A Review Impact of Viral Diseases on Silkworm Bombyx Mori and Its Economic Impact

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***Abstract*—Sericulture is an important agro-based enterprise that contributes substantially to rural livelihoods and economic development, particularly in developing countries. However, the productivity and sustainability of silk production are severely constrained by infectious diseases of the mulberry silkworm, *Bombyx mori*, among which viral diseases are particularly destructive. This review synthesises current knowledge on the major viral pathogens affecting *B. mori*, including *Bombyx mori* nucleopolyhedrovirus (BmNPV), cytoplasmic polyhedrosis virus (BmNPV), denso-viruses (BmDV/ BmBDV), and infectious flacherie virus (Bm IFV). Emphasis is placed on their transmission routes, pathogenic mechanisms, clinical manifestations, host physiological alterations, and impacts on larval survival, cocoon yield, and silk quality. The review further highlights host defence mechanisms involving innate immunity, RNA interference, apoptosis, and major immune-signalling pathways. Conventional and molecular diagnostic approaches, including microscopy, immunological assays, PCR-based detection, biosensors, and lateral flow assays, are discussed in relation to early disease diagnosis. Current disease-management strategies encompassing hygienic rearing, disease-free layings, balanced nutrition, probiotics, molecular diagnostics, and resistant silkworm strains are evaluated. Emerging approaches such as RNA interference, CRISPR/Cas-mediated genome editing, and genomic breeding offer promising opportunities for sustainable disease control. Integrating modern biotechnology with preventive management and continuous surveillance is essential for reducing economic losses and strengthening the long-term sustainability of sericulture.**

***Index Terms*—Bombyx mori, viral infections, sericulture, cocoon yield, economic loss, disease management.**

I. INTRODUCTION

Sericulture is an important agro-based enterprise that contributes substantially to rural employment, income generation, and economic development, particularly in developing countries. The domesticated mulberry silkworm, *Bombyx mori* (Lepidoptera: Bombycidae), is the principal insect species used for commercial silk production. Its productivity depends on successful larval development, efficient utilisation of mulberry leaves, healthy cocoon formation, and production of high-quality silk. However, silkworm rearing is vulnerable to several infectious diseases, among which viral diseases are particularly important because of their high transmissibility, rapid progression, and potential to cause severe crop losses.

Several viruses are recognised as important pathogens of *B. mori*, including *Bombyx mori* nucleopolyhedrovirus (BmNPV), *Bombyx mori* cytoplasmic polyhedrosis virus (BmCPV), *Bombyx mori* densovirus (BmDNV), *Bombyx mori* bidensovirus (BmBDV), and *Bombyx mori* infectious flacherie virus (BmIFV). These pathogens differ in their genome organisation, tissue tropism, replication strategies, and disease manifestations, but collectively cause substantial reductions in larval survival, cocoon production, and silk quality. Recent reviews likewise identify BmNPV, BmCPV and densoviruses among the major viral threats to silkworm production. (R. Zhang, X. Hu, C. Li et al., 2026)

Among these pathogens, BmNPV is considered one of the most destructive viral pathogens of the silkworm and is responsible for grasserie disease. Infection generally occurs through ingestion of virus-contaminated mulberry leaves or contaminated rearing materials. Following entry into the larval midgut, viral replication and dissemination through the haemolymph result in systemic infection involving

tissues such as the fat body, tracheal system, epidermis, Malpighian tubules, silk glands, and gonads. Consequently, infected larvae exhibit characteristic symptoms including lethargy, loss of appetite, body swelling, shiny integument, haemolymph discolouration, loss of body-wall integrity, and eventual death. Lu et al. (2018).

BmCPV primarily infects larval midgut epithelial cells and interferes with digestion and nutrient absorption, resulting in poor growth, developmental abnormalities, and reduced cocoon formation. Densovirus infections also predominantly affect midgut epithelial cells and may cause chronic physiological damage, reduced vitality, stunted growth, and poor cocoon formation. BmIFV is associated with digestive disorders and may occur with bacterial or other enteric infections, increasing disease severity.

The epidemiology and severity of viral diseases are influenced by interactions among pathogen virulence, host genotype, environmental conditions, nutrition, and rearing practices. High temperature and humidity, overcrowding, inadequate sanitation, poor-quality nutrition, and contaminated mulberry leaves can favour pathogen multiplication and transmission. Viral pathogens may spread horizontally through contaminated leaves, rearing equipment, and the rearing environment, while vertical transmission through infected eggs can contribute to persistence across generations.

