Analysis of Genetic Variations And Specific Locus of Banjar Hulu Tribe Through Short Tandem Repeat (STR) Locus Combine Dna Index System (Codis) in Nuclear DNA

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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 are 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 stages 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. Result of the study show THO1 allele 9.3 locus, D3S1358 allele 12 locus, and D16S539 allele 12 locus, D8S1179 allele 12 locus are typical marker for Banjar Hulu tribe. Banjar Hulu tribe have specific loci and alleles.

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

Introduction

Indonesia is a maritime country that has more than 17,000 islands between the Pacific Ocean and the Indian Ocean. Indonesia has 730 regional languages and various tribes, Indonesia is one of the most diverse countries on earth in terms of ethnicity, linguistics and genetics.[1-4] Based on the 2010 Indonesian Population Census there are 1,300 ethnic categories with various sub-tribal details.[5] Ethnic diversity is distributed on various islands in Indonesia, most of which are found on five major islands, namely Sumatra, Kalimantan, Java, Sulawesi and Papua.[6-8] Kalimantan Island is divided into five provinces, one of them is South Kalimantan Province. Most of the population in the South Kalimantan region is the Banjar tribe.[9] South Kalimantan has several disaster-prone areas. The disaster consisted of floods, whirlwinds, fires, landslides, and forest fires. Disasters in South Kalimantan are increasing every year and have an impact on society and destruction. Disasters can leave corpses that may be intact, half intact, decomposed, separated in fragments, burned to ash, half burned, buried or a combination of various conditions. so that it is necessary to use identification methods that have a high degree of accuracy and resistance to various

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conditions, such as DNA testing.[4]

Identification through DNA analysis has several advantages over other identification methods because DNA testing is more specific, more stable, can be propagated in vitro and distributed throughout the body cells. In the aspect of forensic medicine, DNA profile analysis also plays a role in the identification of the perpetrators of murder, sexual violence, victims of mutilation, victims of mass disasters and determination of offspring.[10]

In population studies, analysis of genetic variations based on DNA profiles plays a role in analyzing human origins, migration, and evolution. It also can be used to find out the genetic structure, variation and affinity of a population.[11] From the point of view of forensic genetics, population is defined as a group of humans from the same common ancestor.[12] When discussing in the context of populations, there are differences in DNA sequences known as polymorphisms that can occur in the part of the DNA that encodes or the part that does not encode the protein. DNA polymorphisms can also refer to very diverse parts of chromosomes from one individual to another.[13]

Genetic variation is a genetic difference between individuals which is inherited from one generation to the next, so that it can be used as a differentiator between one individual and another individual.[14-17] Conversely, if there are two people whose DNA profiles are similar, it could be that the kinship between the two people is very close, maybe one mother, one grandmother, or one ancestor, therefore DNA polymorphism can be used in making genetic maps of a population.[11,18] The existence of a genetic map of a population obtained from different DNA profiles can help track the similarities between victims and existing data.[4] The purpose of the analysis of variations genetic (polymorphism) in the case of forensics is to find a DNA profile that has a high level of discrimination, ideally it will produce a unique DNA profile for each individual. This is very useful for matching biological evidence from the scene of a crime to the identity of someone with a high degree of trust and can be a very strong forensic evidence.[12,19]

In October 1998, the Federal Bureau of Investigation (FBI) began a DNA mapping project using the Combine DNA Index System (CODIS). This index is not a database of criminal records but is a system that provides genetic information that is needed to match medical evidence with suspected victims or perpetrators. The FBI has recommended DNA analysis using the CODIS STR loci in the identification process.[4]

Until now the genetic variation data and specific STR loci for identification of the Banjar Hulu tribe is unknown. By conducting DNA analysis through the STR CODIS locus, it is expected to be able to find and explain the genetic variation of the Banjar Hulu tribe, and the specific STR loci for identification of the tribe. The existence of genetic variation data is expected to help the process of identification of forensics of unknown individuals, especially in the event of a mass disaster that occurred in Kalimantan. The aim of the study are 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)

