



Bacterial Pathogens of Silkworm: Impacts and Management Strategies

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ABSTRACT

Bacterial diseases affecting silkworms are collectively known as flacherie. It is one of the infectious diseases reported to cause huge crop loss upto tune of 27–35% with significant cocoon yield reduction of 11 to 15 kg 100 dfls⁻¹ annually. It is caused by a wide variety of bacteria belonging to different genera viz. *Aeromonas*, *Bacillus*, *Enterobacter*, *Pseudomonas*, *Serratia*, *Streptococcus*, and *Staphylococcus*. The poor quality mulberry leaf with low protein, sucrose or high cellulose makes silkworms comparatively more susceptible to infection by pathogens. Many factors viz., improper rearing house, faulty rearing practises, improper disinfection and hygiene, poor quality of nutrition, host susceptibility, host population density, synergistic association of pathogens and host population density lead to bacterial disease outbreak in the silkworm population. The silkworms appear physiologically weak and flacherie outbreak elicits a heavy toll on sericulture every year. The growth of affected silkworm larvae becomes stunted, flaccid and larvae develop different colours, depending on the species of bacteria involved in causing the infection, become rotten and foul smelling. Microscopic tools help in detection of silkworm pathogens and play a significant role in the management aspects. Many prophylactic measures are adopted to reduce the disease outbreak in silkworms. Antibiotics such as erythromycin, kanamycin, streptomycin, chloramphenicol, Aureomycin, neomycin and tetracycline have been reported to be suppressive against bacterial disease of digestive system. The plant extracts bearing anti-microbial activity can be used to control bacterial diseases in silkworm, *B. mori*.

KEYWORDS: Antibiotics, *Bacillus thuringiensis*, bacterial, disease, flacherie, septicemia toxicosis

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1. INTRODUCTION

Bacterial diseases which affect silkworms are collectively known as flacherie which is a syndrome identified by flaccidity, loose elasticity, softening and rotting of larval body (Karthikairaj et al., 2014; Park et al., 2024). Flacherie is considered as most dreadful disease in India identified often causes dysentery in silkworm (Saad et al., 2019; Satish et al., 2024). It may be caused by synergistic effect of different bacteria with viruses such as nuclear polyhedrosis virus (NPV), cytoplasmic polyhedrosis virus (CPV), infectious flacherie virus (IFV), denonucleosis viruses (DNV) (Aruga, 1971; Chitra et al., 1975). Many causal agents may be responsible for mixed infection to cause flacherie (Halo et al., 2016; Tayal and Chauhan, 2017). During primary infection, the physiological state of the host is altered which often originates secondary infection in the host organism (Suraporn et al., 2025). The primary infection is mostly caused by virus whereas bacteria cause the secondary infection. Flacherie is an infectious disease reported to cause huge crop loss upto tune of 27-35 % with significant cocoon yield reduction of 11 to 15 kg 100 dfls⁻¹ annually (Chakravorty and Pandey, 2005; Selvakumar and Savithri, 2012). Savanurmah et al. (1992) reported the flacherie as the most pre-dominant (47.9%) among the diseases of silkworms of *B. mori*. Flacherie is prevalent to the extent of 22.33% to 43.05% throughout the year (Sivaprasad et al., 1995). Samson et al. (1990) reported bacterial flacherie to be highest (57.2%) followed by cytoplasmic polyhedrosis virus (27.88%), nuclear polyhedrosis virus (5.00%), pebrine (2.32%) and muscardine (0.48%) in a three year detailed survey on incidence of silkworm diseases in sericulture. In a commercial rearing, bacterial flacherie incurred loss of 48.9% (Shashidhar et al., 2018). Under different physiological stress conditions, the bacterial propagation and multiplication encourages the flacherie disease development (Mohanta et al., 2015). However, some adverse environmental conditions viz., high temperature, high humidity, polluted air and starvation (Samson et al., 1981) are the predisposing factors for flacherie disease development and cocoon crop loss (Hossain et al., 2017). Kumari et al. (2001) reported that with the increase in temperature the metabolic activities of 4th and 5th instar silkworms get accelerated while as the dip in optimal temperature slacken the growth of 4th and 5th instar silkworms which proves the sensitivity of silkworms to temperature fluctuations (Chopade and Raghavendra, 2021). Kumari et al. (2001) reported that exposure of high temperature to 5th instar silkworms reduces their survivability. Flacherie incidence in Jammu and Kashmir was studied by chisti et al. (1991) and the result of the study shown that the intensity of infection was 3-8% in worms reared scientifically and 12-35% in worms reared under unhygienic conditions. The disease incidence was

mostly reported in 4th and 5th instars (Manimegalai, 2010). Bhat et al. (2016) reported that disease incidence % was maximum in 5th instar. *Bacillus thuringiensis* is a detrimental bacterium which is considered to be causal organism of flacherie. An extreme level of risk to sericulture is enforced when flacherie is caused by *B. thuringiensis* (Smith, 1999). Even low concentration (0.01%) of bacterial infection in silkworm larvae leads to convulsions and causes more than 50% mortality during 4th instar (Aruga, 1994; Attia et al., 2025). Hence flacherie disease pose a serious challenge to sericulture and it is little bit difficult to manage the disease effectively and eliminate the pathogen load from rearing environment (Park et al., 2024).

2. CAUSAL ORGANISM

A wide range of bacteria belonging to different genera viz., *Aeromona*, *Bacillus*, *Enterobacter*, *Pseudomonas*, *Serratia*, *Streptococcus* and *Staphylococcus* are reported to be the causal organisms of flacherie disease (Parbin et al., 2024). The other causes of flacherie such *Proteus vulgaris*, *Proteus inconstana*, *Proteus morganii*, *Aerobacter aerogenes*, *Micrococcus flavus* and *micrococcus* species were reported by, many authors from time to time. A bacterial species, coccus and spore forming bacterium *Bacillus bombycis* in addition to a number of pathogenic bacteria including *Bacillus cubonianus* were reported to cause flacherie disease in silkworm (Santha et al., 2007). The flacherie is the most vulnerable disease when it is caused by bacterium, *B. thuringiensis*. *B. thuringiensis* is a spore forming gram-positive and soil inhabiting bacterium (Nazar et al., 2020) can be found on surface of leaves, midgut of lepidopteran caterpillars and in aquatic environment (Dashora et al., 2017). Many bacteria viz., *Bacillus* spp., *Bacillus thuringiensis*, *Micrococcus* spp., *Pseudomonas* spp., *Streptococcus bombycis* and *Serratia marcescens* are reported to be associated with flacherie as well which weaken silkworm immunity (Table 1). Therefore, causes significant cocoon crop losses in sericulture (Javaid et al., 2021). *Bacillus megaterium* and *Bacillus ellenbachii* are also reported to be the causal organism of flacherie disease in silkworm (Santha et al., 2007). A chronic type of flacherie known as 'gattine' in French and 'macilenze' in the Italian is caused by *Streptococcus bombysis* which is isolated from the

Table 1: Different types of flacherie and their causal agents

Sl. No.	Flacherie disease	Causal agent	Pathogen shape	reference
1.	Bacteremia	<i>Streptococcus faecium</i>	Spherical	Park et al., 2024
2.	Septicaemia	<i>Serratia marcescens</i>	Rod-shaped	Hanh et al., 2024
3.	Toxicosis	<i>Bacillus-thuringiensis</i>	Rod-shaped	Kumar et al., 2016

intestine (Das, 2008; Santha et al., 2008). 'Khuto' disease (multi-bacterial dysentery) was caused by feeding silkworm with leaves grown in shade and deficient in chlorophyll (Das, 2008). In southern china, the spore forming bacterium was isolated from pupae of silkworm (Liang et al., 2015). *Bacillus mycoides* infected into the body and *Bacillus laterosporus* administered were found pathogenic to silkworm (Nesa et al., 2020). Nakasuji and Kodama (1969) found *Aerobacter cloacae* and *Achromobacter superficialis* to be pathogenic to silkworm. *Streptococcus faecalis*, *Streptococcus faecium*, *Serratia piscatorum*, *Serratia marcescens*, *Proteus vulgaris*, *Proteus inconstans*, *Proteus morgani*, *Aerobacter aerogenes*, *Micrococcus flavus* and *micrococcus* species were some of the other pathogenic bacteria species (Santha et al., 2007). Chitra et al. (1974) isolated seven bacteria species from flacherie infected worms and distinguished bacterial disease broadly into two classes such as those that are restricted to the intestine (*Achromobacter cloacae*, *Archromobacter superficialis*, *Archromobacter delmarvae*, *Pseudomonas boreopolis*, *Pseudomonas ovalis*, *Escherichia freundii*, and *Staphylococcus albus*) and those that enter into the haemolymph (*Aerobacter cloacae*, *Archromobacter delmarvae*, *Achromobacter sepeficialis*) and to both (septicaemia). The flacherie (sappe) disease might be a syndrome where multiplicity of pathogens is involved (Mohanta et al., 2013). Investigations conducted by Vasantharajan and Munirathnamma (1978) indicated the presence of *Serratia marcescens* in Kenchu disease of silkworm could cause a lethal infection when associated with *Staphylococcus* species. It is reported several septic bacteria causing septicaemia in silkworm from cocoons and out of the septic bacteria isolated, *Serratia* was most abundant (Park et al., 2024). Bacteria belonging to different genera were isolated viz., *Bacillus*, *Staphylococcus* and *serratia* from diseased silkworm (Priyadarshini et al., 2008). The first time *Streptococcus faecalis* was reported from diseased silkworm in India (Priyadarshini et al., 2008).

