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Original Article

The Vital Importance of Forensic DNA Fingerprinting in Mass Casualty Victim Identification: A Case Study of Unlocking Identities

Rajesh Kumar[1], Lakshmikant[2], Pawan Kumar Prajapati[3], Neha Gupta[4], Kunwar Veer Vikram Srivastav[5]

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ABSTRACT

Background: A mass disaster is defined as an event (railway, naval, air, motorway, earthquake, flooding accidents and so on), results in a large number of fatalities (greater than 12 people) that need to be identified. These victims are called as mass disaster victims and the process of identification of these victims is known as disaster victim identification (DVI). Mass disaster can be classified in three type's vig. Open system, closed system and mixed system. In cases of mass disaster, the scene of disaster can often result in highly inter and intra mixing, decomposition, contamination and fragmentation of the remains of mass disaster victims. The result of traditional identification methods, like anthropological, odontological and X-ray examinations are often difficult to use as they are based on a unique set of physical characteristics. Hence, DNA profiling became a gold standard in disaster victim identification, mass-casualty incidents (MCIs) and any criminal case where the biological sample is highly fragmented or degraded.

Aim & Objective: This case study is based on the disaster victim identification (DVI) method using currently available molecular techniques of DNA profiling for the 11 unknown disaster victims/mass-casualty incident victims reported by the police. We identified all 11 dead bodies using five multiplex PCR amplification kits (GlobalFiler™, PowerPlex® Fusion 5C, Investigator *Argus X*-12 QS System, Yfiler® Plus and PowerPlex® Y23 System PCR Amplification Kit).

Author's Affiliation:

[1] Rajesh Kumar, Deputy Director, State Forensic Science Laboratory, Jaipur 302016, Rajasthan, India.

[2] Lakshmikant , Forensic Scientist, Guyana Forensic Science Laboratory, Guyana, South America.

[3] Pawan Kumar Prajapati, Senior Scientific Assistant, Regional Forensic Science Laboratory, Bhagalpur 812004, Bihar, India.

[4] Neha Gupta, Research Scholar, Institute of Medical Sciences, Banaras Hindu University, Varanasi 221005, Uttar Pradesh, India.

[5] Kunwar Veer Vikram Srivastav, Senior Scientific Assistant, Regional Forensic Science Laboratory, Muzaffarpur 842001, Bihar, India.

Corresponding Author:

Kunwar Veer Vikram Srivastav, Senior Scientific Assistant, Regional Forensic Science Laboratory, Muzaffarpur 842001, Bihar, India.

E-mail: kunwarsrivastav678@gmail.com

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Material: In the present case study, 11 semi-charred unknown bone samples and their relative 11 reference sample (blood sample of the suspect on FTA card) were received properly sealed condition with the sample to maintain the integrity and chain of custody of samples at the DNA Fingerprinting division, State Forensic Science Laboratory, Jaipur, Rajasthan for routine casework analysis.

Result & Conclusion: On the basis of DNA analysis it is concluded that the source of DNA profile obtained from unknown charred bone sample 1, sample 2, sample 3, sample 4, sample 5, sample 6, sample 7, sample 8, sample 9, sample 10 and sample 11 are biologically related with the source of DNA profile obtained from control blood sample on FTA cards sample 16, sample 19, sample 18, sample 12, sample 17, sample 21, sample 13, sample 15, sample 14, sample 22 and sample 20 respectively.

Key Points: Disaster victim identification, Mass-casualty incidents, Anthropological examination and DNA fingerprinting.

Case History: As per police report, a collision between a bus and a truck caused a fire disaster, in which 12 casualties were reported, one body among the 12 bodies, was physically identified by its relative. 22 other people were highly injured. Several fire brigades reached the scene of disaster to extinguish the fire along with Ambulances to aid the injured. The dead bodies were burnt to an extent that they could not be physically identified. The dead bodies were sent for the post mortem. After post mortem procedure,sealed samples of the semi-charred bones were forwarded for DNA analysis to the State Forensic Science Laboratory, Jaipur, Rajasthan. Simultaneously, the police collected all the necessary details of the passengers who were travelling in the bus. 11 relevant control blood samples on FTA cards were also sent for cross matching to the State Forensic Science Laboratory, Jaipur, Rajasthan.