At the molecular level, *B. mori* relies predominantly on innate immune mechanisms to combat viral infections. Antimicrobial peptides, apoptosis, reactive oxygen species, small-RNA-mediated responses, and signalling pathways including Toll, Imd, and JAK/STAT participate in antiviral defence. Studies of silkworm antiviral immunity have further demonstrated the involvement of multiple cellular and molecular pathways and have emphasised the complex interaction between viral replication and host defence mechanisms (Li et al., 2018).

The consequences of viral infection extend beyond larval mortality. Disease outbreaks can reduce cocoon yield, shell weight, filament length, and silk quality while increasing expenditure on disease prevention, sanitation, and replacement of infected batches. Consequently, viral diseases have implications not only for individual rearers but also for the productivity and economic sustainability of the sericulture sector.

Early and accurate diagnosis is therefore a critical component of disease management. Conventional diagnostic methods based on symptom observation and microscopy are useful but may be inadequate for detecting latent or early infections. Molecular techniques such as polymerase chain reaction (PCR), quantitative PCR, loop-mediated isothermal amplification (LAMP), and other nucleic-acid-based assays provide improved sensitivity and specificity. Recent advances have also introduced field-compatible diagnostic platforms, including lateral-flow assays and other rapid molecular approaches, facilitating earlier detection and disease containment. A recent comprehensive review highlights the increasing importance of molecular diagnostics for detecting BmNPV, BmCPV, BmIFV, BmBDV and other silkworm pathogens. (Deepika I et al. 2024)

Disease management traditionally relies on disease-free layings, strict hygiene, disinfection of rearing facilities, proper disposal of infected larvae, environmental management, and continuous disease surveillance. However, advances in molecular biology and biotechnology are opening new possibilities for sustainable disease control. RNA interference, genomic selection, molecular markers, transgenic approaches, and CRISPR/Cas-based genome editing are being investigated for developing virus-resistant silkworm strains. Recent research particularly emphasises the identification of resistance-associated genes and the integration of multi-omics approaches with molecular breeding to enhance BmNPV resistance.

In this context, the present review provides a comprehensive assessment of the major viral diseases affecting *B. mori*, with emphasis on their causative agents, transmission mechanisms, pathogenesis, clinical manifestations, host defence responses, physiological effects, diagnostic approaches, and economic consequences. It further evaluates conventional preventive measures and emerging molecular and biotechnological strategies for disease management. An integrated approach combining hygienic rearing, disease surveillance, early molecular diagnosis, appropriate nutrition, resistant silkworm strains, and modern biotechnology is essential for minimising disease-associated losses and strengthening the long-term sustainability of sericulture.

II. MAJOR VIRAL DISEASES OF SILKWORM

1 Nucleopolyhedrovirus (BmNPV)

Nucleopolyhedrovirus is the most destructive viral pathogen affecting silkworms and is responsible for grasserie disease. Infected larvae typically exhibit body swelling, fragile integument, and accumulation of milky hemolymph. The virus replicates extensively within host tissues, leading to systemic infection and death (Suraporn et al., 2024).

Causative agent:

The major causative agent of grasserie disease, i.e. BmNPV, is the destructive viral pathogen of Bombyx mori, which belongs to the genus Alphabaculovirus of the Baculoviridae family. This virus has a circular double-stranded DNA genome of approximately 128 kb with rod-shaped nucleocapsids. Characteristic polyhedral occlusion bodies are produced by the virus which protects it outside the host and facilitate oral transmission during the infection.

Occurrence and incidence:

When silkworm feeds on mulberry leaves contaminated by BmNPV the grasserie disease is caused.(Jiang and Xia, 2014). The Occlusion Bodies (OBs) are responsible for causing infection in the host. These OBs are the proteinaceous structures which act as an infectious unit of NPV which contains virons (viral particles). First symptoms are observed after 5-7 days of infection and till that silkworm shows no symptoms more than ⅔ of incubation period. The symptoms include shiny appearance of the skin, inter segmental swelling, haemolymph turning milky white.The bodies of diseased larvae gets hanged sometimes with head facing downwards towards its claws. Gradually most of the organs get degenerated and liquefied and the silkworm dies with integument getting fragile and rupturing, releasing liquefied tissues of the pupa (Nataraju et al., 2005). The dead diseased pupae and moth release the infectious OBs, which can cause infection to the healthy silkworms by contaminating the silkworm rearing environment, rearing house, etc.

