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ORIGINAL ARTICLE

Genetic identification of newborns in Peru: a pilot study

Identificación genética de recién nacidos en Perú: un estudio piloto

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Abstract

Objective: To determine the feasibility of genetic identification in a group of newborns from a public hospital in Lima, Peru. **Material and Method:** Descriptive cross-sectional study, carried out by the National Registry of Identification and Civil Status of Peru, on live newborns and their mothers, from the Carlos Lanfranco La Hoz Hospital (Puente Piedra, Lima) during January. 2015. The samples were collected in FTA (Fast Technology for Analysis of nucleic acids) cards that allowed a direct analysis by PCR (Polymerase Chain Reaction) and capillary electrophoresis of 21 STR markers (Short Tandem Repeats), including the amelogenin marker for gender determination. **Results:** 44 mothers and 45 newborns were included (there was a twin birth). The probability of maternity was higher than 99.9% in all cases. There were no difficulties in the sampling or in transporting the material. The obtained biological material was enough to collect DNA to identify the newborn. **Conclusions:** The genetic identification procedure was possible to perform in this hospital. Stages of the process that could be improved were identified for the eventual application of this procedure on a larger scale in Peru.

Keywords:
Biometric identification; genetic identification; Polymerase Chain Reaction; DNA; Peru; Newborn

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Introduction

Identification is an inherent right of the newborn, recognized both in Peru[1] and internationally[2]. Currently, footprints are used to identify the newborn, as well as fingerprints from eight months, however, these do not guarantee a reliable identification[3].

In Peru, despite the efforts to ensure the mother-child relationship through the registration of the newborn and the use of identification bracelets with identical numbers on the mother and child in the delivery room, cases of newborn identity violations caused by change mistakes, loss, break, alteration or neglect during the placement of these bracelets have been evidenced.

In this sense, the described situation generates windows of vulnerability that can be used for child trafficking, commit identity frauds against the vulnerable group of newborns, against the Peruvian State and against Peru's legal security.

DNA analysis for identification is frequently used worldwide in the field of criminalistics, forensics, and biological investigation of paternity[4]. However, it can also be used for civil identification purposes, as is the case in Kuwait[5].

Based on the above, the Registry of Identification and Civil Status of Peru (RENIEC) presents this pilot study that aims to determine the feasibility of genetic identification to a group of newborns from a public hospital in Lima, Peru.

Material and Method

Design and study population

Descriptive cross-sectional study of a population of live newborns and their mothers of the Carlos Lanfranco La Hoz Hospital located in the Puente Piedra district, Lima, during January 2015. As it was a pilot study, the selection of participants was carried out using a non-probabilistic and convenience sampling and therefore 45 newborns (including twins) and 44 mothers were selected. The inclusion criteria of the participants were newborns of both sexes who had their Birth Certificate Registration and/or DNI (National Identity Document) registration for the first time at the hospital with both parents present and of legal age. The exclusion criteria were parents who did not want to participate and mothers who had a bone marrow transplant and/or received a blood transfusion in the last six months, events that could eventually generate genetic profiles of the donor.

Data collection tool

The RENIEC developed the Genetic Identification Management System in three main modules: i) Consent Registry (signed informed consent); ii) Liability of biological samples delivery (chain of custody), and iii) Genetic Identification Registry; in addition to the registry of responsible persons.

Sample taking

A blood sample was obtained from the newborn through a heel stick, and in the case of the mother, two drops of blood were taken from her index finger. Both samples were obtained on separate FTA cards (includes barcode). FTA cards contain a chemically treated matrix that lyses a wide variety of tissues (e.g. blood, saliva, etc.). After the cells lysis, the released DNA binds to the card where the matrix protects the nucleic acids from harmful agents that could produce degradation, thus reducing their degradation[6].

