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## Genetic analysis a major tool in crime scene investigation in pharmacological evidences

Puja Kumari and Suneetha V.

*School of Bioscience and Technology, VIT University, Vellore, Tamil Nadu, India*

### ABSTRACT

*With the increase in development and genetic test, the concerns regarding the uses of genetic information has also increased. The advances in DNA (deoxyribonucleic acid) technology over the past 25 years had led to spectacularly precise forensic identification techniques, although some applications have also release arguments regarding genetic privacy. Current molecular forensic work is pushing these technologies even further by scrutinizing extremely damaged DNA and by announcing RNA techniques to forensic science.*

**Key words:** Genetic analysis, crimescene, pharmacological evidences, DNA

### INTRODUCTION

The process of studying and researching in fields of science that involve genetics and molecular biology is known as genetic analysis. It can be used generally to describe methods used in and resulting from the sciences of genetics and molecular biology, or to applications resulting from this research. It can be done to identify genetic or inherited disorders and also to make a differential diagnosis in certain somatic diseases such as tumor.

**STR PROFILE :-** short tandem repeats (STRs) are an individual's profile of markers that the standard genetic forensic test use in crime labs across the world. These are genetic sequences similar to minisatellites, although the repeating DNA sequence in STRs is greatly shorter. STRs are equally changeable among individuals: with each additional STR locus a forensic scientist scrutinizes, the odds become ethereality small that two people will have the same STRs at all loci. CODIS with STR profiles taken from biological samples found at a crime scene can be queried by Criminal investigators. If the crime-scene sample matches a profile in the offender database, this information can lead police to a likely suspect, or absolve an virtous suspect.

### MATERIAL AND METHODS

#### DNA analysis methods:

- Single nucleotide polymorphism
- Restriction fragment length polymorphism
- Dideoxy method
- Variable number tandem repeats
- Short sequence repeats
- Polymerase chain reaction
- Blotting techniques
- Mitochondrial dna
- Low copy number
- Y chromosome analysis

## ESTIMATION OF DNA

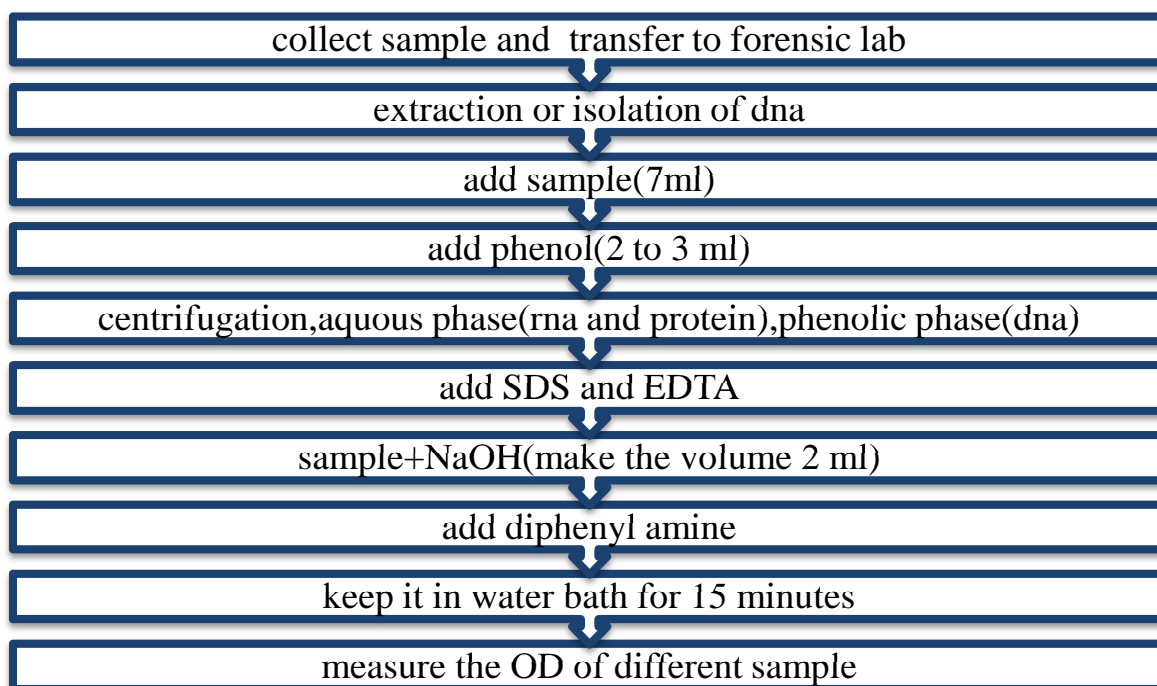
| Distilled H <sub>2</sub> O (500mg/ml) | Concentration (mg) | NaOH(5Mm) | Diphenyl Amine Reagent(ml) | Water bath (min) | O.D 600nm |
|---------------------------------------|--------------------|-----------|----------------------------|------------------|-----------|
| 0.1                                   | 50                 | 1.9       | 2                          | 15-20            |           |
| 0.2                                   | 100                | 1.8       | 2                          | 15-20            |           |
| 0.3                                   | 150                | 1.7       | 2                          | 15-20            |           |
| 0.4                                   | 200                | 1.6       | 2                          | 15-20            |           |
| 0.5                                   | 250                | 1.5       | 2                          | 15-20            |           |
| 0.6                                   | 300                | 1.4       | 2                          | 15-20            |           |
| 0.7                                   | 350                | 1.3       | 2                          | 15-20            |           |
| 0.8                                   | 400                | 1.2       | 2                          | 15-20            |           |
| 0.9                                   | 450                | 1.1       | 2                          | 15-20            |           |
| 1                                     | 500                | 1.0       | 2                          | 15-20            |           |