Infection and Transmission

The primary route of infection is oral ingestion of occlusion bodies attached to contaminated mulberry leaves or rearing equipment. After entering the alkaline environment of the larval midgut, the occlusion bodies dissolve, releasing occlusion-derived virions. These virions infect midgut epithelial cells and subsequently produce budded virions that disseminate through the haemolymph to systemic organs including:

Fat body → Tracheal system → Epidermis → Malpighian tubules → Silk glands → Gonads

The extensive replication of BmNPV eventually destroys host tissues, causing systemic infection and death.

Symptomatology of Nuclear polyhedrosis:

During the early part of the disease, no symptoms are noticed except the worms being slightly sluggish. Initially, the skin shows an oily and shining appearance. The external symptoms of the BmNPV disease of silkworm in the fourth and fifth instar larva, which are visible about a week after infection, include the following: Swelling of inter segmental regions Larvae become lethargic and loose appetite Shining and yellowing body Hyperactivity Crawling around trays and hanging Rupturing of the skin White ooze filled with polyhedra Crawling around the periphery of the rearing tray Death of worms Diseased larvae loose the clasping power of abdominal legs, except the caudal legs by which it hangs with the head downwards. Rotting and secondary infections. Nuclei of cells of various tissue contain polyhedral bodies. The larva becomes restless and impatient, causing fatigue (Krishnamohan,1986). Epidermal cells and cells of all infected tissue become abnormal. If infection occurs in the early instars, the worms fail to spin the cocoons and die, whereas if the infection occurs at later stages, the worms could spin the cocoons but subsequently die inside, producing melted cocoons, and the affected cocoons become unfit for reeling (Chitra C 1975).

BmNPV detection:

In order to stop the spread of the disease, the detection of BmNPV is required by taking suitable preventive steps and some control measures, and for certification in National and International trade. Diagnostic procedures are essential to allow rapid detection of inoculum. The level at which the disease becomes apparent depends to a large extent on the ability of the

observer to recognise the disease. Many times the disease is recognised once it reaches epidemic levels (lethal). Then it is too late to apply a control measure once the symptoms start to appear. It is necessary for the insect pathologists to generate sensitive and portable assays which can rapidly diagnose the disease before it is lethal, as the absence of disease symptoms does not guarantee absence of pathogen or freedom from pathogen-induced mortality. The present most common methodologies for BmNPV detection include microscopy, in vivo assays and nucleic acid-based analysis (Joshi and Raja, 2016). Other tech-niques that have been developed to detect BmNPV include Enzyme-Link Immunosorbent Assay (ELISA) (Vanapruk et al., 1992), DNA hybridization (Attathom et al., 1994), colloidal textile dye-based dipstick immunoassay (Nataraju et al., 1994), protein-A linked monoclonal antibody latex agglutination test (PALMAL) (Shamim et al., 1995) and viral DNA transfection (Martinex-Zubiaur et al., 2016). The nucleus-based analysis technique Polymerase Chain Reaction (PCR) and sequencing for BmNPV detection can be complicated by external factors. For example, prior to analysis, a sample clean-up stage is required as the original stock inoculum may contain high levels of fats, carbohydrates, etc. There can be possibilities of variations due to transportation of samples, processing and testing conditions, which can make the data unreliable. The best technology to detect the presence and amount of a pathogen in any kind of environment is the use of biosensors and Lateral Flow Assay (LFA). A biosensor is a device that can report the presence or activity of analytes using a biomolecular component providing specificity to the sensor by binding or interacting with the analyte and can cause a detectable change in mass, fluorescence, electric charge, or refractive index, and a transducer element, able to transform this interaction into a suitable electronic signal. The Lateral Flow Assay (LFA) is a paper-based platform for the detection and quantification of analytes in complex mixtures, where the sample is placed on a test device, and the results are displayed within 5-30 min. Because LFAs are cheap to produce, easy to use, and can detect diseases easily, they are widely accepted by users (Koczula and Gallotta, 2016) and are convenient for field use because they require no refrigeration and have a long shelf life. For the Polymerase Chain Reaction, LFAs are categorised into Lateral Flow Immunoassays (LFIAs), which use only antibodies as recognition elements, and Nucleic Acid LFAs (NALFAs) (Connelly et al., 2008). Both these techniques are developed for ‘on-site’ diagnostics for performing outside the laboratory, which is capable of testing and yielding results without any trained personnel, laboratory equipment, or reagents.

2. Cytoplasmic Polyhedrosis Virus (CPV):

CPV can be transmitted between various hosts, including insects of the orders Lepidoptera, Hymenoptera and Coleoptera and can generate crystal polyhedra in the cytoplasm of the midgut epithelium of infected insects (Belloncik 1989).