Obtaining the genetic profile

The biological samples analysis was carried out by the Laboratory of Molecular Biology and Genetics (LABIMOG) of the Institute of Legal Medicine and Forensic Sciences of the Public Prosecutor's Office. The genetic profile determination was made by direct amplification of the genetic markers of non-coding DNA of proteins with the GlobalFiler™ Express kit according to the manufacturer's indications (Life Technologies), previously validated. The used kit included 21 autosomal STR markers, one STR marker, and one InDel marker on the Y, and amelogenin (sex-specific marker) chromosomes. Only 20 STR markers and amelogenin were used for the analysis (D8S1179, D21S11, D7S820, CSF1PO, D3S1358, TH01, D13S317, D16S539, D2S1338, D19S433, vWA, TPOX, D18S51, D5S818, FGA, D2S441, D22S1045, D10S1248, D1S1656, and D12S391) without including the STR marker and the InDel one on the Y chromosome.

The amplification of STR markers, known as Polymerase Chain Reaction (PCR), was performed using the multiplex amplification technique, in which all markers were amplified simultaneously. PCR amplification products were detected by the capillary electrophoresis with fluorescence detection technique in the Applied Biosystems™ 3500 Genetic Analyzer.

Following capillary electrophoresis, the data were imported into the GeneMapper® ID-X v1.1 genetic classification software, where the genetic profile was observed. First, the sizes of the different DNA fragments that make up the internal standard used in each sample were reviewed. Then, the allele assignment of the positive control whose genetic profile is previously known was reviewed. In addition, it was reviewed that the negative control and the blank one did not present

peaks in order to rule out contamination. The genetic profiles had to be corroborated with a standard reference marker, therefore, the sizes of the observed peaks (more than 50 RFU), quality, concentration, presence or absence of interferences, and possible null alleles were evaluated.

Finally, after successfully passing the quality control tests, and only in that case, the profiles were exported from the GeneMapper® ID-X v1 software. The frequency of a given genetic profile was calculated using the Familias v3.1.9[7] software; in addition, a comparison was made between all the generated genetic profiles, and the maternity index was calculated using the Familias v3.1.9[7] software.

Hardy-weinberg equilibrium

For a population to be in the equilibrium of Hardy-Weinberg (H-W) must meet three conditions: that the population is large enough, that mating occurs by chance, and that there are no mutations, no genetic drift or natural selection. This predicts that the allelic frequencies of a population will remain in equilibrium across generations[8]. In order to assess that loci are in Hardy-Weinberg equilibrium, the expected heterozygosity (EH) and the observed one (OH) according to Hardy-Weinberg equilibrium were compared using a 0.05 significance level with the Arlequin v3.5.2.2 software in mothers and newborns. Hernandez and Trejo[9] define OH as "the relative frequency of heterozygous individuals observed in the sample for any of the loci" and the EH as "the probability that two alleles that were taken at random from the population are different".

Registration and storage of the genetic profile

The generated genetic profiles are considered as sensitive personal information, so it is necessary to protect them. To this end, an alphanumeric representation of each was created and they were registered in two dissociated databases (DB): i) The genetic profile and the indicated alphanumeric representation were recorded in the DB of the laboratory, ii) The same alphanumeric representation was recorded in the DB of the RENIEC with all personal data such as name, date of birth, address, etc. In this way, the recorded information in each DB would not make it possible to identify a person; and only by court order could the two DBs be used together to obtain personal information.

The laboratory database consisted of genetic profiles linked to 40-character alphanumeric codes. The 40-character codes were a representation of the genetic profiles, obtained the compressed and encrypted coding of the genetic information through the SHA 1 (Secure Hash Algorithm) algorithm[10]. This algorithm had the characteristic of being irreversible (by 2015), that is, the genetic profile could not be obtained directly from the generated alphanumeric code.

In the RENIEC database there was the 40-character alphanumeric code linked to the personal data of newborns (DNI, names and surnames, date of birth, place of birth, mother's data -DNI, names, and surnames- and father's data -DNI, names, and surnames-), and the personal data of mothers (DNI, names and surnames, date of birth, place of birth).

Identification authentication tests

Alphanumeric code authentication

A (1:1) verification was performed in order to corroborate that the person is who he or she claims to be. For this purpose, the alphanumeric code was used where the personal data of the newborn and the personal data of the mother were appropriately linked. The alphanumeric code generated by the RENIEC was used and verified through the Genetic Identification Register that the person was who he or she claimed to be.

