DOI: https://doi.org/10.53350/pjmhs22164861

**ORIGINAL ARTICLE**

# Recent Advances in DNA Analysis for Criminal Cases with the Applications of Forensic Sciences, A Comparative Study

ABDULLAH[1], SHAHID IQBAL[2], MUHAMMAD IKRAM ALI[3], ABDUL SAMAD[4], AISHA RASHEED[5], IJAZ AZIZ[6]
[1]*Lecturer at Forensic Department Bacha Khan Medical College Mardan KPK. Pakistan.*
[2]*Assistant Professor Forensics Department Bacha Khan Medical College Mardan KPK. Pakistan.*
[3]*Assistant Professor, Department of Forensic Medicine & Toxicology, Ziauddin University Karachi Pakistan.*
[4]*Associate Professor, Department of Forensic Medicine and Toxicology, Liaquat University of Medical & Health Sciences, Jamshoro Sindh, Pakistan.*
[5]*Assistant Professor, Department of Forensic Medicine and Toxicology, Liaquat University of Medical & Health Sciences, Jamshoro Sindh, Pakistan.*
[6]*Assistant Professor, Department of Forensic Medicine, Mekran Medical College, Turbat, Baluchistan.*
*Corresponding author:Ijaz Aziz: Email: ijazaziz62@gmail.com, Cell: 03134344367*

## ABSTRACT

**Aims and objectives:** The aims and objectives of this study were to describe the use of forensic DNA analysis for reliable investigation of different criminal cases.

**Conclusion:** In current study DNA and fingerprints data of 63 employees was collected through oral swab and powder dactyloscopy technique. All comparative analysis of different individuals were negative except two workers, their RT-PCR data was positive and completely matched with the suspects data. Suspect's data were collected from crime scene through hair follicles and surface markers.

**Keywords**: Deoxyribonucleic acid, Polymerase chain reaction, Dactyloscopy

## INTRODUCTION

The use of deoxyribonucleic acid (DNA) in criminal justice testing is referred as forensic DNA analysis [2]. When people commit crimes, they might leave evidence behind, which usually includes biological materials containing DNA [4]. The deoxyribonucleic acid can recover from hair, bone, saliva, semen and skin for the matching to DNA of a suspect. In case of evidence matches to the latent print obtained from the crime scene, the match can give proof regarding that person's commitment to the crime [7]. DNA can be extracted from a variety of sources. Now-a-days DNA can be recovered from fingerprints by applying modern theorem of forensic sciences. Recent advancements in DNA analysis includes quality assurance of DNA testing, storage pretreatment, sample collection, DNA extraction and DNA quantitation are very common [6].

In 1981 first time Forensic DNA analysis or DNA profiling was introduced and with the passage of time this technique has been devalued so vast in all over the world for the criminal justice [5]. It is a powerful tool for crack the cases on crime scenes. In this era forensic science mainly focus on genetic material to address queries about legal issues, such as civil and criminal cases [8]. Despite the fact that each person possesses 99.9% of human DNA sequences, forensic investigators only require 0.1 percent of the DNA's unique sequences. In the criminal justice system, this analysis is extremely important [9].

The molecular size of DNA affected by number of factors, because of these circumstances collection and preservation of biological material and is very difficult. Mostly DNA effected by endonucleases and exonucleases which are very common in nature [11]. Regularly Forensic scientists are researching the safest methods for sample collection and preserving techniques of DNA from incidental locations. The cotton swab is an important tool for gathering DNA evidence for forensic investigation [18]. Polymerase chain reaction (PCR) is a molecular biology technique for amplifying DNA segments by making numerous copies under controlled conditions using DNA polymerase enzymes [13].

DNA extraction is very important step in forensic sciences because through this step the amount of DNA measured which is found in the sample for analysis [16]. DNA extraction is the process of extracting nucleic acids from proteins and other biological components in a cell. There are three types of forensic DNA laboratories i.e. pre-laboratory, laboratory, and post-laboratory. In pre-laboratory, the extraction and amplification of DNA performed and in post-laboratory separation of nucleotides and sequencing of different nitrogen bases occurred [18].

## MATERIALS AND METHODS

**Study design:** A robbery in an office was reported. A project tender was stolen, finger prints and other DNA identification samples from crime scene was collected. Criminal DNA strand was analyzed on RT-PCR while finger prints through powder dactyloscopy. DNA samples of 63 employees were collected and compared with the suspect DNA. This study was conducted for identification of criminals through modern DNA analysis technologies.