INTRODUCTION

Disaster is defined as "a sudden ecological phenomenon of sufficient magnitude to require external assistance" by World Health Organization (WHO)[1]. According to the Center for Research on the Epidemiology of Disasters (CRED), disaster is "an event which overwhelms local capacity, necessitating a request to a national or international level for external assistance; an unforeseen and often sudden event that causes great damage, destruction and human suffering"[2,3] The term "disaster originates from French word "desastre"[4,5]. According to the cause, disaster can be of two types, natural and manmade. Natural disasters are tragic and unavoidable and it is the result of interaction between natural forces and humans. Manmade disasters are also known as technological disaster which is directly related and caused by humans. On the basis of availability of victim manifested disaster it can be classified into an open, closed and mixed (combination of both) disaster.

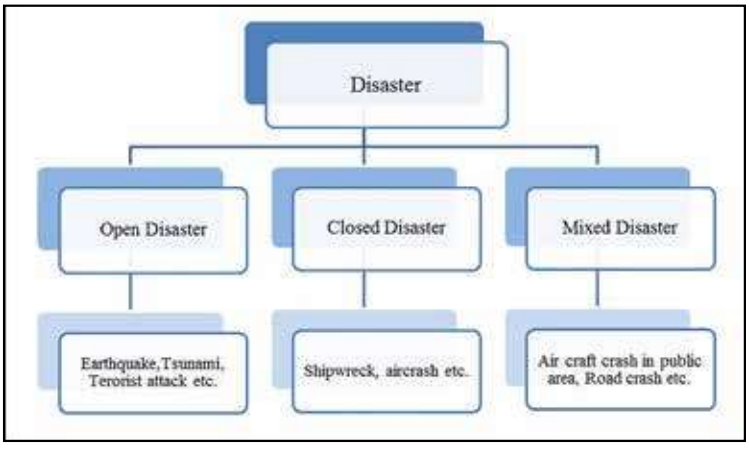

Figure 1: Classification of disaster on the basis of availability of victim manifest

Mass disaster victim's identification is very critical because of the conditions at the scene of disaster. Many times the remains of the victims at the scene are highly inter and intra mixed, decomposed, contaminated and fragmented. The result of traditional identification methods, like anthropological, odontological and X-ray examinations are often difficult to use as they are based on a unique set of physical characteristics are often difficult to use. That's why the DNA profiling became a gold standard in disaster victim identification, mass-casualty incidents (MCIs) and in criminal cases where the biological sample is highly fragmented or degraded. However, limitedness, degradation, non-homogenous character of biological material and lack of reference samples are the unavoidable possible problems of DVI through genetic fingerprinting[1]. DNA fingerprinting is a great discovery of late 20th century and it is a boon for forensic investigation. DNA fingerprinting is an application of core sciences but this technique has revolutionized all the forensic fraternity. DNA or genetic materials of all individuals are as unique as a fingerprint of an individual that's why it is called as DNA fingerprint and the method for its identification, DNA fingerprinting/DNA profiling. DNA fingerprinting is an in-situ technique used to determine the identity of a person based on their nucleotide sequences of certain regions of human DNA. DNA fingerprinting or DNA profiling was discovered by Sir Allec Jeffry[6–8].

MATERIAL AND METHODS

In the present case study, 11 semi-charred unknown bone samples and their relative 11 reference sample (blood sample of the suspect on FTA card) were received properly sealed condition with the sample to maintain the integrity and chain of custody of samples at the DNA Fingerprinting division, State Forensic Science Laboratory, Jaipur, Rajasthan for routine casework analysis. As per discussion with higher authority this case was taken on top priority. Samples were collected and forwarded according to the guidelines of the laboratory. Control blood samples on FTA cards of the disaster victim's related were collected after obtaining written informed consent and as per the declaration of Helsinki [9] and following the laboratory guidelines.

