

**KARAKTERISASI GENETIK DUA POPULASI KAPUK RANDU (*Ceiba
pentandra* (L.) Gaertn.) DI SUMATERA BARAT BERDASARKAN
PENANDA *INTERNAL TRANSCRIBED SPACER* (ITS)**

TESIS

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FAKULTAS MATEMATIKA DAN ILMU PENGETAHUAN ALAM

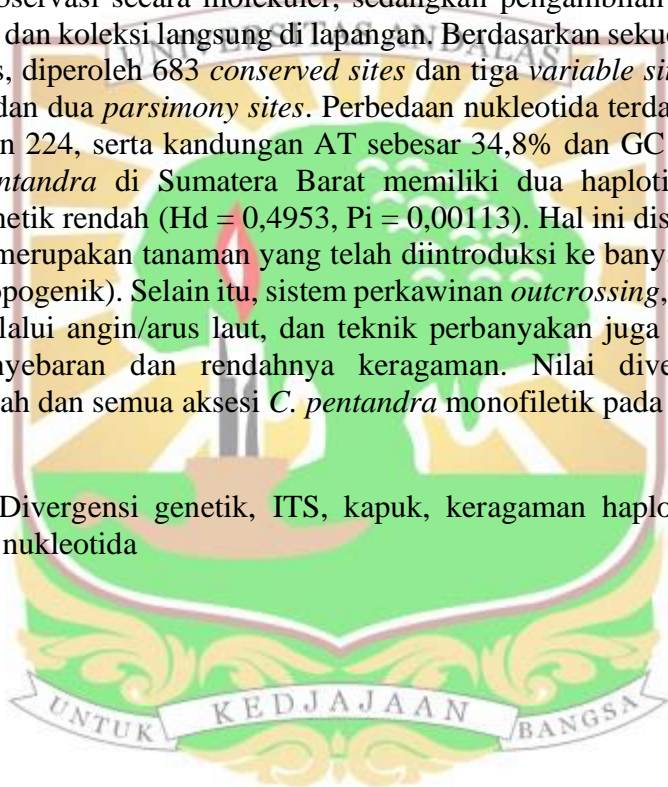
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ABSTRAK

Kapuk randu (*Ceiba pentandra* (L.) Gaertn.) merupakan tumbuhan asli daerah tropis Amerika Tengah, Amerika Selatan, Karibia, dan Afrika Barat. Tanaman ini telah diintroduksi dan dibudidayakan ke banyak wilayah tropis, termasuk Indonesia. Namun, beberapa daerah terjadi penurunan populasi termasuk di Sumatera Barat. Penelitian ini bertujuan untuk menganalisis karakteristik sekuen, keragaman haplotip, dan divergensi genetik beberapa aksesori *C. pentandra* pada dua populasi di Sumatera Barat (Pesisir Selatan dan Tanah Datar) berdasarkan penanda *internal transcribed spacer* (ITS). Penelitian dilakukan dengan metode deskriptif berdasarkan observasi secara molekuler, sedangkan pengambilan sampel dengan metode survey dan koleksi langsung di lapangan. Berdasarkan sekuen *C. pentandra* yang dianalisis, diperoleh 683 *conserved sites* dan tiga *variable sites*, dengan satu *singleton site* dan dua *parsimony sites*. Perbedaan nukleotida terdapat pada urutan ke 64, 149, dan 224, serta kandungan AT sebesar 34,8% dan GC sebesar 65,2%. Aksesori *C. pentandra* di Sumatera Barat memiliki dua haplotip dengan nilai keragaman genetik rendah ($H_d = 0,4953$, $P_i = 0,00113$). Hal ini disebabkan karena *C. pentandra* merupakan tanaman yang telah diintroduksi ke banyak wilayah oleh manusia (antropogenik). Selain itu, sistem perkawinan *outcrossing*, penyebaran biji (dispersal) melalui angin/ arus laut, dan teknik perbanyakan juga memungkinkan perluasan penyebaran dan rendahnya keragaman. Nilai divergensi genetik tergolong rendah dan semua aksesori *C. pentandra* monofiletik pada subklaster yang sama.

Kata kunci: Divergensi genetik, ITS, kapuk, keragaman haplotip, keragaman nukleotida



ABSTRACT

Kapok (*Ceiba pentandra* (L.) Gaertn.) is native to the tropics of Central America, South America, the Caribbean, and West Africa. This plant has been introduced and cultivated in many tropical regions, including Indonesia. However, some areas have experienced population declines, including West Sumatra. This study aims to analyze the sequence characteristics, haplotype diversity, and genetic divergence of several *C. pentandra* accessions in two populations in West Sumatra (Pesisir Selatan and Tanah Datar) based on internal transcribed spacer (ITS) markers. The research was conducted with descriptive methods based on molecular observations, sampling with survey methods, and direct collection in the field. Based on the analyzed *C. pentandra* sequences, 683 conserved sites and three variable sites were obtained, with one singleton site and two parsimony sites. Nucleotide diversity was found in the 64th, 149th, and 224th sequences, and the AT content was 34.8% and the GC content was 65.2%. Accessions of *C. pentandra* in West Sumatra have two haplotypes with low genetic diversity values ($H_d = 0.4953$, $P_i = 0.00113$). This is because *C. pentandra* is a plant that has been introduced to many areas by humans (anthropogenic). In addition, the outcrossing mating system, dispersal of seeds through wind or sea currents, and propagation techniques also allow for the expansion of distribution and low diversity. Genetic divergence values are low, and all *C. pentandra* accessions are monophyletic in the same subcluster.

Keywords: Genetic divergence, haplotype diversity, ITS, kapok, nucleotide diversity