3. PATHOGENICITY OF BACTERIA TO SILKWORM

The pathogenicity of bacteria depends on the mode of infection and the type of bacteria involved in causation of disease. Lysenko (1958) found that different strains of *Streptococcus faecalis* were more pathogenic than *Streptococcus faecium*. The isolates of bacteria such as *Aerobacter cloacae*, *Archromobacter superficialis*, *Achromobacter delmarvae*, *Staphylococcus albus*, *Escherichia freundii*, *Pseudomonas ovalis* and *Pseudomonas boreopolis* when fed to the silkworm caused flacherie with different rates of mortality (Chitra et al., 1973). Chitra et al. (1974) reported that severe bacterial flacherie was observed during moulting periods and when silkworms were ready for spinning which often leads to severe mortality.

Anitha et al. (1994) found that *Serratia* species is less toxic than *Bacillus* and *staphylococcus* and the pathogenicity of *Staphylococcus* comparatively higher than both, *Bacillus* and *serratia* species. The septic bacteria including *Pseudomonas* sp., *Serratia marcescens*, *Proteus* sp., *Streptococcus faecalis*, *Aeromonas* sp., and *Bacillus* sp were found highly pathogenic to silkworm and caused Septicaemia in silkworm. The pathogenicity of *Serratia* showed a high mortality at high humidity and causes death within 18 hours of post infection (Santha et al., 2007). The human pathogenic bacteria were studied with silkworm infection models (Matsumoto and Sekimizu, 2019) viz *Staphylococcus aureus* and *Pseudomonas aeruginosa* (Kaito et al., 2002), *Streptococcus pyogenes* (Kaito et al., 2005), pathogenic *Escherichia coli* (Miyashita et al., 2012), *Listeria monocytogenes* (Castillo et al., 2016), *Serratia marcescens* (Ishii et al., 2012), and *Vibrio cholerae* (Kaito et al., 2002). The injection of extracellular toxins, α -toxin and β -toxin of different *B. thuringiensis*, exotoxin A (*S. aureus*), diphtheria toxin (*P. aeruginosa*) or hemolysin (*B. cereus*) were reported to kill silkworms (Hossain et al., 2006; Usui et al., 2009). The toxins of *Bacillus thuringiensis* acts by producing a protein that blocks the digestive system of larvae and induce vacuolation of midgut cells, swelling and vacuolation in mitochondrial cells and tissues of malpighian tubules in *Bombyx mori* (Zou et al., 2024). The vacuolation and nuclear condensation in other insects due to *B. thuringiensis* was also reported (Pandey et al., 2009; Badr and Darwish, 2024).

4. DIFFERENT GENERA OF BACTERIA AFFECTING SILKWORM

The entomopathogenic bacteria quickly infect and easily multiply in silkworm body and causes reduction in silk production. The various genera of bacteria have been found to infect silkworms include *Bacillaceae*, *Pseudomonadaceae*, *Enterobacteriaceae*, *Streptococcaceae*, *Micrococcaceae*, *Paenibacillaceae*, *S. marcescens* and *S. entomophila*. Some of the bacteria such as *S. marcescens* and *S. entomophila* impair the feeding behavior and growth of lepidoptera insects. They proliferate in gut of insects and secrete large amounts of proteolytic enzymes such as β -hemolysins, elastases, and chitinases. The bacterial diversity of silkworm gut was proved by the presence of *Serratia marcescens*, *Pseudomonas aeruginosa*, and *Bacillus halotolerans* isolated from the diseased larvae (Javaid et al., 2021).

The microbiota in the silkworm gut was investigated by dilution culture method of intestinal juice at different developmental stages and 253 strains of bacteria belonging to 16 genera were isolated (Sun et al., 1996). Lu et al. (1999) studied the intestinal content of the healthy silkworm larvae and adult moths and reported 89 *Enterococcus* species isolates by utilizing numerical taxonomy of bacteria.

Different bacterial populations belonging to different genera viz., *Arthrobacter*, *Lactobacillus*, *Pseudomonas*, *Escherichia*, *Micrococcus*, *Bacillus* and *Staphylococcus* were identified (Yuan et al., 2006). Xiang et al. (2010) reported the presence of many predominant genera viz., *Brevundimonas*, *Stenotrophomonas*, *Enterobacter*, *Aeromonas*, *Brevibacterium*, *Citrobacter*, *Escherichia*, *Klebsiella*, *Pseudomonas*, *Agrobacterium* and *Staphylococcus* in the silkworm gut.

Lu et al. (2003) reported that the distribution of intestinal bacteria changes with respect to the state of health of the silkworm and it was reported that the number of bacterial species of the genus *Enterococci* increases in silkworms which are already infected with *Nosema bombycis* and causes the epidemic disease pebrine in silkworms. The members of the many bacteria such *Proteobacteria* and *Firmicutes* phyla are present in many lepidopteran insects viz., armyworms, mosquitoes and silkworms. The intestinal bacterial microbiota of insects share similar characteristics and there are differences in the composition and diversity of bacterial microbiota in different insects, stated that the diversity of gut bacteria in insects can be affected by environment, habitat, diet and developmental stage. Tian et al., 2007 reported the predominant genera in the bacterial microbiota of silkworm strain (Dongting×Bibo) were *Brevundimonas*, *Stenotrophomonas*, *Enterobacter* and *Staphylococcus*. Xiang et al. (2007) reported *Enterococcus* and *Thermus* as the predominant genera in the C108 and SCN2 strains of silkworm. Sun et al. (2016) reported the presence of predominant genera viz., *Enterococcus*, *Delftia*, *Ralstonia*, *Pelomonas*, *Tepidimonas*, *Aurantimonas*, *Pseudomonas*, *Aspromonas* and *Staphylococcus* in strain Daizo.

5. ISOLATION AND PURIFICATION OF BACTERIA

Pathogenic bacteria causing flacherie in silkworms are isolated from diseased larvae (Selvakumar, 2013). The diseased larvae are disinfected in 2% sodium hypochlorite for 3 to 5 minutes and the bacterial strains are collected from the gut. The gut material is suspended in sterile saline water and spread on agar medium incubating at 37 degree Celsius overnight for bacterial culture (Li et al., 2022). Streak plate method is used to purify the bacterial culture (Liang et al., 2015). The bacterial strains once isolated can be permanently stored in 15% glycerol for future (Javaid et al., 2021). The cadavers showing bacterial infections are surface sterilized with mercuric chloride (0.1%) and washed three times in distilled water. The larvae are titrated in sterile water blanks with glass rod. Using the inoculation needle, a loopful of the suspension is taken and streaked on Nutrient Agar medium and incubated at room temperature (Govinda et al., 1998). After growth of bacterial pathogens in nutrient

agar medium, the isolated pathogens are sub-cultured using streak plate method. The bacterial colonies are purified by streaking on the plate. The isolated single colonies of bacteria are separated by picking and streaked on nutrient agar slants. Once the bacteria attain good growth, the slants are stored in refrigerator at 4°C for further studies (Robert et al., 2002). Anitha et al. (1994) collected infected silkworm of various larval development stages and studied the morphology of bacteria. They reported about 28% of bacteria showed a similar morphology consisting of big gram positive rods with endospores while as 28% consisted of gram-positive cocci morphology, which were seen in clusters while about 34% of cases showed gram-negative tiny rods (Table 2). The biochemical activity and characteristic morphological study identified different bacteria viz., *Bacillus* sp., *Staphylococcus* sp and *Serratia* sp (Table 3 and 4) (Lakshmi and Jamil,

Table 2: Identification of bacteria in diseased silkworms (Aneja, 1996)

Bacteria	Gram's staining	Shape	Motility	spore
<i>Bacillus subtilis</i>	+	rods	+	+
<i>Streptococcus pneumoniae</i>	+	cocci	—	—
<i>Staphylococcus aureus</i>	+	cocci	—	—
<i>Escherichia Coli</i>	—	rods	+	—
<i>Pseudomonas fluorescence</i>	—	rods	+	—
<i>Bacillus cerus</i>	+	rods	+	—
<i>Klbsiella cloacae</i>	—	rods	—	—

‘+’ indicates ‘positive and ‘—’ indicates ‘negative’

2002). Anitha et al. (1994) isolated pathogenic bacterium from 125 samples of faecal materials and dusts have been characterized as *Streptococcus faecalis*. Several strains of *Streptococcus faecalis* and *Streptococcus faecium* based on physiological characters were isolated (Santha et al., 2007). Javaid et al. (2021) isolated some bacterial strains showing close relevance with *Serratia* species, *Bacillus* species and *Pseudomonas* spp. Approximately 83.3% of strains were found resistant to Penicillin, Tetracycline, Amoxicillin, Ampicillin, and Erythromycin. Aneja (1996) identified predominant colonies from four samples by various tests which includes biochemical tests, colony morphology, motility, sugar fermentation and staining properties.

