

INTISARI

ANALISIS FILOGENETIK KAMBING PERANAKAN ETAWA KEPALA HITAM DAN COKELAT ASAL KULON PROGO BERDASARKAN SEKUENS *DISPLACEMENT LOOP* DNA MITOKONDRIA

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Penelitian ini bertujuan untuk menganalisis hubungan kekerabatan genetik dan menentukan haplogrup kambing Peranakan Etawa (PE) kepala hitam dan cokelat asal Kulon Progo berdasarkan sekuens daerah *Displacement Loop* (D-Loop) DNA mitokondria. Sampel yang digunakan berupa darah kambing PE sebanyak 40 sampel, dengan enam sampel terpilih untuk dilakukan sekuensing, yaitu K6, JH7, JH10, B5, B7, dan B8. Isolasi DNA dilakukan menggunakan Geneaid Genomic DNA Mini Kit, kemudian daerah D-Loop diamplifikasi menggunakan metode *Polymerase Chain Reaction* (PCR) dengan primer PE-DL-F dan PE-DL-R. Produk PCR divisualisasikan menggunakan elektroforesis gel agarosa 1,5% dan dilanjutkan dengan sekuensing metode Sanger. Analisis data dilakukan menggunakan software MEGA versi 12 melalui alignment Clustal W, analisis jarak genetik metode *pairwise distance* model Kimura2-parameter, dan konstruksi pohon filogenetik metode *Maximum Likelihood Tree* dengan bootstrap 1000 kali. Hasil penelitian menunjukkan bahwa amplifikasi daerah D-Loop menghasilkan fragmen sepanjang 556 bp. Analisis sekuens menunjukkan adanya satu situs polimorfik pada posisi 16492 berupa mutasi transversi A-C pada sampel B5. Komposisi rata-rata basa nukleotida terdiri atas timin (29,7%), sitosin (28,1%), adenin (24,7%), dan guanin (17,4%). Nilai jarak genetik antar sampel berkisar antara 0,000–0,0036 yang menunjukkan hubungan kekerabatan dekat. Analisis filogenetik menunjukkan seluruh sampel kambing PE berada dalam haplogrup B bersama kambing lokal Asia Tenggara dan Asia Timur seperti kambing Samosir dan Kosta, dengan nilai bootstrap 91–95%. Berdasarkan hasil penelitian dapat disimpulkan bahwa kambing Peranakan Etawa (PE) asal Kulon Progo kepala hitam dan cokelat memiliki hubungan kekerabatan genetik yang dekat dengan kambing lokal Indonesia lainnya dan termasuk ke dalam haplogrup B yang tersebar di wilayah Asia Tenggara dan Asia Timur.

Kata kunci: D-Loop, DNA mitokondria, filogenetik, haplogrup, kambing Peranakan Etawa

ABSTRACT

PHYLOGENETIC ANALYSIS OF BLACK-HEADED AND BROWN-HEADED PERANAKAN ETAWA GOATS FROM KULON PROGO USING MITOCHONDRIAL DNA DISPLACEMENT LOOP SEQUENCES

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This study aimed to analyze the genetic relationship and determine the haplogroup of black- and red-headed Peranakan Etawa (PE) goats from Kulon Progo based on mitochondrial DNA (mtDNA) *Displacement Loop* (D-Loop) region sequences. The samples used were blood samples from 40 PE goats, with six selected samples sequenced, namely K6, JH7, JH10, B5, B7, and B8. DNA isolation was performed using the Geneaid Genomic DNA Mini Kit, followed by amplification of the D-Loop region using the *Polymerase Chain Reaction* (PCR) method with PE-DL-F and PE-DL-R primers. PCR products were visualized using 1.5% agarose gel electrophoresis and subsequently sequenced using the Sanger method. Data analysis was conducted using MEGA version 12 software through Clustal W alignment, genetic distance analysis using the Kimura2-parameter *pairwise distance* model, and phylogenetic tree construction using the *Maximum Likelihood Tree* method with 1000 bootstrap replications. The results showed that D-Loop region amplification produced a fragment length of 556 bp. Sequence analysis identified one polymorphic site at position 16492 in the form of an A-C transversion mutation in sample B5. The average nucleotide base composition consisted of thymine (29.7%), cytosine (28.1%), adenine (24.7%), and guanine (17.4%). Genetic distance values among samples ranged from 0.000 to 0.0036, indicating close genetic relationships. Phylogenetic analysis revealed that all PE goat samples belonged to haplogroup B together with Southeast and East Asian local goats such as Samosir and Kosta goats, with bootstrap values ranging from 91–95%. Based on the results of this study, it can be concluded that black- and brown-headed Peranakan Etawa (PE) goats from Kulon Progo exhibit close genetic relationships with other indigenous Indonesian goat populations and belong to haplogroup B, which is widely distributed throughout Southeast and East Asia.

Keywords: D-Loop, haplogrup, mitochondrial DNA, Peranakan Etawa goat, phylogenetic.