Family relationship

For this pilot study, an allele comparison was made between the newborn and all mothers who participated in the study (comparison 1:n), since the newborn has obtained one allele from the mother and one allele from the father, making this comparison with the used 20 STR type markers. They were calculated with the Likelihood Ratio (LR) and the maternity probability (W) based on the Hispanic frequencies provided by the GlobalFiler by Life Technologies for Forensic or Paternity 2013 manual.

Likelihood Ratio (LR)

The LR is calculated using the quotient of two probabilities (H1/H2), where H1 is the probability of obtaining the child's genotype assuming that "X" is the mother and H2 is the probability of the child's genotype assuming that his/her mother is any woman other than X (the mother assigned in the maternity)[11]. The software Familias v3.1.9[7] was used for this calculation.

Maternity Probability

Maternity probability was calculated by dividing the obtained value of the (LR) by (LR+1) since it is assumed that H1 and H2 prior probabilities are equal and the result was expressed as a percentage ((LR/LR+1)*100)[11].

Ethical considerations

The study was approved by the Ethics Committee of the Carlos Lanfranco La Hoz Hospital. Both parents previously signed an informed consent form, which was written following UNESCO recommendations[12].

The genetic data were irreversibly dissociated from identifiable persons. In addition, the biological sample was accompanied by the chain of custody form, in which the individualization of all persons who had the biological sample in their charge was recorded. Finally, all biological samples were removed, thus guaranteeing the data confidentiality.

Results

A total of 89 individuals were included (44 mothers and 45 newborns, due to one of the mothers had twins, both male).

Allelic frequencies of mothers and children

The genetic marker allelic frequencies indicate the number of times an allele is observed in the population regarding the total number of alleles of that marker and it is represented as a fraction or percentage. Among the analyzed genetic markers, it was observed that the most polymorphic loci (or genetic systems or genetic markers) had 11 alleles and the less polymorphic had five (Table 1).

Very frequent alleles were observed in the studied population of mothers and children for some genetic markers such as allele 10 of the marker D2S441 (67.00%), allele 15 of the marker D3S1358 (59.85%), allele 11 of the marker D5S818 (56.06%), allele 7 of the marker TH01 (54.27%), allele 8 of the marker TPOX (50.00%), allele 15 of the marker D22S1045 (46.97%), and allele 14 of the marker D10S1248 (43.18%). When comparing the most frequent allelic frequencies of the studied population with the Hispanic frequencies provided by the GlobalFiler manual, it is observed that the most frequent alleles of the markers coincide with those identified in this study with the exception of markers D12S391 (allele 18), D13S317 (allele 12), D16S539 (allele 11), D18S51 (allele 17), D21S11 (allele 30), FGA (allele 24) (Table 2).

There are also rare or infrequent alleles in the study population such as allele 9 of the marker D8S1179, allele 27 of the marker D21S11, allele 11 of the marker D3S1358, allele 8 of the marker TH01, allele 8 of the marker D16S539, allele 16 and 21 of the marker D2S1338, allele 8.2 and 12.2 of the marker D19S433, allele 19 and 20 of the marker vWA, allele 10 of the marker TPOX, allele 11 and 19 of the marker D18S51, allele 14 of the marker D5S818, allele 18 and 28 of the marker FGA, allele 11.3 and 13 of the marker D2S441, allele 13 and 14 of the marker D22S1045, allele 10 of the marker D10S1248, allele 15.3 and 18 of the marker D1S1656, allele 15 and 25 of the marker D12S391, and allele 15 and 25 of the marker D12S391. All the above alleles are present in the 0.76% of the studied population. When comparing the obtained results with the Hispanic frequencies provided by the GlobalFiler manual, it is observed that the less frequent alleles that coincide correspond to the markers D5S818 (allele 14), D8S1179 (allele 9), TH01 (allele 10) while the less frequent alleles of the rest of the markers do not coincide (Table 2).

