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COMPARATIVE ANALYSIS OF GENETIC FINGERPRINTING AND TRADITIONAL DNA TESTING

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Abstract:

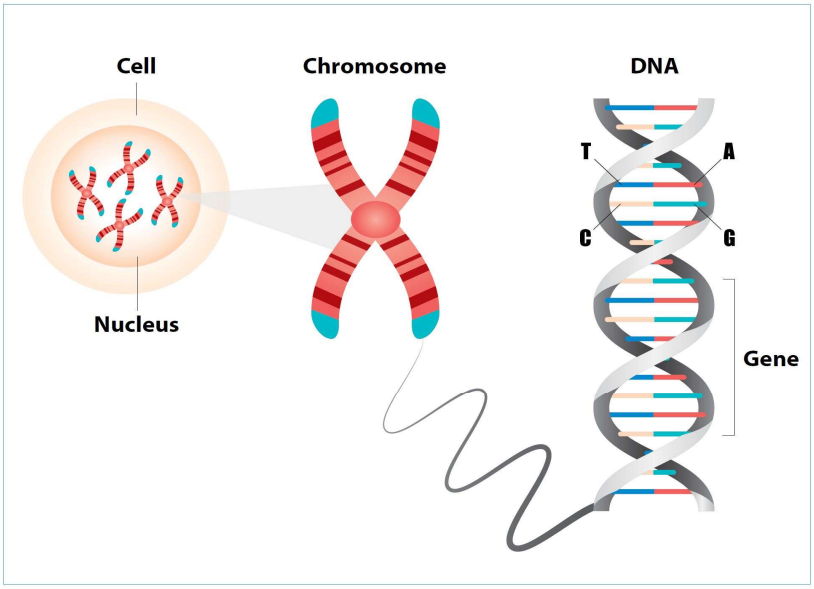
Genetic fingerprinting and traditional DNA testing are two methods used in forensic science and paternity testing to identify individuals based on their unique genetic profiles. This essay provides a comparative analysis of these two techniques, focusing on their methodologies, applications, accuracies, advantages, and limitations.
Genetic fingerprinting, also known as DNA profiling, involves the analysis of specific DNA segments to create a unique genetic profile for each individual. Traditional DNA testing, on the other hand, typically focuses on identifying specific genetic markers to establish relationships or genetic predispositions.
The paper highlights the differences between these two techniques and explores the implications of using one over the other in various forensic and paternity testing scenarios.

Keywords: genetic fingerprinting, DNA profiling, traditional DNA testing, forensic science, paternity testing, genetic markers, accuracy, advantages, limitations

1.2 1. Introduction

DNA testing has become increasingly important in many disciplines these days, be it in forensic science, in determining the paternity of a child, or just studying the origin of a particular individual or population group. To put it simply, DNA testing is the process by which a person's unique DNA is determined (Daniel Bober & A. Longmire, 2004). In essence, everyone's DNA is unique (unless the person happens to have an identical twin) and so, DNA analysis can be used to identify a person just like a fingerprint, only much more accurately. While this technology has been around for quite some time and is somewhat misunderstood in general by the public, new advances in technology and the increased utility of such tests are starting to push them into the public eye, mostly through interactions with the law. It is for this reason that a descriptive analysis of the two main methods of DNA testing, the traditional Restriction Fragment Length Polymorphism (RFLP) and the more recently developed Short Tandem Repeat (STR) analysis will be done.
Indeed, as the technology of DNA testing becomes simpler and less costly, the use of such testing is anticipated to become as common as checking for fingerprints or blood type. This will undoubtedly lead to more and more cases where a person's DNA is tested and will then want to

know exactly what that test reveals. This will not be an easy question to answer. DNA testing is based on a relatively simple genome. There are only four different components of DNA. But, there is a staggering 3.2 billion of these components in the human genome (Reddy et al., 2009). To add diversity into the DNA pool, the arrangements of these components vary all the way from one person to another. While most people do share about 99.9% of the same DNA, it is enough variety to pinpoint individuals. Currently, a DNA test does not look at the entire genome however. It



