

Abstract

Based on the 2010 Indonesian Population Census, there are 1,300 ethnic categories with various sub-tribal details. Ethnic diversity is important in terms of identification, such as natural disasters, accidents, crime, and the discovery of unidentified corpses that may come from various tribes. Forensic Medicine views genetic diversity and variation as one of the challenges in identification. Genetic variation and kinship in Banjar Hulu tribe have never been done. The aim of the study is to identify and analyze the genetic variation of Banjar Hulu tribe through nucleus DNA examination of short tandem repeat (STR) Loci combined DNA index system (CODIS). This study is a descriptive observational study that aims to explain the genetic variation of Banjar Hulu tribe. The design of this study is cross-sectional. This study was conducted in two stages, the first stage is to obtain information on family tree from the study subjects conducted by interview. Then the second stage is to draw blood from the study subjects' criteria. Blood is drawn from peripheral vein. Then, there will be DNA examination and analysis of genetic variation. Results of the study show THO1 allele 9.3 locus, D3S1358 allele 12 locus, and D16S539 allele 12 locus, D8S1179 allele 12 locus are typical markers for Banjar Hulu tribe. Banjar Hulu tribe have specific loci and alleles.

Keywords: *Banjar Hulu tribe, STR, CODIS.*