DNA *Barcoding* Ulat Sutra Eri *Samia ricini* (Boisduval, 1854) di Yogyakarta Berdasarkan Gen Mitokondria *16S*

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INTISARI

Serikultur Eri merupakan budidaya ulat sutra yang relatif baru dan berpotensi dikembangkan di Indonesia. Ulat sutra Eri (*Samia*) merupakan ulat sutera non-murbei domestikasi, anggota Saturniidae yang dibudidayakan untuk menghasilkan sutera komersial. Salah satu tempat serikultur ulat sutra Eri di Indonesia terletak di Kulon Progo, Yogyakarta yang memiliki empat tipe *morphs*, yaitu *white zebra, yellow zebra, white spotted,* dan *greenish spotted*. Namun, penelitian mengenai informasi genetik spesies ulat sutra Eri di Indonesia belum pernah dilakukan. Identifikasi spesies secara molekuler dapat dilakukan menggunakan DNA *barcoding* menggunakan gen mitokondria *16S*. Oleh karena itu, pada penelitian ini dilakukan identifikasi dan analisis filogenetik antar *morphs* ulat sutra Eri budidaya di Yogyakarta menggunakan gen mitokondria *16S*. Tahapan penelitian yang dilakukan terdiri dari ekstraksi DNA, amplifikasi DNA, elektroforesis, purifikasi, dan sekuensing. Analisis data dilakukan menggunakan *software* GeneStudio, MEGA, dan DnaSP. Hasil analisis similaritas dengan NCBI BLAST menunjukkan bahwa empat sampel *morphs* ulat sutra Eri yang dibudidayakan di Yogyakarta adalah *Samia ricini* dengan nilai persentase sebesar 98.20%—99.74% terhadap sekuen dari *Genbank*. Analisis filogenetik menunjukkan empat *morphs* ulat sutra Eri di Yogyakarta tidak menunjukkan adanya perbedaan spesies. Analisis variasi genetik antara individu menunjukkan jarak genetik diantara individu ulat sutra Eri sebesar 0,00-0,11 dengan terdapat 13 haplotipe,nilai *haplotype diversity* (Hd) sebesar 0,88421, dan *nucleotide diversity* (π) sebesar 0,0188.

Kata kunci : DNA *barcoding*, filogenetik, gen *16S, Samia ricini*

DNA Barcoding of Eri Silkworm *Samia ricini* (Boisduval, 1854) In Yogyakarta Based on *16S* Mitochondrial Gene

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ABSTRACT

Eri sericulture is a relatively new silkworm cultivation that has the potential to be developed in Indonesia. The Eri silkworm (*Samia*) is a domesticated non-murbei silkworm, member of Saturniidae that is cultivated to produce commercial silk. One of the Eri silkworm sericulture sites in Indonesia is located in Kulon Progo, Yogyakarta which has four types of morphs, including white zebra, yellow zebra, white spotted, and greenish spotted. However, research on the genetic information of Eri silkworm species in Indonesia has never been conducted. Molecular species identification can be done using DNA barcoding using the *16S* mitochondrial gene. Therefore, this study aimed to identify and analyze phylogenetic between morphs of cultivated Eri silkworm in Yogyakarta using the *16S* mitochondrial gene. The research stages included DNA extraction, DNA amplification, electrophoresis, purification, and sequencing. Data analysis were conducted using GeneStudio, MEGA, and DnaSP software. The results of similarity analysis with NCBI BLAST showed that the four samples of Eri silkworm morphs cultivated in Yogyakarta were *Samia ricini* with percentage similarity value of 98.20%-99.74% compared to sequences from Genbank. Phylogenetic analysis showed that the four morphs of Eri silkworm in Yogyakarta showed no species differences. Analysis of genetic variation between individuals showed genetic distance between Eri silkworm individuals of 0.00-0.11 with 13 haplotypes, a haplotype diversity (Hd) value of 0.88421, and a nucleotide diversity (π) of 0.0188.

Keywords: DNA barcoding, phylogenetics, *16S* gene, *Samia ricini*