INTISARI

IDENTIFIKASI MOLEKULAR KUSKUS (Phalangeridae) ASAL PAPUA BERDASARKAN SEKUEN GEN PENYANDI *NADH Dehydrogenase 3* (ND3)

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Kuskus merupakan salah satu hewan berkantung endemik yang terancam punah akibat perburuannya yang meningkat. Salah satu upaya untuk menjaga eksistensi kuskus adalah dengan konservasi. Identifikasi spesies kuskus relatif sulit pada tingkat morfologi sehingga perlu dilakukan identifikasi spesies kuskus di tingkat genetik molekular. Penelitian ini bertujuan untuk mengidentifikasi kuskus asal Papua berdasar sekuen gen penyandi *(ND3)*serta mengetahui kekerabatannya dengan kuskus lain dalam famili Phalangeridae.

Sebanyak delapan sampel kuskus didapatkan dari lima daerah di Papua, yaitu satu sampel dari Topo Nabire (I.), dua sampel dari Wanggar Nabire (2. dan 4.), tiga sampel dari Nabire (2A, Papua Lama A, dan Papau IA), satu sampel dari Yaro Nabire (3.), dan satu sampel dari Pulau Sentani (Totol Sentani Papua). Sampel diisolasi DNA, diamplifikasi dengan teknik PCR. Produk PCR (1035 bp) disekuensing. Hasil sekuensing gen *ND3* (347 bp) dianalisis keragaman genetik antar spesies kuskus lain dari *Genbank* menggunakan program MEGA 7.00.

Kuskus asal Papua terdiri dari kelompok *Spilocuscus* dan *Phalanger*. Kuskus Nabire, Wanggar Nabire Coklat Garis Hitam, Yaro Nabire, Pulau Sentani, dan Topo Nabire teridentifikasi sebagai *S. maculatus*(jarak genetik 0,6-1,5% terhadap *S. maculatus*). Kuskus Wanggar Nabire Kelabu Tuateridentifikasi sebagai *Phalanger sp.* (jarak genetik 10,4% terhadap *P. vestitus*). Sebanyak 66 nukleotida dan 8 asam amino sebagai penanda genetik padakuskus Nabire, Wanggar Nabire Coklat Garis Hitam, Yaro Nabire, dan Topo Nabire dengan kuskus Wanggar Nabire Kelabu Tua, serta terdapat 5 nukleotida dan 2 asam amino sebagai penanda genetik pada kuskus Pulau Sentani dengan kuskus Nabire, Wanggar Nabire Coklat Garis Hitam, Yaro Nabire, dan Topo Nabire.

Kata kunci: gen ND3, kuskus, *Phalanger*, *Spilocuscus*, PCR

ABSTRACT

MOLECULAR IDENTIFICATION OF CUSCUS (Phalangeridae) FROM PAPUA BASED ON *NADH Dehydrogenase 3* (ND3) GENE SEQUENCES

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Cuscus is one of the endemic marsupial mammals which threatened to extint due its increased hunting activity by people. One of the efforts to maintain the existence of cuscus is by conservation. Species identification of cuscus is relatively difficult to do by seeing the morphology, so it is needed to identify cuscus at the level of genetic molecular. The goal of this research is to identify cuscus from Papua based on ND3 gene sequences and also knowing the genetic relationship among another cuscuses in the Phalangeridae.

Eight samples of cuscus is obtained from five region in Papua, one sample is from Topo Nabire (I.), two samples is from Wanggar Nabire (2. dan 4.), three samples is from Nabire (2A, Papua Lama A, dan Papau IA), one sample is from Yaro Nabire (3.), and one sample is from Sentani Island (Totol Sentani Papua). Samples is treated by DNA isolation, DNA amplification by PCRA 1035 bp PCR product is then sequenced. Product of sequenced ND3 gene (347 bp) is analyzed in genetic variety among species from *Genbank*using MEGA 7.00.

Cuscus from Papua consist of *Spilocuscus* and*Phalanger*group. Nabire, Wanggar Nabire Coklat Garis Hitam, Yaro Nabire, Pulau Sentani, and Topo Nabire cuscuses are identified as *S. maculatus*(genetic distance of 0,6-1,5% with *S. maculatus*). Wanggar Nabire Kelabu Tua cuscus is identified as *Phalanger sp.* (genetic distance of 10,4% with *P. vestitus*). As many as 66 nucleotides and 8amino acids can be used as genetic markers between Nabire, Wanggar Nabire Coklat Garis Hitam, Yaro Nabire, and Topo Nabire cuscuseswith Wanggar Nabire Kelabu Tua cuscus and as many as 5 nucleotidesand 2 amino acids can be used as genetic markers between Sentani Island cuscus with Nabire, Wanggar Nabire Coklat Garis Hitam, Yaro Nabire, and Topo Nabire cuscuses.

Keywords: ND3 gene, cuscus, *Phalanger*, *Spilocuscus*, PCR