Methods

This type of study is descriptive observational which is one type of study that aims to provide an explanation and real facts in the field that depend on the situation about the genetic variation of the Banjar Hulu Tribe. The design of this study is cross sectional or momentary because each sample is only examined once. The population of this study is the Banjar Hulu Tribe. The sample size is calculated by the Lemeshow formula (1997). From the sample size calculation, the minimum number of samples needed for the Banjar Hulu Tribe is 35 people. The sampling technique with Probability Proportional to Size (PPS) is a sampling technique that highly considers the size of the group or population. The sample of this study came from the Banjar Hulu Tribe who lived in Banua Kepayang Village, Labuan Amas Selatan District, Hulu Sungai Tengah, South Kalimantan Province.

The sample of this study has an inclusion and exclusion criteria.

Inclusion criteria, namely:

1. Men or women who agree to be the subject of study

2. Minimum age 21 years old.

3. Healthy born and inner

4. A native descendant who has ties up to 3 generations above with the Banjar Hulu Tribe.

Exclusion Criteria, namely:

1. Men or women who have a phobia of needles

2. Men or women who have indications of psychiatric disorders

Sampling was carried out in Banua Kepayang Village, Labuan Amas Selatan District, Hulu Sungai Tengah Regency, South Kalimantan Province. The study was conducted at the Laboratory of Genetics of the Institute of Tropical Disease (ITD) Airlangga University Surabaya, March 2018 to September 2018. This study was conducted in two stages, first obtaining information on the family tree from study subjects conducted by interview, then the second stage was carried out by taking blood on study subjects that fit the criteria. Before conducting the study, an ethics feasibility test must first be conducted and declared to have passed an ethics feasibility test.

At the time of the interview, the subjects were given an explanation of the study procedures and filled out informed consent. Then the subjects were interviewed and genealogy drawing was made from the subject. Blood sampling is performed on eligible subjects. Blood sample is taken from peripheral blood from vein mediana cubiti. Then blood sample is analyzed and DNA examination is done.

The selection of DNA extraction method with DNAzol because this method is practical and easy to implement. Measuring the level and purity of DNA through the UV-Spectrophotometer. For PCR DNA amplification TR and GM nuclei used STR CODIS primers (CSF1PO, D18S51, D21S11, D21S11, D3S1358, FGA, D8S1179, D5S818, D7S820, D13S317, D16S539). On DNA PCR results that have been amplified using STR CODIS primers were electrophorized using a polyacrilamide composite gel to determine the success of DNA amplification and continued analysis of each electrophoresis result. Data were analyzed based on the frequency of the allele description of each locus.