simply looks at specific loci in the human genome where there is diversity. The current tests being used in the courts were set up by the FBI and look at a varied loci in the human genome to the spec of each person. The test output's what are called RFL accounts where the tester is matching the banding pattern of a sample of DNA against a number of these RFL account profiles. The output can be phrased in such a way to make it seem like there is a good match or not such a good match, but in reality, without going into statistical computations, no one match should be considered as conclusive evidence. The profiles just give the expected frequency by chance of a match. Isn't that a big enough odds one might say? Not when one is dealing with a national population. Because of this, most current analyses look for several banding patterns to be in common before such a match is considered of evidentiary value. However, this does not mean that a single match should be taken lightly for this reason. It is still possible, even though it is incredibly remote.

Fig1 : Genetic testing

1.3 2. Historical Development of DNA Testing

DNA testing has undergone steady refinement since its inception in the 1980s, with simpler methods gradually giving way to sophisticated ones. The earliest approaches were based on variable number tandem repeats; however, these produced DNA profiles that were ultimately too imprecise for any sort of commercial application. By the mid-1990s, the shift was already towards 13-core short tandem repeat (STR) analysis, a method that greatly improved the accuracy of genetic examination. And this is the tendency that has remained ever since: though numerous further refinements have been made, the underlying tripartite character of the STR analysis has yet to be displaced by any newer technology (N. Mandape et al., 2024). There have been parallel opportunities for DNA testing. Apart from the famous PCR-based genetic fingerprinting, paternity tests have been available since the early 1970s working on the basis of ABO blood groups. And

of these, the latter was far more regularly used—two of the key discoverers of the polymerase chain reaction worked at the industry that did most to commercialize paternity tests—indeed, by 1985, it was estimated that up to 37,000 ABO tests were being carried out in the UK each year, mostly litigation (Swalec & Alexander Moseley, 2011). Indeed, the flurry of interest in DNA testing in the early 1980s owed most to its potential use in proving non-paternity, especially where, as in the US, huge sums of child support could be at stake—although, conversely, the 13th Amendment would shield alleged fathers from slavery if the only evidence of paternity was to prove a genetic link to the child based on a high degree of biometric certainty, which is what genetically extreme testing could offer.

1.4 3. Principles of Genetic Fingerprinting

The scientific investigation of a malleable biological substance that could uniquely identify persons has prompted a dichotomous divide about the validity of a crime-matching technique that has been heavily complexified by violent lobbying on all sides. The admixture of scientific evidence into jurisprudence has a convoluted and oftentimes counterintuitive structure. Given its objectivity, scientific data can engender an air of authority that belies the potential for procedural lapse, confounding variables, sampling bias, and outright misinterpretation. The eloquent rhetoric that emerges from the courtroom on the part of barristers and expert witnesses is most certainly present in academic discourses on ethical, political, and even scientific grounds. Thus, legal and ethical postulations are largely jettisoned in the interest of outlining genetic fingerprinting in the manner one might find in a scientific treatise or laboratory manual (Robert Landry et al., 2008). In the early 1980s, pioneering work began on the RFLPs, or restriction fragment length polymorphisms, which present unique patterns in each individual. Nonetheless, a less erudite procedure, relying upon similarly unique but much shorter sequences termed STRs, supplanted this earlier technique in the mid-1990s and became the modern benchmark of genetic fingerprinting. This overhauled procedure examines specific STR regions to obtain a genetic profile at thirteen core loci. Perhaps the climacteric mutation in genetic fingerprinting methodologies was base code or capillary electrophoresis, introduced in the late 1990s and still greatly undersigned as the procedure par excellence. Additionally, supplemental changes, including bolstered database anchorage and threshold adjustability, have had a far-reaching impact on the objectivity and cogency of results emanating from forensic laboratories and have fomented metastasis in the debate over admissibility. Ruminations upon the applied science of individual identification should remain contingent upon an astute appreciation of the scientific practice underlying the technology. Primacy of place thus proceeds to an examination of the conceptions of genetic variability that undergird genetic fingerprinting, followed by a technical elucidation of forensic procedures and their evolution in recent years. True, almost all living organisms have comparable fundamental components at a cellular level. Still, the nuclear DNA that exists in every human cell is suffused with an almost incalculable number of genetic elements. Manifestation of this information is discerned in the variable regions of DNA. These three billion base pairs codify 20,000 to 25,000 genes, but they likewise encompass around three million differential base pairs, accounting for approximately 1.5% of the whole. At first glance, this magnitude of discrepancy would appear to dispose of the desired unique individuation; however, the large majority of putative variance in the genome is due to single nucleotide polymorphisms, most of which will be very common and will not present the neotype variation required for forensic prosecution. However, there are regions of the genome that are polymorphic due to structural anomalies.