6. MODE OF ACTION

The proliferation of *S. aureus* indicated that the killing effect of bacteria requires bacterial growth in silkworm. The killing effect of *P. aeruginosa* to *C. elegans* has two

Table 3: Biochemical analysis for identification of bacteria (Aneja, 1996)

Bacteria	Catalase	Coagulase	Starch hydrolysis	Lipid hydrolysis	Gelatin hydrolysis
<i>Bacillus subtilis</i>	—	—	—	—	—
<i>Streptococcus pneumoniae</i>	—	—	—	—	—
<i>Staphylococcus aureus</i>	+	+			
<i>Escherichia coli</i>	—	—	—	—	—
<i>Pseudomonas fluorescense</i>	—	—	—	—	+
<i>Bacillus cereus</i>	—	—	—	—	—
<i>Klbsiella cloacae</i>	—	—	—	—	—

‘+’ indicates ‘positive and ‘—’ indicates ‘negative’

Table 4: Characterization of bacteria for carbohydrate metabolism (Aneja, 1996)

Bacteria	Glucose	Lactose	Sucrose	Mannitol
<i>Bacillus subtilis</i>	+	—	+	—
<i>Streptococcus pneumoniae</i>	—	+	—	—
<i>Staphylococcus aureus</i>	+	+	—	+
<i>Escherichia coli</i>	+	+	+	+
<i>Pseudomonas fluorescense</i>	—	—	—	+
<i>Bacillus cereus</i>	+	—	+	+
<i>Klbsiella cloacae</i>	+	+	+	—

‘+’ indicates ‘positive and ‘—’ indicates ‘negative’

different modes of action. One is ‘fast killing’ which is caused by exotoxins secreted into the culture medium and another one ‘slow killing’ which occurs after proliferation of bacteria in the insect bodies (Kaito et al., 2002). The bacterial toxins are stimulated to active form by silkworm gut enzymes. The activated toxin binds to the receptor and subsequently gets inserted into the membrane and causes leakage of ions and small molecules (Chen et al., 2020). The silkworms become weak, the metabolism become inactive which causes imbalance in body functions. As the digestive fluid of silkworm gut weakens, the bacteria devoured together with mulberry leaf multiplies in the digestive tract and takes nutrition from the body of the silkworm which destroys the membranous tissue of the intestine (Yuan et al., 2023). The mortality in the larval stages of *B. mori* is attributable to eight genotypes of *Bacillus thuringiensis* within 3 hours of post inoculation when *B. thuringiensis* endotoxin cause damage to gut lining cause gut paralysis and the larval death in silkworm occurs due to starvation

(Bhowmik, 2014). The beta endotoxin of *Staphylococcus aureus*, *Bacillus cereus* and *Pseudomonas aeruginosa* causes toxidermia and septicemia disease and eventually death of the silkworm larvae.

The bacteria multiply in silkworm while undergoing different developmental stages inside the body. A typical growth curve shows different phases of growth which includes lag phase, exponential phase and stationary phase.

6.1. Lag phase

It is the latent period or equilibrium phase before the bacterial cell division. It is most poorly understood growth phase and controlled by unknown regulatory mechanism. The lag phase has been assumed to allow the adaptations for exploitation of new environmental conditions and the bacterial cells begin accordingly. This phase is not characterized by physiological or biochemical criteria but it is supposed to be the active phase of bacteria (Madigan et al., 2000).

6.2. Exponential phase

This phase represents the processes of cell divisions and the cessation of divisions respectively. Many factors influence the exponential phase which includes nutrient availability, presence or absence of inhibitory factors and environmental conditions (Navarro-Llorens et al., 2010). The exponential bacterial growth physiology and replication involves DNA synthesis, transcription and translation process for synthesis of DNA-RNA-Protein and some necessary biomolecules (Rolfe et al., 2012).

6.3. Stationary phase

At this stage growth cessation occurs but cells remain metabolically active. This phase comes after exponential growth and conditions become unfavorable for growth of bacteria and they stop replication. This phase leads to many physical and molecular changes. The physical changes includes changes in cell structure, they become spherical in shape and smaller in size surrounded with a rigid cell envelope, the cell wall becomes highly cross-linked,

membrane fluidity gets reduced and cells are activated to the stringent response mechanism to survive (Jaishankar and Srivastava, 2017). During this division, the rate of cell division is directly proportional to the rate of cell death. After this comes the death phase of bacteria and cells lose viability.

The contaminated mulberry leaves with bacteria, exuviae of bacterial infected silkworm, excreta of infected silkworms, pest infested mulberry leaf contains bacterial pathogens and get introduced into a healthy population (Mondal et al., 2025). The unhygienic leaves and wet leaves may consist of bacterial pathogens which get inoculated into silkworm. The physiological starvation is caused when silkworms are fed with unhygienic and poor nutritive mulberry leaves due to which silkworms does not produce anti-bacterial factor (Mir et al., 2018; Dai et al., 2025). The bacteria propagating on the unhygienic rearing environment gets ingested with leaf into the silkworm body and causes flacherie outbreak (Dai et al., 2025). The toxins produced by microorganisms viz., *Staphylococcus aureus* and *Pseudomonas aeruginosa*, provide a selective growth advantage to bacteria in silkworm rearing environments. The toxins produced by bacteria aid in combating the immune system of host silkworm and securing nutrients for better growth. *Staphylococcus aureus* produces different types of components which enhance the virulence of bacteria by contributing in different mechanism viz., surface associated adhesions, exoenzymes, capsular polysaccharides and exotoxins (Cheung et al., 2021).

Bacteria infect silkworms through two different ways viz., ingestion or wounding. Ingestion refers to entry of bacteria into the midgut of silkworm through mulberry leaves which are contaminated by it (Miyashita et al., 2015). Infection through wounds is caused when bacteria directly invades the haemocoel through wounds on body surface (Wang et al., 2022). The bacterial species causing disease in silkworm mainly belongs to genus *Bacillus*. Some of the bacillus species causing disease in silkworm are *Bacillus cubonius*, *Bacillus bombysepticus*, *Bacillus mycoides*, and *Bacillus leterosporus*. There is one another possible mode of transmission of bacterial disease in silkworm which refers to transovarial transmission and persistence of latent infection in the silkworm eggs. However, no such mode of bacterial infection transmission has been reported earlier in silkworm. Rai et al. (2013) found a bacterium *B. subtilis* which was isolated from the eggs of silkworms and was found prevalent in progeny eggs laid by infected females. It is probably the first report transovarial transmission of *Bacillus* species in insects which confirms the bacteria inoculated to parents are transmitted to progeny eggs. It indicates the transovarial transmission of bacteria is observed in silkworm, if it survives till the adult stage.

The bacteria invade the silkworm body through mouth or integument and proliferate in the digestive organs of silkworm. Though different pathogens multiply in different parts of the body and the host succumbs to infection in shorter period (Deb et al., 2021). In case of septicaemia, the bacteria penetrate the haemolymph through membranous cells of the alimentary canal of silkworm and propagate into large numbers causing septicaemia disease (Yup-Lian, 1991). Due to damage of midgut membrane, the silkworm starves which makes it wander aimlessly and causes death (Trager, 2012). The cephalothoracic region becomes translucent and in the advanced stage even the posterior region becomes translucent and the larvae show symptoms of diarrhoea and develop foul smell (Mallikarjuna and Balasaraswathi, 2023).

The infection of bacteria lowers the gut pH and provides congenial conditions for growth of other pathogens. Due to faster multiplication of bacteria in gut, the peritrophic membrane degenerates and blocks the absorption of nutrients which causes stoppage of feeding and sluggishness in silkworms (Rajakumari et al., 2007). A change in blood pH also leads to general paralysis in silkworms and leads to leakage of gut contents into the haemocoel. In 1970, the production of 'late moult' in silkworm rearing was found to be associated with bacterial septicaemia. The changes in protein and fat content in haemolymph and intestinal part of the 5th instar larvae was reported when infected with *Serratia marcescens* (Guo-Ping and Xi-Jie, 2011). The carbohydrate content was found to be lower in intestines and higher in haemolymph (Sam et al., 1994). The bacteria disintegrate fat body, trachea and other tissues (FuKuda and Lwashita, 1988). The bacteria multiplies in attached specific tissue surfaces and releases different components such as immunosuppressive factors, special metabolites and toxin proteins which results in the rapid death of host silkworm (Zhang et al., 2023). The silkworm cadavers infected with bacteria shows slow growth, sluggishness, body shrinkage, oral and anal discharge, swelling of thorax, rupturing of skin, loses appetite and elasticity and oozes a brown fluid with foul smell (Gudimalla et al., 2020). *B. thuringiensis* produces crystal protein or Cry protein that gets attached to epithelial layer of midgut and rupture it (Mullins, 1985; Nazar et al., 2019). The ruptured midgut and larval body liquefies. The haemocyte number significantly decreases and signs of rupture integument increase (Broderick et al., 2010). The bacteria, *Serratia marcescens*, were isolated from exuvium of the cocoons the same bacteria was smeared on body surface of 5th instar larvae before cocooning. It confirms the fact that bacteria adheres to the body surface of silkworms and gets introduced into cocoons when infected in 5th instar. It causes infection, death, and putrefaction in cocoons within an extremely short time (Enomoto et al., 1987).

7. HOST RANGE

Microbes have symbiotic association with various insect hosts and their interactions lead complementary to high pathogenic responses. *Bacillus thuringiensis* is a soil dwelling micro-organism found to infect a range of lepidopteran insects including *Spodoptera littoralis*, *Helicoverpa armigera*, *Spilarctia obliqua* and *Bombyx mori* as well. The vigorous feeding on infected leaves ingests *B.thuringiensis* toxins which influences the larval stage of susceptible worms (Thakur et al., 2015). Other than bacillus species, there are many bacteria which infect a wide range of lepidopteran insects. *Serratia marcescens* isolated from the gut of *Rhynchites bacchus* were found to cause mortality in the same host and silkworm *B. mori* as well. The species of genus *Pseudomonas*, *Bacillus*, *Staphylococcus*, *Enterobacter* and *Enterococcus* are found to be most widespread and infect a range of insect hosts. In lepidopteran insects, the gut bacterial families belong to proteobacteria phylum. Around 60% of the lepidopteran species were screened for the presence of bacteria belonging to enterobacteriaceae, bacillaceae, pseudomonaceae, staphylococaceae and enterococcaceae families (Voirol et al., 2018). For instance, the pathogenicity is caused by *Enterococcus* bacteria present in the midgut of *Manduca sexta* Linnaeus (Mason et al., 2011). Also, *Enterobacter cloacae* which is commonly found in the intestines of insects when administered orally to *Spodoptera litura* causes alterations in the intestinal microbial community and leads to pathogenicity (Thakur et al., 2015). The oral administration of *Flavobacterium* species, *Klebsiella* species and *Serratia marcescens* has been confirmed to be pathogenic to insects (Zhang et al., 2020).