Cytoplasmic Polyhedrosis Disease of Silkworm

The BmCPV causes major damage to the sericulture industry, which is a major pathogen of silkworm. The CPV disease is caused by an occluded double-stranded RNA virus that multiplies in the cytoplasm of columnar cells of midgut epithelium. The disease shows symptoms like flaccid body, paleness of skin, vomiting, etc

Causative agent:

This virus of silkworm, i.e. Bombyx mori Cytoplasmic Polyhedrosis Virus (BmCPV) belongs to the CPV subfamily consisting of 19 distinct species (electropherotypes) of the Cypovirus genus of the Reoviridae family (Shapiro A.2005, Graham RI 2006). The virus particle is globular, 60-70 nm in size, icosahedral, hexahedral; each capsomer extends outwards to form a four-jointed projection, the tip of which carries a globular body concealing the two distal joints. The capsid consists of two icosahedral coats linked to a tubular structure at the opposing apices and a core at the centre of the capsid. BmCPV tends to infect epithelial and columnar cells of the midgut of the silkworm. The infected silkworms show symptoms like hypogenesis, emaciation and sluggishness, and when the infection increases, white wrinkles are observed in the posterior part of the midgut, which is the major symptom of CPV disease (Magnoler A. 1974).

Occurrence and Infection

Occurrence of this disease is throughout the year, while severity is observed more during the summer and rainy season. Incidence of diseases differs from

region to region, crop to crop and even farmer to farmer in the same crop (Kumari KV et al., 2001). Crop losses are mainly observed more in the tropics than in temperate regions, around 30% (Sengupta K, 1988). The weather conditions greatly influence the outbreak of BmCPV disease during the rearing period.

Infection and Transmission

Infection mainly occurs orally as the virus and polyhedra enter the digestive tract when the mulberry leaves are swallowed by the silkworm. The virions get lined up in rows and get enclosed to form polyhedral proteins in the cytoplasm. After entering the body, the BmCPV first parasitises the tubular cells at the junction of the mid and hind gut to form a milky white fold. The milky white portion increases in the midgut region, impairing its digestive and absorptive functions, turning the whole body of the worm into milk white colour, forming large quantities of host proteins to form viral and polyhedral proteins, which causes disturbances in nucleic acid and protein metabolism. This results in the decrease of free amino acid content of the haemolymph, the digestive fluids and tissues and there even occurs an absence of some amino acids, leading to physiological dysfunction. The tubular cells get packed with polyhedra, which causes the cells to swell and finally burst. The polyhedra and viral particles also get released into the cavity of the intestine, which are then excreted in the faeces with a milk white colour.

Symptomatology of Cytoplasmic Polyhedrosis

Symptoms of the disease occur slowly. Small worms infected with less virus do not show any symptoms until the fifth instar. If infection occurs at the first instar, then symptoms are observed at the second and third instars; if at the second instar, then the symptoms at the third and fourth instars; if at the third or fourth instar, then symptoms appear in the fifth instar and if in the fifth instar, then no symptoms are seen. Larvae show symptoms like sluggishness, loss of appetite, cease feeding and sometimes diarrhoea and vomiting gut juice and Stunted growth and development. The head becomes disproportionately large and translucent, and the body shrunken. There is frequent expulsion of semi-solid and whitish faecal matter. The midgut gets chalky white and opaque. Infected pupae appear to be smaller than the healthy ones, and infected moths lay fewer eggs and have a short life span. On dissection, the midgut of infected larvae appears to be whitish and opaque instead of green and transparent, which is of the healthy larvae. Anal region is solid, and rectal protrusion is noticed occasionally. If infection occurs at the adult larva stage, then a transparent thorax is observed with body atrophy and vomiting and diarrhoea. The disease is often affected by factors like temperature, humidity and quantity and virulence of the virus. The infection usually occurs at the third and fourth instar, and the onset of disease at the fifth instar, which occurs mainly during summer and autumn rearing seasons.

Disease Detection

To detect the disease, dissection can be performed by tearing open the body wall rostrally to the caudal horn and finding a milky white circular prominence in the posterior part of the midgut. Dissecting out tissue from the caudal part of the midgut and pressing specimens should be prepared to observe under a 400-600x microscope. If the disease has been caused, then there will be the presence of polyhedra.

3. Densovirus (DNV):

Densovirus infection results in chronic disease characterised by slow growth and reduced vitality. Although mortality rates may vary, the overall productivity and quality of silk are adversely affected (Khan et al., 2023).

Densovirus infection is another economically significant viral disease affecting commercial silkworm production. Earlier classified within the family Parvoviridae, several silkworm densoviruses are now classified under the family Bidnaviridae because of their unique bipartite linear DNA genome. These viruses specifically infect the epithelial cells of the larval midgut.