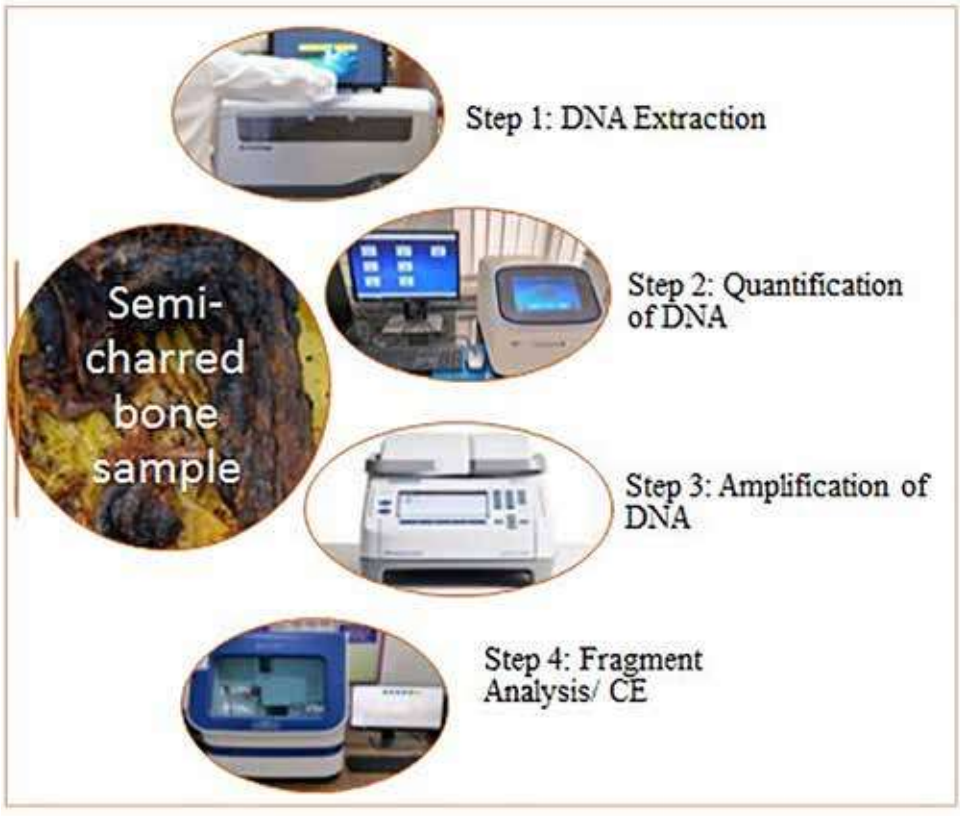

Figure 2: Process of DNA Profiling from semi-charred bone samples.

DNA Extraction

The seized all partially semi-charred bones of unknown deceased were found intact inside the glass jars. Before the processing bones, all the bone samples were marked as 1 to 11 and the control blood samples were also marked as 12 to 22. Then, the whole surface of bones were first cleaned with running water to remove major dirt material and then the bones surface were treated with sodium hypo chloride for the removing of tissue debris and at last washed with ethanol for removing all the surface contamination, then took over night for drying properly. Next day, all the bone samples were slightly peeled off using a sterile surgical knife in the shaft (body) portion of the femur and other long bones. After wiping off of peeled material on the shaft, the shaft was broken into small pieces and broken pieces of the bones are converted into fine powdered form. The powdered form of the femur and long bones were subjected to DNA isolation using the bone DNA extraction kit (Promega, CA, USA) for processing and DNA IQ™ chemistry for purification of DNA on Maxwell® RSC 48 instrument (Promega, CA, USA) according to the recommendations of the manufacturer.

DNA Quantitaion/Quantification

Quantity and quality of isolated DNA from unknown semi-charred bone samples were performed by using the Quantifiler™Trio DNA Quantification Kit (Applied Biosystems) as per recommendations of the manufacturer except the half reaction volume. We prepared a master mix with half reaction volume of 9 µL(5µL of Quantifiler™ THP PCR reaction mix and 4µL of Quantifiler™ Trio Primer Mix) for each samples. After preparation, we dispensed 9µL of the master mix into the wells of the PCR reaction plate. Further, 1µL of standard solutions, 1µL Quantifiler™ THP DNA Dilution Buffer to the NTC tubes, and 1µL of DNA samples were dispensed individually into the wells of the PCR reaction plate. The quantification was performed on Applied Biosystems® QuantStudio™ 5 Real-Time PCR System using the HID Real-Time PCR Analysis Software version-1.3[10].The control blood samples on FTA card were directly subjected to amplification[11].

DNA Amplification/PCR

We used five PCR amplification kits in this case.

