Paternity Test Through Kinship Analysis and Cell Free Fetal DNA (Cff-DNA) as a Forensic Identification Technique

by Arofi Kurniawan

Submission date: 03-Apr-2023 02:13PM (UTC+0800)
Submission ID: 2054358941
File name: Scopus_12-2022_Paternity_Test_Through_Kindship_Analysis.pdf (1.15M)
Word count: 6017
Character count: 23028

Paternity Test Through Kinship Analysis and Cell Free Fetal DNA (Cff-DNA) as a Forensic Identification Technique

Ahmad Yudianto[1,3]*, Arofi Kurniawan[1,4], Fery Setiawan[4], Abdul Hadi Furqoni[3,4], Beta Novia Rizky[2]

1. Department of Forensics and Medicolegal-dr.Soetomo Hospital, Faculty of Medicine, Universitas Airlangga, Indonesia.
2. Department of Forensic Odontology, Faculty of Dentistry, Universitas Airlangga, Indonesia.
3. Human Genetics Study Group, Institute of Tropical Disease, Universitas Airlangga, Indonesia.
4. Department of Pathology Oral Maxillofacial, Faculty of Dental Medicine, Universitas Airlangga, Surabaya, Indonesia.

Abstract

The application of kinship analysis and cell-free fetal DNA (cff-DNA) analysis can be found in forensic identification processes, mainly on (civil or criminal) parentage testing, disaster victim identification, missing person identification, and familial searching (Butler, 2006; 2015). So far, paternity tests using kinship analysis and cell-free fetal DNA (cff-DNA) as a forensic identification examination are still not widely known.

This study aims to analyze the application of kinship analysis and cff-DNA analysis in paternity examination tests. This study is observational laboratory research with a one-shot research design. The extracted DNA sample was measured for its DNA contents and purity. The average DNA contents were 575 ± 4.33 ng/µl with the purity range of 1.035-1.82 while the average DNA contents for maternal plasma DNA (cff-DNA) were 75 ± 2.31 ng/µl with the purity range of 1.12-1.56. The highest allele frequency was on allele 31 of the D21S11 locus (64.375%). All the examined STR CODIS loci showed that allele sharing was dominated by two allele sharing with a percentage higher than 50%.

The 13 STR CODIS loci has the highest percentage of two allele sharing. Based on this finding, it is recommended that paternity tests can be performed through kinship line by using siblings' DNA in case the DNA from the parents are unavailable, and the use of cff-DNA as a non-invasive method in paternity test examination.

Experimental article(J Int Dent Med Res 2022; 15(4): 1434-1441)

Keywords: Paternity test, kinship analysis, cff-DNA, Human and Mortality.

Received date: 21 June 2022 **Accept date:** 19 July 2022

Introduction

A paternity test is a valid legal procedure in determining parentage. Up until today, the solution for paternity problems is often determined by assessing similar aspects or the dissimilar aspects of a child and his/her alleged father. The similar aspects here refer to the characteristics of iris color, hair, unique gesture and way of speaking, and body stature.[1]

The unavailability of information originating from both parents during the identification process is one of the problems in forensic DNA analysis, especially in a paternity test.[2,3] Therefore, a comparison originating from close family or relatives such as biological siblings is required as one of the solutions in the forensic DNA analysis process.

Paternity tests can be conducted before an individual is born. DNA test can be conducted by using chorionic villi sampling (CVS) at the 10th-13th week of pregnancy or by using amniocentesis at the 14th-24th week of pregnancy. Inside a mother's body, molecules are transferred from the mother to the fetus and vice versa. Studies on this two-way molecular transfer have been developed and one of the topics with the most rapid development is cell-free fetal DNA (cff-DNA).[4]

The principles of forensic DNA examination are based on the comparison of alleles originating from the victims or perpetrators with the comparing sample from their family or relatives (kinship analysis). It is common in cases

*Corresponding author:
Ahmad Yudianto,
Department of Forensic Medicine and Medicolegal-dr.Soetomo Hospital, Faculty of Medicine Universitas Airlangga, Indonesia
St. Mayjen Prof. Dr. Moestopo No. 47, Surabaya, Indonesia
E-mail: yudi4n6sby@yahoo.co.id

such as unborn child disputes, paternity disputes, or in forensic DNA analysis on mass disaster victims or war victims. In these conditions, a comparison originating from a close family line is required as a means in the forensic DNA analysis process, for example, the siblings of the victim or perpetrator in case the information from parents or descendants is unavailable.

