

ABSTRACT

*Molecular Genetic Analysis of Bima Horse (*Equus caballus*) Based on Cytochrome B Sequences*

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*Bima horse is an indigenous horse of Indonesia which is consider an endangered species. Based on statistical data done by the local government of West Nusa Tenggara, its population was 65.998 in 2008, and drop into 9.703 in the year of 2009. Conservation efforts must be done to save this species, either by in-situ or ex-situ approaches. Morphological approaches are not sufficient, and a more basic approach need to be done, which is based on its genetic character. The aim of this study is to analyse the relationship between local Bima horses based on cytochrome b sequence of *Equus caballus*.*

Research samples as blood were collected from horses of 2 different areas in Western Nusa Tenggara, Panda and Kalaki villages of district Palibelo, Bima region. DNA obtained from the blood were used to run PCR reaction to amplify cytochrome b region by using CYTBECF and CYTBECR primers. A 371 bp fragment was produced and continued with sequence analysis. The resulting sequence was then compared with sequences database of Genbank.

*Sequence analysis with MEGA 5.05 detecting 35 different nucleotide sites and 1 different amino acid site between Bima horse and *E. caballus*. Genetic distance using Kimura 2-parameter based on nucleotide sequence of cytochrome b, the genetic distance among samples is 3.1%, and the genetic distance of 0.2% was obtained based on amino acids sequence. Phylogenetic analysis based on nucleotides and amino acids sequences by employing Neighbour-Joining method with 1000 bootstrap value revealed that cytochrome b could be used to study the relatedness of Bima horses, and it is shown that Bima horses are closely related to each other.*

Keywords : *Equus caballus*, DNA, cytochrome b, PCR, sequence of DNA