Results and Discussion

In the results of this study it is known that the Banjar Hulu Tribe has a variety of alleles at several loci. At the TPOX locus the Banjar Hulu tribe has a dominant allele of allele 8 and 9 of 91.43% and the lowest allele of allele 6 and 7 of 0%. The THO1 locus of the Banjar Hulu tribe has a dominant allele, which is allele 9.3 as much as 100% and the lowest allele is allele 10.3 and allele 11 is as much as 2.86%. The Banjar Hulu tribe has a distribution of all alleles at the THO1 locus, namely alleles 8.3, 9, 9.3, 10, 10.3 and 11. The Banjar Hulu FGA locus found dominant alleles, namely allele 21 as much as 40% and the lowest allele was 18.3, allele 19.3, allele 20.2, allele 21.2, allele 23, allele 23.1, allele 23.3 , and allele 25.2 as much as 0%. At the CSF locus of the Banjar Hulu Tribe, it is known that the dominant allele is allele 29.2 as much as 45.7% and the lowest allele is seen in allele 8, allele 10.3, allele 11 and allele 28.2 which is as much as 0%. Locus D5S818 have a dominant allele of the Banjar Hulu tribe, namely allele 11 as much as 77.14%. The lowest allele is in allele 9 as much as 2.86%. The Banjar Hulu tribe has all the alleles at the D5S818 locus as can be seen in the picture. The VWA locus have a dominant allele that is the allele of the Banjar Hulu 16 Tribe as much as 91.43% while the lowest allele is found in alleles 13 and 15.1 which is as much as 0%. Locus D18S51 Banjar Hulu tribe has two dominant alleles namely 15 and 16 alleles as much as 37.14% and the lowest alleles are allele 9, 13, 18 and 20 as much as 0%. The D21S11 locus have a dominant allele in the Banjar tribe that is allele 31 as much as 42.86% and the lowest allele at allele 34 as much as 0%. The D3S1358 locus has a dominant allele that is allele 16 in the Banjar Hulu Tribe by 100% and does not have an allele 15.2 at the D3S1358 locus. Locus D13S317 have a dominant allele that is allele 8 as much as 97.14% in the Banjar Hulu Tribe. The Banjar Hulu tribe has more varied alleles at locus D12S317 allele 8; 8.1; 9; 10; 11; 12. The lowest allele is in allele 11 and allele 12 as much as 2.86%. The D8S1179 locus in the Banjar Hulu Tribe has 100% of alleles 12 and 11.43% of alleles 13. The D16S539 locus of the Banjar Hulu tribe has a dominant allele that is allele 11 as much as 82.86% and the lowest allele is in the 10 allele and 13.1 allele as much as 2.86%. At the D16S539 locus the Banjar Hulu tribe has a greater allele variation of 10; 11; 12; 13; 13,1; 13,3. The D7S870 locus in the Banjar Hulu tribe has a dominant allele that is allele 9 (34.29%). 7.3 alleles; 8 and 12.1 never appeared in the Banjar Hulu tribe at the D7S870 locus.

Based on the results of study that has been done, the Banjar Hulu tribe has loci and alleles that are owned by everyone in the population, namely locus THO1 allele 9.3, locus D3S1358 allele 16 and locus D8S1179 allele 12. Alleles at these loci are typical markers for the tribe Banjar Hulu. So, to be able to determine an individual is a member of the Banjar Hulu tribal community must refer to the existence of these three loci / alleles.

The Banjar Hulu tribe does not have alleles 6 and alleles 7 at the TPOX locus, alleles 18.3, 19.3, 20.2, 21.2, 23, 23.1, 23.3, 25.2 at the FGA locus, alleles 8, 10.3, 11 at the CSF locus, alleles 9, 13, 18 , 20 at the D18S51 locus, allele 34 at the D21S11 locus, allele 15.2 at the D3S1358 locus, alleles 7.3, 8, 12.1 at the D7S870 locus. Whereas at several loci, the Banjar Hulu tribe has alleles that are normally distributed. At THO1 locus has distribution on all alleles, at allele 8.3, 9, 9.3, 10, 10.3, 11, locus D5S818 at allele 9, 10, 11, 12, 13, 14, 15, 16, locus D13S317 at allele 8, 8.1, 9, 10, 11, 12, locus D8S1179 at allele 12 and allele 13, locus D16S539 at alleles 10, 11, 12, 13, 13.1, 13.3.

The characteristic of the Banjar Hulu tribe that is not found in the Dayak Bukit and Dayak Ngaju tribes are at the FGA locus namely allele 18, 20.1, 21.1, 21.3, 22.3, 27, CSF locus at allele 21, 31.2, 32, D5S818 locus at allele 9, D18S51 locus at allele 16.1, 18.2, D21S11 locus at allele 30.1, D13S317 locus at allele 9, D18S51 locus at allele 16.1, 18.2, D21S11 locus at allele 30.1, D13S317 locus at allele 9, D18S51 locus at allele 16.1, 18.2, D21S11 locus at allele 30.1, D13S317 locus at allele 9, D18S51 locus at allele 16.1, 18.2, D21S11 11 and 12, D16S539 locus at allele 13.1, D7S870 locus at allele 8.1.