Objectives to explain the application of kinship analysis and cell-free fetal DNA (cff-DNA) analysis can be found in forensic identification processes, particularly on parentage testing (civil or criminal), disaster victim identification, missing person identification, and familial searching.[5,6] So far, paternity tests using kinship analysis and cell-free fetal DNA (cff-DNA) as a forensic identification examination are still not widely known.

Materials and methods

Research Samples

This research was observational laboratory research with a one-shot study design. The respondents of this study consisted of 20 women in the second and third trimesters of pregnancy and their two biological children. This study obtained ethical clearance from the Faculty of Dentistry Universitas Airlangga Number 275/HRECC.FODM/VI/2020. This study was conducted at the Human Genetics Study Group, the Institute of Tropical Diseases, Universitas Airlangga.

Sample Preparation

Twenty samples of respondents' peripheral blood were stored in tubes and labeled A (mother), B (Child 1), and C (Child 2) to indicate the blood samples from mothers and biological children.

DNA Extraction

For pregnant women's blood samples: the blood samples were centrifuged at 1600 rpm for 10 minutes. The supernatant was moved into Eppendorf tubes and was centrifuged at 1600 rpm for 10 minutes. The supernatant was removed and the DNA was extracted while for children 1 and 2's blood sample, the DNA was extracted. The DNA extraction process of the 20 peripheral blood samples was carried out using the DNAzol method.[7] 50 µl distilled water was added to the isolated DNA pellets.

DNA Amplification

The DNA amplification was conducted through the Polymerase Chain Reaction (PCR) process (PowerPlex® 21Systems, Promega, USA) targeting specific DNA sequences to produce a number of replications of the isolated DNA. The amplification of the 80 samples used 13 primers of Short Tandem Repeats [STR]-Combined DNA Index System [CODIS] (TPOX, D3S1358, FGA, D5S818, CSFIPO, D7S820, D8S1179, THOI, vWA, D13S317, D16S539, D18S51, D21S11) and Amelogenin (Amel) x:106bp,y:112bp. The amplification adjustment for D3S1358, FGA, D8S1179, D18S51,and D21S11 was: 96 °C- 2 minutes, followed by [94 °C-1 minute, 60 °C-1 minute, 70 °C-1.5 minutes for 10 cycles], [90 °C-1 minute, 64 °C- 1 minute, 70 °C-1.5 minutes for 25 cycles]. The adjustment for CSF1PO was 96 °C-2 minutes, followed by [94 °C-1 minute, 64 °C-1 minute, 70 °C-1.5 minutes for 10 cycles], [90 °C-1 minute, 64 °C- 1 minute, 70 °C-1.5 minutes for 30 cycles]. The amplification adjustment for D5S818, D7S820, and D13S317 was 96 °C- 1 minute, followed by [94 °C-30 seconds, 60 °C-30 seconds, 70 °C-45 seconds for 10 cycles], [90 °C-30 seconds, 64 °C- 30 seconds, 70 °C-45 seconds for 30 cycles]. The amplification adjustment for D16S539 was 96 °C-1 minute, followed by [94 °C-1 minute, 59 °C-1 minutes, 72 °C-1.5 minutes for 25 cycles] and 72 °C-1 minutes. All DNA templates were stored at 4 °C temperature.[8]

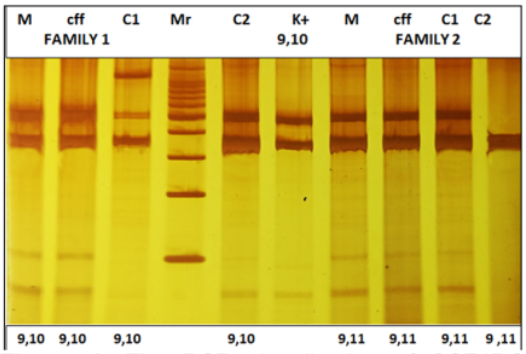

Figure 1. The PCR visualization of CSF1PO locus (321 bp-357 bp) Mr (marker 100 bp), M (mother), cff (cell-free fetal), C1 (Child 1), C2 (Child 2).

Electrophorese Gel

The visualization of PCR results was conducted through vertical electrophoresis using 6% polyacrylamide agarose gel [PAGE] [Bio-Rad Mini-PROTEAN®] with Silver nitrate staining (Figure 1).

Allele Sample

The reading of PCR visualization on the electrophoresis gel resulted in alleles at each locus with K562 as the control (Table 1).

The alleles were matched with family members (the father, the mother, and the children) and the value of allele frequency (Table 2).

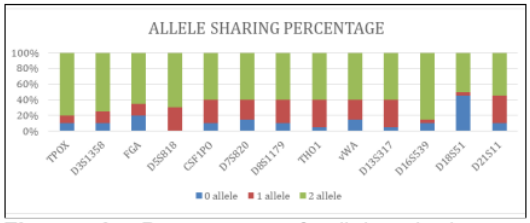

Figure 2. Percentage of allele sharing on biological children.

