

ABSTRAK

IDENTIFIKASI MOLEKULER *Amblyomma* sp. PADA BIAWAK AIR ASIA DI YOGYAKARTA BERDASARKAN SEKUEN DNA MITOKONDRIA GEN CYTOCHROME OXIDASE C SUBUNIT 1

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Biawak air Asia merupakan salah satu jenis biawak yang tersebar luas di Indonesia dan memiliki nilai konservasi, ekologi, maupun ekonomi. Biawak sering kali ditemukan dalam kondisi terinfestasi caplak yang dapat merugikan kesehatan biawak dan menjadi vektor penyakit. Beberapa caplak keras yang menginfestasi biawak di D. I. Yogyakarta belum dapat teridentifikasi. Tujuan diadakannya penelitian ini adalah untuk menentukan identitas caplak keras pada biawak secara morfologi dan molekuler serta menganalisis hubungan kekerabatan dengan spesies lainnya. Identifikasi molekuler dilakukan dengan marka DNA mitokondria gen cytochrome oxidase subunit 1. Sampel DNA diisolasi dan diamplifikasi dengan menggunakan teknik *Polymerase Chain Reaction (PCR)* menggunakan primer LCO 1490 dan HCO 2198. Hasil PCR kemudian di sekuensing untuk mengetahui urutan dari basa nukleotida dengan perangkat lunak MEGA 11.0. Analisis hasil sekuensing dibandingkan dengan data lainnya yang diperoleh dari *GenBank*. Penentuan jarak genetik dilakukan berdasarkan sekuen nukleotida menggunakan metode kimura 2-parameter dengan hasil yang didapatkan 2,4%. Konstruksi pohon filogenetik berdasarkan sekuen gen COI menggunakan metode *Neighbour-Joining* dengan 1000 pengulangan *bootstrap*. Sampel biawak yang digunakan dalam penelitian ini memiliki afiliasi genetik terdekat dengan *Amblyomma varanense* dengan persentase tingkat kemiripan 97,58%.

Kata kunci : Caplak keras, biawak air Asia, DNA mitokondria, nukleotida, sekuensing

ABSTRACT

MOLECULAR IDENTIFICATION OF *Amblyomma* sp. FROM ASIAN WATER MONITOR LIZARDS IN YOGYAKARTA BASED ON MITOCHONDRIAL DNA CYTOCHROME C OXIDASE SUBUNIT I (COI) GENE SEQUENCE

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The Asian water monitor (*Varanus salvator*) is one of the widely distributed lizard species in Indonesia and has conservation, ecological, and economic importance. Water monitors are often found infested with ticks, which can negatively affect their health and act as vectors of disease. Several hard ticks infesting water monitors in the Special Region of Yogyakarta have not yet been identified. This study aimed to determine the identity of hard ticks infesting water monitors using morphological and molecular approaches, as well as to analyze their phylogenetic relationships with other species. Molecular identification was performed using the mitochondrial DNA marker of the cytochrome oxidase subunit I (COI) gene. DNA samples were isolated and amplified using the Polymerase Chain Reaction (PCR) technique with LCO1490 and HCO2198 primers. The PCR products were subsequently sequenced to determine the nucleotide sequence using MEGA 11.0 software. Sequencing results were compared with reference data obtained from GenBank. Genetic distance was calculated based on nucleotide sequences using the Kimura 2-parameter method, yielding a value of 2.4%. Phylogenetic tree construction based on the COI gene sequence was performed using the Neighbor-Joining method with 1000 bootstrap replicates. The tick sample obtained from the water monitor showed the closest genetic affiliation with *Amblyomma varanense* with the percentage of identity value of 97.58%.

Key words : Hard ticks, Asian water monitor, mitochondrial DNA, nucleotides, sequencing