In addition, it should be mentioned that only alleles 8.2 of the marker D19S433, allele 11 of the marker D3S1358, allele 20.3 of the marker D12S391, and allele 29.2 of the marker D21S11 appear in the studied population (Table 2).

Hardy-weinberg equilibrium

All loci were found to have high heterozygosity (higher than 57% in newborns and mothers). In the case of newborns, the lowest value was 57% (loci D3S1358 and D5S818) and the highest value was 91% (D2S1338), while in the case of mothers, the lowest value was 57% (loci D3S1358 and D2S441) and the highest value was 87% (locus D18S51). The analyzed loci are in Hardy-Weinberg equilibrium (p-value> 0.05) considering Bonferroni correction by multiple comparisons[13].

Maternity probability

The average probability found among 44 mothers and 45 newborns was 99.9990 + 0.0003, which was higher than 99.9% in all cases (Table 3).

Discussion

This pilot study demonstrates that the genetic identification of newborns in a public hospital in Lima is feasible since the protocols and procedures were properly applied, which is verified by obtaining a probability of motherhood higher than 99.9% in all cases and which was considered as a measure of quality assurance. According to Ma et al.[14], obtaining a probability higher than 99.9% confirms the biological relationship between two individuals, which is in accordance with the obtained results.

A similar pilot study conducted at a hospital in Spain shows that genetic identification was feasible, using a quick and easy protocol and known materials to health professionals. A minimum blood amount was enough to obtain the DNA for the determinations[15].

Another study carried out in Spain compared the identification method of fingerprints and genetic identification of the newborn, finding that no fingerprint taken from 30 newborns had value for identification, on the contrary, the obtained sample for genetic identification of the newborn was enough to perform molecular tests, making a proper identification of 30 children included in the study[16].

Table 1. Allelic frequencies in the mother-child pair for 132 individuals (44 mothers and their respective children)

Alleles	D8S1179	D21S11	D7S820	CSF1PO	D3S1358	TH01	D13S317	D16S539	D2S1338	D19S433	vWA	TPOX	D18S51	D5S818	FGA	D2S441	D22S1045	D10S1248	D1S1656	D12S391	Alleles
6						0.2576															6
7						0.5227								0.1591							7
8			0.0455			0.0076	0.0530	0.0076				0.5000									8
8.2										0.0076											8.2
8.3																					8.3
9	0.0076		0.0530	0.0303		0.0606	0.3030	0.2273				0.0379		0.0379							9
9.3						0.1439															9.3
10	0.0530		0.3182	0.2348		0.0076	0.1591	0.2955				0.0076		0.0530		0.6667		0.0076			10
11	0.0379		0.3788	0.3106	0.0076		0.1515	0.2500				0.3182	0.0076	0.5606		0.1970	0.0303		0.0227		11
11.3																0.0076					11.3
12	0.1667		0.1742	0.3182			0.1212	0.1818		0.0227		0.1364	0.1061	0.0985		0.0303		0.0303	0.0303		12
12.2										0.0076											12.2
13	0.3636		0.0303	0.0758			0.1136	0.0379		0.1136			0.1591	0.0833		0.0076	0.0076	0.2879	0.1742		13
13.2										0.1439											13.2
14	0.2273			0.0303	0.0152		0.0985			0.3106	0.0152		0.2424	0.0076		0.0606	0.0076	0.4318	0.1061		14
14.2										0.0455											14.2
15	0.1136				0.5985					0.1970	0.0682		0.1742			0.0303	0.4697	0.1818	0.1288	0.0076	15
15.2										0.0758											15.2
15.3																			0.0076		15.3
16	0.0303				0.2045				0.0076	0.0455	0.3712		0.1061				0.4394	0.0606	0.1667	0.0152	16
16.2										0.0303											16.2
16.3																			0.0152		16.3
17					0.1288				0.1439		0.3561		0.1515				0.0455		0.0227	0.0455	17
17.3																			0.2955		17.3
18					0.0455				0.1667		0.1742		0.0303		0.0076				0.0076	0.2273	18
18.3																			0.0227	0.0152	18.3
19									0.2879		0.0076		0.0076		0.1061					0.2348	19
20									0.1212		0.0076		0.0152		0.0758					0.2879	20
20.3																				0.0076	20.3
21									0.0076						0.1061					0.0985	21
22									0.0455						0.0682					0.0303	22
23									0.1591						0.0379						23
24									0.0455						0.1742					0.0227	24
25									0.0152						0.2424					0.0076	25
26															0.1364						26
27		0.0076													0.0379						27
28		0.0227													0.0076						28
29		0.1742																			29
29.2		0.0076																			29.2
30		0.1591																			30
30.2		0.0303																			30.2
31		0.0682																			31
31.2		0.2121																			31.2
32.2		0.2197																			32.2
33.2		0.0758																			33.2
34.2		0.0227																			34.2
Alleles	D8S1179	D21S11	D7S820	CSF1PO	D3S1358	TH01	D13S317	D16S539	D2S1338	D19S433	vWA	TPOX	D18S51	D5S818	FGA	D2S441	D22S1045	D10S1248	D1S1656	D12S391	Alleles
N	132	132	132	132	132	132	132	132	132	132	132	132	132	132	132	132	132	132	132	132	N

