INDIAN INSTITUTE OF TECHNOLOGY GUWAHATI
SHORT ABSTRACT OF THESIS

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SHORT ABSTRACT

For centuries, sericulture has been a major agronomic practice in Asia. India is one of the largest producers of silk in the world with exports to ~50 countries, earning foreign exchanges of over 2000 crores per year. Muga silk is one of the unique, golden colored commercial silk produced in India. It is spun by *Antheraea assamensis* Helfer, commonly known as muga silkworm, which is a multivoltine, polyphagous Lepidopteran silkmoth endemic to the Brahmaputra valley of Assam and adjoining hilly areas of Northeast India. Due to its unique physical properties, the muga silk and its core constituent proteins- fibroin and sericin, have found a special place in the commercial and scientific domain with prospective applications in the field of biomedical sciences, skincare, tissue engineering and so on. The field of "mugaculture" is vulnerable to numerous biotic and abiotic threats due to the semidomesticated nature of the muga silkworm. Pathogens like Nosema which cause pebrine in silkworms are one of the major biotic challenges to silk yield every year. Another biotic factor that affects this field is diseased host plants which invariably affects the rearing process of the silkworm as it is an herbivore (folivore). To tackle these vagaries of mugaculture, it is pertinent to identify the key players involved in silk biosynthesis and molecular defense from pest and pathogens in *A. assamensis.* However, genomic information on these species is scarce, thereby hindering in-depth studies on these molecular aspects.

The current study aimed to address this necessity using next-generation sequencing technology. Here, we sequenced, assembled and annotated the de novo transcriptomes of *A. assamensis* and two of its host plants, *Machilus bombycina* and *Litsea citrata*. We identified candidate transcripts involved in silk biosynthesis, allelochemical detoxification and microbial defense in the muga silkworm. We also identified

key transcripts involved in biomolecular defense against microbes and herbivores in the two host plants. We performed comparative analysis of differential expression of two developmental stages of *A. assamensis* larvae (4th & 5th instar) which led to identification of differentially expressed biological processes in the muga silkworm. We were also able to observe the biological processes differentially expressed in the muga silkworm with respect to host plant variation. We parallelly studied the Nosema genus, which includes microsporidian pathogens infecting silkworms, to identify transporters which are the key molecules for sustaining its obligate intracellular life. Using the whole proteomes of four microsporidian pathogens of Nosema genus, we predicted the whole transportomes of *Nosema apis, N. antheraea, N. bombycis* and *N. ceranae*, and associated nutritional scenario. These transportomes constituted a source of potential molecular targets for biocontrol of these eukaryotic pests. Finally, we constructed an online database, named MugaSeqDB (http://mugaseqdb.in) for dissemination of the molecular data derived in this entire study. The primary information in MugaSeqDB is the transcriptomic information of *A. assamensis, M. bombycina* and *L. citrata*. In summary, our study was able provide molecular insights to some of the key molecular processes in muga silkworm and its associated biota. The resources generated by this study expanded the periphery of existing genomic data on these species as well as laid the groundwork for future genetic investigation and improvement towards a better sustainable future of mugaculture.