1. **GlobalFiler™ PCR Amplification Kit (For the amplification of Autosomal STR Markers)**

   Amplification of the 24 STRs locus (GlobalFiler™ PCR Amplification Kit) which included AMEL, D13S317, D7S820, D5S818, CSF1PO, D1S1656, D12S391, D2S441, D10S1248, D18S51, FGA, D21S11, D8S1179, vWA, D16S539, TH01, D3S1358, D2S1338, D19S433, DYS391, TPOX, D22S1045, SE33 and a Y-specific Y_{indel} (insertion/deletion locus) by Verti™ Thermal Cycler (Thermo Fisher Scientific, CA, USA-Thermo) according to their recommendations except for half-reaction volume[12–14].

2. **PowerPlex® Fusion 5C PCR amplification Kit (For the amplification of Autosomal STR Markers)**

   Amplification of the 24 STRs locus using PowerPlex® Fusion 5C PCR amplification kit (Promega) which included 22 CODIS (D3S1358, D1S1656, D2S441, D10S1248, D13S317, PENTA-E, D16S539, D18S51, D2S1338, CSF1PO, PENTA-D, TH01, vWA, D21S11, D7S820, D5S818, TPOX, D8S1179, D12S391, D19S433, FGA, D22S1045), one sex determining loci AMELOGENIN (AMEL) and one Y-specific DYS391 was performed by Verti™ Thermal Cycler (Thermo Fisher Scientific, CA, USA-Thermo) according to their recommendations except for half-reaction volume[15].

3. **Investigator *Argus X*-12 QS System (For the amplification of X-STR Markers)**

   Amplification of the X-STRs markers using Investigator Argus X-12 QS Kit contains primers for one gender determining loci AMELOGENIN (AM) and 12 X-STR markers (DXS7132, DXS7423, DXS8378, DXS10074, DXS10079, DXS10101, DXS10103, DXS10134, DXS10135, DXS10146, DXS10148 and HPRTB) and one autosomal STR marker Amplification was performed by Verti™ Thermal Cycler (Thermo Fisher Scientific, CA, USA-Thermo) according to recommendations of the manufacturer.

4. **Yfiler® Plus PCR Amplification Kit (For the amplification of Y-STR Markers)**

   Amplification of the Y-STRs markers using Yfiler® Plus PCR Amplification

Kit which consists of 27 Y-specific STRs loci (DYS19, DYS385a/b, DYS389I/II, DYS390, DYS391, DYS392, DYS393, DYS437, DYS438, DYS439, DYS448, DYS456, DYS458, DYS635 (Y GATA C4), Y GATA H4, DYS460, DYS481, DYS533, DYF387S1a/b, DYS449, DYS518, DYS570, DYS576 and DYS627) in a 6-dye chemistry was performed by Verti™ Thermal Cycler (Thermo Fisher Scientific, CA, USA-Thermo) according to recommendations of the manufacturer[16].

5. **PowerPlex® Y23 System PCR Amplification Kit (For the amplification of Y-STR Markers)**

   Amplification of the Y-STRs markers using PowerPlex® Y23 System PCR Amplification Kit consists of 24 Y-specific STRs loci (DYS19, DYS385a/b, DYS389I/II, DYS390, DYS391, DYS392, DYS393, DYS437, DYS438, DYS439, DYS448, DYS456, DYS458, DYS635, Y-GATA-H4, DYS481, DYS533, DYS549, DYS570, DYS576 and DYS643) in a 5-dye chemistry was performed by Verti™ Thermal Cycler (Thermo Fisher Scientific, CA, USA-Thermo) according to recommendations of the manufacturer[17].

Fragment Analysis and Data Interpretation (DI)

Capillary electrophoresis is used for the separation and detection of amplified fragments (amplicons) by using an ABI 3500xL Genetic Analyzer (Thermo Fischer, Scientific, CA, USA).

For the separation of amplified DNA by PowerPlex® Fusion 5C PCR amplification Kit and PowerPlex® Y23 System PCR Amplification Kit, 1 µL of the PCR products or allelic ladder (AL) were diluted in 10 µL of the mixture of 0.5 µL of WEN ILS (Internal Lane Standard)–500 Size Standard and 9.5 µL of Hi-Di™Formamide (Thermo Fischer, Scientific, CA, USA).