Pathogenesis

Following oral infection, viral replication occurs mainly in the nuclei of midgut epithelial cells, causing degeneration of digestive tissues. Unlike BmNPV, densovirus infection progresses more slowly but produces persistent physiological damage. Studies have shown that susceptibility is strongly influenced by the nsd-2 gene, which encodes a putative amino acid transporter acting as a viral receptor. Resistant silkworm strains carrying recessive nsd-2 alleles exhibit significantly lower infection rates, making this

gene an important target for breeding disease-resistant varieties.

Symptomatology of Densovirus:

Reduced appetite, Stunted growth, Transparent thoracic region, Soft body, delayed development, Digestive dysfunction, Poor cocoon formation. Mortality varies according to viral strain and host genotype but may reach significant levels under intensive rearing conditions.

In silkworm, flacherie disease is caused by Bombyx mori densovirus (BmDNV). The BmDNV was previously divided into type-1 (BmDNV-1) and type-2 (BmDNV-2 and-Z) based on differences in their virulence toward silkworms, serological characteristics and genomic structures (Watanabe 1978,1986; Seki 1984). The genus is Iteravirus of BmDNV-1, while BmDNV-2 and- Z come under the Bidensovirus genus of the subfamily Densovirinae, or parvovirus-like viruses. At present, BmDNV-1 has been reassigned to the Iteradensovirus genus and has been renamed BmDV [8]. On the other hand, BmDNV-2 and-Z were excluded from the Parvoviridae family because of their bipartite genome structure and a DNA polymerase motif within their genomes. These viruses belong to the Bidensovirus genus, Bidnaviridae family and are designated as *B. mori bidensovirus* (BmBDV) (Adams 2012).

Infection:

It is observed that BmDV and BmBDV multiply only in the columnar cell nuclei in the larval midgut epithelium with no pathological changes in the other tissues (Shimizu 1975; Seki 1983; Watanabe1976). Silkworms infected with BmDV show hypertrophic nuclei in the columnar cells, markedly stained with the Feulgen reaction of methyl green, observed under histopathological studies of the midgut epithelium (Watanabe1976). The degenerated columnar cells are eventually liberated into the midgut's lumen (Watanabe1976; Ito 2013). In the BmBDV infection, almost identical features were observed in the midgut (Seki 1983). However, the course of BmDV infection is significantly different from BmBDV infection. Larvae infected with BmDV show major symptoms of flaccid body, and death of larvae occurs within 7 days postinfection (DPI) (Ito 2013; Watanabe1988). The BmBDV infection shows no external symptoms until 6-7 DPI, and death occurs within 10-20 DPI (Watanabe 1988; Ito 2016). These results suggest that BmBDV infection is acute, whereas BmDVs infection is chronic (Watanabe 1988).

4. Bombyx mori Densovirus (BmDVs)

Bombyx mori Densoviruses (BmDVs) are mainly classified into two types, type I and type II, based on their genetic constituents. BmDVs are DNA viruses. To date, three isolates of BmDV have been reported. They are: (1) BmDV-1(Ina isolate),

(2) BmDV-2 (Saku isolate and Yamanashi isolate) and finally

(3) BmDV-Z (Zhenjiang isolate).

BmDV-1 contains a single-stranded DNA that is about 5 kb in length. On the contrary, BmDV-2, possessing a split genome, comprises two types of single-stranded linear DNA molecules. BmDV-2 (Yamanashi isolate) and BmDV-Z (Zhenjiang isolate) contain two ssDNA molecules which are 6.0 and 6.5 kb in length. BmDV type I was found to have a higher pathogenicity to silkworm than type II. As per previous classification, BmDV-1, -2 and -Z were all classified into the genus named Bidensovirus. However, recently BmDV-2 and BMDV-Z have been excluded from the family of Parvoviridae due to their unique bipartite genome and the presence of a DNA polymerase motif of their own (Wang et al., 2007; Ito, 2008; Kadono-Okuda, 2010).

Symptomatology of Densovirus:

Flacherie causes massive loss in silk yield and is one of the most widespread and fatal diseases of the silkworm. It occurs when silkworms feed on mulberry leaves contaminated by viruses. The midgut columnar cells get infected, where the infected cells carry hypertrophied nuclei in which the virus multiplies. Anorexia and lethargy are observed, leading to body flaccidity and inhibition of moulting or metamorphosis. BmDV-infected larvae become whitish and progressive paralysis occurs (Meynadier et al., 1964; Chao et al., 1985). Death occurs within 2-20 days depending on the DV isolate, larval stage, virus concentration, and the way of infection: natural (epidemic)or experimental (per os or inoculation) transmission. BmDV per os infected larvae show major symptoms of body flaccidity, with death usually occurring after 7 days.

