

**Variasi Intra- dan Inter- populasi *Troides helena* (Lepidoptera: Papilionidae)
di Gunung Merapi dan Gunung Api Purba Nglanggeran
Berdasarkan Sekuen Gen COI, ND5 DAN EF-1 α**

ABSTRAK

Rusaknya habitat, fragmentasi habitat dan perdagangan spesies merupakan penyebab utama kepunahan spesies. Erupsi Gunung Merapi yang terjadi dua kali dalam 10 tahun terakhir berdampak pada penyusutan jumlah individu beberapa spesies, termasuk *T. helena*. Hal ini melatarbelakangi dilakukannya penelitian mengenai variasi *T. helena* secara morfologis dan genetik. Penelitian ini dilakukan untuk mengetahui variasi molekular intra dan inter populasi *Troides helena*. Variasi morfologis diperoleh dari pengukuran 33 karakter morfologis dilakukan. Haplotipe dan pohon filogenetik diperoleh dari sekuensing 3 gen yakni, ND5 (*NADH dehydrogenase subunit 5*), COI (*Cytochrome C Oxidase Subunit I*) dan EF-1 α (*Elongation Factor 1-Alpha*). Data hasil sekuensing disejajarkan menggunakan software MEGA, penentuan haplotipe menggunakan program Network 4612 dan analisis populasi dilakukan menggunakan program DNAsp. Hasil analisis PCA memperlihatkan bahwa karakter yang berkontribusi dalam variabilitas spesies meliputi: panjang total, ukuran sayap beserta panjang venasi sayap, panjang antenna dan panjang kaki. Plot PCA memperlihatkan pemisahan antara populasi Nglanggeran dan Gunung Merapi, namun terdapat satu grup yang beranggotakan individu Merapi dan Nglanggeran yang saling tumpang tindih. Dendrogram yang dihasilkan juga terbagi atas tiga kelompok besar. Sekuens gen ND5 memiliki diversitas haplotipe dan diversitas nukleotida terbesar dibandingkan dua gen lainnya, namun nilai estimasi aliran gen (F_{st} dan N_m) signifikan dihasilkan oleh sekuen gen EF-1 α . Pohon filogenetik Maximum likelihood dan Neighbor Joining yang terbentuk memperkuat hasil haplotipe yang diperoleh. Disimpulkan dari analisis molekular bahwa terdapat aliran materi genetik antara dua populasi tersebut.

Kata kunci. *Troides helena*, variasi molekular, haplotipe.

**Variation intra- and inter-population of *Troides helena* (Lepidoptera: Papilionidae) from Merapi Mountain and Ancient Volcano Nglanggeran
Based on Gene Sequence of ND5, COI and EF-1 α**

ABSTRACT

Habitat destruction, fragmentation and trade of butterflies are the major cause of species extinction. Since Merapi eruption happened twice in lately ten years had effect on decrease of the individu number of some species, including *Troides helena*, it interested to investigate the morphological and genetic variation *T. helena*. The purpose of this study is to determine variation within and between population of *T. helena*. The morphological measurement was conducted using 3 morphological traits. Haplotypes and phylogeny was obtained with sequences of three protein-coding genes: two mitochondrial (ND5 NADH dehydrogenase subunit 5; COI Cytochrome C Oxidase Subunit I), and one nuclear (EF-1 α Elongation factor 1-alpha). Sequence data was aligned using MEGA software, constructed of haplotypes using Network 4612 program and population analysis using DNAsp program. The PCA results that the characters contributing largely to the species variability were those related to total length of *T. helena*, wing size including length of wing venation, antenna length and leg length. The two dimensional plot of PCA showed separation between population from Nglanggeran and Merapi, but one group unable to distinguish among these populations. Dendogram of CA revealed three major group that supported the PCA grouping. Sequence of ND5 gene has the largest of haplotype and nucleotide diversity. Meanwhile, significant of Fst and Nm value that revealed genetic drift and gene flow was given from sequence of EF1 α . Maximum likelihood and Neighbor Joining phylogenetic tree supported the haplotype data. Molecular data revealed there is possibility to change of genetic material between two populations.

Keyword: *Troides helena*, molecular variation, haplotype