For the separation of amplified DNA by Investigator Argus X-12 QS PCR amplification Kit 1 µL of PCR product or allelic ladder (AL) was diluted in the mixture consisting 0.5 µL of DNA Size Standard 550 (BTO) (Qiagen, Germany) and 12 µL of Hi-Di™ Formamide (Thermo Fischer, Scientific, CA, USA).

For the separation of amplified DNA by GlobalFiler™ PCR Amplification Kit and Yfiler® Plus PCR Amplification Kit, 1 µL of the PCR products or allelic ladder (AL) were diluted in 0.4uL GeneScan™ 600 LIZ™ Size Standard v2.0 and 9.6 uL HiDi™ Formamide (Thermo Fischer, Scientific, CA, USA).

One allelic ladder was used for each run. In ABI 3500xL Genetic Analyzer (Thermo Fischer, Scientific, CA, USA), we used 36 cm long capillary, POP-4 (Performance Optimizer Polymer) for the separation of amplified DNA/amplicons and allelic ladder was used for the detection/identification of denatured DNA fragments. The obtained raw data were interpreted by the system software-Gene Mapper ID-X version- 1.6. The analytical threshold for Autosomal STR, Y-STR and X-STR markers was 100 Relative Fluorescence Unit (RFU).

RESULTS AND DISCUSSION

In the present case study, examinations of all 11 bones and control blood on FTA cards were done. All the observations of study are mentioned in Table 1, 2, 3, 4, 5 & 6.

Table 1: One view result/observation of present study

Sr.No.	Unknown semi-charred bone sample(s)		Biologically related to control blood sample on FTA card(s)		Relation of control blood sample on FTA card(s) to deceased	Useful kit(s)
1	Sample 1	Male	Sample 16	Male	Brother of Deceased	Investigator *Argus X*-12 QS System
2	Sample 2	Female	Sample 19	Female	Sister of Deceased	Investigator *Argus X*-12 QS System
3	Sample 3	Male	Sample 18	Female	Mother of Deceased	GlobalFiler™ system
4	Sample 4	Male	Sample 12	Male	Son of Deceased	PowerPlex® Y23 System
5	Sample 5	Female	Sample 17	Male	Son of Deceased	GlobalFiler™ system
6	Sample 6	Male	Sample 21	Male	Brother of Deceased	PowerPlex® Y23 System

Sr.No.	Unknown semi-charred bone sample(s)		Biologically related to control blood sample on FTA card(s)		Relation of control blood sample on FTA card(s) to deceased	Useful kit(s)
7	Sample 7	Male	Sample 13	Male	Son of Deceased	GlobalFiler™ system & Yfiler® Plus system
8	Sample 8	Female	Sample 15	Male	Father of Deceased	GlobalFiler™ system
9	Sample 9	Male	Sample 14	Male	Brother of Deceased	Yfiler® Plus system
10	Sample 10	Male	Sample 22	Male	Brother of Deceased	PowerPlex® Y23 System
11	Sample 11	Female	Sample20	Female	Mother of Deceased	PowerPlex® Fusion 5C system

Table 2: Showed, allelic data analysis of Investigator *Argus X*-12 QS PCR Amplification System, X,Y seen at AMEL marker of sample 1 and sample 16 it means the source of sample 1 and sample 16 are male. All the X-STRs are same in sample 1 and sample 16. The half set of allele of DNA profile was obtained from sample 1 is accounted in the DNA profile obtained from sample 16 at locus D21S11. X,X seen at AMEL marker of sample 2 and sample 19 it means the source of sample 2 and sample 19. The half set of alleles of DNA profile was obtained from sample 2 are accounted in the DNA profile obtained from sample 19.