**Duration of study:** 6 months

**Sample size:** 63 individuals

**Sampling technique:** DNA oral swab test and finger prints.

**Sample analyzing techniques:** RT-PCR and Dactyloscopy

**Specimens Collected from the crime scene (SCCS):** Hairs and fingerprints

**Statistical Data analysis:** Raw data was presented Bio-statistically through SPSS and p-test applied for comparative analysis of each parameter.

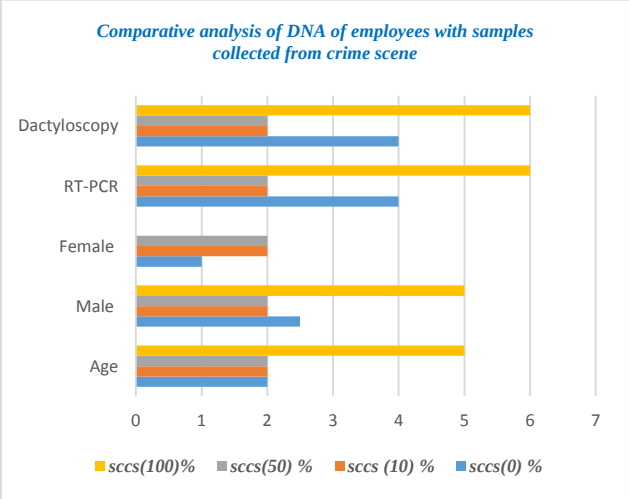
## RESULTS

Table1: Comparative analysis of DNA of employees with samples collected from crime scene

| Parameters | Mean ± SD Percentage Of 63 individuals | Mean ± SD Matching Percentage with SCCS (0) | Mean ± SD Matching Percentage with SCCS (10) | Mean ± SD Matching Percentage with SCCS (50) | Mean ± SD Matching Percentage with SCCS (100) |
|---|---|---|---|---|---|
| Age | 20.40± 22.10 | 98±01 | Negative | Negative | 2.1±0.01 |
| Male | 50.21±0.10 | 98±01 | Negative | Negative | 2.1±0.01 |
| Female | 13.1±1.03 | 98±01 | Negative | Negative | Negative |
| RT-PCR | 63.01±1.04 | 98±01 | Negative | Negative | 2.01±0.01 |
| Dactyloscopy | 62.01±1.02 | 98±01 | Negative | Negative | 2.1±0.01 |

In this study after robbery in an office, finger prints and other DNA identification samples from crime scene was collected. Criminal DNA strand was analyzed on RT-PCR while finger prints through powder dactyloscopy. On the other hand DNA samples of 63 employees were also collected and compared with the suspect DNA. The percentage mean standard deviation of RT-PCR and powder dactyloscopy of each person was concluded. It has seen only the DNA of two male employee (2.01±0.01) showed

significant (P<0.005) similarities with the DNA of that specimen which was collected from the crime scene.




Figer-1: Graphical Presentation

## DISCUSSION

DNA analysis has powers which is not available in most other forensic fields. With the help of DNA sequencing and matching of the culprit and the victim in violent crimes like murder and rape cases it works efficient solution [19]. DNA testing will improve in terms of speed, accuracy, and sensitivity. Probabilistic techniques of conveying complex outcomes will necessitate the use of software as well as more in-depth consideration of the meaning of the data obtained. As our understanding of human genomic information grows, we will need to address genetic privacy problems today and in the future [18].

This expansion has occurred as a result of successful lobbying efforts by inventors of DNA databases and software, sellers of DNA testing kits, and victim advocates in federal and state legislatures in the world [20]. The success and advancement in DNA testing gives a new strength in the field of sample backlogs and data interpretation [13]. Due to increased sensitivity in PCR tests and the information content of profiles created, more data is accessible from biological materials. In any scientific endeavor, successful research is reliant on adequate, long-term financing. Mitochondria has its own DNA and it is located inside the cells [14].

In present study DNA data of 63 employees was collected by oral swab and powder dactyloscopy technique. Most of the case were negative except two workers, their RT-PCR data was positive and completely matched with the suspects data. Out of 63 individuals, 50 were male while 13 were female. DNA and fingerprints specimens of suspect were collected through hair follicles and different surfaces from crime scene for comparative study.