3.1. STR Analysis

Short tandem repeats (STRs) have become one of the most accepted methods of genetic fingerprinting. An STR region is any section of the DNA that shows multiple repeated basepairs of 10-50 basepairs long on each chromosome. Most human chromosomes contain STR segments that are mostly, but not absolutely identical. This lack of absolute identity contributes to a high degree of individual genetic variation between humans. Very early in studying the human genome, searching for such repeated sequences was favored because of their high-level of differentiation between individuals. The method is now based on pouring a primer into a solution of the cut chromosomal DNA, while also adding DNA polymerase and numerous nucleotide bases. The debate then stirs, since the primer is "designed to" catch anywhere specific sequences of the chromosomes. Within minutes, millions of replicated DNA strands have been created, 1 base longer than each other. Many samples of these replicated fragments are run on a gel with known standard lengths the fragments migrate to. The banding pattern of these samples is compared to that of the unknown and a match is determined by percentage fine strayings (Keerti & Ninave, 2022). However, STR fingerprints produced is a low percentage of a false positive match. These limitations were addressed with the advent of new European STRs involving longer sequences of DNA. Simulation analysis of these new STRs indicated a much lower percentage of false identities. Thus, the current trial was able to demonstrate validation. An important function was enhanced access services, so that lawyers could seek experts to consult with and indeed to testify in court. Moreover, this was the first attempt to compare a current trial with a database of previously conducted trials in categorical terms. These comparisons revealed that struck discovery rates were far from the active word in favor of results that finalize a case quickly.