Locus	Sample 1	Sample 2	Sample 16	Sample 19
AMELOGENIN	X,Y	X,X	X,Y	X,X
DXS10103	18	16,19	18	17,19
DXS8378	8	11,12	8	12,12
DXS10101	32.2	28.2,31	32.2	28.2,31.2
DXS10134	35	35,41.3	35	38,41.3
DXS10074	17	15,18	17	15,18
DXS7132	14	14,14	14	14,14
DXS10135	28	25,26	28	22,26
DXS7423	15	14,16	15	16,16
DXS10146	29	28,41.2	29	27,41.2
DXS10079	18	15,18	18	15,18
HPRTB	13	13,14	13	13,14
DXS10148	25.1	18,28.1	25.1	18,18
D21S11	29,32.2	32.2,32.2	28,32.2	32.2,32.2

Table 3: Showed, allelic data analysis of GlobalFiler™ PCR Amplification Kit, the half set of alleles of male DNA profile obtained from sample 3 and sample 7 respectively are accounted in the female DNA profile obtained from sample 18 and male DNA profile obtained from sample 13. The half set of alleles of female DNA profile obtained from sample 5 and sample 8 respectively are accounted in the male DNA profile obtained from sample 17 and sample 18. Amelogenin marker of sample 3 shows X,Y which indicates that the particular sample is from male source, marker Y-indel and DYS391 supports above statement. THO1 shows homozygosity. Sample 5 is from female origin and Y-indel& DYS391 did not call also. Four markers are homozygous in sample 5. Nine markers are homozygous in sample 7 that is male and sample 8 is also male and shows homozygosity at three autosomal markers.

Locus	Sample3	Sample 5	Sample 7	Sample 8	Sample 13	Sample 15	Sample 17	Sample 18
D3S1358	14,16	15,16	15,16	15,18	16,17	15,18	15,15	14,16
vWA	15,18	18,18	16,16	16,18	14,16	18,18	16,18	15,16
D16D539	9,11	11,12	11,11	8,11	11,13	8,9	11,13	9,12

Locus	Sample3	Sample 5	Sample 7	Sample 8	Sample 13	Sample 15	Sample 17	Sample 18
CSF1PO	11,12	10,12	10,12	11,11	10,11	11,11	7,10	7,11
TPOX	8,11	8,10	9,11	8,10	8,11	9,10	8,11	8,11
Y-indel	2	-	2	-	2	2	2	-
Amelogenin	X,Y	X,X	X,Y	X,X	X,Y	X,Y	X,Y	X,X
D8S1179	13,14	12,14	10,10	10,15	10,15	15,15	10,11	13,15
D21S11	30.2,31.2	29,30.2	30,30	30.2,33.2	28,30	32.2,32.2	29,30.2	30.2,31.2
D18S51	13,17	13,14	14,14	14,22	12,14	14,20	13,16	13,17
DYS391	10	-	10	-	10	10	10	-
D2S441	12,14	10,10	10,11	11,14	11,11	10,11	10,11	14,14
D19S433	14,15	14,15	13,15	15,16	12,15	15,15.2	12,15	12,15
THO1	6,6	6,7	6,6	6,9.3	6,6	7,9.3	6,6	6,8
FGA	23,26	20,23	23,24	21,22	23,24	22,23	23,24	20,26
D22S1045	15,16	11,15	15,15	16,16	15,15	16,16	11,11	16,16
D5S818	10,11	11,12	11,11	10,10	11,11	10,11	12,13	10,12
D13S317	8,11	12,13	9,12	8,11	9,12	10,11	12,14	9,11
D7S820	9,10	12,12	9,12	8,11	9,9	8,10	11,12	9,10
SE33	8,19	28.2,29.2	25.2,30.2	28.2,30.2	13,25.2	17,28.2	18,29.2	8,19
D10S1248	13,13	13,17	14,15	14,15	14,15	14,14	13,16	13,16
D1S1656	12,18.3	14,14	11,16.3	8,16.3	11,11	12,16.3	14,15	11,12
D12S391	17,24	19,21	18,18	19,20	18,19	16,19	19,19	17,19
D2S1338	18,25	19,20	23,25	19,24	24,25	24,24	19,19	18,20

Table 4: Showed allelic data analysis of PowerPlex® Fusion 5C PCR amplification Kit, the half set of alleles of female DNA profile obtained from sample 11 are accounted in the female DNA profile obtained from sample 20. Sample 11 and sample 20 both are female origin, contains seven and two homozygous marker respectively.