For the purposes of forensic identification, the presence of THO1 locus allele 9.3, locus D3S1358 allele 16 and locus D8S1179 allele 12 which are always present in the population of the Banjar Hulu Tribe is very significant. Likewise the TPOX locus at allele 6 and allele 7, FGA locus at alleles 18.3, 19.3, 20.2, 21.2, 23, 23.1, 23.3, 25.2, CSF locus at alleles 8, 10.3, 11, locus D18S51 alleles 9, 13, 18, 20, locus D21S11 allele 34, locus D3S1358 allele 15.2, locus D7S870 allele 7.3, 8, 12.1 which are not found in the population of the Banjar Hulu tribe.

In the results of this study, it is known that the Banjar Hulu tribe has 376 heterozygous alleles and 79 homozygous alleles, this shows that the Banjar Hulu tribe has a heterogamous pattern of marriage. This is in accordance with Daud (1997) which states that the Banjar tribe has an exogamous pattern of marriage.[5]

The Banjar Hulu tribe are the inhabitants who inhabit in the valley area of river branches from the Negara river that flows into the Meratus Mountains.[20] In the beginning their settlement area was a distance from each other, around the settlement there was also a Dayak tribe settlement.[21] Concentration of a large population is located on the banks of the river, at river cliffs that are relatively higher than the surrounding area in the form of swamps. The Banjar Hulu tribe inhabit the Negara, Tabalong, Batang Alai, Labuan Amas, Amandit, Tapin and Martapura areas.[5]

The pattern of exogamic Banjar Hulu marriages is strongly influenced by the teachings of the Islamic religion they profess.[22,23] Unlawful women are married by men because of hereditary ties consisting of mothers, grandmothers of both fathers and mothers, daughters and their offspring, sisters in line or one father / one mother, daughter, and sister's daughter. In addition to being related to kinship, there is also a prohibition on marrying brothers and sisters. The *Mahram* for men are mother-in-law, stepmother, stepmother, daughter-in-law, stepdaughter, and sister-in-law.[24]

Marriage is something that is considered sacred by the Banjar tribe.[5] When a man has reached the time to get married, then the closest family will hold a process of *Basusuluh*, which is a process to obtain information about the desired prospective wife, which is generally based on the choice of the man with the family's consent.[25] There are four things that are the object of the *Basusuluh* namely about her religion, offspring, ability to manage the household and the beauty of her face. About religion, does she come from a descendant who is devout in practicing her religion (Islam). About his descendants, whether she comes from a good offspring, kind, and patient and responsible. About the ability of her household, whether she comes from a rich or underprivileged family, About the beauty of his face, how is her physical condition. The influence of the teachings of Islam and traditionalism causes Banjarese very rarely married to his closest relatives.[26]

Geographical and cultural factors, especially marital patterns, as described above can explain the uniqueness and diversity of the genetic identity of the Banjar Hulu tribe and the allele patterns that tend to be more heterozygote.

Conclusion

Based on the analysis of the genetic variation of the Banjar Hulu tribe through examination of the nuclei locus of the short tandem repeat (str) combine DNA index system (CODIS), it was concluded that the Banjar Hulu tribe has the characteristics of the presence of THO1 locus at allele 9.3, D3S1358 locus at allele 16 and D8S1179 locus at allele 12, so that the existence of alleles at these loci is a reference to determine the individuals who come from the tribe.

This study has study limitations, so suggestions for further studyers need to do further study with a number of different regions to get genetic variation data from the Banjar Hulu tribe and also need to do study on other tribes to get data on genetic variation of the population inhabiting the island of Borneo .

Ethical Clearance: Taken from Medical Faculty of Lambung Mangkurat University Ethical Review Board (No. 615/KEPK-FKUNLAM/EC/III/2018)

Source of Funding: Self-Funding

Conflict of Interest: None

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