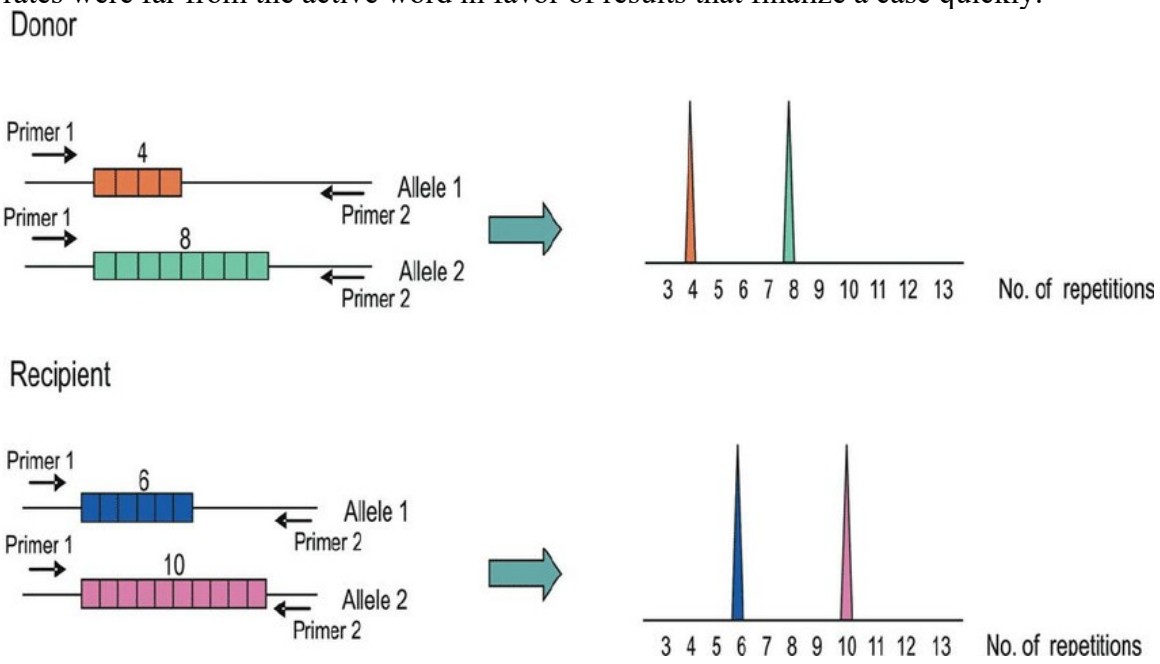


Fig2: Principles of STR analysis. STRs loci comprise repetitive sequences of 2-7 bp; which are a highly polymorphic characteristic. In the example, for this locus, the receptor has alleles with 6 and 8 repetitions, unlike the donor, which has 4 and 8 repetitions. The STRs are amplified by PCR with fluorescent primers flanking the interest region. PCR products are separated according to size by electrophoresis in automated sequencer and proportion of each peak may be quantified according to its area.

3.2. PCR Techniques

In the rapidly evolving field of genetic analysis, one of the most fundamental processes is that of the polymerase chain reaction (PCR). For forensic DNA analysis, and a growing legion of other applications, this process is used to amplify specific DNA sequences present in minute quantities in a mixture of template DNA. An understanding of the PCR process and its implications is essential for an appreciation of how genetic fingerprinting works and the manner in which laboratory validation samples are performed (McDonald et al., 2024).

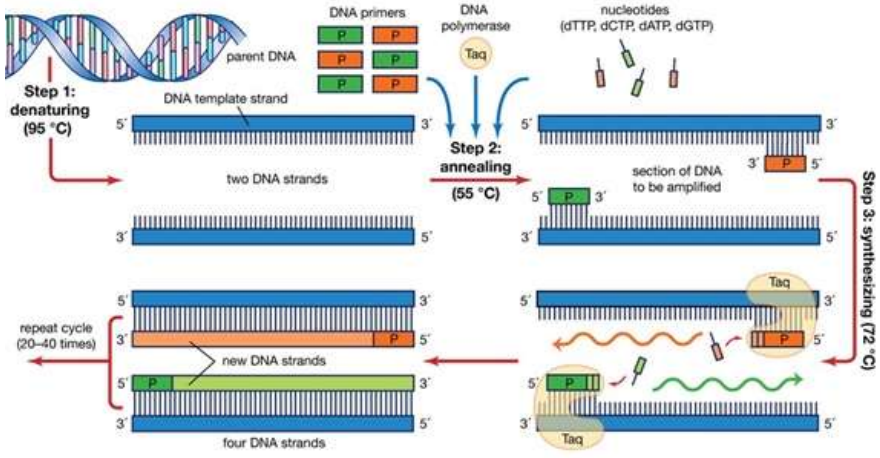
Extraction of the DNA from the sample is the initial step in the analysis process. This is usually done by a method known as organic extraction which separates the genetic material from the remainder of the sample and can be done by various means. The PCR process itself involves the hybridization of two oligonucleotide primers to a denatured template, followed by the replication of that sequence by a heat-stable DNA polymerase. Through the repeated cycles of separate DNA strands, annealing of primers, and extension by Taq polymerase, the target sequence is replicated million-fold in a few hours. Though the advances and advantages of this process are significant, and extend to scientific disciplines beyond forensic science, the focal point of this section is the PCR procedures of genetic fingerprinting, additional validation tests, and traditional DNA testing methods. In addition to the traditional methods, the main focus here is on the newer fluorescent technologies that represent the current state of the practice in the profession.