The analysis was based on the frequency of allele sharing based on kinship analysis between the biological siblings at every STR CODIS locus by assessing the use of allele sharing (Figure 2).

Results

The extracted DNA samples were measured for their DNA contents and purity range. The average value of biological children's DNA contents was 675 ± 5.35 with a purity range of 1.05-1.86. The average value of pregnant women's DNA contents was 4.75 ± 3.31 ng/µl with the purity range of 1.02-1.78 while the average value of maternal plasma DNA (cff-DNA) was 75 ± 2.31 ng/µl with the purity range of 1.12-1.56.

The PCR amplification through the primers of 13 STR-CODIS loci and the visualization of PCR results through Polyacrylamide Agarose Gel (PAGE) with silver nitrate staining are presented in the figure 1.

Discussion

The genetic materials of an individual are inherited from his/her parents with each of his/her parents contributing 50% of genetic materials (as presented in Table 1). Since the nuclear DNA is inherited from the father and the mother, it can be said that nuclear DNA is inherited according to the Mendelian way. The first Mendel's law (the segregation of allelic genes) discusses the principles of allelic segregation during gamete formation. Gamete formation occurs through meiosis where the homologous pairs are decoupling and segregated. The alleles of a gene freely segregate from diploid to haploid.[9,10,11] Table 2 presents the frequency of the allele in this study, namely on D21S11 allele 31 (64.375%).

In genetics, alleles are the alternative forms of genes in certain loci that are related to the expression of certain traits (phenotype). Alleles are formed as the result of variations in nitrogen base sequences caused by mutation. In an individual, allele pairs determine the genotype of the individual. The term 'allele' exists as the result of the use of the term *allelomorph* in Mendel's *Principles of Heredity*.[5,9,12]

Individuals with the same allele at a locus are said to have a homozygote genotype while individuals with different alleles are heterozygote genotypes. Since genotypes are expressed into certain phenotypes, alleles may cause different appearances among individuals within a population.[5,6]

A paternity test is a DNA test aimed to determine whether a man is the biological father of a child. Family dispute cases, in the form of doubting parents, are increasingly popular in Indonesian society.[2]

Therefore, a paternity test uses parents as the comparison where the results are statistically close to 100% or about 99.99%.[13] The unavailability of information originating from a father, a mother, or a child that can be used as a comparison in forensic DNA examination becomes a problem in forensic DNA examination.[14] Unlike DNA testing with parental DNA as the comparison, the accuracy rate of personal identifications using siblings' information is not close to 100%.[15]

The finding of this study indicates that the alleles of STR CODIS loci with the

highest percentage are TPOX allele 9 [34.375%], D3S1358 allele 17[35%], FGA allele 21[35.625%], D5S818 allele 11[32.5%], CSF1PO allele 9 [35.75%], DS820 allele 9[38.12%], D8S1179 allele 12[50%], THOI allele 9[27%], vWA allele 18[22.25%], D13S317 allele 8[43.75%], D16S539 allele 10[29.375%], D18S51 allele 16[34.375%], and D21S11 allele 31[64,375%] (Table 2).

The principle of identification examination through DNA is based on the process of allelic comparison between the victim or the perpetrator and alleles from the family line, especially parents, following the Mendelian laws.[16,17,18] In case the parental or descendant line is unavailable, a comparison with close family line is needed as one of the methods taken in an identification examination through DNA, namely biological siblings (i.e. full brother or full sister). The use of siblings as the comparison is one of the identification methods known as kinship analysis. Similar to a paternity test, the kinship analysis of an identification process using siblings as the comparison also has a possibility of mismatched profile in the examined DNA loci .[10,15,19,20,21]

Allele sharing plays a significant role in kinship analysis. Wenk, Traver, and Chiafari (1996) stated that in determining full siblings, allele sharing was very useful in defining kinship relationships when the two alleles were interrelated.[22] Statistically, full siblings had the probability of two exact alleles as much as 0.25 (25%). This value was as high as not having a shared allele (zero allele sharing) while the probability of one shared allele was 50%.[15] The findings of this study support the theory proposed by O'Connor (2011) above. All examined STR CODIS loci show that 2-allele sharing is dominant with an average value higher than 50% (Figure 2).