8. SYMPTOMS OF BACTERIAL FLACHERIE

The symptoms caused by different bacteria are a typical and are of general type. The growth becomes stunted and the larvae become flaccid (Plate 1). The dead larvae develop different colours, depending on the species of bacteria involved in causing the infection, become rotten and foul smelling (Yup-Lian, 1991; Zhang et al., 2020). The silkworms appear physiologically weak and flacherie outbreak elicits a heavy toll on sericulture every year (Aruga, 1994). The silkworms affected with flacherie lose appetite and become sluggish. At the beginning, no colour change



Plate 1: Flacherie infected silkworms

occurs but infected silkworms turn flaccid later with vibrant discolouration and larvae turn dark brown. Larvae wriggle in pain due to rapid pulsation of dorsal vessel. Vomiting brown fluid is also a symptom, excreta becomes soft and sticks to the rearing bed. During moulting, skin is not shed properly. A change in physiological state, alternation in biochemical constituents and haemolymph composition is reported in flacherie infected larvae which is often observed with stoppage of feeding by infected larvae (Pawar and Ramakrishnan, 1977; Begum et al., 2004). In case of septicemic flacherie, larvae turn red or brown in colour depending upon the pathogen infected to silkworm and causes diarrhoea in severe infections (Santha et al., 2007). *B. thuringiensis* causes shrinking and softening of larval body. Hence, it is also known as as shrinking disease, softening disease or faecal disease. *Bacillus thuringiensis* in silkworm cause abrupt halting of feeding, head movements, spasms, tremors, paralysis, distress, sudden collapse of body and death in case of acute bacterial toxicosis. Death may occur within ten minutes to a few hours (Yup-Lian, 1991). Shortly after death, the silkworm is extended and appears hard for touch with the head retracted so as to assume a hook-shaped appearance. Gradually, the dead silkworm becomes black and rotten, exuding a foul smelling dark brownish fluid (Santha et al., 2007). Chronic bacterial toxicosis is caused by ingestion of small quantity of *Bacillus thuringiensis* crystal toxin (Mitsuhashi and Miyamoto, 2020). The thorax and abdominal tip become transparent and the silkworms are often motionless among the litter. After 10 to 12 hours of infection, the larvae become sluggish, lose clasping power, body turn flaccid and eventual death of larvae (Anitha et al., 1994; Mallikarjuna and Balasaraswathi, 2023). Silkworm infected with bacteria cocci exhibits body shrinkage, skin softness, stunted growth and turn light brown in color (Santha et al., 2007).

9. SUSCEPTIBILITY OF SILKWORMS TO BACTERIAL INFECTION

Silkworms are susceptible to bacterial infections and degree of susceptibility may vary with race and larval instar (Anusha and Bhaskar, 2018). Infection with some bacterial pathogens causes high mortality and maximum deaths occur during moulting and just before spinning. Also irrespective of the age of infection, mortality is maximum in the final instar. The susceptibility of fifth instar larvae to infection is more or less in the same (Tayal and Chauhan, 2017). The younger larvae show varying degree of susceptibility (Rahmathulla, 2012; Tayal and Chauhan, 2017). Kumari et al. (2001) investigated sensitivity of 4th and 5th instar silkworms towards temperature fluctuations. With the increase in temperature, the metabolic functions also increase while as with the decrease in temperature, the

metabolism of silkworms is totally shaken. A stress factor is generated in silkworms when temperature goes higher or lowers than 25°C and it enhances the susceptibility of silkworm to viral infections (Steinhaus, 1958). Kato (1989) investigated that high temperature exposure to 5th instar larvae declines the survival rate of silkworms. The most susceptible instar is third instar as revealed by maximum mortality due to infection at this instar (Santha et al., 2007). The susceptibility of silkworm to bacterial infection is governed by the nutritive factors (Zha et al., 2021). The poor quality mulberry with low protein, sucrose or high cellulose makes silkworms comparatively more susceptible to infection by pathogens (Urbanek et al., 2022). The rise in silkworm rearing temperature accelerates the development of bacterial disease (Huang et al., 2009). *Aerobacter cloacae* and *Staphylococcus albus* are observed to be more lethal to late age larvae than to early instar larvae and the reverse is true with *Escherichia freundii*. A silkworm exposed to small doses of *B. thuringiensis*, *Var alesti* leads to chronic infection, but on exposure to higher temperature of around 30°C rapidly develops into fatal bacteriosis (Paudel et al., 2021; Sun et al., 2022). High temperature and humidity leads to dysfunction of alimentary canal, which in turn leads to *Enterococcus* multiplication (Santha et al., 2007).

10. DETECTION OF BACTERIAL DISEASE IN SILKWORM

There is no such process in detection of this disease, it is detected by observing the symptoms of disease (Chopade et al., 2021). Morphologically the disease can be identified by presence of soft and lethargic larvae which rapidly stop feeding and rot (Yadav et al., 2016). The larvae with retarded growth vomit gut juices excrete semi-solid faeces and the inner content of gut turn blackish color which emit foul smell (Sakthivel et al., 2012). However for the early detection of disease the microscopic study is important. Direct microscopical and bacterioscopic examinations are carried out to exclude the risk of the presence of pathogens. The developmental stages of silkworm, egg and larval stage are subjected to microscopy and examinations in sericulture. The molecular tools play a profound role in detection of silkworm pathogens in sericulture. These tools have revolutionized the detection of microbes due to its special attributes viz., early and timely detection, high accuracy and sensitivity, superior specificity and rapid interpretation and analysis. The primary step to detect pathogens relies on the identification of pathogen to control infectious diseases in sericulture. The preparatory steps such as genomic Deoxyribo nucleic acid (DNA) and Ribonucleic acid (RNA) extraction by lyses of tissue sample are required to detect the pathogen. The traditional protocols or commercially available kits are used to achieve the preparatory process.

After preparatory the quantification of extracted genomic DNA or RNA is required (Deepika et al., 2024). The 16S rRNA gene is common to all prokaryotes. It is often used as a marker for identifying bacterial species (Schmidt et al., 1994). Hence it is a powerful tool to detect and identify a particular bacteria infecting silkworm. The restriction pattern of 16S rRNA gene amplification of bacterial gut metagenomic DNA of silkworm was used to detect the bacterial population infecting silkworm. Some advanced techniques viz., scanning electron microscopy, florescent microscopy, and phase contrast microscopy and transmission electron microscopy are also used for diagnosis of silkworm diseases (Rabha et al., 2024). However these techniques are sophisticated, expensive and requires technically sound personnel for the maintenance of high costs equipments. These factors limit the use advanced microscopic techniques for diagnosis of silkworm pathogens. The immunological techniques viz., Enzyme linked immunoassay (ELISA), immuno-diffusion assay, immunofluorescence assay are widely used for detection of *Nosema* (pebrine) and infectious flacherie virus in sericulture. However no work has been done with detection of bacterial pathogens using immunological diagnostics in sericulture. However, more advanced molecular techniques possess remarkable attributes to be utilized for detection of pathogens. Polymerase chain reaction (PCR) is an efficient detection technique for initial diagnosis of disease. It has been widely utilized for detection of different pathogens including bacteria as well. *Bacillus* species and *Pseudomonas* species are detected through PCR (Subrahmanyam et al., 2023). Unlike PCR, other molecular techniques like restriction fragment length polymorphism (RFLP), Enzyme linked immunosorbent assay (ELISA), western blotting, lateral flow assay (LFA) are also used to detect bacterial pathogens affecting silkworm (Deepika et al., 2024). Restriction fragment length polymorphism (RFLP) analysis and nucleic acid fingerprinting can help to detect differences in the genomes of closely related microbial species. Additionally, it can detect the involvement of a particular pathogen in disease outbreak.

11. MANAGEMENT OF BACTERIAL DISEASE

Improper disinfection of rearing house and environment causes the build-up of bacterial pathogens in the rearing environment and this can be destabilizing factor (Trivedy et al., 2011). Thorough disinfection of rearing room and rearing equipments with recommended general disinfectant is essential to ensure elimination of pathogens from the rearing environment before initiation of rearing (Davies and Wales, 2019). Different bed disinfectant are used in silkworm rearing to curb the bacterial diseases which includes vijetha, hydrated lime, active lime, captan,

Resham Keed Oushad (RKO), Ankush, Jyothi, Labexetc (Shashidhar et al., 2018). The application of chemical based and season specific bed disinfectant 'Sanjeevni' for control of bacterial flacherie is recommended in sericulture. Use surface disinfected quality eggs and rear the early instar of silkworms under optimum conditions. In order to prevent the outbreak of bacterial flacherie, the silkworm should be reared on nutritive mulberry leaves under hygienic and congenial rearing conditions (Gupta and Dubey, 2021). Application of silkworm body and rearing bed disinfectants as per recommended schedule and quantity prevent the spread of bacterial diseases (Habeanu et al., 2024; Chauhan and Tayal, 2017). It is essential to provide required bed space as per the instar in addition to ventilation. In order to prevent flacherie and thatteroga in silkworm rearing, the rearing trays and equipments or tools used for silkworm rearing are to be dipped in an effective disinfectant solution for 10 minutes (Dingle et al., 2005; Tayal and Chauhan, 2017). Ensuring good cross ventilation helps in reducing humidity between the rearing beds. Dusting of slaked lime before resumption of silkworms is helpful in keeping the humidity low especially during moulting reduces the pathogen build-up in the rearing environment (Singh, 2010). Use of antibiotics to suppress bacterial flacherie, especially bacterial disease of digestive organ is found to be effective (Darvekar et al., 2024). Antibiotics such as erythromycin, kanamycin, streptomycin, chloramphenicol, Aureomycin, neomycin and tetracycline have been reported to be suppressive against bacterial disease of digestive system (Kahn, 2016; Montali et al., 2020). Enriching the mulberry leaves with 0.1% gentamycin was found to reduce flacherie (Nanda et al., 2024). As a prophylactic measure, ampicillin at the rate of 500 ppm can be used to treat mulberry leaves and fed to silkworms during the first feeding of 3rd and 5th instars to manage bacterial flacherie in order to harvest better cocoon crops (Manimegalai and Chandramohan, 2008). The plant extracts bearing anti-microbial activity can be used to control bacterial diseases in silkworm, *B. mori*. The botanicals are used to control the bacterial infections in silkworm. Many plants viz., aloe vera, neem, viscum album, were found possess anti-microbial activity (Yusuf et al., 2013; Ujjwala et al., 2006).