Locus	Sample 11	Sample 20
AMELOGENIN	X,X	X,X
D3S1358	14,15	15,16
D1S1656	13,15	13,15
D2S441	10,10	10,10
D10S1248	13,13	13,15
D13S317	11,11	11,13
PENTA-E	5,10	10,11
D16S539	9,11	9,11
D18S51	14,15	14,16
D2S1338	18,25	18,24
CSF1PO	10,10	10,11
PENTA-D	9,14	10,14

Locus	Sample 11	Sample 20
TH01	7,9.3	7,9.3
vWA	17,17	16,17
D21S11	28,28	28,29
D7S820	8,10	8,10
D5S818	10,11	10,11
TPOX	10,11	11,11
DYS391	-	-
D8S1179	13,15	13,14
D12S391	23,24	23,24
D19S433	13,16	13,15
FGA	25,25	20,25
D22S1045	11,15	11,15

Table 5: Showed allelic data analysis ofYfiler® Plus PCR Amplification Kit; same male DNA profiles were obtained from sample 7 and sample 13. The alleles of male DNA profile was obtained from sample 9 is matching with the male DNA profile obtained from sample 14.

Locus	Sample 7	Sample 9	Sample 13	Sample 14
DYS576	15	16	15	16
DYS389I	12	12	12	12
DYS635	21	21	21	21
DYS389II	29	29	29	29
DYS627	17	20	17	20
DYS460	11	11	11	11
DYS458	17	16	17	16
DYS19	15	15	15	15
YGATAH4	11	10	11	10
DYS448	19	19	19	19
DYS391	10	10	10	10
DYS456	13	13	13	13
DYS390	23	24	23	24
DYS438	9	9	9	9
DYS392	11	11	11	11
DYS518	37	36	37	36
DYS570	20	15	20	15
DYS437	15	15	15	15
DYS385	13,19	13,18	13,19	13,18
DYS449	32	30	32	30

Locus	Sample 7	Sample 9	Sample 13	Sample 14
DYS393	12	12	12	12
DYS439	12	12	12	12
DYS481	22	23	22	23
DYF387S1	38,39	37,37	38,39	37,37
DYS533	10	10	10	10

Table 6: Showed allelic data analysis of PowerPlex® Y23 System PCR Amplification Kit, same male DNA profile was obtained from sample 4 and sample 12. The alleles of male DNA profile obtained from sample 6 is matching with the male DNA profile obtained from sample 21. Same male DNA profile was obtained from sample 10 and sample 22.

Locus	Sample 4	Sample 6	Sample 10	Sample 12	Sample 21	Sample 22
DYS576	20	16	15	20	16	15
DYS389I	13	12	12	13	12	12
DYS448	20	-	21	20	-	21
DYS389II	29	28	29	29	28	29
DYS19	16	15	14	16	15	14
DYS391	10	10	10	10	10	10
DYS481	24	20	22	24	20	22
DYS549	12	14	11	12	14	11
DYS533	12	9	11	12	9	11
DYS438	11	10	10	11	10	10
DYS437	14	15	16	14	15	16
DYS570	17	18	16	17	18	16
DYS635	23	21	21	23	21	21
DYS390	26	22	22	26	22	22
DYS439	11	12	12	11	12	12
DYS392	11	11	12	11	11	12
DYS643	10	11	11	10	11	11
DYS393	13	14	12	13	14	12
DYS458	16	17	18	16	17	18
DYS385a/b	11,14	13,14	14,16	11,14	13,14	14,16
DYS456	15	15	15	15	15	15
Y_GATA_H4	12	12	10	12	12	10

CONCLUSION

DNA fingerprinting/profiling/typing is very fruitful for disaster victim identification. New technologies and commercially available multiplex PCR kits are very helpful for providing the DNA report in short period. Nowadays, new technologies ruled out the problem of quantity and quality of DNA. Due to advance technology and hard work of our team we provide DNA report of this case in just 3 working days.

On the basis of DNA analysis it is concluded that the source of DNA profile obtained from unknown charred bone sample 1, sample 2, sample 3, sample 4, sample 5, sample 6, sample 7, sample 8, sample 9, sample 10 and sample 11 are biologically related with the source of DNA profile obtained from control blood sample on FTA cards sample 16, sample 19, sample 18, sample 12, sample 17, sample 21, sample 13, sample 15, sample 14, sample 22 and sample 20 respectively.

Disclosure of conflict of interest

All authors declared that they have no conflict of interest and no any financial support.