Allele sharing is a genetic variation an individual inherits from his/her parents. All individuals are part of a population as the result of mating between individuals and have the same gene pool. A gene pool is a collection of genes/alleles in a population.[10]

Hardy-Weinberg equilibrium principle states that the frequency of genes and genotypes will remain constant through generations in an equilibrium population. This can be found in a large population with randomized marriage and there is no attempt to regulate certain traits.[11,23,24,25]

Conclusions

All examined STR-CODIS loci have the highest percentage of two allele sharing (percentage above 50%. Based on this finding, it is recommended that paternity tests can be conducted using sibling line or kinship line in case the parental line is unavailable. This study also recommends the use of cell-free fetal DNA as a non-invasive method in paternity examination.

Declaration of Interest

The authors declare that there are no conflicts of interest.

		STR CODIS													
Family	Kode	TPOX	D3S1358	FGA	D5S818	CSF1PO	D7S820	D8S1179	THO1	vWA	D13S317	D16S539	D18S51	D21S11	Amel
1	A1	8,9	16,17	21,24	11,12	9,10	9,11	12,13	8,9	15,18	8,8	11,11	15,16	29,31	106, 112
	B1	8,10	16,16	21,24	11,12	8,10	9,11	12,13	9,10	16,17	8,8	11,11	15,16	30,31	106
	C1a	8,8	16,16	21,21	12,12	8,10	9,11	12,12	9,10	15,17	8,8	11,11	15,16	30,31	106, 112
	C1b	8,9	16,16	21,24	11,12	9,10	9,11	12,13	9,10	15,17	8,8	11,11	15,15	31.31	106, 112
2	A2	9,10	15,17	21,22	10,12	9,10	8,8	11,12	11,13	19,20	8,9	10,11	14,15	29,31	106, 112
	B2	8,9	16,17	21,24	9,10	8,9	9,10	10,11	9,10	18,19	8,10	11,13	15,15	30,31	106

	C2a	8,9	17,17	21,21	10,10	9,9	8,9	11,11	9,11	19,19	8,8	11,11	15,15	31,31	106
	C2b	8,9	15,17	21,22	10,12	8,9	8,9	11,11	9,11	19,19	8,9	11,11	15,15	31,31	106
3	A3	8,9	15,17	20,24	9,11	8,8	8,9	9,10	8,9	15,17	8,11	9,11	14,16	29,32	106, 112
	B3	9,10	16,17	22,24	11,11	9,10	9,10	11,12	8,10	18,19	9,10	9,10	16,16	30,32	106
	C3a	9,10	16,17	24,24	11,11	8,9	9,9	10,11	8,8	17,18	9,11	9,9	16,16	32.32	106, 112
	C3b	9,10	16,17	24,24	11,11	8,9	8,9	10,12	8,9	17,18	8,9	9,9	16,16	29,30	106, 112
4	A4	9,9	16,18	22,24	8,9	9,10	8,11	9,12	11,13	20,21	9,11	10,11	15,16	31,32	106, 112
	B4	9,10	17,18	21,22	10,12	9,11	9,10	12,13	11,12	16,18	9,11	10,10	16,17	29,31	106
	C4a	9,9	18,18	22,22	9,10	9,9	9,11	12,12	11,11	16,20	9,9	10,10	16,16	31,31	106, 112
	C4b	9,9	18,18	21,24	9,10	9,11	8,9	12,12	11,11	16,20	9,9	10,10	16,16	31,31	106
5	A5	8,10	16,17	20,21	11,13	8,12	9,11	10,12	8,12	16,17	9,11	9,11	14,17	29,31	106, 112
	B5	8,9	17,17	22,24	9,11	9,10	9,11	9,12	9,11	18,20	11,11	8,10	16,17	30,31	106
	C5a	8,8	17,17	21,22	11,11	9,12	9,9	12,12	8,9	16,18	11,11	8,9	14,16	31,31	106, 112
	C5b	8,8	17,17	21,22	11,11	9,12	9,9	12,12	8,9	16,18	11,11	8,9	17,17	31,31	106
6	A6	7,10	15,18	21,21	9,11	8,9	8,10	11,12	8,9	19,20	8,9	11,13	14,15	29,31	106, 112
	B6	10,11	16,17	22,23	11,11	10,11	9,11	12,13	10,13	18,19	10,12	10,12	15,15	30,31	106
	C6a	7,11	16,18	21,22	11,11	8,11	8,9	12,12	8,10	19,19	9,10	11,12	15,15	30,31	106, 112
	C6b	10,11	16,18	21,23	11,11	8,11	9,10	12,12	8,10	19,19	9,10	11,12	15,15	31.31	106, 112
7	A7	9,10	16,17	20,21	10,12	10,11	8,11	11,13	11,12	17,19	8,8	11,11	14,16	29,31	106, 112
	B7	8,9	15,17	22,24	11,13	9,10	9,10	10,12	9,10	17,20	8,9	10,10	16,16	30,31	106
	C7a	8,9	17,17	21,22	11,12	10,10	9,11	11,12	9,11	17,17	8,8	10,11	16,16	31,31	106
	C7b	8,9	15,17	21,22	11,12	9,11	8,9	11,12	9,11	17,19	8,8	10,11	16,16	31,31	106, 112
8	A8	9,10	17,19	22,24	10,12	9,11	9,11	12,13	11,12	15,17	8,9	9,11	14,17	31,32	106, 112
	B8	8,9	16,18	21,23	9,11	10,11	9,11	12,13	10,11	20,21	8,10	8,10	16,17	29,31	106
	C8a	8,9	17,18	21,24	9,10	9,11	9,9	12,12	11,11	15,21	8,8	8,9	14,16	31,31	106, 112
	C8b	8,9	17,18	21,24	9,10	9,11	9,9	12,13	11,11	15,21	8,9	8,9	17,17	31,31	106, 112
9	A9	11,13	16,18	22,23	11,12	8,10	9,11	11,12	8,13	16,17	9,11	11,13	14,15	29,31	106, 112
	B9	11,12	17,17	21,24	10,11	9,10	9,11	12,13	9,10	18,20	9,11	10,12	15,15	30,31	106
	C9a	11,11	16,17	21,24	11,11	8,9	9,9	12,12	8,9	16,18	9,9	11,12	15,15	31,31	106
	C9b	11,11	16,17	21,24	11,11	8,9	9,9	12,12	8,9	16,18	9,9	11,12	15,15	31,31	106, 112
10	A10	10,11	15,17	20,24	9,11	8,12	9,11	11,13	8,11	15,18	9,11	10,11	15,16	31,32	106, 112
	B10	9,10	16,18	19,22	11,13	8,10	11,11	10,12	8,9	16,17	11,11	10,10	16,17	29,31	106
	C10a	10,10	15,18	20,22	11,11	8,8	11,11	11,12	8,8	15,17	11,11	10,10	16,16	31,31	106, 112
	C10b	9,11	16,17	20,22	9,13	8,8	11,11	11,12	8,8	15,17	11,11	10,10	16,16	31,31	106, 112
11	A11	11,13	15,17	19,21	10,12	9,10	8,8	12,13	8,9	15,17	9,11	9,11	14,17	29,31	106, 112