12. CONCLUSION

Bacterial flacherie is most outrageous disease causing significant economic losses in sericulture. Many bacterial species are causal organisms. Different diagnosis strategies have been developed, among which the artificial tools using sensors are most reliable to detect the pathogen presence. The implementation of precautions and prevention strategies can be adopted for healthy cocoon crop production. The modern techniques like feeding of

antibiotic fortified leaves and application of botanical bed disinfectants may help to sustain healthy cocoon production and promote smart sericulture.

13. REFERENCES

- Aizawa, K., Takasu, T., Kurata, K., 1961. Isolation of *Bacillus thuringiensis* from the dust of silkworm rearing houses of farmers. *Journal of Sericultural Science Japan* 30, 451–455.
- Aneja, K.R., 1996. Methods of obtaining pure culture of microorganisms. In: experiments in microbiology, plant pathology, tissue culture and mushroom cultivation (2nd edn.). International (P) Ltd. New Delhi, 139–153.
- Angus, T.A., 1956. General characteristics of certain insect pathogens related to *Bacillus cereus*. *Canadian Journal of Microbiology* 2(2), 111–121.
- Anitha, T., Sironmani, P., Meena, P., Vanitha, R., 1994. Isolation and characterization of pathogenic bacterial species in the silkworm, *Bombyx mori* L. *Sericologia* 34(1), 971–02.
- Anusha, H.G., Bhaskar, R.N., 2018. Identification of new pathogenic bacteria (*Alcaligenes faecalis*) and assessment of pathogenicity with mixed infection on rearing and cocoon parameters of silkworm (*Bombyx mori* L.). *Research on Crops* 19(1), 120–126.
- Aruga, H., 1994. Principles of sericulture (1st edn.). 9054102543 CRC press. ISBN-13. 978-9054102540
- Attia, R.G., Moustafa, M.N., Ma'moun, S.A., Sayed, H., Abdel-Haleem, D.R., 2025. Mechanisms of some *Lactobacillus* sp. for enhancing the growth of mulberry silkworm, *Bombyx mori* larvae, and their role as biocontrol agents against diseases. *Egyptian Journal of Biological Pest Control* 35(1), 1–11.
- Ayoade, F., 2014. Isolation, Identification, antibiogram and characterization of bacterial pathogens of the Silkworm, *Bombyx mori* in South-west Nigeria. *Journal of Biological Sciences* 10.3923/jbs.2014.
- Badr, S.M.S., Darwish, A.M.A., 2024. Anatomical and cytological studies on the cotton leaf worm *Spodoptera littoralis* (Biosd.) larva infected with some bio-insecticides. *Journal of Umm Al-Qura University Applied sciences* 10(2), 245–256.
- Bhat, S.A., Nooruddin, S., Ganai, N.A., Sahaf, K.A., Malik, M.A., 2016. Susceptibility of different silkworm breeds to nuclear polyhedrosis and bacterial flacherie under natural conditions. *Applied Biological Research* 18(1), 85–88.
- Bhowmik, A., 2014. Development of a cost effective medium for enhanced production of *Bacillus thuringiensis* δ -endotoxin (Doctoral dissertation, BRAC University).
- Broderick, N.A., Raffa, K.F., Handelsman, J., 2010.

- Chemical modulators of the innate immune response alter gypsy moth larval susceptibility to *Bacillus thuringiensis*. BMC Microbiology 7(10), 129.
- Cappellozza, S., Saviane, A., Tettamanti, G., Squadrin, M., Vendramin, E., Paolucci, P., Squartini, A., 2011. Identification of *Enterococcus mundtii* as a pathogenic agent involved in the “flacherie” disease in *Bombyx mori* L. larvae reared on artificial diet. Journal of Invertebrate Pathology 106(3), 386–393.
- Castillo, Y., Suzuki, J., Watanabe, K., Shimizu, T., Watarai, M., 2016. Effect of vitamin A on *Listeria monocytogenes* infection in a silkworm model. PLoS One 11, e0163747.
- Chakravorty, D., Pandey, P.N., 2005. Silk worm crops. APH Publishing. SBN-10. 8176488917.
- Chen, B., Zhang, N., Xie, S., Zhang, X., He, J., Muhammad, A., Shao, Y., 2020. Gut bacteria of the silkworm *Bombyx mori* facilitate host resistance against the toxic effects of organophosphate insecticides. Environment International 143, 105886.
- Cheung, G.Y., Bae, J.S., Otto, M., 2021. Pathogenicity and virulence of *Staphylococcus aureus*. Virulence 12(1), 547–569.
- Chitra, C., Karanth, N.G.K., Vasantharajan, V.N., 1974. Studies on “Sappe” disease of the silkworm, *Bombyx mori*: II. Effect of age of larvae on the manifestation of the disease. Journal of Invertebrate Pathology 24(2), 248–252.
- Chisti, M.Z., Sahaf, K.A., Khan, M.A., 1991. Occurrence of bacterial disease (Flacherie) of silkworm, *Bombyx mori* in Jammu and Kashmir State. Indian Journal of Sericulture 30(1), 54–55.
- Chopade, P., Raghavendra, C.G., 2021. Assessment of diseases in *Bombyx mori* silkworm—A survey. Global Transitions Proceedings 2(1), 133–136.
- Dai, T.M., Qiu, J.F., Luo, C., Cui, W.Z., Liu, K., Li, J.L., Xu, S.Q., 2025. The circadian clock affects starvation resistance through the pentose phosphate pathway in silkworm, *Bombyx mori*. Insect Science 32(1), 55–68.
- Darvekar, A., Shivdasani, H., Nashikkar, N., Bundle, S., Rai, M., Rathod, M., 2024. Prevalence of *Enterococcus mundtii* in the fat body and its effect on the development of silkworm, *Bombyx mori* L. Journal of Applied Bioscience 50(2), 268–278.
- Das, D., 2008. Studies on some biochemical profiles of muga silkworm, *Antheraea assama* WW (Lepidoptera: Saturniidae) and their relation to the disease bacteriosis in the Cooch Behar Districts of West Bengal (Doctoral dissertation, University of North Bengal).
- Dashora, K., Roy, S., Nagpal, A., Roy, S.M., Flood, J., Prasad, A.K., Muraleedharan, N., 2017. Pest management through *Bacillus thuringiensis* (Bt) in a tea-silkworm ecosystem: status and potential prospects. Applied Microbiology and Biotechnology 101, 1795–1803.
- Davies, R., Wales, A., 2019. Antimicrobial resistance on farms: a review including biosecurity and the potential role of disinfectants in resistance selection. Comprehensive Reviews in Food Science and Food Safety 18(3), 753–774.
- Deb, S., Sinha, A.K., Saha, A.K., 2021. Studies on synergistic effects of different chemicals on nuclear polyhedrosis (grasserie disease) of silkworm, *Bombyx mori* Linnaeus. African Journal of Biological Sciences 3(4), 104–113.
- Deepika, I., Ramesh, K.V., Kumar, I., Singh, A., Debnath, R., Dubey, H., Subrahmanyam, G., 2024. Molecular diagnostics in sericulture: A paradigm shift towards disease diagnosis in silkworms. Entomologia Experimentalis et Applicata 172(5), 372–382.
- Dingle, J.G., Hassan, E., Gupta, M., George, D., Anota, L., Begum, H., 2005. Silk production in Australia. A report for the Rural Industries Research and Development Corporation, 105.
- Dong, X., Lu, P., Cao, W., Zhang, C., Zhu, F., Meng, X., Chen, K., 2017. Study of the toxicity of *Bacillus cereus* on silkworm (*Bombyx mori*) and the relevant proteome. Invertebrate Survival Journal 14(1), 129–139.
- Enomoto, B.S., Moriyama, H., Iwanami, S., 1987. Septicemia occurrence in cocoons as related to silkworm rearing conditions. Japanese Agricultural Research Quarterly 21(2), 117–121.
- Entry, I.P.O., 1993. Bacterial Infections: bacillacea. Insect Pathology 84(4).
- Fast, P.G., Angus, T.A., 1965. Effects of parasporal inclusions of *Bacillus thuringiensis* var sotto Ishiwata on the permeability of the gut wall of *Bombyx mori* L. larvae. Journal of Invertebrate Pathology 7, 29–32.
- Faust, R.M., 1977. Toxins of *Bacillus thuringiensis*: Mode of action. Biological regulation of vectors: The saprophytic and aerobic bacteria and fungi. Washington: US Department of Health, Education, and Welfare, 31–48.
- Faust, R.M., 1984. Nature of pathogenic process of *Bacillus thuringiensis*. In: Pathogens of invertebrates: Application in biological control and transmission mechanisms. Boston, MA: Springer US, pp. 91–141.
- Faye, I., Wyatt, G.R., 1980. The synthesis of antibacterial proteins in isolated fat body from cecropia silk moth pupae. Experientia 36, 1325–1326.
- Glare, T.R., O’Callaghan, M., 1998. Environmental and health impacts of *Bacillus thuringiensis israelensis*. Report for the Ministry of Health, 57.
- Glaser, R. W., 1924. A bacterial disease of silkworms. Journal of Bacteriology 9(4), 339–355.
- Goswami, J., Gogoi, D.K., Rasid, N., Handique, B.K.,

