

INTISARI

Analisis Kekerabatan Caplak Anjing *Rhipicephalus sanguineus* Berdasarkan Sekuen DNA Ribosomal (rDNA) Regio ITS2

Alan Chandrasaputra

Caplak *Rhipicephalus sanguineus* merupakan ektoparasit dari hewan kesayangan seperti anjing serta memiliki distribusi yang luas. Luasnya distribusi anjing membuat perannya sebagai hospes dan penyebar *R. sanguineus* berakibat pada distribusi caplak *R. sanguineus* yang luas pula. Di Indonesia, penyebaran *R. sanguineus* termasuk memiliki cakupan distribusi yang luas serta memungkinkan caplak *R. sanguineus* memiliki variasi genetik pada susunan materi genetiknya. Analisis genetik hubungan kekerabatan akan membantu pemetaan genetik caplak *R. sanguineus* serta variasi genetik yang ada di Indonesia.

Sampel diperoleh dari caplak yang terdapat di Banda Aceh, Bekasi, dan Sleman. Isolasi DNA dilakukan dengan menggunakan Genomic® *DNA Mini Kit (Tissue)* GT 100. Hasil isolasi kemudian diamplifikasi dengan primer BO2F dan BO2R dengan teknik PCR. Sampel kemudian dilakukan sekuensing di PT. Genetika Science, Jakarta. Analisis data dilakukan dengan *Molecular Evolutionary Genetic Analysis* (MEGA) versi 6.06. Pohon filogenetik dianalisis dengan metode *Neighbor-Joining* dan nilai *bootstrap* 1000.

Produk PCR yang dihasilkan berukuran 1079 bp. Sampel caplak isolat Aceh memiliki hubungan kekerabatan yang identik dengan jarak genetik 0,0000 (0%) dengan data *R. sanguineus* dari *Genbank*. Sedangkan, sampel caplak isolat dari Bekasi memiliki jarak genetik lebih besar sebesar 0,0082 (0,82%) bila dibandingkan dengan data *Genbank* dan berjarak genetik lebih kecil dengan *R. turanicus* sebesar 0,0041 (0,41%) dan bukan termasuk *R. sanguineus*.

Kata Kunci: *Rhipicephalus sanguineus*, anjing, rDNA, ITS-2, distribusi geografis, sekuensing, *Polymerase Chain Reaction* (PCR)

ABSTRACT

Phylogenetic analysis of Dog Ticks *Rhipicephalus sanguineus* Based on ITS2 Ribosomal DNA sequence

Alan Chandrasaputra

Rhipicephalus sanguineus is an ectoparasite of dog that has spread widely because of dog wide distribution as a companion animal. The wide distribution of *R. sanguineus* will increase the chance of genetic variation between different geographical locations. This study is to analysis the genetic variation and to help genetic mapping of *R. sanguineus* in Indonesia and to assist genetic mapping and identification of Indonesian ticks of *R. sanguineus*

Tick genetic analysis was done by sequencing the ribosomal DNA of the ITS2 region. Through sequencing method, the amplified DNA from polymerase chain reaction (PCR) amplification was sequenced. The sample were obtained from Aceh, Bekasi, and Sleman. The isolation process was done by using isolation kit from Genomic® DNA Mini Kit (Tissue) GT100. The primers that were used for amplification were BO2F and BO2R. The samples were through sequencing process in PT. Genetics Science, Jakarta. The data analysis was performed with the version 6.06 of Molecular Evolutionary Genetics Analysis (MEGA) program. The phylogenetic tree was then analyzed by Neighbor-Joining method with 1000 bootstrap values.

The PCR product is 1079 bp of partial ITS2 regio. Tick sample from Aceh has identic genetic distance by 0,0000 (0,00 %) with *R. sanguineus* from Genbank which means they are identic and can be grouped as *R. sanguineus*. Meanwhile, the sample from Bekasi has higher genetic distance 0,0082 (0,82%) with the other samples of *R. sanguineus* and *Genbank* data. The sample from Bekasi is grouped together with *R. turanicus* and most likely not included into *R. sanguineus* species.

Keyword: *Rhipicephalus sanguineus*, dog, rDNA, ITS-2, geographic distribution, sequencing, polymerase chain reaction (PCR).