	B11	11,12	16,18	21,23	9,11	9,11	8,8	12,13	10,13	18,19	11,11	8,10	16,17	30,31	106
	C11a	11,11	15,18	21,21	9,10	9,9	8,8	12,12	8,10	17,18	11,11	8,9	14,16	31,31	106, 112
	C11b	11,11	16,17	21,21	9,10	9,11	8,8	12,13	8,10	17,18	11,11	8,9	17,17	31,31	106, 112
12	A12	11,13	16,17	20,24	10,12	9,11	8,9	12,13	11,12	20,21	8,8	11,13	14,15	29,31	106, 112
	B12	11,12	16,16	19,22	9,11	10,11	8,10	12,13	9,10	16,18	8,8	10,12	15,15	30,31	106
	C12a	11,11	16,16	20,22	9,10	9,11	8,8	12,12	9,11	16,20	8,8	11,12	15,15	30,31	106
	C12b	11,11	16,16	20,22	9,10	9,11	8,9	12,13	9,11	16,20	8,8	11,12	15,15	31.31	106
13	A13	9,10	16,17	22,24	10,12	8,10	8,11	11,12	8,13	15,18	8,9	10,11	15,16	29,31	106, 112
	B13	8,9	17,17	21,23	9,10	9,10	9,10	12,13	9,10	16,17	8,10	10,10	16,17	30,31	106
	C13a	8,9	17,17	21,24	10,10	8,9	9,11	12,12	8,9	15,17	8,8	10,10	16,16	31,31	106, 112
	C13b	8,9	17,17	21,24	10,12	8,9	8,9	12,12	8,9	15,17	8,9	10,10	16,16	31,31	106, 112
14	A14	8,9	15,18	22,23	9,11	8,12	9,11	11,13	8,11	16,17	8,8	9,11	14,17	29,31	106, 112
	B14	9,10	16,17	21,24	11,11	8,10	9,11	10,12	8,9	18,20	8,8	8,10	16,17	30,31	106
	C14a	9,10	16,18	21,24	11,11	8,8	9,9	11,12	8,8	16,18	8,8	8,9	14,16	30,31	106, 112
	C14b	9,10	16,18	21,24	11,11	8,8	9,9	11,12	8,8	16,18	8,8	8,9	17,17	31.31	106
15	A15	9,9	17,19	21,24	8,9	9,10	9,11	12,13	11,13	15,18	9,11	9,11	14,17	28,30	106, 112
	B15	9,10	16,18	21,24	10,12	9,11	11,11	12,13	11,12	16,17	9,11	8,10	16,17	30,31	106
	C15a	9,9	17,18	21,21	9,10	9,9	11,11	12,12	11,11	15,17	9,9	8,9	14,16	30,30	106, 112
	C15b	9,9	17,18	21,24	9,10	9,11	11,11	12,13	11,11	15,17	9,9	8,9	17,17	30,31	106
16	A16	9,10	16,18	21,22	8,9	8,12	8,9	11,12	8,12	19,20	9,11	10,11	15,16	31,32	106, 112
	B16	8,9	17,17	21,24	10,12	8,10	8,10	10,11	9,11	18,19	11,11	10,10	16,17	29,31	106
	C16a	8,9	16,17	21,21	9,10	8,8	8,8	11,11	8,9	19,19	11,11	10,10	16,16	31,31	106, 112
	C16b	8,9	16,17	21,22	9,10	8,8	8,9	11,11	8,9	19,19	11,11	10,10	16,16	31,31	106, 112
17	A17	11,13	15,17	20,24	10,12	9,10	9,11	9,10	11,13	17,19	8,8	9,11	14,17	29,31	106, 112
	B17	11,12	16,18	19,22	9,10	9,11	9,11	11,12	9,10	17,20	8,8	8,10	16,17	30,31	106
	C17a	11,11	15,18	20,22	10,10	9,9	9,9	10,11	9,11	17,17	8,8	8,9	14,16	31,31	106
	C17b	11,11	16,17	20,22	10,12	9,11	9,9	10,12	9,11	17,19	8,8	8,9	17,17	31,31	106, 112
18	A18	10,11	16,17	22,24	8,9	8,12	9,11	11,13	8,9	16,17	8,9	11,13	14,15	29,31	106, 112
	B18	9,10	16,16	21,23	10,12	9,10	11,11	10,12	9,10	18,20	8,10	10,12	15,15	30,31	106
	C18a	10,10	16,16	21,24	9,10	9,12	11,11	11,12	9,10	16,18	8,8	11,12	15,15	30,31	106, 112
	C18b	9,11	16,16	21,24	9,10	9,12	11,11	11,12	9,10	16,18	8,9	11,12	15,15	31.31	106, 112
19	A19	11,13	15,18	21,24	9,11	8,12	9,11	12,13	11,13	19,20	8,11	9,11	14,17	31,32	106, 112
	B19	11,12	16,17	21,24	11,13	8,10	11,11	12,13	9,10	18,19	9,10	8,10	16,17	29,31	106
	C19a	11,11	16,18	21,21	11,11	8,8	11,11	12,12	9,11	19,19	9,11	8,9	14,16	31,31	106
	C19b	11,11	16,18	21,24	9,13	8,8	11,11	12,13	9,11	19,19	8,9	8,9	17,17	31,31	106, 112