Early PCR was a cumbersome process performed by batch that involved a step block type of machine in which little more than a single sample could be processed. Analysis of the results was conducted by pouring a gel and looking at after electrophoresis was completed. It was necessary to wait a long time between the submission of evidence samples and the issuance of DNA profiling results. Both technological advancements have spurn the rise of real-time PCR instruments that simultaneously amplify and size fractionate the amplified DNA. A range of other applications has resulted from PCR technology, such as microbial detection, food safety, sex determination, pathogen detection, malignant transformation analysis, oncogenic mutation, gene expression analysis, and more. The ability of PCR to amplify minute quantities of genetic material has revolutionized these applications, and continues to have impact across an extensive range of scientific disciplines.

Fig3: The three-step process of the polymerase chain reaction.

1.5 4. Principles of Traditional DNA Testing

DNA, the main carrier of genetic information, is a macromolecule that codes for all biologic traits. Derived from each parent, it uniquely distinguishes every individual. DNA replication is



responsible for genetic inheritance, sharing approximately 99.9% of its sequence among all humans. However, the remaining 0.1% exhibits polymorphism. This variation can be exploited to uniquely differentiate every person. Although only 3 million base pairs comprise this 0.1%, it encompasses genes that collectively comprise over 30,000 loci. While the vast majority of these 30,000 loci have not yet been genetically mapped, approximately 2-4% of the genome consists of 87 sequences that adequately discriminate individuals (Robert Landry et al., 2008). The procedures for DNA extraction, quantification, amplification, and electrophoretic separation comprise the laboratory techniques to analyze such sequences. For genetic informatics analysis, sampling blood and saliva is most common. However, DNA extracted from hair, teeth, or damaged and old biological materials can also prove useful. As these genetic procedures necessarily destructively modify the analyzed biological samples, their analysis using standard methods is a one-time event. Although lab procedures can be repeated, sampling more biological material is required for re-analysis. Further, DNA is present in a high proportion in the vast majority of cells, often constituting the primary genotyping material. Since no universally nondestructive procedures for harvesting cell DNA are standard, the techniques to avoid multiple captures involve statistical analysis of earlier gathered genetic prints of distinct objects. Given the great complexity and laboriousness of laboratory procedures, it is incredibly difficult and time-consuming to collect a sufficient database for exact analysis. Under many conditions, it means that only parametric inference can be implemented. Despite their nonparametric nature, non-exact statistical analogs are nonetheless feasible and can outperform standard parametric techniques, especially when the latter are based on erroneous models. Determination of whether two samples originate from the same source enables various practical applications, from convicting criminals to solving medical problems. The majority of these fast coherent methods were developed with the PCR in mind. Since PCR amplification has become common laboratory practice, DNA analysis has evolved conventional methods. Apparently, significant advances in genetic methods make necessary a detailed comprehension of the entire scope of DNA typing, including the older techniques.

4.1. RFLP Analysis

Restriction Fragment Length Polymorphism (RFLP), one of the first forms of DNA fingerprinting techniques, was patented in 1983 by Alec Jeffreys and used for a forensic case to establish the innocence of Colin Pitchfork in the United Kingdom in 1988. RFLP became the gold standard for proving innocence and guilt until the mid-1990s when advances in DNA technology led to alternative genotyping methods. RFLP is still considered, however, the most accurate & reliable test for forensic purposes (Robert Landry et al., 2008). Often times, restriction fragment length polymorphism analysis is used synonymously with traditional DNA testing, even among those who should know better. The invention of RFLP was a technology development that allowed DNA samples to be manipulated in a way that allowed identifying conceptualized points of comparison. DNA evidence has been used only rarely in cases of rape and murder until the advent of RFLP. Prior to the development of this technology, there was no safe way of stabilizing a sample of DNA continuously taken from a contaminated environment, and comparing an individual's DNA profile against this valuable evidence-containing sample risked losing the contamination detection tool and raised the possibility of relying on evidence that may contain the informed DNA examiner's DNA. The advent of RFLP "eliminated much of the subjectivity from DNA testing (Reddy et al., 2009)." With RFLP, the accuracy of results is based mostly on the quality of the sample, as testing is easy to do and remarkably consistent in its methodology. And though these procedures are somewhat time-consuming, the likelihood of generating a mistaken result is very low and unlikely to be sustained.

