

## ABSTRACT

*Bombyx mori*, commonly known as the domestic silkworm, is a fascinating insect of great economic significance. It belongs to the family *Bombycidae* within the order Lepidoptera. Despite its critical role in silk production, the silkworm, *Bombyx mori*, is susceptible to various bacterial diseases that can have detrimental effects on sericulture. Common bacterial diseases in silkworms include bacterial flacherie, grasserie, bacterial wilt, enterococcal infections, and staphylococcal infections, which can result in substantial economic losses in the sericulture industry. Several bacterial pathogens pose significant threats to silkworm population. *Bacillus thuringiensis*, *Bacillus cereus*, *Clostridium perfringens*, *Staphylococcus aureus*, *Enterococcus faecalis*, *Pseudomonas aeruginosa*, *Serratia marcescens* and *Staphylococcus aureus* are just few examples of bacterial strains that can infect silkworm.

In current study, pathogenic bacteria were isolated from diseased silkworm larvae. Isolates were characterized through traditional microbiological techniques, including microscopy, colony morphology, and gram staining, etc. Pathogenicity was checked by blood agar test. Molecular techniques, such as DNA extraction through phenolchloroform method was used and 16S rRNA gene sequencing was employed for precise taxonomic classification. The identified bacterial species predominantly belonged to genera commonly associated with silkworm infections, such as *Bacillus*, *Enterococcus*, *Pseudomonas*, and *Serratia*. The resistance developed in these pathogenic strains against various antibiotics was checked through well diffusion method.

This work offers valuable insights into the molecular basis of silkworm-pathogen interactions, which can potentially inform strategies to enhance the health and productivity of silkworm populations in the sericulture industry.

**Key words:** Pathogenic bacteria, DNA extraction, 16S rRNA sequencing, Colony morphology, Antibiotic resistance