20	A20	9,9	17,19	21,22	10,12	9,10	8,8	11,12	8,13	17,19	8,9	11,13	14,15	29,31	106,112
	B20	9,10	16,18	21,24	9,11	9,11	8,8	10,11	9,10	17,20	8,10	10,12	15,15	30,31	106
	C20a	9,9	17,18	21,21	9,10	9,9	8,8	11,11	8,9	17,17	8,8	11,12	15,15	31,31	106,112
	C20b	9,9	17,18	21,22	9,10	9,11	8,8	11,11	8,9	17,19	8,8	11,12	15,15	31,31	106,112

Table 1. STR allele profile of 20 families.

Allele	Frequency	Allele	Frequency
TPOX		**THOI**	
7	0,01250	8	0,25250
8	0,17500	9	0,27000
9	0,34375	10	0,10750
10	0,18125	11	0,27000
11	0,22500	12	0,05000
12	0,03125	13	0,05000
13	0,03125		
D3S1358		**vWA**	
15	0,09375	15	0,12750
16	0,33125	16	0,10750
17	0,35000	17	0,19500
18	0,20625	18	0,22250
19	0,01875	19	0,19500
		20	0,10250
		21	0,05000
FGA		**D13S317**	
19	0,03750	8	0,43750
20	0,08750	9	0,25625
21	0,35625	10	0,06250
22	0,22500	11	0,23750
23	0,05000	12	0,00625
24	0,24375		
D5S818		**D16S539**	
8	0,02500	8	0,13125
9	0,21250	9	0,16875
10	0,25625	10	0,29375
11	0,32500	11	0,28125
12	0,14375	12	0,08750
13	0,03750	13	0,03750
CSF1PO		**D18S51**	
8	0,23250	14	0,13750
9	0,35750	15	0,31875
10	0,20250	16	0,34375
11	0,15750	17	0,20000
12	0,05000		
D8S1179		**D21S11**	
9	0,02500	28	0,00625
10	0,08750	29	0,12500
11	0,23125	30	0,16875
12	0,50000	31	0,64375
13	0,15625	32	0,05625
D7S820			
8	0,25000		
9	0,38125		
10	0,05625		
11	0,3125		