4.2. Southern Blotting

The clarity derives from the controlled circumstances of a courtroom (DR Croning et al., 2010). The watching jurors acknowledge defiled guilt across the defendant's face as the fingerprint samples match the trail of evidence. The purity of the case lies in the fingerprinting technology. Begin with isolation of human genomic DNA from cheek cells; treat the sample with restrictive enzymes to produce DNA fragments of varying lengths. Genomic DNA analysis proceeds with gel electrophoresis. Load samples into the agarose trench, and apply a charge for 45 minutes. Ethidium bromide binds to the DNA and makes the bands visible under UV light. Gels of the DNA fragments are transferred to a membrane using Southern blotting. This technique owes its success to capillarity – small fragments move upward faster, and probes are added to detect the fragments of interest. Blotting is used to detect or identify an individual's disorder. In each case, Southern blotting is a central investigatory technique. Restriction enzymes and gel electrophoresis are used to separate the DNA into fragments – the following Southern blotting allows a gene, or portion be singled out. Hybridized probe is used to detect the gene (or specific sequence) in a sample (blot). This has wide applications, in both the medical and legal professions. It is useful for fingerprinting, paternity cases, and to smoothly establish genetic relationships. Interestingly, Southern blotting is still the best method for understanding complex genomes, even under significant study. It is a wonderful example of the interplay between scientific investigation and technological advances. There is a good appreciation of the technique, what it is used for, and why it is still important. The limits are also appreciated; it is difficult with degraded DNA, bacterial contamination, and low-quality probes. Despite the greater time involved, the technique is appreciated for the detail it can yield. Implement natural links between Southern blotting and gel electrophoresis.

1.6 **5. Applications in Forensic Science**

DNA analysis has become an everyday necessity in the field of forensic science. Using new techniques in DNA analysis, offenders can be quickly found and removed from society. Most importantly, everyday people who are wrongly accused of a crime can also be easily cleared as suspects (John Pittera et al., 2010). Traditional DNA testing involves comparing DNA band patterns produced when DNA samples undergo electrophoresis. Repeats in DNA sequence are discovered in the process. A minute quantity of DNA is needed for the comparison. Genetic fingerprinting is particularly useful in cases in which detection is needed for early prevention of a situation's severity. A particular group of family members, rapists, or set of suspects is detected from a vast array of tested individuals. With traditional DNA testing, a large group of sampled individuals must be tested before an offender is found. This can be due to a lack of suspects or because a large area is being tested. Genetic fingerprinting can be useful in a large habitat that is being monitored because results are produced more quickly.

The reliability of this testing has been exhibited on the popular television show Law and Order. Those who are accused of a crime are subjected to a DNA test and then cleared or tagged as a suspect. Many times in recent events, the DNA analysis is the deciding factor in convicting a person of a crime. For hours or days, suspects are held in interrogation, and their DNA is usually taken before they are even charged with a crime. Regardless if the person admits to committing the criminal offense or not, the suspect is usually found through this type of evidence. DNA handling, however, is not an easy task (James McCormick & Lee White, 2011). Specially trained people are usually asked to handle the evidence. Techniques are usually used so that the test is tampered with as little as possible while being conducted. Timing is also very delicate. DNA can disappear and degrade quickly if not preserved with delicate care. Because of this, many of the

latest techniques in DNA analysis have evolved into on the site testing. These people are specially trained to handle the methods that would usually take a laboratory to perform.