Source: self made.

Table 2. Comparison of allelic frequencies between the studied population and the Hispanic population

Alleles	Population studied (n = 132)	Hispanic Population (n = 368)	Alleles	Population studied (n = 132)	Hispanic Population (n = 368)	Alleles	Population studied (n = 132)	Hispanic Population (n = 368)	Alleles	Population studied (n = 132)	Hispanic Population (n = 368)	Alleles	Population studied (n = 132)	Hispanic Population (n = 368)
Marker D8S1179			Marker D21S11(continuation)			Marker D3S1358			Marker D16S539			Marker D19S433 (continuation)		
8	*	0.0068	34.2	0.0227	0.0014	9	*	0.0014	6	*	0.0014	11.2	*	0.0027
9	0.0076	0.0027	35	*	0.0027	11	0.0076	*	8	0.0076	0.0204	12	0.0227	0.0842
10	0.0530	0.0951	36	*	0.0014	12	*	0.0014	9	0.2273	0.1019	12.2	0.0076	0.0149
11	0.0379	0.0503	38	*	0.0014	13	*	0.0041	10	0.2955	0.1576	13	0.1136	0.1848
12	0.1667	0.1250	Marker D7S1179			14	0.0152	0.0910	11	0.2500	0.3179	13.2	0.1439	0.0693
13	0.3636	0.3315	7	*	0.0109	15	0.5985	0.3465	12	0.1818	0.2418	14	0.3106	0.3071
14	0.2273	0.2323	8	0.0455	0.1250	16	0.2045	0.0269	13	0.0379	0.1440	14.2	0.0455	0.0462
15	0.1136	0.1141	9	0.0530	0.0829	17	0.1288	0.1793	14	*	0.0122	15	0.1970	0.1304
16	0.0303	0.0353	10	0.3182	0.2514	18	0.0455	0.0992	15	*	0.0027	15.2	0.0758	0.0679
17	*	0.0680	10.3	*	0.0014	19	*	0.0082	Marker D2S1338			16	0.0455	0.0408
Marker D21S11			11	0.3788	0.2938	Marker TH01			16	0.0076	0.0380	16.2	0.0303	0.0217
24	*	0.0027	11.3	*	0.0014	6	0.2576	0.2717	17	0.1439	0.1780	17	*	0.0054
26	*	0.0041	12	0.1742	0.1902	7	0.5227	0.3274	18	0.1667	0.0652	17.2	*	0.0041
27	0.0076	0.0149	13	0.0303	0.0394	8	0.0076	0.0870	19	0.2879	0.1753	Marker vWA		
28	0.0227	0.1141	14	*	0.0041	9	0.0606	0.1277	20	0.1212	0.1386	11	*	0.0014
28.2	*	0.0014	Marker CSF1PO			9.3	0.1439	0.1712	21	0.0076	0.0367	12	*	0.0027
29	0.1742	0.2106	7	*	0.0095	10	0.0076	0.0149	22	0.0455	0.0652	13	*	0.0014
29.2	0.0076	*	8	*	0.0054	Marker D13S317			23	0.1591	0.1427	14	0.0152	0.0652
30	0.1591	0.2717	9	0.0303	0.0258	8	0.0530	0.0897	24	0.0455	0.0883	15	0.0682	0.0978
30.2	0.0303	0.0177	10	0.2348	0.2514	9	0.3030	0.1630	25	0.0152	0.0543	16	0.3712	0.3057
31	0.0682	0.0516	11	0.3106	0.2745	10	0.1591	0.0965	27	*	0.0014	17	0.3561	0.2717
31.2	0.2121	0.1114	11.1	*	0.0014	11	0.1515	0.2283	28	*	0.0014	17.3	*	0.0014
32	*	0.0136	12	0.3182	0.3791	12	0.1212	0.2745	Marker D19S433			18	0.1742	0.1807
32.2	0.2197	0.1250	13	0.0758	0.0462	13	0.1136	0.1005	8.2	0.0076	*	19	0.0076	0.0639
33	*	0.0014	14	0.0303	0.0054	14	0.0985	0.0476	10	*	0.0041	Marker TPOX		
33.2	0.0758	0.0530	15	*	0.0014	Marker D16S539			11	*	0.0163	6	*	0.0054