- Subrahmanyam, G., Bora, P.P., Das, R., Raju, P.L.N., 2021. Development of a Muga disease early warning system—a mobile-based service for seri farmers. *Current Science* 121(10), 1328–1334.
- Gudimalla, P., Akula, S., Kuntamalla, S., 2020. Isolation, identification, and characterisation of pathogenic bacteria from the gut tissue of silkworm (*Bombyx mori* L.) and its management using Phyto essential oils. *International Journal of Entomology Research* 5(2), 67–69.
- Guo-Ping, K., Xi-Jie, G., 2011. Overview of silkworm pathology in China. *African Journal of Biotechnology* 10(79), 18046–18056.
- Gupta, S.K., Dubey, R.K., 2021. Environmental factors and rearing techniques affecting the rearing of silkworm and cocoon production of *Bombyx mori* Linn. *Acta Entomology and Zoology* 2(2), 62–67.
- Habeanu, M., Gheorghe, A., Dinita, G., Mihalcea, T., 2024. An in-depth insight into the profile, mechanisms, functions, and transfer of essential amino acids from mulberry leaves to silkworm *Bombyx mori* L. *Pupae and fish. Insects* 15(5), 332.
- Haloi, K., Kalita, M.K., Nath, R., Devi, D., 2016. Characterization and pathogenicity assessment of gut-associated microbes of muga silkworm *Antheraea assamensis* Helfer (Lepidoptera: Saturniidae). *Journal of Invertebrate pathology* 138, 73–85.
- Handique, B.K., Das, P.T., Goswami, J., Goswami, C., Singh, P.S., Prabhakar, C.J., Raju, P.L.N., 2016. Expansion of sericulture in India using geospatial tools and web technology. *Current Science* 111(8), 1312–1318.
- Hanh, N.T., Ngoc, P.M., Tuan, H.M., 2024. Isolation and identification of the *Serratia marcescens* causing septicemia in the silkworms from Yen Bai province and prevention measures. *Vietnam Journal of Biotechnology* 22(2), 278–288.
- Hao, J., Gao, Y., Xue, J., Yang, Y., Yin, J., Wu, T., Zhang, M., 2022. Phytochemicals, pharmacological effects and molecular mechanisms of mulberry. *Foods* 11(8), 1170.
- HD, Y.K., Reddy, N.N., 2024. Sericulture–Soil to Silk. *Advances* 69, 85.
- Honee, G.J.E.M., 1992. The specificity of *Bacillus thuringiensis* crystal proteins. Wageningen University and Research. <https://doi.org/10.18174/200968>.
- Hossain, M.S., Hamamoto, H., Matsumoto, Y., 2006. Use of silkworm larvae to study pathogenic bacterial toxins. *The Journal of Biochemistry* 140, 439–444.
- Hossain, Z., Chakraborty, S., Gupta, S.K., Saha, A.K., Bindroo, B.B., 2017. Silkworm disease incidence trends during the years 1992–2011 in the Murshidabad district of West Bengal, India. *International Journal of Tropical Insect Science* 37(4), 259–270.
- Huang, L., Cheng, T., Xu, P., Cheng, D., Fang, T., Xia, Q., 2009. A genome-wide survey for host response of silkworm, *Bombyx mori* during pathogen *Bacillus bombysepticus* infection. *PloS one*, 4(12), e8098.
- Hurst, M. R., 2016. Non-spore-forming bacterial entomopathogens: Their toxins, hosts and the environment: why be a pathogen. In: *The Rasputin effect: when commensals and symbionts become parasitic. Advances in Environmental Microbiology* Cham: Springer, 169–220.
- Imtiyaz, A., Sahaf, K.A., Bhat, S.A., Gul, S., Rafiq, I., Buhroo, Z.I., Maqbool, S., 2021. Studies on mulberry pest (*Glyphodes pyloalis* Walker) as an alternate host to the pathogens of silkworm (*Bombyx mori* L.) diseases. *Plant Archives* 21(1), 2463–2468.
- Ishii, K., Adachi T., Imamura, K., 2012. *Serratia marcescens* induces apoptotic cell death in host immune cells via a lipopolysaccharide- and flagella-dependent mechanism. *Journal of Biological Chemistry* 287, 36582–36592.
- Islam, T., Qadir, J., 2024. Antiviral activity of red fluorescent proteins in silkworm, *Bombyx mori* L. *Journal of Scientific Agriculture* 8, 100–103.
- Jaishankar, J., Srivastava, P., 2017. Molecular basis of stationary phase and applications. *Frontiers in Microbiology*, 8, 2000.
- Javaid, A., Hussain, M., Aftab, K., Malik, M.F., Umar, M., Iqbal, T., 2021. Isolation and characterization of bacteria associated with silkworm gut under antibiotic-treated larval feeding. *Brazilian Journal of Biology* 84, e249664.
- Kahn, L.H., 2016. One health and the politics of antimicrobial resistance. JHU Press. <https://doi.org/10.3201/eid2304.161871>
- Kaito, C., Akimitsu, N., Watanabe, H., Sekimizu, K., 2002. Silkworm larvae as an animal model of bacterial infection pathogenic to humans. *Microbial pathogenesis* 32(4), 183–190.
- Kaito, C., Kurokawa, K., Matsumoto, Y., 2005. Silkworm pathogenic bacteria infection model for identification of novel virulence genes. *Molecular Microbiology* 56, 934–944.
- Kato, M., 1989. Study on the resistance of silkworm, *Bombyx mori*, to high temperature. *Proceedings of 6th International Congress, SABRAO* 2, 953–956.
- Karthikairaj, K., Isaiarasu, L. and Sakthivel, N., 2014. Efficacy of some herbal extracts on microbes causing flacherie disease in mulberry silkworm, *Bombyx mori* L. *Journal of Biopesticides* 7, 89.
- Kashyap, L., Goswami, T.N., Patel, V.K., Sharma, R.K., 2017. *Bacillus thuringiensis* and insect pest management. In: *Biopesticides and Bioagents*. Apple Academic Press, 331–369.

- Krishnakumar, R., 1998. Influence of weather and rearing techniques on mulberry silk worm crops in Kerala (Doctoral dissertation, Department of Agricultural Entomology, College of Agriculture, Vellayani).
- Kumar, D.S., Tarakeswari, M., Lakshminarayana, M., Sujatha, M., 2016. Toxicity of *Bacillus thuringiensis* crystal proteins against eri silkworm, *Samia Cynthia ricini* (Lepidoptera: Saturniidae). *Journal of Invertebrate Pathology* 138(1), 116–119.
- Kumari, K.M., Rajan, R.K., Himantharaj, M.T., Nataraj, B., Rekha, M., 2001. Influence of temperature and relative humidity on the rearing performance and disease incidence in CSR hybrid silkworms, *Bombyx mori* L. *International Journal of Industrial Entomology and Biomaterials* 3(2), 113–116.
- Lakshmi, V.V.N.S., Jamil, K., 2002. Biochemical basis for the occurrence of microbial diseases in silkworm, *Bombyx mori* L. (Lepidoptera: Bombycidae). *Journal of Entomological Research* 26(1), 11–22.
- Li, G., Cai, M., Zheng, X., Xie, X., Zhu, Y., Long, Y., 2022. Impact of disinfectants on the intestinal bacterial symbionts and immunity of silkworm (*Bombyx mori* L.). *Environmental Science and Pollution Research* 29(52), 79545–79554.
- Liang, X., Fu, Y., Liu, H., 2015. Isolation and characterization of enzyme-producing bacteria of the silkworm larval gut in bioregenerative life support system. *Acta Astronautica* 116, 247–253.
- Lu, X.M., Huang, S.K., Wang, F.W., 2003. Distribution of the Enterococci isolated from intestine of the pebrine infected silkworm. *Science of Sericulture* 29(2), 151–156.
- Lu, X.M., Jin, W., Qian, Y.H., Gong, C.L., 1999. Distribution of the enterococci isolated from the intestine of the Silkworm, *Bombyx mori*. *Science of Sericulture* 25(3), 158–162.
- Lysenko, O., 1958. ‘*Streptococcus bombycis*’, its Taxonomy and Pathogenicity for Silkworm Caterpillars. *Microbiology* 18(3), 774–781.
- Madigan, M.T., Martinko, J.M., Parker, J., 2000. *Brock biology of microorganisms*. Prentice-Hall, Upper Saddle River, NJ. pp. 135–162.
- Mahalingam, C.A., Muruges, K.A., Shanmugam, R., 2010. Grasserie disease incidence on silkworm and development of botanical based management strategy. *Trends in Biosciences* 3(2), 212–215.
- Mallikarjuna, G., Balasaraswathi, S., 2023. Mulberry silk insect. In *Commercial Insects*. CRC Press. pp. 17–48.
- Manimegalai, S., 2009. Bacterial pathogens of mulberry silkworm *Bombyx mori* and their management strategies. *Sericologia* 49(4), 401–420.
- Manimegalai, S., 2010. A review on the larval resistivity and disinfection of the nuclear polyhedrosis virus of mulberry silkworm, *Bombyx mori* L. in India. *Revue des Vers a Soie Journal of Silkworms*, 297.
- Manimegalai, S., Chandramohan, N., 2008. Antibiotics for the management of bacterial flacherie of silkworm, *Bombyx mori* L. *Madras Agricultural Journal* 95(jan-jun), 1.
- Mason, K.L., Stepien, T.A., Blum, J.E., Holt, J.F., Labbe, N.H., Rush, J.S., Raffa, K.F., Handelsman, J., 2011. From commensal to pathogen: translocation of enterococcus faecalis from the midgut to the hemocoel of manduca sexta. *mBio*, 2, e00065–11. <https://doi.org/10.1128/mBio.00065-11>.
- Matsumoto, T., Zhu, Y.F., Kurisu, K., 1985. Mixed infection with infections flacherie virus and bacteria in *Bombyx mori*. *The Journal of Sericultural Science of Japan* 54(6), 453–458.
- Matsumoto, Y., Sekimizu, K., 2019. Silkworm as an experimental animal for research on fungal infections. *Microbiology and Immunology* 63, 41–50.
- Milner, R.J., 1994. History of *Bacillus thuringiensis*. *Agriculture, Ecosystems & Environment* 49(1), 9–13.
- Mir, A.H., Qamar, A., 2018. Effects of starvation and thermal stress on the thermal tolerance of silkworm, *Bombyx mori*: existence of trade-offs and cross-tolerances. *Neotropical Entomology* 47, 610–618.
- Mitsuhashi, W., Miyamoto, K., 2020. Interaction of *Bacillus thuringiensis* Cry toxins and the insect midgut with a focus on the silkworm (*Bombyx mori*) midgut. *Biocontrol Science and Technology* 30(1), 68–84.
- Miyashita, A., Iyoda, S., Ishii, K., Hamamoto, H., Sekimizu, K., Kaito, C., 2012. Lipopolysaccharide O-antigen of enterohemorrhagic *Escherichia coli* O157:H7 is required for killing both insects and mammals. *FEMS Microbiology Letters* 333, 59–68.
- Mogili, T., Sarkar, T., Gnanesh, B.N., 2023. Mulberry breeding for higher leaf productivity. In *The Mulberry Genome*. Cham: Springer International Publishing, pp. 57–114.
- Mohanta, M.K., Saha, A.K., Saleh, D.K.M.A., Hasan, M.A., 2013. Bioefficacy of some plant extracts against pathogenic bacteria isolated from diseased silkworm larvae. *University Journal of Zoology* 32, 9–14.
- Mohanta, M.K., Saha, A.K., Saleh, D.K.M.A., Islam, M.S., Mannan, K.S.B., Fakruddin, M., 2015. Characterization of *Klebsiella granulomatis* pathogenic to silkworm, *Bombyx mori* L. *3 Biotech* 5, 577–583.
- Mondal, R., Das, D., Mandal, A.K., 2025. Antibiotic Stewardship in Silkworms: Navigating the Pros and Cons. *Bacteria* 4(1), 2.
- Montali, A., Berini, F., Brivio, M.F., Mastore, M., Saviane,