Most forensic laboratories have a set timeframe when samples are collected, transported, and analyzed. DNA samples must usually be analyzed the same day they are collected. There are many methods in which DNA can be tested. Over the last decade, DNA testing has blossomed. In 1985, DNA analysis was non-existent. In 2004, people are being cloned every day. Common techniques that are usually used are automated DNA sequencing using fluorescent tags, restriction enzyme analysis, and the use of radiation to match codes. Genetic fingerprinting relies heavily on the comparison of DNA. Standard DNA analysis virtually eliminates any risk of mistakes. Only blood, hair, or ova can be compared and are analyzed using the same tests. Common DNA analysis tests are hair bulge coloration, ABO/ antibody detection, fluoro-immunoassay, and a comparison of DNA, and those methods can be used on saliva, hair, blood, or other DNA carrying substances. Traditional DNA tests use one-third the methods of genetic fingerprinting and have a low-profile, although very high cost. DNA analysis takes a little amount of time and can compare far more DNA than any other test. The top nuclear laboratories in the world when dealing with DNA testing are the FBI, an Australian Centre for DNA Analysis, and the Varanase Memorial Institution of Genetic Engineering. In the growing field, DNA analysis takes the field of genetics and mixing it with archeology has provided scientists with a method to learn about ancient societies. Analyses are done by simply exuming the body and comparing its DNA with other dead societies. Model societies that could be analyzed the same way would be Roman gladiators and Native American tribes. Traces of ancient DNA have been found in many countries, such as Germany, Austria, and Italy. Genetically, the Solomon Islanders are roughly of the same society as the people of Vanuatu, which caused a great deal of controversy in the world of archeology. This attempt was one of the first obtained from DNA testing to reignite the study of ancient societies. The growing nature of DNA analysis will only further progress the accuracy of genetic fingerprinting. On June 19th, 2002, the FBI will finally begin so-called "paternity testing" or DNA evidence tests so that people will no longer be put to death solely on "eye witness" accounts. In the world of Law and Order this drastically changes the series. No longer will detectives be quite the best murderers. Of course, it will be a long time before the DNA labs could ever hope to catch someone with the blood of a costo Rican Chutacabra.

1.7 6. Applications in Paternity Testing

Usually done as required by child welfare agencies, to establish legal parentage and to claim the child's inheritance resulting from his father/mother die, but often also simply to establish the relationship between a parent and his child. The method used is the "traditional" DNA testing using many bands analysis because public laboratories in Indonesia do not have DNA sequencing facilities that can discriminate between similar sized bands ((S. (Djaja) Atmadja & (Evi) Untoro, 2008)).

Apa itu vro? Genetic fingerprinting, or DNA fingerprinting or DNA profiling (DNA fingerprinting). Application of DNA testing in establishing blood relationship to claim inheritance ever since while ago worldwide often used to establish family relationships, parentage and disputed racial origin or ethnic groups. Versatility is because genetic fingerprinting using (probe) is not necessarily specific. A large amount of repetitive DNA families allows a relatively simple DNA probe to hybridize to unrelated families DNA of the same DNA fingerprint patterns ((John Pittera et al., 2010)). Due to his inferiority, these types of DNA fingerprinting and the method of weight analysis from the pattern of bred DNA bands have been abandoned in developing this DNA application. Because his DNA application is perceived as an expert and public laboratory, here

discussed what is called a genetic fingerprinting as DNA fingerprinting is only DNA short tandem repeat (STR) or microsatellite DNA test. DNA short tandem repeat or microsatellite DNA test is currently used mostly for paternity testing that public opinion by the tendency is uncertain of its uniqueness. Generated DNA bands are the same between people who are not blood related (non-hybrid), especially before they were put into the database to prove potentially the same "genetic fingerprint". Determine existence alleged father or "biological" father who was confirmed (confirm) father of the child, rather than exclusion except in cases of mutation, the highest paternity index will be obtained. The pattern of adult patterns is the pattern of children who match considering every band on a 15-17 profile.

1.8 **7. Accuracy and Reliability Comparison**

Genetic fingerprinting is the new darling of the media, but it is not enough to simply be new and well-publicized for a technology to be suitable for all purposes. With hundreds of papers in the medical literature attesting to the excellent record of traditional DNA testing, any comparison must be made with an awareness of both sides of the debate. Genetic fingerprinting is more discriminatory than traditional DNA testing, but analyst proficiency is a major factor in the efficacy of its use. Results will be variable and subjective, even when the same criteria are used. Genetic fingerprinting is new and so less literature is available on levels of acceptance and validation than for traditional DNA testing. Genetic fingerprinting may now constitute a theoretically excellent tool for investigating extra-pair paternity, but whether or not it can be employed for such research with any real confidence is another matter (H. Kaye, 1991).

