

Research Paper

ISOLATION AND CHARACTERIZATION OF GUT-BACTERIA OF MUGA SILKWORM (ANTHERAEA ASSAMENSIS HELFER) COLLECTED FROM DIFFERENT LOCALITIES OF ASSAM

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ABSTRACT

Muga silkworm (*Antheraea assamensis Helfer*) producing golden-yellow silk is a semi-domesticated, multivoltine, sericigenous insect endemic to North-east India. *A. assamensis* primarily feeds on Som (*Persea bombycina* Kost) leaves, the major ingredients of which being pectins, cellulose, starch, xylan, lipid and fatty acids. Gut microflora of muga silkworm synthesize digestive enzymes and play a functionally significant role by degrading the leaf contents to provide better nutritional uptake by the silkworm and eventually improve the productivity. In the present study, bacteria were isolated from the gut of muga silkworm larvae collected from different localities of Assam by culture dependent technique using Nutrient Agar and Brain Heart Infusion Agar media. The 12 bacterial isolates comprised of eight gram positive rods, two gram negative rods, one gram positive coccus and one gram negative coccus. Further biochemical characterization of the gut-bacteria was carried out by using rapid identification kit (Himedia Ltd., Mumbai). On the basis of biochemical characteristics, the dominant gut-bacteria identified were *Bacillus* sp., *Proteus* sp., *Escherichia coli etc. In-vitro* screening of the isolates were done by amylase, pectinase, xylanase, lipase and cellulase test. The positive results revealed the possible influence of gut-bacteria on digestion and utilization of leaf carbohydrates, lipids and fatty acids for better productivity of Muga.

Key words: Amylase, *Antheraea assamensis*, cellulase, gut microflora, pectinase, xylanase.

INTRODUCTION

Muga silkworm (*Antheraea assamensis* Helfer) is a semi-domesticated, multivoltine, sericigenous insect endemic to North-east India. It produces the natural glistering golden-yellow silk of good economic value. Initially, Muga silk production was confined to the state of Assam and later, adopted by other North Eastern states and certain parts of West Bengal. Muga silkworm life cycle include four stages *viz.*, egg, larval instars, pupa within cocoon and adult moth. The larvae primarily feed on the leaves of Som (*Persea bombycina*) and Soalu (*Litsea polyantha* Juss) plants belonging to the family, Lauraceae. The major components of *P. bombycina* leaves are carbohydrate, pectins, cellulose, starch, xylan, lipid and fatty acids (Sharma and Devi, 1997; Singh *et al.*, 2000; Yadava and Goswami, 1992; Dutta *et al.*, 1997;

Choudhury et al., 1998).

The entire insect gut contains diverse groups of microorganisms that are potential source of digestive enzymes (Zhang and Brune, 2004) and metabolites (Wilkinson and Disloyalty, 2001). They play significant role in nutrition, immunity, growth and reproduction (Brand *et al.*, 1975, Brune *et al.*, 1995; Moran *et al.*, 2005). The bacterial community harboured by mid guts of Lepidopteran insects produces digestive enzymes and help in digestion of leaf constituents such as cellulose, xylan, pectin and starch (Dillon and Dillon, 2004). Different types of cellulose, xylan, pectin and starch degrading microflora have been isolated and characterized from 5th instar larvae of *B. mori* (Khayade and Marathe, 2012). *Streptomyces noursei*, is a potential gut bacteria