

ABSTRAK

IDENTIFIKASI MOLEKULER CAPLAK KERAS (Ixodidae) PADA ULAR SANCA KEMBANG (*Malayopython reticulatus*) BERDASARKAN GEN COI

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Ular sanca kembang (*Malayopython reticulatus*) merupakan reptil yang memiliki peranan ekologis penting serta banyak dipelihara sebagai hewan eksotik. Namun, pemeliharaannya sering dihadapkan pada permasalahan kesehatan berupa infestasi caplak keras (Ixodidae). Identifikasi caplak secara morfologis memiliki keterbatasan akibat kemiripan karakter antarspesies, sehingga diperlukan pendekatan molekuler yang lebih akurat. Penelitian ini bertujuan untuk mengidentifikasi spesies caplak keras yang menginfestasi *Malayopython reticulatus* berdasarkan analisis gen *cytochrome c oxidase* subunit I (COI). Sampel caplak dikoleksi dari satu ekor ular di Kabupaten Bantul, Daerah Istimewa Yogyakarta. Identifikasi dilakukan secara morfologis dan dilanjutkan dengan analisis molekuler meliputi ekstraksi DNA, amplifikasi gen COI menggunakan teknik *polymerase chain reaction* (PCR) dengan primer LCO1490 dan HCO2198, elektroforesis, purifikasi, dan sekuensing DNA. Data sekuens dianalisis menggunakan program MEGA 12 dengan membandingkan data *GenBank*. Hasil penelitian menunjukkan bahwa caplak secara morfologis termasuk genus *Amblyomma*. Amplifikasi PCR menghasilkan fragmen DNA berukuran ± 709 bp. Analisis molekuler menunjukkan perbedaan basa nukleotida paling rendah dengan *Amblyomma varanense* (8–12 basa) serta nilai jarak genetik terendah (0,015–0,023). Komposisi nukleotida didominasi oleh basa A+T, dan analisis rasio transisi–transversi serta pohon filogenetik menunjukkan kedekatan kekerabatan yang tinggi dengan *Amblyomma varanense* dibandingkan spesies lain. Secara umum, caplak yang menginfestasi *Malayopython reticulatus* di Kabupaten Bantul teridentifikasi sebagai *Amblyomma varanense* melalui analisis gen COI.

Kata kunci: caplak keras, *Amblyomma varanense*, COI, PCR, filogenetik

ABSTRACT

MOLECULAR IDENTIFICATION OF HARD TICKS (Ixodidae) ON THE RETICULATED PYTHON (*Malayopython reticulatus*) BASED ON THE COI GENE

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The reticulated python (*Malayopython reticulatus*) is a reptile with significant ecological roles and is widely kept as an exotic pet. However, its management is often challenged by health issues, specifically infestations of hard ticks (Ixodidae). Morphological identification of ticks is frequently limited by interspecies character similarities, necessitating a more accurate molecular approach. This study aims to identify the hard tick species infesting *M. reticulatus* based on the analysis of the *cytochrome c oxidase* subunit I (COI) gene. Tick samples were collected from a snake in Bantul Regency, Special Region of Yogyakarta. Identification was performed morphologically and followed by molecular analysis, including DNA extraction, COI gene amplification via *polymerase chain reaction* (PCR) using LCO1490 and HCO2198 primers, electrophoresis, purification, and DNA sequencing. Sequence data were analyzed using MEGA 12 software by comparison with *GenBank* database entries. The results showed that the ticks morphologically belonged to the genus *Amblyomma*. PCR amplification produced a DNA fragment of approximately 709 bp. Molecular analysis revealed the lowest nucleotide base differences with *Amblyomma varanense* (8–12 bases) and the lowest genetic distance values (0.015–0.023). The nucleotide composition was dominated by A+T bases. Furthermore, transition-transversion ratio analysis and phylogenetic tree construction indicated a high genetic closeness to *Amblyomma varanense* compared to other species. In conclusion, the ticks infesting *Malayopython reticulatus* in Bantul Regency were identified as *Amblyomma varanense* through COI gene analysis.

Key words: hard ticks, *Amblyomma varanense*, COI, PCR, phylogenetic