

INTISARI

ANALISIS KERAGAMAN GENETIK KUSKUS (*Phalangeridae*) ASAL MALUKU BERDASARKAN SEKUEN GEN PENYANDI NADH DEHYDROGENASE SUBUNIT 4L

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Kuskus merupakan marsupial dimana salah satu penyebarannya di Maluku. Satwa tersebut memiliki karakter morfologi yang mempesona sehingga menjadi target perburuan masyarakat. Sampai saat ini penelitian mengenai kuskus masih terbatas pada penelaahan tentang taksonomi, morfologi, dan ekologi. Oleh karena itu, diperlukan penelitian identifikasi secara molekuler untuk membantu konservasinya. Tujuan dari penelitian ini adalah untuk mendapatkan sekuen nukleotida dan keragaman genetik dari gen ND4L mitokondria pada kuskus asal Maluku.

Sampel DNA diisolasi dari 11 kuskus asal delapan daerah di Maluku, yaitu Pulau Ambon, Pulau Seram, Pulau Tobelo, Pulau Geser, Pulau Gorom, Pulau Haruku, Kepulauan Manipa, dan Pulau Lakor kemudian diamplifikasi menggunakan primer ND34LF dan ND34LR dengan teknik *Polymerase Chain Reaction* (PCR) menghasilkan produk amplifikasi sebesar 1035 *basepair* (bp), kemudian dilakukan sekuensing. Hasil sekuensing sebesar 279 nukleotida (nt) selanjutnya dianalisis menggunakan program MEGA versi 6.06 yang dibandingkan dengan spesies kuskus dari *Genbank*.

Hasil analisis memperlihatkan bahwa sampel kuskus asal Tobelo Ternate Maluku Utara (coklat muda garis hitam), Tanah Amahai Seram Selatan (totol), Soya P. Ambon (totol), Kepulauan Manipa Maluku (kelabu), Allang P. Ambon (kelabu), Larike P. Ambon (coklat garis hitam), Lakor Maluku Barat (coklat garis hitam), dan P. Gorom Maluku (putih) merupakan spesies *S. maculatus* dengan jarak genetik berkisar 0,3%-1,7%. Sampel asal Allang P. Ambon (putih) dan P. Geser (putih) kemungkinan juga masih kelompok *Spilocuscus sp.* dengan jarak genetik 9,4%, sedangkan sampel kuskus asal Kariu P. Haruku (coklat garis hitam) kemungkinan teridentifikasi sebagai *Phalanger sp.* dengan jarak genetik 7,9%.

Kata kunci : Kuskus, Maluku, ND4L, Gen, Molekuler, Sekuensing

ABSTRACT

ANALYSIS OF CUSCUS GENETIC DIVERSITY (Phalangeridae) ORIGINATED FROM MALUKU BASED ON GENE SEQUENCES CODING FOR NADH DEHYDROGENASE SUBUNIT 4L

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Cuscus is a member of marsupial which has spread across the globe, including in Maluku, Indonesia. These animals have a fascinating morphological characters which often be the target for hunters. Until now, research related to cuscus is still limited to the study of taxonomy, morphology, and ecology. Therefore, further research is needed to aid the identification of molecular conservation. The purpose of this study is to obtain nucleotide sequences and genetic diversity from ND4L mitochondria genes in cuscus originated from Maluku.

DNA samples were isolated from eleven cuscus originated from eight regions in the Maluku such the island of Ambon, Seram, Tobelo, Geser, Gorom, Haruku, Manipa, and Lakor. Next, the samples were amplified using primer ND34LF and ND34LR with *Polymerase Chain Reaction* (PCR) technique that result in products of 1035 *basepair* (bp) and later be sequenced. The result from sequencing 279 nucleotides (nt) are then analyzed using MEGA program version 6.06 and later will be used in comparison to the cuscus species from *Genbank*.

The result shows that the sample originated from Tobelo Ternate in North Maluku (light brown with black line), Tananahu Amahai South Seram (spots), the island of Soya Ambon (spots), Manipa Maluku Islands (gray), Allang in the island of Ambon (gray), Larike in the island of Ambon (brown black line), Lakor in the west Maluku (brown black line), and Gorom in the island of Maluku (white) are categorized as a *S.maculatus* species with genetic distances ranging from 0.3% - 1.7%. Samples from Allang in the island of Ambon (white) and the island of Geser (white) are categorized in *Spilocuscus sp.* group with genetic distance of 9.4%, while sample from Kariu the island of Haruku (brown black line) is identified as a *Phalanger sp.* with genetic range of 7.9%.

Keywords: Cuscus, Maluku, ND4L, Gene, Molecular, Sequencing