DNA+Diphenyl amine

Dark blue color

**Protocol**

- 5mM NaOH ,diphenyl amine reagent(glacial acetic acid,H<sub>2</sub>SO<sub>4</sub>, diphenyl amine powder).
- Different aliquot of standard was taken.
- Volume was made upto 2ml with 5mM NaOH.
- 2ml of diphenyl amine was added and tubes were kept in boiling water bath for 15 min.Then we have to measure the O.D.

**Rna analysis methods:**

- RNA interference (RNAi)
- RNA-dependent RNA polymerase (RdRp)
- Reverse transcription
- Polymerase chain reaction

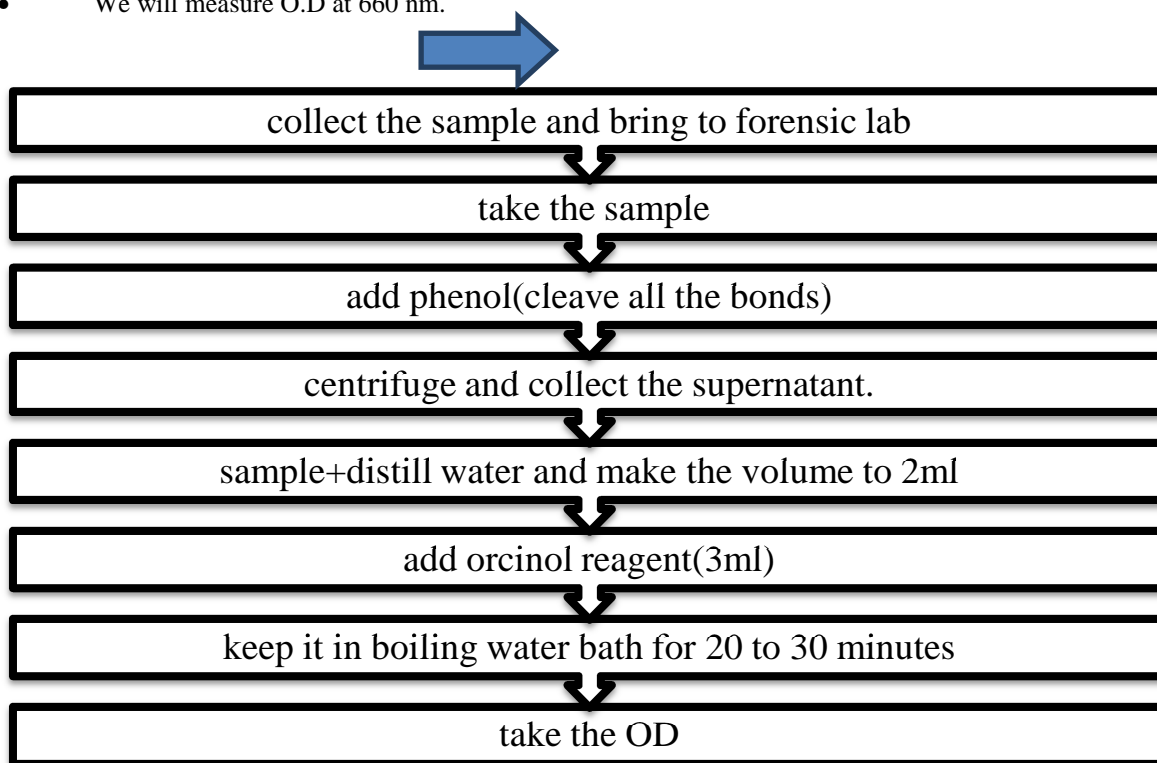
## RNA estimation

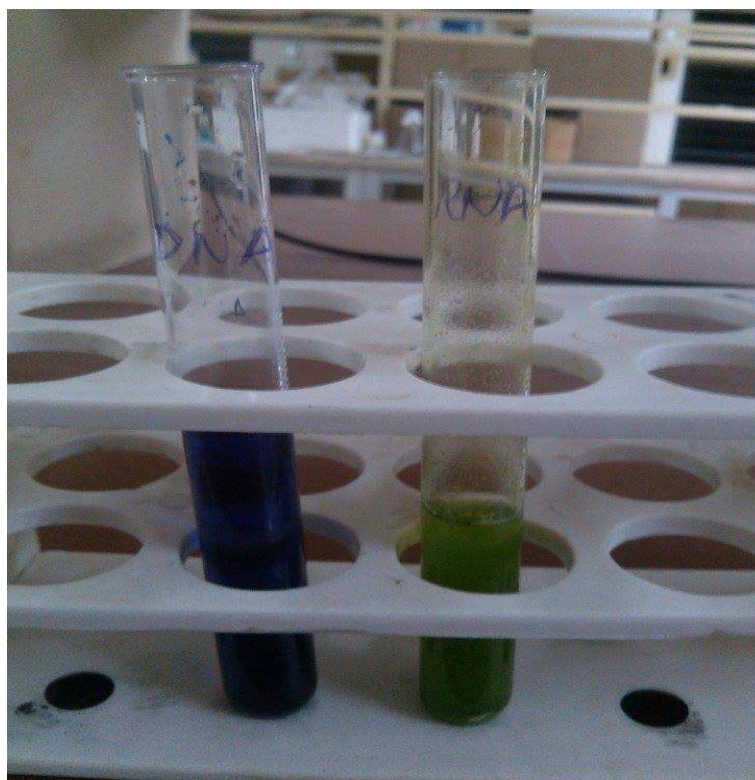
| Standard | Distilled H <sub>2</sub> O | Orcinol reagent | Boiling water bath(>100°c) | O.D at 660nm |
|----------|----------------------------|-----------------|----------------------------|--------------|
| 0.1      | 1.9                        | 3ml             | 20-30 min                  |              |
| 0.2      | 1.8                        | 3ml             | 20-30 min                  |              |
| 0.3      | 1.7                        | 3ml             | 20-30 min                  |              |
| 0.4      | 1.6                        | 3ml             | 20-30 min                  |              |
| 0.5      | 1.5                        | 3ml             | 20-30 min                  |              |
| 0.6      | 1.4                        | 3ml             | 20-30 min                  |              |
| 0.7      | 1.3                        | 3ml             | 20-30 min                  |              |
| 0.8      | 1.2                        | 3ml             | 20-30 min                  |              |
