



Cultivable and Non Cultivable Bacteria Associated with the Gut of *Antheraea assamensis* (Muga Silkworm)

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ABSTRACT: *Antheraea assamensis* Helfer, the golden-yellow silk producer silk moth, is semi-domesticated insect species endemic to North East India, around which the whole of sericulture industry depends. A multitude of bacteria have been isolated from the guts of several insect species. Inherited intracellular insect endosymbionts may manipulate host reproduction or provide fitness benefits to their hosts. The gut microbiotas are associated with several physiological functions including digestion, absorption, degradation of toxic metabolites, semiochemical production and resisting the colonization of entomopathogens (Dillon and Dillon, 2004). To determine the composition of gut bacteria of *A. assamensis*, we applied culture dependent and culture independent techniques. Culture dependent technique includes the identification of gut bacterial by using 16SrRNA gene amplicons. It was observed that the gut composed of diverse community of bacteria; some of the predominant were identified as *Bacillus safensis*, *Alcaligenes aquatilis*, *Serratia nematodiphila*, *Salmonella enteric*, *Bacillus flexus*, *Serratia marcescens*, *Pseudomonas stutzeri*, *Alcaligenes faecalis*. For identification of non culturable gut bacteria we focused on metagenomic analysis of V3 region of 16sRNA by using next generation sequencing (Illumina Miseq). The metagenomic analysis revealed that community of gut bacteria belonging to *acinetobacteria*, *alphaproteobacteria*, *betaproteobacteria*, *gammaproteobacteria*, *clostridia*, and *bacteroidia* are most predominant than others. Our results demonstrated that a core bacterial community exist in the insect gut, which may contribute to the host physiology and could play a role in conferring host resistance to diseases. © 2016 iGlobal Research and Publishing Foundation. All rights reserved.

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