ABSTRACT

SURIANA. Morphometry and Genetics Diversity of Wild Silk Moth *Cricula trifenesstrata* Helfer (Lepidoptera: Saturniidae). Under direction of: DEDY DURYADI SOLIHIN, RONNY RACHMAN NOOR dan ACHMAD MACHMUD THOHARI.

The study was conducted to describe morfometry, life cycle, fibroin and cytochrome C oxidase subunit I (COI) gene characteristics of *Cricula trifenesstrata*. Morphometry data were obtained from 3 locations at Campus IPB Darmaga area, namely in the parking area Graha Widya Graduation (GWW), Bara Tomb Complex, and Animal House C Fapet. Observations were done on the duration and timing of life cycle, viability, morphology, anatomy, and nine morphological traits, namely cocoon weight (CW), shell cocoon weight (SCW), cocoon length (CL) cocoon width (CWD), pupae weight (PW), pupae length (PL), pupae width (PWD), thorax length (TL), and wingspan (WS). Data were analyzed descriptively, and discriminant analysis were also performed. Molecular data obtained from genomic DNA extracted from silk glands of larvae. Genomic DNA was amplified and sequenced, and then characterized in order to describe the number and type of nucleotide, the number and types of amino acids on proteins fibroin and COI. Characterization results compared with fibroin and COI genes sequences of other silk moth available in GenBank and using it to constructed phylogenetic tree. The results showed that *C. trifenesstrata* spend $51.0 \pm 7.3$ days for one life cycle. All morphological traits significantly affected the grouping by location in each stage of development. The prediction accuracy for the parameter grouping cocoon, pupae and imago were 93.6%, 83.3%, and 92.7% respectively, with the biggest differentiator: CW, PW, and WS respectively. The partial fibroin gene consists of first exon coding region with 42 nucleotides (14 amino acids), an introns (113 nucleotides) and partial coding region of second exon with 831 nucleotides (277 amino acids) long. The comparison with other silk moth showed that fibroin gene were conserved on *C. trifenesstrata*, but very diverse with other species. Nucleotides 25th (C), 35th (T) of the first exon, and 12th amino acids (valine) were diagnostic for the species *C. trifenesstrata*. Nucleotide of second exon encoding 277 amino acids that were dominated by the amino acid alanine (27.8%) and glycine (21.66%). Nucleotide introns were very diverse, more than 70% nucleotide of A and T. The partial COI gene of *C. trifenesstrata* size of 595 nucleotides, encoded 198 amino acids. There was no difference nucleotide sequence of intra species *C. trifenesstrata*, but showed 23.7% diversity with other silk moth. Nucleotide dominated by thymine and adenine bases (± 70%). There are 25 nucleotide diagnostic for *C. trifenesstrata*. Sequenced of 198 amino acids, showed only 10% variation between species of silk moth. Amino acid 107th (valine) and 138th (treinonin) are amino acid diagnostic for *C. trifenesstrata*.

Key word: Wild silk moth, *C. trifenesstrata*, morphometry, fibroin gene, COI, nucleotide and amino acid diagnostics.