- A., Cappellozza, S., Tettamanti, G., 2020. A silkworm infection model for in vivo study of glycopeptide antibiotics. *Antibiotics* 9(6), 300.
- Mullins, D.E., 1985. Chemistry and physiology of the haemolymph. In *Comp. Insect Biochemistry and Physiology*. Press, N.Y. 3: 355–400. <https://doi.org/10.1016/B978-0-08030804-3.50015-7>.
- Nakano, H., Tahara, S., Iizuka, T., Mizutani, J., 1987. A defense mechanism against pathogenic bacteria in the digestive tracts of silkworm larvae *in vitro* evidence of the formation of caffeoquinone, a true antibacterial substance, and synergism of amino compounds. *Agricultural and biological chemistry* 51(2), 549–555.
- Nanda, P., Nadaf, H.A., Vishaka, G.V., Rathore, M.S., Kaushik, R., Mishra, S., Selvakumar, T., 2024. Know how on essential chemicals used in Tasar sericulture. *International Journal of Advanced Biochemistry Research* SP-8(3), 701–710
- Nataraju, B., Balavenkatasubbaiah, M., Baig, M., Singh, B. D., Sengupta, K., 1991. A report on the distribution of *Bacillus thuringiensis* in sericultural areas of Karnataka, India. *Indian Journal of Sericulture* 32, 103–105
- Navarro-Llorens, J., Tormo, A., Martinez-Garcia, E., 2010. Stationary phase in gram-negative bacteria. *FEMS Microbiology Reviews* 34, 476–495
- Nesa, J., Sadat, A., Buccini, D. F., Kati, A., Mandal, A.K., Franco, O.L., 2020. Antimicrobial peptides from *Bombyx mori*: a splendid immune defense response in silkworms. *RSC Advances* 10(1), 512–523.
- Ohba, M., Aizawa, K., Furusawa, T., 1979. Distribution of *Bacillus thuringiensis* serotypes in ehime prefecture: Japan. *Applied Entomology and Zoology* 14(3), 340–345.
- Pandey, S., Joshi, B.D., Tiwari, L.D., 2009. Histopathological changes in the midgut of *Spodoptera litura* larvae on ingestion of *Bacillus thuringiensis* delta endotoxin. *Archives of Phytopathology and Plant Protection* 42, 376–383.
- Parbin, H., Chutia, B.C., Koushik, S., Ahmed, A., Hazarika, G., Borah, P., 2024. Antimicrobial activity of *Ligilactobacillus salivarius* against pathogenic bacteria *Staphylococcus aureus*, *Proteus vulgaris* and *Bacillus thuringiensis* Causing Flacherie in Silkworm. In: *Proceedings of the Zoological Society*, pp. 1–4. New Delhi: Springer India.10.1007/s12595-024-00540-6.
- Park, J.W., Park, S.K., Jeong, C.Y., Kwon, H.G., Lee, J.H., Kang, S.K., Kim, S.R., 2024. Microbial community changes in silkworms suspected of septicemia and identification of *Serratia* sp. *International Journal of Molecular Sciences* 25(7), 3957.
- Paudel, A., Furuta, Y., Higashi, H., 2021. Silkworm model for *Bacillus anthracis* infection and virulence determination. *Virulence* 12(1), 2285–2295.
- Priyadarshini, P., Mahalingam, C.A., Shashidhar, K.R., 2008. Identification and characterization of bacterial pathogens in silkworm, *Bombyx mori* L. *Current Biotica* 2(2), 181–192
- Rahmathulla, V.K., 2012. Management of climatic factors for successful silkworm (*Bombyx mori* L.) crop and higher silk production: a review. *Psyche: A Journal of Entomology* 2012(1), 121–234.
- Rahmathulla, V. K., Tilak, R., Rajan, R.K. 2006. Influence of moisture content of mulberry leaf on growth and silk production in *Bombyx mori* L. *Caspian Journal of Environmental Sciences* 4(1), 25–30.
- Rai, M.M., Gore, D.G., Rathod, M.K., Khurad, A.M., 2013. Evidence of transovarial transmission of *Bacillus subtilis* in the silkworm, *Bombyx mori* L. *Journal of Pharmacy Research* 7(4), 318–323.
- Rajakumari, D.S., Padmalatha, C., Das, S.S.M., Ranjitsingh, A.J.A., 2007. Efficacy of probiotic and nutraceutical feed supplements against Flacherie disease in mulberry silkworm, *Bombyx mori* L. *Indian Journal of Sericulture* 46(2), 179–182
- Rolfe, M.D., Rice, C.J., Lucchini, S., Pin, C., Thompson, A., Cameron, A.D., Hinton, J.C., 2012. Lag phase is a distinct growth phase that prepares bacteria for exponential growth and involves transient metal accumulation. *Journal of Bacteriology* 194(3), 686–701.
- Saad, M.S., Elyamani, E.M., Helaly, W.M., 2019. Controlling of bacterial and fungal diseases that contaminating mulberry silkworm, *Bombyx mori* by using some plant extracts. *Bulletin of the National Research Centre* 43, 1–9.
- Sakthivel, S., Angaleswari, C., Mahalingam, P.U., 2012. Isolation & Identification of bacteria responsible for flacherie in silkworm. *Journal of microbiology & biotechnology Research* 2(6), 91–93.
- Sam, D.C., Sasidharan, T.O., Samson, M.V., 1994. Infectivity of *Serratia marcescens* to the silkworm, *Bombyx mori* L. (Lepidoptera :Bombycidae) ,and its effect on certain biochemical constituents in the haemolymph and gut. *Sericologia* 34(2), 275–281.
- Samson ,M.V., 1995. Flacherie in *Bombyx mori* L. *Indian Silk* 33(11), 31–32.
- Samson M.V., Nataraju B., Baig M., Krishnaswamy, S., 1981. Starvation of *Bombyx mori* L. on cocoon crop and incidence of loss due to diseases. *Indian Journal of Sericulture* 20, 42–47.
- Samson, M.V., 1987. Bacterial diseases of silkworm, *Bombyx mori*, Ph.D. Thesis, Univ. of Mysore, 137.
- Santha, P. C., Bhargava, S. K., Sindagi, S. S., Kamble, C.K.,