| 0.9      | 1.1                        | 3ml             | 20-30 min                  |              |
| 1        | 1.0                        | 3ml             | 20-30 min                  |              |

RNA(Ribose)+Orcinol(yellow)-----Furfural(green color)

## Protocol

- Different aliquot of standard was taken.
- Volume was made upto 2ml with distilled water.
- 3ml of Orcinol reagent was added and tubes were kept in boiling water bath for 20-30 mins.
- We will measure O.D at 660 nm.





**FIGURE 1 DNA AND RNA REACTION**

**Methods of protein analysis**

- Protein immunostaining
- Protein immunoprecipitation
- Western blotting
- Bca assay
- Spectrophotometry
- Enzyme assay

**GENETIC ANALYSIS CASES**

| Case           | Date and year             | Incident      | Country        |
|----------------|---------------------------|---------------|----------------|
| Isabella kerr  | Sept, 1935                | Murder        | Scotland       |
| Lynda mann     | 1987                      | Murder & rape | England        |
| Sister Abhaya  | 27 <sup>th</sup> mar,1992 | Murder        | India          |
| Texas girl     | 19995                     | Murder & rape | Texas          |
| Leanne tiernan | August 2001               | Murder        | West Yorkshire |

**RESULTS AND DISCUSSION**

Case study:- The **Sister Santhi Case** is an investigation into the 1993 death of a Catholic nun who was found dead in water in St Pius X convent in Kottayam, India. She was 20 years old at the time of her death and a member of St. Paul's Congregation for women under the Catholic Archeparchy of Kottayam, Kerala in India.