## REFERENCES


1. Alotaibi, S. S., Sayed, S. M., Alosaimi, M., Alharthi, R., Banjar, A., Abdulqader, N., et al. (2020). Pollen molecular biology: Applications in the forensic palynology and future prospects: A review. Saudi J. Biol. Sci. 27, 1185–1190.
2. Ansorge, W. J. (2009). Next-generation DNA sequencing techniques. N. Biotechnol. 25, 195–203.
3. Arenas, M., Pereira, F., Oliveira, M., Pinto, N., Lopes, A. M., Gomes, V., et al. (2017). Forensic genetics and genomics: Much more than just a human affair. PLoS Genet. 13:e1006960.
4. Borsting, C., and Morling, N. (2015). Next generation sequencing and its applications in forensic genetics. Forensic Sci. Int. Genet. 18, 78–89.
5. Botstein, D., White, R. L., Skolnick, M., and Davis, R. W. (1980). Construction of a genetic linkage map in man using restriction fragment length polymorphisms. Am. J. Hum. Genet. 32, 314–331.
6. Budowle, B., and van Daal, A. (2008). Forensically relevant SNP classes. Biotechniques 60:610.
7. Butler, J. M. (2012). “Non-human DNA,” in Advanced Topics in Forensic DNA Typing, ed. J. M. Butler (San Diego: Academic Press), 473–495.
8. Butler, J. M., Coble, M. D., and Vallone, P. M. (2007). STRs vs. SNPs: thoughts on the future of forensic DNA testing. Forensic Sci. Med. Pathol. 3, 200–205.
9. Constantinescu, C. M., Barbarii, L. E., Iancu, C. B., Constantinescu, A., Iancu, D., and Girbea, G. (2012). Challenging DNA samples solved with MiniSTR analysis. Brief overview. Rom. J. Leg. Med. 20, 51–56.
10. Damaso, N., Martin, L., Kushwaha, P., and Mills, D. (2014). F-108 polymer and capillary electrophoresis easily resolves complex environmental DNA mixtures and SNPs. Electrophoresis 35, 3208–3211.
11. Damaso, N., Mendel, J., Mendoza, M., von Wettberg, E. J., Narasimhan, G., and Mills, D. (2018). Bioinformatics Approach to Assess the Biogeographical Patterns of Soil Communities: The Utility for Soil Provenance. J. Forensic. Sci. 63, 1033–1042.
12. Daniel, R., Santos, C., Phillips, C., Fondevila, M., van Oorschot, R. A., Carracedo, A., et al. (2015). A SNaPshot of next generation sequencing for forensic SNP analysis. Forensic Sci. Int. Genet. 14, 50–60.
13. Datwyler, S. L., and Weiblen, G. D. (2006). Genetic variation in hemp and marijuana (Cannabis sativa L.) according to amplified fragment length polymorphisms. J. Forensic Sci. 51, 371–375.
14. Editorial. (2007). Launching Forensic Science International daughter journal in 2007: Forensic Science International: Genetics. Forensic Sci. Int. Genet. 1, 1–2.
15. Finley, S. J., Benbow, M. E., and Javan, G. T. (2015). Potential applications of soil microbial ecology and next-generation sequencing in criminal investigations. Appl. Soil. Ecol. 88, 69–78.
16. Fondevila, M., Borsting, C., Phillips, C., de la Puente, M., Consortium, E. N., Carracedo, A., et al. (2017). Forensic SNP genotyping with SNaPshot: Technical considerations for the development and optimization of multiplexed SNP assays. Forensic Sci. Rev. 29, 57–76.
17. Gettings, K. B., Kiesler, K. M., Faith, S. A., Montano, E., Baker, C. H., Young, B. A., et al. (2016). Sequence variation of 22 autosomal STR loci detected by next generation sequencing. Forensic Sci. Int. Genet. 21, 15–21.
18. Giampaoli, S., Berti, A., Di Maggio, R. M., Pilli, E., Valentini, A., Valeriani, F., et al. (2014). The environmental biological signature: NGS profiling for forensic comparison of soils. Forensic Sci. Int. 240, 41–47.
19. Gill, P., Haned, H., Bleka, O., Hansson, O., Dorum, G., and Egeland, T. (2015). Genotyping and interpretation of STR-DNA: Low-template, mixtures and database matches-Twenty years of research and development. Forensic Sci. Int. Genet. 18, 100–117.
20. Gill, P., Jeffreys, A. J., and Werrett, D. J. (1985). Forensic application of DNA ‘fingerprints’. Nature 318, 577–579. doi: 10.1038/318577a0