BmDVs infect only the columnar cells of midgut epithelium, where they multiply in the nucleus,

developing diarrhoea due to loss of midgut tissue, turning dark brown in colour, making the body flaccid and eventually the larvae die. The nucleoplasm can be studied histopathologically by staining it with DNA-chromophilic methyl green or Feulgen reagent, which shows that Flacherie can be solely caused by the infection of BmDV or by the combined infection of BmDV and NPV. The alimentary canal of the diseased larva appears pale yellow. The virulence of each isotype is different from each other; for example, BmDV-2 only infects the columnar cells of midgut epithelium, while BmDV-Z infect columnar cells of midgut epithelium during the early stage of infection and can also infect goblet cells of midgut epithelium (Wang et al.,2007). When flacherie-diseased silkworms were collected from different sericulture areas of Southern India and screened for BmDV-2 infection through qPCR analysis, high copy numbers of BmDV-2 in the midguts of the flacherie-diseased silkworms ranged from an average of 2.9x105 to 6.4x109. This finding confirmed the presence of viable BmDV-2 in quite high numbers in the field and its widespread association with flacherie disease in *B.mori* (Kadono et al.,2014)

5. Infectious Flacherie Virus (IFV)

IFV is associated with soft and flaccid bodies, retarded growth, making them inactive and vomiting gut juice, with faecal matter appearing soft with high moisture content and sometimes chain type of excreta with rectal protrusion. (Alkesh I. 2016)

Bombyx mori Infectious Flacherie Virus (BmIFV)

Infectious flacherie is primarily caused by Bombyx mori infectious flacherie virus (BmIFV), a positive-sense single-stranded RNA virus belonging to the family Iflaviridae. The disease frequently occurs together with bacterial infections or other enteric viruses, resulting in severe gastrointestinal pathology.

Infection Mechanism

BmIFV infects epithelial cells of the digestive tract after oral ingestion. Viral replication destroys intestinal tissues, disrupts nutrient absorption, and damages gut integrity. Secondary bacterial invasion commonly follows, increasing disease severity and mortality. Environmental stress, particularly high temperature and humidity, greatly enhances disease incidence.

Symptomatology of Infectious Flacherie Virus:

Sudden loss of appetite →Vomiting→ Diarrhoea →Yellowish-brown faeces → Soft and flaccid body → Irregular moulting → Dehydration →Foul-smelling cadaver →Failure to spin normal cocoons →Infected larvae become weak, translucent, and eventually die due to severe disruption of digestive physiology.

Bioassay studies

To study infectivity of the isolated bacteria, a bioassay was conducted during July-August, 2019. All the isolated bacterial strains were inoculated at a concentration of 1× 107 cfu/ml to B. mori (M.Con.4), healthy silkworms on the first day of the III instar by leaf disc method. Enumeration of bacteria was determined by the serial dilution technique. Three replications of fifty larvae were maintained for each treatment. 200µl of inoculum was smeared uniformly on a mulberry leaf disc, measuring 7.5 cm in diameter. Each batch of 50 larvae was fed with 2 such leaf discs. A control batch was also maintained devoid of inoculation but fed with leaves smeared with distilled water. Based on visual symptoms and microscopic examination, mortality caused by flacherie was recorded. Infectivity test was performed based on Koch's postulates to confirm the pathogenicity of the bacterial isolates. Flacherie infected larva from the treatment batches were collected after inoculation, and bacteria were re-isolated and purified following the same methodology as delineated above. (K. Rahul et al., 2020)

Causative agent

Flacherie is commonly caused by Bombyx mori Flacherie Virus (BmFV), Bombyx mori Densonucleosis Virus (BmDV), or bacterial infections caused by Staphylococcus spp., Streptococcus spp., Serratia marcescens and Bacillus thuringiensis, among others. Infection can occur from a single pathogen or from a combination of pathogens. Infection can be primarily caused by contaminated mulberry leaves, faecal matter, body fluids and gut juices of infected larvae [SILKS, India,2025]. Infected larvae show a flaccid body, vomit gut juice and can cause loose faeces with rectal protrusion (Balavenkatasubbaiah M, 2025). Flacherie occurs most commonly in summer and least in winter [Selvakumar T, 2013]. Cappellozza et al. (2011) were the first to report Enterococcus