Table 2. Comparison of allelic frequencies between the studied population and the Hispanic population (continuation)

Alleles	Population studied (n = 132)	Hispanic Population (n = 368)	Alleles	Population studied (n = 132)	Hispanic Population (n = 368)	Alleles	Population studied (n = 132)	Hispanic Population (n = 368)	Alleles	Population studied (n = 132)	Hispanic Population (n = 368)	Alleles	Population studied (n = 132)	Hispanic Population (n = 368)
Marker TPOX (continuation)			Marker D18S51 (continuation)			Marker FGA (continuation)			Marker D10S1248			Marker D1S1656 (continuation)		
7	*	0.0014	23	*	0.0054	27	0.0379	0.0312	8	*	0.0014	18	0.0076	0.0082
8	0.5000	0.4783	24	*	0.0027	28	0.0076	0.0095	9	*	0.0014	18.3	0.0227	0.0448
9	0.0379	0.0802	25	*	0.0014	29	*	0.0041	10	0.0076	0.0014	19.3	*	0.0068
10	0.0076	0.0611	Marker D5S818			30	*	0.0014	11	*	0.0027	**Marker D12S391**		
11	0.3182	0.2636	7	0.1591	0.0530	Marker D2S441			12	0.0303	0.0448	13	*	0.0014
12	0.1364	0.1073	8	*	0.0149	9	*	0.0014	13	0.2879	0.2595	14	*	0.0014
13	*	0.0014	9	0.0379	0.0503	10	0.6667	0.3030	14	0.4318	0.3614	15	0.0076	0.0408
14	*	0.0014	10	0.0530	0.0435	11	0.1970	0.3193	15	0.1818	0.2269	16	0.0152	0.0503
Marker D18S51			11	0.5606	0.3818	11.3	0.0076	0.0462	16	0.0606	0.0774	17	0.0455	0.0734
9	*	0.0014	12	0.0985	0.3016	12	0.0303	0.0380	17	*	0.0231	17.1	*	0.0027
10	*	0.0068	13	0.0833	0.1454	12.3	*	0.0041	Marker D1S1656			17.3	*	0.0122
11	0.0076	0.0122	14	0.0076	0.0095	13	0.0076	0.0190	9	*	0.0014	18	*	0.1970
12	0.1061	0.1046	Marker FGA			14	0.0606	0.2310	10	*	0.0041	18.3	0.0152	0.0217
13	0.1591	0.1141	18	0.0076	0.0068	15	0.0303	0.0340	11	0.0227	0.0394	19	0.2348	0.1875
14	0.2424	0.1630	19	0.1061	0.0761	16	*	0.0041	12	0.0303	0.0938	19.3	*	0.0122
14.2	*	0.0014	20	0.0758	0.0870	Marker D22S1045			13	0.1742	0.0707	20	0.2879	0.1712
15	0.1742	0.1223	20.2	*	0.0027	10	*	0.0068	14	0.1061	0.1128	20.3	0.0076	*
15.2	*	0.0014	21	0.1061	0.1345	11	0.0303	0.0761	14.3	*	0.0027	21	0.0985	0.0870
16	0.1061	0.1291	22	0.0682	0.1440	12	*	0.0095	15	0.1288	0.1549	22	0.0303	0.0679
17	0.1515	0.1793	22.2	*	0.0054	13	0.0076	0.0109	15.3	0.0076	0.0299	23	*	0.0367
18	0.0303	0.0774	23	0.0379	0.1291	14	0.0076	0.0204	16	0.1667	0.1508	24	0.0227	0.0190
19	0.0076	0.0353	23.2	*	0.0041	15	0.4697	0.4348	16.1	*	0.0027	25	0.0076	0.0136
20	0.0152	0.0019	24	0.1742	0.1562	16	0.4394	0.3465	16.3	0.0152	0.0516	26	*	0.0027
21	*	0.0217	25	0.2424	0.1372	17	0.0455	0.0842	17	0.0227	0.0679	27	*	0.0014
22	*	0.0068	26	0.1364	0.0707	18	*	0.0095	17.3	0.2955	0.1576			

