

## **Analysis of DNA Cytochrome Oxidase I (COI) as an Endemic Primate Conservation Effort on Siberut Island, West Sumatera**

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Islands Siberut is the largest island among the Mentawai Islands group, west of Sumatra Island. Island covering an area of 4,480 sq km in the Mentawai Islands group, separated by deep-sea mainland of Sumatra since 500,000 years ago (Whitten, 1980). This condition has maintained the life forms of living things that are separated from the mainland so that in the Mentawai Islands many endemic species are found. Of the existing mammal species, 65% are endemic species. The four types of primates that exist are endemic to the Mentawai Islands. *Hylobates klossii (bilou)*, *Simias concolor (klikobu)*, *Presbytis potenziami (joja)*, and *Macaca pagensis (bokoi)*, are protected species, and are listed on the IUCN (*International Union for Conservation of Nature and Natural Resources*) as threatened species (*vulnerable*) (Whittaker, 2005). So in this study, this paper was created by combining the literature study of Animal Ecology studies with Genetics which will discuss the conservation efforts of endemic primates on Siberut Island, Mentawai Islands, and West Sumatra through DNA analysis of Cytochrome Oxidase I (COI).

This paper will discuss studies in terms of Animal Ecology, namely conservation efforts that aim to protect and preserve endemic primates so that they do not become extinct. While in the genetic study, namely analyzing endemic primates using DNA Barcoding, which can aid conservation and research by assisting field workers in identifying species, helping taxonomists determine species groups needing more detailed analysis, and by facilitating the recognition of the appropriate units and scales for conservation planning. This paper was made using a literature study method that involved reviewing lecturers' journals in related fields of science and other articles that supported the preparation of the paper. The purpose of this paper is to fulfill the final task of the Scientific Article Writing course and provide new innovations in the conservation of endemic primates or other endemic animals.

Human impacts on the environment have rapidly accelerated species extinction via habitat degradation and climate change and the recent report by the Intergovernmental Science-Policy Platform on Biodiversity and Ecosystem Services (IPBES) predicts that climate change has already affected the distribution of nearly half (47% ) of land-mammals (Groves, 2001). Protection is urgently needed but is hampered by the lack of data for a large number of mammal species, subspecies, and populations that face extinction. A typical

example is Asian primates for which 70% of the species are threatened. Effective population management is needed but it requires a robust understanding of species numbers, boundaries, and distributions based on up-to-date information. Unfortunately, this information is lacking for many rare, globally threatened, and elusive mammalian species. Many lack molecular data and collecting this data is difficult because its taxonomy remains unclear and the different color variants of the species make it difficult to determine the boundaries of its ranges (Rizaldi, 2019).

This leaves only two alternative sources of DNA. The first is museum specimens, but the number of samples in museums tends to be small and many were collected in the 19th or early 20th century thus reflecting historical genetic diversity prior to extensive habitat loss. The second is tissue samples obtained from specimens that died of “natural causes” such as road accidents (Roesma, 2020). The problem then arises when these endemic primates need to be classified into each species and then distributed to zoos and rehabilitation centers for further protection. Although identification based on cranial or craniodental measurements has been reported (Groves & Maryanto 2008) these in vivo measurements are practically difficult to perform. Therefore, it is necessary to find a relatively simple and more accurate method for the identification of various species to be explored, one of which is through DNA analysis. Recent advances in DNA-based genetic analysis are using mitochondrial DNA which is suitable for species-level analysis and has been carried out on a variety of target genes (Masters *et al.* 2007).

The encoding genes in the mtDNA genome include the *cytochrome oxidase* subunit I (COI) gene (Nijman, 2019). CO I has been selected to be one of the genes whose sequences are used in *barcoding*. This gene has traits that meet the requirements for use in determining species identity in almost all higher animals. DNA *barcoding* has the advantage of identifying species with a high degree of accuracy compared to morphological observations (Madduppa *et al.*, 2017). DNA *barcodes* based on Cytochrome Oxidase Subunit I (COI) gene markers are widely used in species identification and biodiversity studies (Leatemia *et al.*, 2018).

Thus, the COI gene can be used in conservation efforts because it has many advantages for studying genetic characteristics because it undergoes very few deletions and insertions in its sequences, as well as many parts that are *conserved* so that it can be used as DNA *barcoding* in most species (Hebert *et al.* 2003). The CO I gene can also be used to reconstruct the phylogenetic branch of evolution at the species level (Palumbi, 1996). In addition, the amino acid composition of the protein encoded in the COI gene rarely undergoes substitution so that the COI gene is stable and can be used as a marker for phylogeny analysis, but the bases in the *triple* codon are still changing and are *silent*, i.e. base changes that do not change the type of amino acid. (Herlina, 2013).

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