mundtii as a causative agent of flacherie. In their study, they isolated the pathogen from contaminated mulberry leaves and traced infection to an artificial diet prepared from contaminated leaf dust. (Ayoade et al. 2014) identified Citrobacter freundii, Citrobacter amalomaticus, Bacillus badius, Staphylococcus epidermidis, Staphylococcus marcescens and Enterobacter cloacae as primary bacterial agents responsible for severe infections in silk-rearing regions of southwest Nigeria. Another investigation in Karnataka state of India found Pseudomonas fluorescens, Providencia rettgeri, Streptococcus pneumoniae, Staphylococcus aureus, Bacillus subtilis, Bacillus cereus, Enterobacter aerogenes, Klebsiella cloacae, Providencia vermicola and Escherichia coli in infected silkworm larvae (Swathi HC, 2015). Furthermore, gram-positive bacteria such as Bacillus sphaericus, Bacillus circulans, Bacillus cereus, Paenibacillus macerans, Streptococcus spp., and Staphylococcus epidermidis were identified as major causes of flacherie. These pathogens exhibited resistance to various antibiotics including penicillin, chloramphenicol, quinolones, macrolides, tetracycline and sulphonamides (Gurugulova K I, 2017).

Transmission and Disease Development

Most DNVs are responsible for causing fatal diseases in insects, mostly infecting the larval stages, although pupal stages are also infected in natural populations or due to experimental contamination. (Boemare and Bres, 1969; Suto et al., 1979). Fluctuating temperature and humidity conditions as well as poor quality of mulberry leaf are the main factors causing the disease (K. Kadono-Okuda, 2014). Following entry into the host, viral particles replicate rapidly and spread through the hemolymph to various tissues, including the fat body and silk glands. This systemic infection results in severe tissue damage and eventual mortality (Li et al., 2023).

The successful establishment of viral infection in Bombyx mori depends on the interaction between viral pathogenicity, host susceptibility, environmental conditions, and rearing management. Viral pathogens are highly contagious and spread rapidly under intensive sericulture systems, where thousands of larvae are reared in close proximity. Because silkworms consume large quantities of mulberry leaves during the fifth instar, contaminated foliage serves as the principal route of infection. Once introduced into a rearing house, viral pathogens can rapidly infect an entire batch of larvae, resulting in severe mortality and substantial economic losses.

Host Defence Mechanisms

Silkworms rely on innate immune responses to combat viral infections. These include antimicrobial peptide production, RNA interference (RNAi), and apoptosis. Key signalling pathways such as Toll, Imd, and JAK/STAT are also involved in regulating immune responses (Ayaz et al., 2025).

However, viruses have evolved mechanisms to evade these defences, enabling successful infection and replication within the host. The interaction between silkworm viruses and their host represents a complex molecular "arms race." During infection, viruses manipulate host metabolism to maximise replication, whereas the host activates multiple innate immune mechanisms to restrict pathogen proliferation.

Recent genomic and transcriptomic studies have identified hundreds of genes whose expression changes following viral infection. These include genes involved in immunity, metabolism, apoptosis, oxidative stress, protein degradation, and signal transduction.

BmNPV infection, for example, alters the expression of numerous host proteins associated with: Cell cycle regulation, DNA replication, Protein synthesis, Cytoskeleton organization, Mitochondrial function, energy metabolism, and immune signalling. These alterations create an intracellular environment favourable for viral replication while suppressing normal host defence mechanisms. Viral proteins also interfere with transcription factors responsible for activating antiviral genes, thereby delaying immune responses and increasing viral survival.

Proteomic studies have further demonstrated that BmNPV modifies host lipid metabolism, amino acid biosynthesis, and carbohydrate utilisation, enabling infected cells to meet the high energy demands associated with rapid viral multiplication.

Effects on Silkworm Physiology

The primary cause of Flacherie disease in silkworms is due 3 the physiological weakness of the organism combined with the invasion of pathogenic/ non-pathogenic microbes. Adverse environmental conditions, starvation of silkworms, feeding silkworms with poor-quality mulberry and improper

handling are the major causes for the weakness in silkworms, which, upon causing external injury, can infect the wound with microbes leading to Flacherie. In such physiologically weak larvae, even the non-pathogenic bacteria microflora of the midgut multiply at a faster rate, alter the gut environment and penetrate up to the haemolymph, causing flaccidity. (Alkesh I. 2016)

III. ECONOMIC CONSEQUENCES

1. Decline in Cocoon Yield

When mulberry silkworms are fed without proper nutrition, it is found that if the temperature in the wormhole changes sharply, the productivity (biological, productivity, variety) of the cocoons decreases as a result of the negative impact on the activity of the silkworm. It is also of practical importance that there is a link between silkworm activity and cocoon productivity and that mulberry silkworms, which are necessary for production, produce positive cocoons from new breeds and hybrids. (Ch Bekkamov, 2022).

