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Genetic variation analysis and kinship relationship between Dayak Ngaju tribe and Dayak Bukit tribe through examination of core DNA of Bukit CODIS STR Locus (combine DNA index system) 13 for the purpose of Forensic Identification

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Abstract

Dayak Ngaju tribe lived scattered along the Kapuas and Kahayan river. Meanwhile, the Dayak Bukit tribe lived scattered the mountain and valley area. Kinship between Dayak Bukit and Dayak Ngaju tribe is still under debate. DNA examination is one of the most reliable methods in determining personal identity, community, and kinship relationship. FBI has recommended DNA analysis using 13 short tandem repeat loci, known as CODIS 13 for DNA test. We used the system to identify the difference between Dayak Ngaju and Dayak Bukit tribe and analyze the kinship between these two tribes. There are loci and alleles that always owned by each individual of Dayak Ngaju tribe. The Dayak Ngaju characteristic which cannot be discovered in Dayak Bukit tribe are TPOX allele 6 locus, FGA allele 25.2 locus, CSF allele 8, 10.3, 11 locus, VWA allele 13, 15.1 locus, D18S51 allele 9, 13, 18, 20 locus, D21S11 allele 34 locus, D7S870 allele 12.1 locus. Dayak Bukit tribe has locus and allele that owned by each individual of Dayak Bukit tribe. The Dayak Bukit tribe characteristic which cannot be discovered in Dayak Ngaju tribe are FGA alleles 18.3, 19.3, 21.2, 23, 23.1 locus, CSF allele 28.2 locus, D7S870 allele 7.3 and allele 8 locus. The similarity of Dayak Ngaju tribe and Dayak Bukit tribe lied on 5 dominant loci named THO1 allele 9.3 locus, D5S818 allele 11, VWA allele 16, D3S1358 allele 16, D13S317 allele 8, but these loci are also found in Banjar Hulu tribe. The similarity that only discovered in Dayak Ngaju and Dayak Bukit tribe are located in TPOX allele 7 locus, FGA allele 20.2, 20.3, and D3S1358 allele 15.2. According to the research results above, it can conclude that Dayak Ngaju tribe doesn't have a close kinship to the Dayak Bukit tribe.

Keywords: Dayak Ngaju tribe, Dayak Bukit tribe, Identification, Kinship, CODIS 13

Introduction

Dayak tribe are considered as the original inhabitants of Borneo Island. Dayak tribe is divided into approximately 405 sub-tribes.¹ The Dayak tribe existence's spread throughout the Borneo Island, they lived scattered on the headwaters, highlands, valleys, and foothills. There have been some difference of opinion about the Dayak Bukit (Dayak Meratus) tribe population's origin. According to Tjilik Riwut, The Dayak Bukit tribe population is part of Dayak Ngaju tribe but it is still in doubt because there are differences

in language and beliefs aspect.² Whereas Idwar Saleh argues that the Dayak Bukit tribe is the South of Borneo Island original inhabitants who used to inhabit the coastal area and outskirts of Tabalong river, but due to the arrival of Melayu immigrants in 400-500 A.D. They were excluded to the mountain area.³

The absence of accurate data about different characteristics of these tribes may cause difficulties in further identification. In the aspect of forensic medicine, DNA profile plays a role in identifying the perpetrators and murder victims, sexual violence, mutilation victims,

mass disaster victim, and can be used to determine paternity.⁴

Examination of Short Tandem Repeats (STR) in the core of Deoxyribonucleic Acid (DNA) is often used in the determination of genetic variation and forensic identification. The STR is generally an area that does not encode proteins but has a simple repetition of nucleotide motifs. Alleles at the STR locus are vary greatly depending on the number of its motif units, so that it can be used to study population sub-structure and short-term evolution and also to measure the phylogenetic relationships of its each populations. STR can also used as a marker in observing population proximity from ethnic, linguistic, cultural, and historical population aspects. In 1990, Federal Bureau of Investigation (FBI) began a DNA mapping project using Combine DNA Index System (CODIS). The FBI has recommended DNA analysis using the STR CODIS locuses in the identification process.⁵

By conducting DNA analysis through the STR CODIS locuses, it is expected to be able to find and explain the genetic variation of Dayak Bukit and Dayak Ngaju tribe so that data can be used for the benefit of forensic identification and law enforcement, beside that it can be also be known the kinship between these two tribes.

