INDIAN INSTITUTE OF TECHNOLOGY GUWAHATI
SHORT ABSTRACT OF THESIS

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Antheraea assamensis Helfer, commonly known as the Muga silkworm, is an endemic, economically important Lepidopteran species explicitly found in the northeastern part of India and its neighbouring areas. This semi-domesticated, multivoltine, polyphagous, edible insect produces an economically important, lustrous golden-coloured silk with high tensile strength and durability. The cultivation of Muga silkworm for silk production has been in practice for ages in Assam, a state of India. Due to its extreme durability, magnificent colour and lustre, Muga silk is considered one of the most expensive natural fibers in the world. The fibroin part of the Muga silk is also a promising material for tissue engineering. Unlike mulberry-feeding silkworms, *A. assamensis* is semi-domesticated and can be grown only in outdoor conditions. Lack of genetic variation and low adaptability to changing environmental conditions and limited knowledge of its host plants are the key bottlenecks towards its domestication. The role of gut microbiota in host metabolism, growth, development, nutrition and immune regulation is becoming increasingly evident in humans and other organisms. To date, the gut microbiota of *A. assamensis* has remained largely unexplored. The present work aims to comprehensively identify

and characterize the gut microbial community of *A. assamensis* through a culture-independent approach. The gene expression analysis of the gut microbial community was studied through metatranscriptome analysis. The influence of the host leaf–associated microbiota on larval gut microbial composition and its variation to changes in host plants was also investigated. The results have indicated that the 5th instar larva of *A. assamensis* contains a highly diverse gut microbial community dominated by Proteobacteria, Patescibacteria, Planctomycetota, Chloroflexi, Acidobacteriota and Actinobacteriota. Functional analysis of *A. assamensis* gut microbiome through shotgun metagenomics and metatranscriptomics revealed key associations between the insect and its gut microbial community including host leaf digestion, metabolite detoxification, chitinase production and fat body metabolism. The host leaf-associated microbiota was found to occupy a major portion of the total larval gut microbiota. However, the diversity of the larval gut microbiota was greater than the host leaf-associated microbiota. The findings of this study will illustrate the structure of the gut microbial community of *A. assamensis*, their key interactions with the host organism and the role of host leaf-associated microbiota on the holobiont. The thesis also describes the global metabolome of the host plant leaf, larval gut and silk gland of 5th instar larvae of *A. assamensis* and how the change in the host plant affects the gut and silk gland metabolite composition. For this, larvae reared on Som and Mejankari plants were considered. The results of this experiment identified hundreds of metabolites from the larval gut, silk gland and host plant leaf of *A. assamensis* larvae reared on the two host plants. The identified metabolites can be clustered into different categories like amino acids, sugars, fatty acids, alkaloids, secondary metabolites, pigments vitamins and others. Change in the host plant was found to change the metabolite composition of the larval gut and the silk gland. The findings of this study will help to extend our knowledge of the global metabolomes of the studied samples.