In yellow alleles that are only found in the population studied. Source: self made.

Table 3. Values of Likelihood Ratio (LR) in the samples and probability of maternity *a posteriori*

Mother/son	LR	Percentage (%)
2	4691189.21	99.9999787
3	127294.3	99.9999980
4	43746.89	99.9977142
5	11168.58	99.9910471
6	282673.34	99.9996462
7	45313690.87	99.9999978
8	691778.6	99.9998554
9	1114833.63	99.9999103
10	204468.03	99.9995109
11	1162574990	99.9999999
12	73050.25	99.9986311
13	33077865.1	99.9999970
14	272534640.7	99.9999996
15	63479610.14	99.9999984
16	41314.4	99.9975796
17	52275.18	99.9980871
18	1007811.55	99.9999008
19	5883227.67	99.9999830
20	62292760.1	99.9999984
21*	4036084.19	99.9999752
22	405617.08	99.9997535
23*	4036084.19	99.9999752
24	249839.08	99.9995997
25	85635.09	99.9988323
26	23976075.98	99.9999958
27	192031.7	99.9994793
28	3323408.28	99.9999699
29	257853560.8	99.9999996
30	110493.54	99.9990950
31	32962.71	99.9969664
32	105591175.9	99.9999991
33	2204553.99	99.9999546
34	30280589.61	99.9999967
35	30731378.1	99.9999967
36	167075.47	99.9994015
37	210156.3	99.9995242
38	2763551.13	99.9999638
39	76646.65	99.9986953
40	75843647.6	99.9999987
41	6224.42	99.9839368
42	1619646.25	99.9999383
43	31952169.23	99.9999969
44	72685.3	99.9986242
45	1352441.92	99.9999261

*Twins. Source: self made.

In this study, the sample was taken by health professionals, the used methodology for blood sampling is well known by them, and they should only be trained in taking the blood sample in the FTA cards. Likewise, there were no difficulties in storing and transporting the sample, obtaining sufficient genetic material for processing.

Although no difficulties were observed in the heel blood collection from newborns, it should be noted that one study shows that the umbilical cord blood collection could also be used for the genetic identification of the newborn, with the advantage of avoiding the traumatic effect on children and its possible complications such as infection. This evidence could be taken into consideration for future studies that expand on the found results[17]. In this study, the heel blood sample was used since the same sample taken during the neonatal screening was used, in which blood is collected to screen for the most frequent metabolic and hormonal diseases.