Materials and Method

This type of research is descriptive observational, which is one type of research that aims to provide an explanation and real facts in the field that depending on the situation about the genetic variation of the Dayak Ngaju tribe and Dayak Bukit tribe, and the kinship between these two tribes, with a cross sectional design. The sample consisted of 35 volunteers (18 people from the Dayak Ngaju tribe and 17 people from the Bukit Dayak tribe) aged over 21 years who agreed to donate their blood for genetic studies. All volunteers were asked and confirmed that they were from the Dayak Ngaju tribe or Dayak Bukit tribe along 3 generations. Blood is taken from the arm vein based to the standard protocol for DNA isolation. The laboratory analysis did in Genetic Laboratory of Tropical Disease Center, Faculty of Medicine, Airlangga University. All performed procedure had got the ethical approval from the Ethical Committee of Medical Research, Faculty of Medicine, Lambung Mangkurat University.

DNA is isolated from the blood using the Nucleospin Blood Quick Pure device. Amplification of 13 STR loci was carried out using PCR (Takara) application, with a total volume of 10 µl per tube consisting of 6 µl ddH₂O, 10 µl PCR master mix kit (10x buffer Taq polymerase, dNTP, MgCl₂, primer, Taq DNA Polymerase, ddH₂O), 1 µl primary forward, 1 primary reverse and 2 µl blood genomic DNA with 94° C PCR 1 minute cycle for pre-denaturation, followed by 35 cycles of 94 ° C 1 minute denaturation, 60 ° C 1 minute for strengthening process, and 72 ° C 1 minute for extension, and one cycle 72 ° C for final incubation.

In the PCR result DNA that have been amplified using the primary STR CODIS are carried out electrophoresis using polyacrilamide composite gel to determine the success of these DNA amplification and continued by analysis of each electrophoresis result.

The alleles frequency for each CODIS 13 locus was analyzed to determine the genetic variation and kinship relationship between the Dayak Ngaju tribe and Dayak Bukit tribe.

Results and Discussion

Based on this study results, Dayak Ngaju tribe has loci and alleles that owned by each individual of Dayak Ngaju tribe which are D8S1179 allele 12 locus and D16S539 allele 12 locus. Alleles on these locuses are distinctive markers for Dayak Ngaju tribe. Therefore in order to determine an individual as a member of the Dayak Ngaju tribe population, the alleles at these loci must be present. On the other hand, the Dayak Bukit tribe has their characteristic locus and allele which owned by each individual of Dayak Bukit tribe which are TPOX allele 9 locus, D13S317 allele 8 locus and D8S1179 allele 12 locus. Alleles at these loci are distinctive markers for the Dayak Bukit tribe. Therefore, in order to determine an individual as a member of the Dayak Bukit tribe population, the alleles at these loci must be present.

The distinctive features of the Dayak Ngaju Tribe which cannot be discovered in the Dayak Bukit tribe are the presence of TPOX allele 6 locus, FGA allele 25.2 locus, CSF allele 8, 10.3, 11 locus, VWA allele 13, 15.1 locus, D18S51 allele 9, 13, 18, 20 locus, D21S11 allele 34 locus, D7S870 allele 12.1 locus. The presence of alleles at these loci is very valuable, in order to distinguish the Dayak Ngaju tribe from the Dayak Bukit tribe. While the distinctive characteristics of the Dayak Bukit tribe that cannot be discovered in the Dayak Ngaju

tribe are the presence of the FGA alleles 18.3, 19.3, 21.2, 23, 23.1 locus, CSF allele 28.2 locus, D7S870 allele 7.3, 8 locus. Therefore, the presence of alleles at these loci can distinguish the Dayak Bukit tribe and the Dayak Ngaju tribe.

For forensic identification interest, the presence of D8S1179 allele 12 loci and D16S539 allele 12 locus that always present in the population of the Dayak Ngaju Tribe is very valuable. Similarly with the THO1 allele 8.3 locus, FGA alleles 18, 18.3, 19, 19.2, 19.3, 20, 20.1, 21.1, 21.2, 21.3, 22.3, 23, 23.1, 24.1, 27 locus, CSF alleles 21, 28.2, 29, 29.2, 30, 30.2, 31, 31.2, 32 locus, D5S818 allele 9 and 15 locus, D18S51 allele 14.1, 16.1, 16.2, 18.2 locus, D21S11 allele 28.2, 28.3, 30.1, 30.3 locus, D13S317 allele 11 and 12 locus, D16S539