Table 2. STR Allele Frequencies of the Sample (N=2080).

References

1. Yudianto A. Pemeriksaan Identifikasi Forensik Molekuler. Surabaya: Global Persada Press; 2015:1-45.
2. Syukriani YF. DNA Forensik. Jakarta: Sagung Seto; 2012:45-60.
3. Lu D, Liu Q, Wu W, Zhao H. Mutation analysis of 24 short tandem repeats in Chinese Han population. Int J Legal Med. 2012;126(2):331–5.
4. Prastowo W, Lyrawati D, Andarini S, Mintaroem K. Allele frequencies of STR CODIS 13 of Madura Ethnic from Bangkalan and Probolinggo. Res J Life Sci. 2018; 5(2):116–20. https://doi.org/10.21776/ub.rjls.2018.005.02.5
5. Butler JM. Genetics and genomics of core STR loci used in

human identity testing. J Forensic Sci. 2006:1–48
6. Butler JM. The future of forensic DNA analysis. Philos Trans R Soc Lond BBiol Sci.2015;370(1674): 20140252. https://doi.org/10.1098/rstb.2014.0252
7. Venkanna N, Ravi NV, Naveen, Kiran KD, Purna CGK, Lakshmi NM. Single and double incompatibility at vWA and D8S1179/D21S11 loci between mother and child: Implications in kinship analysis. Clinica Chimica Acta. 2008; 395: 162 –5
8. Omran GA, Rutty GN, Jobling MA. Genetic variation of 15 autosomal STR loci in upper (Southern) Egyptians. Forensic Science International: Genetics. 2009; 3(2): e39-44. https://doi.org/10.1016/j.fsigen.2008.05.007
9. Elvita A, Feldi W, Husni W, Maimanah, Mitha P, Rani PS, Sofi S, Ucky S, Wella Y, Yaoli S, Genetika dasar. FK UNRI; 2008:45-60. http://yayanakhyar.wordpress.com
10. Mangoendidjojo W. Genetika Populasi. Gadjah Mada University Press; 2014:45-60.
11. Artadana IBM, Wina DS. Dasar-dasar Genetika Mendel dan Pengembangannya. Graha Ilmu; 2018:45-60
12. Butler JM, Hill CR. Biology and genetics of new autosomal STR loci useful for forensic DNA Analysis. Forensic Sci Rev. 2012;24(1):15-26
13. Untoro E, Atmadja DS, Pu CE, Wu FC. Allele Frequency of CODIS 13 in Indonesian Population. Legal Medicine. 2009;11(1):S203–S205. https://doi.org/10.1016/j.legalmed.2009.01.007
14. Kido AR, Susukida MO, Fujitani N, Kimura H, Hara M. Allele frequency distributions of four STR loci VWA, TH01, TPOX and F13A01 in three Asian populations (Japanese, Bangladeshis and Indonesians). 2003;1239: 105–8.
15. Connor O. Interpretation of DNA Typing Results for Kinship Analysis. National Institute of Standards and Technology USCIS Working Group on DNA Policy Washington, DC; 2011:1-28.
16. Leclair B, Fregeau CJ, Bowen KL, Fourney RM. Enhanced Kinship Analysis and STR-based DNA Typing for Human Identification in Mass Fatality Incidents: The Swissair Flight 111 Disaster. J Forensic Sci. 2004; 49(5):939-53. www.astm.org
17. Reid TM, Baird ML, Reid JP, Lee SC, Lee RF. Use of sibling pairs to determine the familial searching efficiency of forensic databases. Forensic Science International: Genetics. 2008;2(4):340–2. https://doi.org/10.1016/j.fsigen.2008.04.008
18. Hares DR. Selection and implementation of expanded CODIS core loci in the United States. Forensic Science International: Genetics. 2015;17:33–4. https://doi.org/10.1016/j.fsigen.2015.03.006
19. Maeda K, Murakami C, Irie W, et al. The case of 2 siblings that identified not only by DNA profiling. Forensic Science International: Genetics Supplement Series. 2015;5:e555–e556. https://doi.org/ 10.1016/j.fsigss.2015.09.219
20. Marano LA, Fridman C. DNA phenotyping: current application in forensic sciences. Research and Reports in Forensic Medical Science. 2019;9:1-8; https://doi.org/10.2147/RRFMS.S164090.
21. Sosiawan A, Yudianto A, Furqoni AH, Nzilibili SM Indah N. Full-Sibling Allelic frequency and Sharing among Madurese: STR Technique by 12 locus and the sex-typing amelogenin gene. Egyptian Journal of Forensic Sciences. 2019; 9:38. https://doi.org/10.1186/s41935-019-0143-5
22. Wenk RE, Traver M, Chiafari FA. Determination of sibship in any two persons. Transfusion. 1996;36(3):259–62. https://doi.org/10.1046/j.1537-2995.1996.36396182146.x
23. Chomczynski P, Mackey K, Drews R, Wilfinger W. DNAzol: a reagent for the rapid isolation of genomic DNA. BioTechniques. 1997;22(3):550–3
24. Fung WK, Yang CT, Guo W. EasyDNA: user-friendly paternity and kinship testing program. International Congress Series. 2004; 1261:628-630. doi: 10.1016/S0531-5131(03)01486-9.
25. Krenke BE, Viculis L, Richard ML, et al. Validation of a male-specific, 12-locus fluorescent short tandem repeat (STR) multiplex. Forensic Sci Int. 2005;148(1):1–14.