In Florida, USA, blood sampling on FTA cards is recommended for future determination of the genetic identification of the newborn in cases of doubt. The blood cards of the mother and child are given to the parents and it is recommended that they kept them in a safe place[18].

In the same way, the Spanish Association of Pediatrics recommends the umbilical cord blood collection, always with maternal consent, for the sole purpose of checking the identification of the newborn in case of doubt. The recommended time that these cards can last with biological material is one to five years, although it is reported that they could be valid for genetic identification for up to 15 years[19].

The storage of the blood sample in FTA cards would be appropriate at first in Peru, in order to have the genetic material properly stored for later analysis in case of routine implementation of genetic identification of the newborn, or in case of doubts about his/her identification.

In terms of international experiences in relation to national databases of genetic information, we found that a national biometric registry based on DNA is already in use in Kuwait[5]. A population database with genetic information is also being implemented in the Emirate of Dubai, which will be used mainly for disease prevention and treatment[20]. In China, there is a national DNA database which contains parental data on missing, trafficked, lost or homeless children. A recent study based on this registry recommends the use of more than 18 genetic markers for the correct identification of parents and children[21]. In Peru, this is the first pilot study that evaluates the feasibility of this technology for identification purposes.

In this study, stages of the genetic identification

process were identified that could be improved for future implementation of this technology on a larger scale in Peru, such as automation for obtaining, analyzing, and encrypting genetic profiles. Sampling was easily applied by health personnel, however, the sample collection and storage implies an additional activity in the newborn care by the nurse. In this study, the collection and storage of these cards with the child's blood was carried out by RENIEC staff, hired specifically for this process. A strong institutional collaboration between the Ministry of Health (MINSA) and the RENIEC is therefore necessary in order to replicate this experience in other hospitals in Peru.

Within the limitations of this study is the small number of samples, and the application in a single hospital fully accessible from the city center. However, this hospital has the same logistical and administrative difficulties as other hospitals in Lima and the regions of Peru, which could give an idea of the feasibility of this technique in hospitals of the same or higher level. Another limitation is that many births at the national level take place in first-level care facilities (Health Centers), where the number of personnel and resources are much lower than in Hospitals, so the feasibility of taking samples and transporting them from remote communities to the institution that will carry out the genetic identification should be explored.

In conclusion, genetic identification was feasible to perform jointly between the RENIEC, a hospital and the laboratory (LABIMOG). The RENIEC properly managed the entire process including the consent registration, the liability of biological samples delivery, and the Genetic Identification registration. The sampling protocol was easily applied by trained health personnel, the storage and delivery of biological material were carried out without difficulties to the institution where the genetic identification was determined. The LABIMOG properly processed the sample and obtained the genetic profile. Finally, all this is reflected in the maternity probability, which in all cases was higher than 99.9%.

These results could be useful for the possible implementation of this technique, in order to perform the clear identification of the newborn in case of suspicion or doubts regarding identification, however, it is necessary to conduct an study of assessment of this health technology (HTA) in the Peruvian context, as well as other pilot studies to recommend its implementation on a larger scale for identification by genetic profiles in natural persons to improve the identification process of children, support the legal system, secure identification in case of human trafficking, collaborate in solving problems of paternity (when legally required), and support the forensic system.

Future studies should evaluate the feasibility of other types of biological sampling, because there may be cases in which blood sampling is not authorized in FTA cards, and the study of other technologies for obtaining genetic profiles, as well as include first-level care health facilities, from the Peruvian mountains and jungle, in order to assess the difficulties for the application of this technique at the national level.

Ethical Responsibilities

Human Beings and animals protection: Disclosure the authors state that the procedures were followed according to the Declaration of Helsinki and the World Medical Association regarding human experimentation developed for the medical community.

Data confidentiality: The authors state that they have followed the protocols of their Center and Local regulations on the publication of patient data.

Rights to privacy and informed consent: The authors have obtained the informed consent of the patients and/or subjects referred to in the article. This document is in the possession of the correspondence author.

Conflicts of Interest

Authors declare no conflict of interest regarding the present study.

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