Initially, the local police crime branch declared that the death was a homicide. A petition by the nuns of the congregation led to a new inspection by the Central Bureau of Investigation (CBI). Although the CBI concluded that Santhi was murdered, they requested cessation of the case for lack of evidence; however, the request was rejected by the courts. Seventeen years later, on 9 November 2010, two priests and a nun were arrested by the CBI. On 15 July 2011, charges of murder, destruction of evidence, and disparagement were filed against the three.

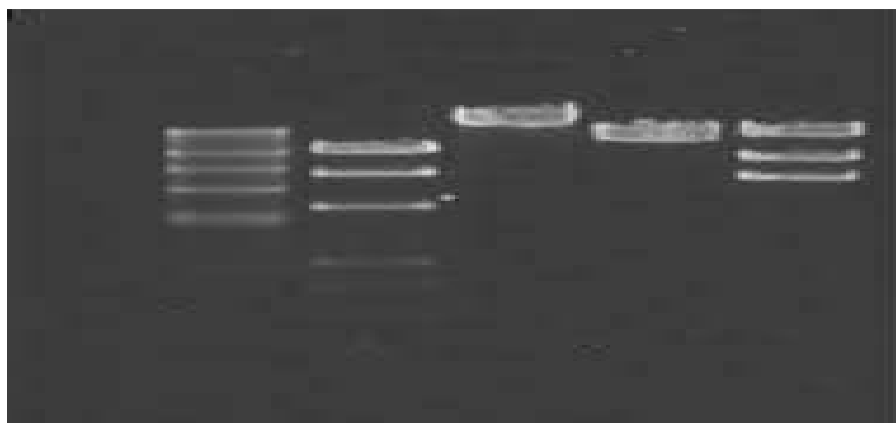


FIGURE 2 DNA Bands

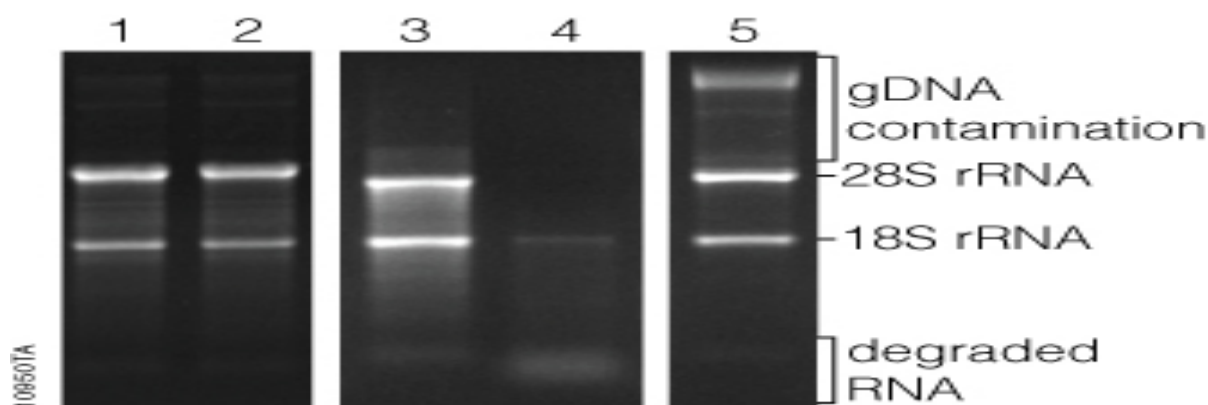


FIGURE 3 RNA bands

### CONCLUSION

The study of genes has proved to be a powerful approach to understanding biological systems. Because genes affect virtually every aspect of the structure and function of an organism, being able to identify and determine the role of genes and the proteins that they encode is an important step in charting the various processes that underly a particular character under investigation. We can do genetic analysis by Isolation of mutants affecting the process under study, Analysis of progeny of controlled matings (“crosses”) between mutants and other discontinuous variants, Biochemical analysis of cellular processes controlled by genes, Microscopic analysis, Analysis of DNA directly.

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