allele 10, 13.1 locus, D7S870 allele 7.3, 8, 8.1, 8.2 locus which cannot be discovered in the Dayak Ngaju tribe population. While the presence of TPOX allele 9 locus, D13S317 allele 8 locus and D8S1179 allele 12 locus that always present in the Dayak Bukit tribe population is very valuable. Likewise with the TPOX allele 6 locus, FGA alleles 18, 20.1, 21.1, 21.3, 22.1, 22.3, 24.2, 25, 25.2, 26, 27 locus, CSF alleles 8, 9, 9.1, 10, 10.1, 10.3, 11, 21, 31.2, 32 locus, D5S818 allele 9 locus, VWA alleles 13 and 15.1 locus, D18S51 allele 9, 13, 14, 16.1, 16.3, 18, 18.1, 18.2, 19, 20 locus, D21S11 allele 29.2, 29.3, 30.1, 31.2, 34 locus, D13S317 allele 11 and 12 locus, D8S1179 allele 13 locus, D16S539 allele 13.1 and 13.3 locus, D7S870 allele 8.1, 9.3, 10.3, 11.1, 12.1 and 13 locus which cannot be discovered in the Dayak Bukit tribe population.

Table 1. STR Codis patterns of Dayak Bukit and Dayak Ngaju tribe

The distinctive features of Dayak Bukit tribe	The distinctive features of Dayak Ngaju tribe	Dayak Bukit and Dayak Ngaju's specific loci with same allele
<ul style="list-style-type: none"> • TPOX allele 6 locus • FGA allele 25.2 locus • CSF allele 8, 10.3, 11 locus • VWA allele 13, 15.1 locus • D18S51 allele 9, 13, 18, 20 locus • D21S11 allele 34 locus • D7S870 allele 12.1 locus 	<ul style="list-style-type: none"> • GA alleles 18.3, 19.3, 21.2, 23, 23.1 locus • CSF allele 28.2 locus • D7S870 allele 7.3, 8 locus 	<ul style="list-style-type: none"> • TPOX allele 7 locus • FGA allele 20.2, 23.3 locus • D3S1358 allele 15.2 locus

In this study, it was known that the Dayak Ngaju tribe had 215 heterozygous alleles and 45 homozygous alleles, indicating that the Dayak Ngaju tribe had heterogamous patterns of marriage. Dayak Ngaju population has exogamous pattern of marriage. While the Dayak Bukit tribe had 214 heterozygous alleles and 42 homozygous alleles, indicating that the Dayak Bukit tribe has a heterogamous pattern of marriage.² Dayak Bukit population has exogamous marriage patterns.⁶

The Dayak Ngaju and Dayak Bukit tribes respectively have specific loci with the same allele which are TPOX allele 7 locus, FGA allele 20.2, 23.3 locus and D3S1358 allele 15.2 locus. Meanwhile, these two tribes also has similarities at the THO1 allele 9.3 locus, D5S818 allele 11 locus, VWA allele 16 locus, D3S1358 allele 16 locus, D13S317 allele 8 locus, D8S1179 allele 12 locus, but the

presence of these loci based on research are also found in the Banjar Hulu tribe.

From the this study results, we know that the Dayak Ngaju tribe does not have a close relationship with the Bukit tribe. The reason that might be the cause of their low level of kinship is geographically separated, where the Dayak Bukit tribe inhabits the highlands of the Bukit Mountains while the Dayak Ngaju Tribe inhabits the watersheds that far from the Bukit Mountains. The Dayak Ngaju tribe lived scattered the Kapuas River and Kahayan Rivers with extensive distribution, mainly in Palangka Raya, Pulang Pisau, Gunung Mas, Kapuas, Katingan, East Waringin City and Seruyan. The Dayak Ngaju villages are scattered along the river with the far distance between villages and scattered, as well as their lamin or betang (Dayak Ngaju houses).² On the other

hand, the Dayak Bukit tribe occupied the forest area of Bukit Mountains. they lived scattered the mountain and valley area between the riverstream. The main villages are villages that have never been abandoned, while the location of their underling village is far apart. Between one underling village and the other are separated by mountains, forests and rivers, with springs as a natural barrier.

Their low level of kinship is in accordance to the previous research which states that the population inhabiting the Bukit mountains is not a Dayak, but coastal Malay residents who migrated into the forest of Bukit Mountain.^{6,7}

Conclusion

Dayak Ngaju tribe has loci and alleles that only owned by each individual in the population, namely D8S1179 allele 12 locus and D16S539 allele 12 locus. Dayak Bukit tribe has the locus and allele that only owned by each individual in the population, namely TPOX allele 9 locus, D13S317 allele 8 locus, D8S1179 allele 12 locus. The presence of these loci and alleles is a distinctive marker for these two tribes. The Dayak Ngaju tribe doesn't have a close kinship with the Dayak Bukit tribe.

Ethical Clearance: This study approved and received ethical clearance from the Committee of Medical Ethics of Medical Faculty, Airlangga University, Indonesia.

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Conflict of Interest: The authors declare that they have no conflict interests.

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