2007. Bacterial flacherie of silkworm, *Bombyx mori* and its control by the application of antibiotics. Journal of Experimental Zoology, India 10(1), 1–7
- Satish, L., Kusuma, L., Suresh, R.V., Moorthy, S.M., Sivaprasad, V., 2024. Application of marker-assisted selection in silkworm breeding for disease resistance. In Biotechnology for Silkworm Crop Enhancement: Tools and Applications. Singapore: Springer Nature Singapore, pp. 109–118.
- Savu, V., Sapcaliu, A., 2024. The Importance of proactive approach to the microscopic laboratory techniques for the prevention and control of major silkworm diseases. Scientific Papers Animal Science and Technologies 57(1), 266–272.
- Schmidt, T.M., Relman, D.A., 1994. Phylogenetic identification of uncultured pathogens using ribosomal RNA sequences. Methods in Enzymology 235, 205–222.
- Selvakumar, T., 2013. Prevalence of flacherie disease and pathogenicity of isolated pathogens in silkworm, *Bombyx mori* (L.) under different environmental conditions. Agricultural Science Digest-A Research Journal 33(4), 253–258.
- Selvakumar, T., Datta, R.K., 2013. Role of bacteria (*Streptococcus faecalis* & *Staphylococcus aureus*), viruses and their combined infection in causation of flacherie under different environmental conditions. Sericologia 53(1), 54–62.
- Selvakumar, T., Savithri, M., 2012. Thermo therapy of infectious flacherie in young age silkworm larvae of *Bombyx mori* L. Journal of Sericulture & Technology 3(1), 62–64.
- Shashidhar, K.R., Thulasiram, K., Haveri, N., 2018. Effectiveness of bed disinfectants on silkworm diseases and cocoon yield under tropical conditions of Kolar district, Karnataka. Journal of Pharmacognosy and Phytochemistry 7(5), 2720–2724.
- Singh, G.P., Baig, M.M., Bajpayi, C.M., 2021. Recent trends in tasar silkworm *Antheraea mylitta* Drury disease management. In Methods in Microbiology 49, 175–200. Academic Press. <http://dx.doi.org/10.1016/bs.mim.2021.05.001>.
- Singh, T., 2010. Principles and techniques of silkworm seed production. Discovery Publishing House.
- Sivaji, M., 2010. Molecular cloning of cry genes specific to dipterans from native *Bacillus thuringiensis* berliner (Doctoral dissertation, Centre for Plant Biotechnology and Molecular Biology, College of Horticulture, Vellanikkara).
- Smith, T., 1999. Pasteur and insect pathogens. Nature structural biology 6(8), 720–720.
- Soares, G.G., 2021. Problems with entomopathogens in insect rearing. In Advances in insect rearing for research and pest management, pp. 289–322. CRC Press.
- Steinhaus E.A., 1958. Stress as factor in insect diseases. Proceedings of Tenth International Congress of Entomology 4, 725–730.
- Steinhaus, E.A., 1958. Crowding as a possible stress factor in insect disease. Ecology, 503–514.
- Stevens, J.M., 1963. Protective effects of several immunizing preparations that produce active immunity in *Galleria mel/onella* (Linnaeus). Journal of Insect Pathology 5, 129–130.
- Subrahmanyam, G., Das, R., Debnath, R., Chutia, M., Ponnuvel, K.M., Sathyanarayana, K., 2023. Characterization of bacterial pathogens in muga silkworm, *Antheraea assamensis* Helfer (Lepidoptera: Saturniidae). Journal of Environmental Biology 44, 479–484.
- Sun, X., Yuan, Q., Du, B., Jin, X., Huang, X., Li, Q., Sima, Y., 2022. Relationship between changes in intestinal microorganisms and effect of high temperature on the growth and development of *Bombyx mori* larvae. International Journal of Molecular Sciences 23(18), 10289.
- Sun, X.Q., Huang, Y.X., Dong, C.J., Liu, Z.H., Zheng, C.W., 1996. Silkworm intestinal part aerobic and facultative anaerobic microorganisms and the study of silkworm with probiotics. Sichuan silk 24 (1), 13–15
- Suraporn, S., Liu, J., Ren, F., Wang, L., Feng, M., Terenius, O., Swevers, L., 2025. Towards a rational basis for the selection of probiotics to improve silkworm health and performance. Insects 16(2), 162.
- Tang, M.A.K., 2002. A comparative study on the nutritional quality of four varieties of healthy and disease affected mulberry leaves and determination of factors associated with the disease. (Doctoral dissertation, University of Rajshahi).
- Tayal, M.K., Chauhan, T.P.S., 2017. Silkworm diseases and pests. Industrial Entomology, 265–289.
- Thakur, A., Dhammi, P., Saini, H.S., Kaur, S., 2015. Pathogenicity of bacteria isolated from gut of *Spodoptera litura* (Lepidoptera: Noctuidae) and fitness costs of insect associated with consumption of bacteria. Journal of Invertebrate Pathology 127, 38–46.
- Tian, Z.H., Hui, F.L., Ke, T., Kan, Y.C., Wen, Z.Z., 2007. Molecular analysis of the bacteria community composition in silkworm midgut. Sericultural Science Magazine 33(4), 592–595.
- Trager, W., 1986. Living together: the biology of animal parasitism. Springer Science & Business Media. ISBN 0306423103
- Trivedy, K., Kumar, S.N., Vinutha, N., Qadri, S.M.H., 2011. *In vitro* testing of common disinfectants used in sericulture to control the growth of fungi in rearing

- houses. Research Journal of Microbiology 6(5), 439.
- Ueda, S., Kimura, R., Suzuki, K., 1975. Studies on the growth of the silkworm, *Bombyx mori* L., 4: Mutual relationships between the growth in the fifth instar larvae and the productivity of silk substance. Bulletin of Sericultural Experiment Station.
- Ujjwala, J.S., Chilkale, N.J., Roymon, M.G., 2006. Anti-microbial activity of extract from aloe vera leaf. Journal of basic and Applied Mycology 5(I & II), 98–99.
- Urbanek, K.A., Bakonyi, T., Ando, I., Kurucz, E., Solymosi, N., Pongrac, P., Bercic, R.L., 2022. The effect of feeding with central european local mulberry genotypes on the development and health status of silkworms and quality parameters of raw silk. Insects 13(9), 836.
- Usui, K., Miyazaki, S., Kaito, C., Sekimizu, K., 2009. Purification of a soil bacteria exotoxin using silkworm toxicity to measure specific activity. Microbial Pathogenesis 46, 59–62.
- Vasantharajan, V.N., Munirathnamma, N., 1978. Studies on silkworm diseases, Epizootiology of septicemic diseases of silkworms caused by *Serratia Marcescens*. Journal of the Indian Institute of Science 60(4), 33.
- Voirol, L.R.P., Frago, E., Kaltenpht, M., Hilker, M., Fatouros, N.E., 2018. Bacterial Symbionts in Lepidoptera: Their diversity, transmission and impact on the host. Frontiers in Microbiology, 1–14.
- Wang, Q., Sun, Z., Ma, S., Liu, X., Xia, H., Chen, K., 2022. Molecular mechanism and potential application of bacterial infection in the silkworm, *Bombyx mori*. Developmental and Comparative Immunology 131, 104381.
- Wani, K.A., Jaiswal, Y.K., 2011. Health hazards of rearing silk worms and environmental impact assessment of rearing households of Kashmir, India. Indian Journal of Public Health Research & Development 2(2), 84–88.
- Watanabe, H., Yutaka K., Yu-Xing, W., Takao, S., 1988. Mulberry pyralid, *Glyphodespyloalis*: Habitual host of non-occluded viruses pathogenic to the silkworm, *Bombyx mori*. Journal of Invertebrate Pathology 52, 401–408.
- Xiang, H., Li, M.W., Zhao, Y., Zhao, L.P., Zhang, Y.H., Huang, Y.P., 2007. Bacterial community in midguts of the silkworm larvae estimated by PCR/DGGE and 16S rDNA gene library analysis. Acta Entomologica Sinica 50(3), 222–233.
- Xiang, Y.Q., Wang, X.Q., Feng, W., 2010. Comparative analysis of the composition of dominant intestinal microflora in silkworm reared with different forages. Acta Ecologica Sinica 30(14), 3875–3882.
- Yadav, S., Singh, H., Kumar, A., Singh, H., 2016. Isolation and identification of bacteria responsible for bacterial flacherie disease in mulberry silkworm (*Bombyx mori* L.) under laboratory condition. Annals of Entomology, 32–34.
- Yuan, S., Sun, Y., Chang, W., Zhang, J., Sang J., Zhao, J., Lou, H., 2023. The silkworm (*Bombyx mori*) gut microbiota is involved in metabolic detoxification by glucosylation of plant toxins. Communications Biology 6(1), 790.
- Yup-Lian, L., 1991. Silkworm diseases, 73–74. Food & Agriculture Org.
- Yusuf, L., Oladunmoye, M.K., Ogundare, A.O., 2013. In-vivo Antibacterial activities of mistletoe (*Viscum album*) leave extract, growing on cocoa tree in Akure North, Nigeria. European Journal of Biotechnology and Bioscience 1(1), 37–42.
- Zha, X.L., Wang, H., Sun, W., Zhang, H.Y., Wen, J., Huang, X.Z., Shen, Y.H., 2021. Characteristics of the peritrophic matrix of the silkworm, *Bombyx mori* and factors influencing its formation. Insects 12(6), 516.
- Zhang, P., Zhao, Q., Ma, X., Ma, L., 2020. Pathogenicity of *Serratia marcescens* to hazelnut weevil (*Curculio dieckmanni*). Journal of Forestry Research 32, 409–417.
- Zhang, Y., Shang, R., Zhang, J., Li, J., Zhu, G., Yao, M., Shen, Z., 2020. Isolation and identification of two *Serratia marcescens* strains from silkworm, *Bombyx mori*. Antonie van Leeuwenhoek 113, 1313–1321.
- Zhang, Y., Zhang, J., Xiao, J., Wang, H., Yang, R., Guo, X., Zheng, Y., Yin, Y., Zhang, X., 2023. comCDE (Competence) operon is regulated by *ccpA* in *Streptococcus pneumoniae* D39. Microbiology Spectrum 11(3), 1–22. e00012–23.
- Zhao, L.N., Ma, Y., Yang, X., Iqbal, A., Ruan, C.C., Zang, L.S., 2020. Identification of *Serratia marcescens* isolated from *Antheraea pernyi* eggs and determination of bacterial pathogenicity and transmission pathway. Journal of Invertebrate Pathology 169, 107297.
- Zhao, P., Hong, S., Li, Y., Chen, H., Gao, H., Wang, C., 2024. From phyllosphere to insect cuticles: silkworms gather antifungal bacteria from mulberry leaves to battle fungal parasite attacks. Microbiome 12(1), 40.
- Zou, H., Gu, H., Cheng, J., Tian, C., Shu, Q., Peng, P., Li, B., 2024. The mechanism of damage to the midgut by low concentration of *Bacillus thuringiensis* in the silkworm, *Bombyx mori*. Insects 15(911), 1–12.