REFERENCES

1. E. Ziętkiewicz, M. Witt, P. Daca, J. Żebracka-Gala, M. Goniewicz, B. Jarząb, M. Witt, Current genetic methodologies in the identification of disaster victims and in forensic analysis, J. Appl. Genet. 53 (2012) 41–60.
2. R. Below, A. Wirtz, D. Guha-Sapir, Disaster category classification and peril terminology for operational purposes, 2009.
3. D. Prevention, P. Commission, Ethiopia: National Information on Disaster Reduction, in: Report for the World Conference on Disaster Reduction, 2004.
4. J.O. Obafunwa, V.O. Ogunbanjo, O.B. Ogunbanjo, S.S. Soyemi, F.A. Faduyile, Forensic odontological observations in the victims of DANA air crash, Pan Afr. Med. J. 20 (2015).
5. H.G. Liddell, A greek-english lexicon, Harper, 1894.
6. P. O'reilly, J.M. Wright, The evolving technology of DNA fingerprinting and its application to fisheries and aquaculture, J. Fish Biol. 47 (1995) 29–55.
7. L. Roewer, DNA fingerprinting in forensics: past, present, future, Investig. Genet. 4 (2013) 1–10.
8. G.K. Chambers, C. Curtis, C.D. Millar, L. Huynen, D.M. Lambert, DNA fingerprinting in zoology: past, present, future, Investig. Genet. 5 (2014) 1–11.
9. J. Hedman, R. Ansell, A. Nordgaard, A ranking index for quality assessment of forensic DNA profiles forensic DNA profiles, BMC Res. Notes. 3 (2010). https://doi.org/10.1186/1756-0500-3-290.
10. E.K. Graham, J. Drobac, J. Thompson, M. Loten, A. Gopalakrishnan, Evaluation of the PowerQuant® System on the QuantStudioTM 5 Real-Time PCR System, (2018).
11. R.K. Kumawat, P. Shrivastava, D. Shrivastava, G.K. Mathur, S. Dixit, Genomic blueprint of population of Rajasthan based on autosomal STR markers, Ann. Hum. Biol. 47 (2020) 70–75.
12. M.J. Ludeman, C. Zhong, J.J. Mulero, R.E. Lagacé, L.K. Hennessy, M.L. Short, D.Y. Wang, Developmental validation of GlobalFilerTM PCR amplification kit: a 6-dye multiplex assay designed for amplification of casework samples, Int. J. Legal Med. 132 (2018) 1555–1573.
13. N. Gouveia, P. Brito, A. Serra, F. Balsa, L. Andrade, M. São Bento, P. Cunha, V. Bogas, V. Lopes, M.J. Porto, Direct amplification of reference samples with Globalfiler® PCR Amplification Kit, Forensic Sci. Int. Genet. Suppl. Ser. 5 (2015) e135–e137.
14. A. Kumar, R. Kumar, R.K. Kumawat, P. Shrivastava, R. Yadav, G. Chaubey, Population genetic data of 22 autosomal STR loci for the Scheduled Caste population of Rajasthan India, Ann. Hum. Biol. 48 (2021) 598–604.
15. H.K. Mahmood, N.F. Salman, D.H. Hasan, K.M. Salih, M.A. Sadiq, B.T. Mohammad, M.K. Mohammed, S.M. Nahi, S.S. Baqir, Validation of Half-Reaction Volumes of the Promega PowerPlex® Forensic Amplification Kits (PowerPlex® 18D Systems, PowerPlex® 21System, PowerPlex® Fusion System and PowerPlex® Y23 System) in STR Analysis, Arab J. Forensic Sci. Forensic Med. 2 (2020) 152–158.
16. S. Gopinath, C. Zhong, V. Nguyen, J. Ge, R.E. Lagacé, M.L. Short, J.J. Mulero, Developmental validation of the Yfiler® Plus PCR Amplification Kit: An enhanced Y-STR multiplex for casework and database applications, Forensic Sci. Int. Genet. 24 (2016) 164–175.
17. J.M. Thompson, M.M. Ewing, W.E. Frank, J.J. Pogemiller, C.A. Nolde, D.J. Koehler, A.M. Shaffer, D.R. Rabbach, P.M. Fulmer, C.J. Sprecher, Developmental validation of the PowerPlex® Y23 System: a single multiplex Y-STR analysis system for casework and database samples, Forensic Sci. Int. Genet. 7 (2013) 240–250.