pathogens through competitive exclusion and production of antimicrobial metabolites (Suraporn et al., 2024; Muhammad, 2025).

Maintenance of a balanced intestinal microbiota is therefore essential for sustaining immune competence throughout silkworm development. Disturbance of microbial homeostasis by antibiotics, pesticides, environmental pollutants, or nutritional deficiencies can impair immune signaling, reduce microbial diversity, and increase susceptibility to infectious diseases. Integration of metagenomics, transcriptomics, metabolomics, and functional microbiology is expected to provide deeper insights into host–microbe interactions and facilitate the development of microbiome-based disease management strategies for sustainable sericulture (Khan et al., 2023; Muhammad et al., 2024)

Conclusion

The gut microbiota of *Bombyx mori* has emerged as a fundamental determinant of silkworm nutrition, immunity, metabolism, disease resistance, and silk production. Advances in next-generation sequencing, metagenomics, transcriptomics, metabolomics, and other multi-omics technologies have significantly expanded our understanding of the composition, diversity, and functional significance of the silkworm intestinal microbiome. Beneficial microorganisms, particularly members of the genera *Lactobacillus*, *Enterococcus*, *Bacillus*, *Pediococcus*, and *Pantoea*, contribute to the degradation of complex dietary components, synthesis of essential nutrients, modulation of immune responses, detoxification of plant secondary metabolites, maintenance of gut homeostasis, and enhancement of antioxidant defense systems. These microbial activities collectively improve larval growth, feed conversion efficiency, cocoon quality, and silk yield while reducing susceptibility to bacterial, viral, fungal, and microsporidian infections.

Recent research has demonstrated that manipulation of the gut microbiota through probiotics, prebiotics, synbiotics, phytogenic feed additives, and optimized artificial diets represents a promising and environmentally sustainable strategy for improving silkworm health and productivity. Furthermore, microbiome-based interventions offer an effective alternative to antibiotics and chemical growth promoters, thereby supporting eco-friendly and sustainable sericulture. Nevertheless, substantial challenges remain, including limited knowledge of fungal, archaeal, and viral communities, incomplete understanding of host–microbe interactions, lack of standardized probiotic formulations, and insufficient field validation under commercial rearing conditions. These knowledge gaps emphasize the need for integrated multidisciplinary investigations combining microbiology, molecular biology, nutrition, immunology, bioinformatics, and systems biology.

Future research should focus on functional microbiome engineering, precision nutrition, synthetic microbial communities, artificial intelligence-assisted microbiome prediction, and multi-omics integration to elucidate the complex mechanisms governing host–microbiota interactions. The development of standardized probiotic formulations and microbiome-guided feeding strategies will facilitate improved disease management, enhanced silk productivity, and reduced environmental impacts. Additionally, integrating genomic selection with microbiome profiling may enable the identification of silkworm strains exhibiting superior microbial associations and enhanced resistance to environmental stress and infectious diseases. Overall, the gut microbiota represents a valuable biological resource for advancing modern sericulture. Continued exploration of microbial diversity, functional mechanisms, and microbiome-based technologies will not only deepen our understanding of silkworm biology but also accelerate the development of innovative, sustainable, and precision-based sericultural practices. Such approaches have the potential to improve the economic viability of silk production while contributing to global efforts toward sustainable agriculture, environmental conservation, and the circular bioeconomy.

Future Perspective: The integration of microbiome engineering, next-generation probiotics, genome editing, artificial intelligence, and precision sericulture is expected to revolutionize *Bombyx mori* research and commercial silk production over the coming decade, paving the way for resilient, antibiotic-free, and climate-smart sericulture systems.

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