2. Deterioration of Silk Quality

Silk deterioration involves the molecular scission of fibroin chains, which leads to the loss of structural integrity, processes influenced by environmental stressors such as temperature, humidity and pollutants, as well as potentially by manufacturing variables. (Ibrahim Elrefaey et al.,2026)

3. Increased Production Costs

The limited contribution of agriculture cooperatives in supporting and improving the economics of natural silk production. This limitation has led to decreased productivity, increased Production Costs and weakened competitiveness both locally and globally. (Abdel Hamed E. 2025)

4. Broader Economic Impact

At an industry level, viral diseases disrupt silk supply chains, affect pricing, and reduce overall production, thereby impacting rural economies dependent on sericulture (Singh et al., 2024).

Factors Influencing Disease Outbreaks:

Environmental conditions such as high humidity and temperature, along with poor hygiene, overcrowding, and inadequate nutrition, significantly increase susceptibility to viral infections (Das et al., 2023). Proper management practices are essential to minimise disease incidence.

IV. DISEASE MANAGEMENT STRATEGIES

1 Preventive Practices

Maintaining hygienic rearing conditions, using disease-free layings, and regular disinfection are critical preventive measures (Suraporn et al., 2024).

2 Nutritional and Biological Approaches

Balanced nutrition and the use of probiotics can enhance silkworm immunity and improve resistance to viral infections (Bhuvana et al., 2024).

3 Genetic and Biotechnological Interventions

The sequencing of genomes of major silkworm pathogens has opened new avenues for understanding their biology and identifying novel control targets. Transcriptomic and proteomic studies of infected silkworms have revealed how pathogens like *N. bombycis and B. bassiana* manipulate host pathology, including hijacking metabolic pathways and suppressing immune responses (HU et al., 2021; Lu et al, 2021)

V. FUTURE DIRECTIONS

Future research should focus on the production of fully sustainable silk that are not only economically viable but also ecologically sound and socially equitable, which will require a multi stakeholder approach, involving Researchers, extension workers policy makers and farmers to conduct create and implement integrated pest and disease management strategies that are tailored to local conditions and needs, ensuring the long-term health and prosperity of the global silk industry. (Likhit Kumar R, 2026)

VI. CONCLUSION

Viral diseases represent a persistent and economically significant constraint to *Bombyx mori* rearing, with major consequences for larval survival, cocoon productivity, silk quality, and the profitability of sericulture. Among the principal viral pathogens, *Bombyx mori* nucleopolyhedrovirus (BmNPV), cytoplasmic polyhedrosis virus (BmCPV), densoviruses (BmDV/BmBDV), and *Bombyx mori*

infectious flacherie virus (BmIFV) exhibit diverse pathogenic mechanisms and transmission patterns, but collectively pose a substantial threat to successful silkworm production. Their rapid dissemination under intensive rearing conditions, together with the influence of host susceptibility and environmental factors, underscores the complexity of effective disease management.

Sustainable control of viral diseases requires a comprehensive and integrated disease-management framework rather than reliance on any single intervention. Conventional measures, including the use of disease-free layings, strict rearing-house hygiene, regular disinfection, appropriate environmental management, balanced nutrition, and continuous disease surveillance, remain fundamental components of disease prevention. These approaches should be strengthened through the application of sensitive and rapid molecular diagnostic technologies capable of detecting infections at an early stage, before the development of severe clinical disease and widespread transmission.

Recent advances in molecular biology, genomics, and biotechnology have expanded opportunities for developing more precise and sustainable strategies for viral disease control. RNA interference, genomic and molecular breeding, probiotics, and CRISPR/Cas-mediated genome editing offer promising avenues for enhancing antiviral responses and developing disease-resistant silkworm strains. Nevertheless, these emerging technologies should be viewed as complementary tools that must be integrated with established biosecurity and rearing practices.

Future progress in sericulture will therefore depend on the convergence of preventive management, early molecular diagnosis, host-resistance breeding, biotechnology, and farmer-level disease surveillance. Such an integrated, evidence-based approach can improve disease preparedness, minimise production losses, enhance cocoon and silk quality, and strengthen the resilience and economic sustainability of the sericulture sector. Continued research into host–virus interactions, resistance mechanisms, field-deployable diagnostics, and sustainable antiviral interventions will be essential for developing effective disease-management systems and ensuring the long-term productivity of *B. mori* cultivation.

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