

## ABSTRAK

### IDENTIFIKASI MOLEKULER CAPLAK KERAS PADA ULAR SANCA BATIK BERDASARKAN GEN 12S Ribosom RNA

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Ular Sanca Batik (*Malayopyhton reticulatus*) merupakan jenis ular yang memiliki nilai konservasi, nilai ekologi, dan mampu mendukung kegiatan ekonomi. Ular sering terinfestasi caplak keras sehingga merusak kulit dan berakibat menurunkan nilai jual dan dapat menularkan agen penyakit baik ke manusia maupun hewan lainnya. Banyak jenis caplak keras yang belum teridentifikasi berparasit pada ular di wilayah Daerah Istimewa Yogyakarta dan Jawa Tengah. Tujuan dari penelitian ini adalah untuk mengidentifikasi dan menentukan runutan basa nukleotida caplak keras yang menginfestasi ular sanca batik di Daerah Istimewa Yogyakarta dan Jawa Tengah. Analisis molekuler dilakukan untuk mendukung keakuratan dari pemeriksaan caplak keras secara morfologi. Identifikasi morfologi dilakukan dengan mikroskop menunjukkan caplak tersebut termasuk spesies *Amblyomma varanense* dan molekuler dilakukan dengan DNA mitokondria gen 12S rRNA. Sampel caplak berasal dari ular daerah Bantul, Daerah Istimewa Yogyakarta dan Magelang. Sampel caplak diisolasi DNANYA dengan menggunakan GenAid Extraction Kit. Amplifikasi DNA dilakukan menggunakan teknik *Polymerase Chain Reaction* (PCR) menggunakan primer *forward* Tick12SRNAF1 dan *reverse* Tick12SRNAR1. Hasil dari proses PCR yaitu produk ampikon berukuran 680 bp. Sampel kemudian di sekuensing untuk menentukan runutan nukleotida. Analisis data dilakukan dengan perangkat lunak MEGA 11.0 dibandingkan dengan data lain dari GenBank. Jarak genetik berdasarkan sekuen nukleotida ditentukan dengan metode Kimura 2-parameter. Hasil yang didapatkan yaitu jarak genetik interspesies terkecil yaitu 0% dan jarak terbesar 17,3%. Konstruksi pohon filogenetik berdasarkan sekuen gen 12S rRNA menggunakan metode *Neighbour-Joining* dengan nilai bootstrap 1000. Sampel caplak *Amblyomma varanense* setelah di alignment memiliki kerabat dekat dengan *Amblyomma gervaisi*.

**Kata kunci** : Caplak keras, ular sanca batik, DNA mitokondria, nukleotida, sekuensing

## ABSTRACT

### MOLECULAR IDENTIFICATION OF HARD TICKS ON RETICULATED PHYTHON BASED ON 12S Ribosom RNA GENE

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Reticulated Python (*Malayopython reticulatus*) is a type of snake that has conservation value, ecological value, and is able to support economic activities. Snakes are often infested with hard ticks that damage the skin and result in lower sales value and can transmit disease agents to both humans and other animals. Many types of hard ticks have not been identified as parasites on snakes in the Special Region of Yogyakarta and Central Java. The purpose of this study was to identify and determine the nucleotide base sequence of hard ticks that infest reticulated pythons in the Special Region of Yogyakarta and Central Java. Molecular analysis was carried out to support the accuracy of the morphological examination of hard ticks. Morphological identification was carried out by microscopy showing that the tick belonged to the *Amblyomma varanense* species and molecular identification was carried out based on mitochondrial DNA 12S rRNA gene. The tick samples came from snakes from the Bantul area, the Special Region of Yogyakarta and Magelang. The tick samples were isolated from their DNA using the GenAid Extraction Kit. DNA amplification was carried out using the Polymerase Chain Reaction (PCR) technique using forward Tick12SRNAF1 and reverse Tick12SRNAR1 primers. The results of the PCR process are amplicon product measuring 680 bp. The sample is then sequenced to determine the nucleotide sequence. Data analysis was performed with MEGA 11.0 software compared to other data from GenBank. Genetic distances based on nucleotide sequences were determined by the 2-parameter Kimura method. The results obtained were the smallest interspecies genetic distance of 0% and the largest distance of 17.3%. Phylogenetic tree construction based on the 12S rRNA gene sequence using the Neighbor-Joining method with a bootstrap value of 1000. The samples of *Amblyomma varanense* ticks after alignment have close relatives with *Amblyomma gervaisi*.

**Keywords :** Hard ticks, reticulated python, mitochondrial DNA, nucleotide, sequencing