Paternity Test Through Kinship Analysis and Cell Free Fetal DNA (Cff-DNA) as a Forensic Identification Technique

ORIGINALITY REPORT

13%	12%	5%	0%
SIMILARITY INDEX	INTERNET SOURCES	PUBLICATIONS	STUDENT PAPERS

PRIMARY SOURCES

1	www.karyailmiah.trisakti.ac.id Internet Source	2%
2	journals.athmsi.org Internet Source	2%
3	journal.ugm.ac.id Internet Source	2%
4	news.unair.ac.id Internet Source	1%
5	www.promega.com Internet Source	1%
6	pubmed.ncbi.nlm.nih.gov Internet Source	1%
7	hrcak.srce.hr Internet Source	<1%
8	itd.unair.ac.id Internet Source	<1%
9	Jörn Bullerdiek. "Ten Pulmonary Chondroid Hamartomas With Chromosome 6p21	<1%

	Breakpoints Within the HMG-I(Y) Gene or Its Immediate Surroundings", Journal of the National Cancer Institute, 1996 Publication	
10	hdl.handle.net Internet Source	<1 %
11	jjbs.hu.edu.jo Internet Source	<1 %
12	www.sciencegate.app Internet Source	<1 %
13	Molecular Pathology in Clinical Practice, 2007. Publication	<1 %
14	Bustamante-Aragones, A.. "New strategy for the prenatal detection/exclusion of paternal cystic fibrosis mutations in maternal plasma", Journal of Cystic Fibrosis, 200811 Publication	<1 %
15	e-journal.unair.ac.id Internet Source	<1 %
16	actamedicaphilippina.upm.edu.ph Internet Source	<1 %
17	tede2.pucrs.br Internet Source	<1 %
18	pagepress.org Internet Source	<1 %

19	repositorio.bc.ufg.br Internet Source	<1 %
20	"Abstracts of the 26th Annual Scientific Meeting of Indonesian Heart Association 2017 (26th ASMIHA), Jakarta, Indonesia, April 20–23, 2017", European Heart Journal Supplements, 2017 Publication	<1 %
21	"Advances in Forensic Haemogenetics", Springer Science and Business Media LLC, 1994 Publication	<1 %
22	Ahmad Yudianto, Indah Nuraini M., Abdul Hadi Furqoni, Simon Martin Manyanza Nzilibili, Pudji Harjanto. "The use of touch DNA analysis in forensic identification focusing on Short Tandem Repeat-Combined DNA Index System loci THO1, CSF1PO and TPOX", Infectious Disease Reports, 2020 Publication	<1 %
23	Sozer, . "Terminology", DNA Analysis for Missing Person Identification in Mass Fatalities, 2014. Publication	<1 %

Exclude quotes	Off	Exclude matches	Off

Exclude bibliography On

Paternity Test Through Kinship Analysis and Cell Free Fetal DNA (Cff-DNA) as a Forensic Identification Technique

GRADEMARK REPORT

FINAL GRADE

/0

GENERAL COMMENTS

Instructor

PAGE 1

PAGE 2

PAGE 3

PAGE 4

PAGE 5

PAGE 6

PAGE 7

PAGE 8