The conclusion indicates that in the context considered genetic fingerprinting fell well short of traditional DNA testing in terms of an ability to detect foreign sperm. In general terms the debate over the comparative merits of genetic fingerprinting and traditional DNA testing will significantly split the scientific community, as artefacts prominent in one view are not so in the other. Method of comparative assessment are deliberated on and a proforma for a more objective comparison of the two techniques is devised. The terms 'accuracy' and 'reliability' are kept quite distinct in the comparisons drawn between genetic fingerprinting and traditional DNA testing. A methodology is therefore established so that it is no longer possible to claim that one might have been critiqued more than the other. It is clear that the same experiment can be performed with both techniques; for example, expert witnesses regard genetic fingerprinting on radioactive detection as not sufficiently sensitive and suggest using an ethidium bromide method. It is known that the radioactive detection technique can pick up no size match equivalent to a molecule smaller than 3 or 4 kb; this is the extreme range at which disparities can sometimes occur with the traditional method, but this would still clear 80–90% of disputed cases. At the best of times the ethidium bromide detection system is extremely unlikely to reliably detect a size match outside the 2.5–4 kb range, and disparity can be as low as 25% with a 50% polymorphic kinase. In addition, findings from other research indicate that even the 2.5 estimate might be generous; found that the smallest detectable size difference was about 3 kb.

1.9 **8. Cost Analysis**

There are significant differences in the costs between a genetic fingerprinting kit for swab testing, currently costing about $500 and a traditional basic kit with eight core STR markers for amplification testing, while database costs and analysis time costs have bigger variance. Setup costs for the equipment and initial training must be taken into account as well. The cost per sample depends on the reagents and the personnel spending time on setting up the test and analyzing the results. The amplification test for DNA profile has a fixed cost of about $21 for reagents, with the main variable cost being personnel spending time on the procedure. In the case of the swab kit for

detecting the presence of biological materials, the fixed reagent cost for each kit is about $15, while the only further fixed cost is the analysis of the databases, costing about $5 per result. The personnel-related costs consist of the operators collecting the samples and analyzing the results, who are different in the two methods and only the analysis labor is included in the genetic fingerprinting cost calculation. The database comparison of the genetic fingerprints is automatically done and free to use with the genetic fingerprinting kit, while in the case of the DNA profile proper manual analysis is needed and the time-consuming gene mapping serves as a barrier to wider use of these tests. The biggest part of the costs is the initial setup, which mainly consists of the equipment costs. These are based on the cheap end of the tools (moderate quality shop), resulting in $1,503 for the swab test and $17,015 for the amplification test. The analysis can only be done if the samples reach the research laboratory and if the related person agrees to take part in the test, and the higher investment in equipment can be a hindrance in the previous step, not to mention the relatively scarce number of locations. On the other hand, the results are not always accurate in case of genetic fingerprinting. In addition, law laboratories cannot determine the blood relationship while the family court is not allowed to reveal the genetic origin of the donors (Th. Martinsohn et al., 2018). Nonetheless, in the case of average effects, the swab test becomes affordable in fewer cases, because the fine has to be very large to outweigh the deposition and analysis costs. Besides, the costs are always borne by the designated offender in the criminal cases. On the other hand, suspects could be deterred by the greater likelihood of the discovery of biological material if the investigative authority uses this method. Another problem is the data management cost of the criminal test, because although the result is negative in all other cases, the test itself is still revealing intimate information, which could easily be abused. Amplicon tests need a relatively small total amount of equipment investment, so it only becomes cheaper to carry a test than an average fine in special around half of the cases, or even the majority if the case Norm Distribution of penalties in civil matters. The disease of cost management of such tests could be exacerbating the social problems created by the discrimination against low-income people. Given such harsh restrictions, it is not possible to carry out the tests, even if they would have considered the long-term perspective. Individually though, the short-term expenses can be expected to outweigh the benefits. As a result, the average effect of the implementation of ameliorated genetic tests could be to stratify the population not only genetically and income wise but also in term of equal treatment (Budowle et al., 2022). Spread in TouchDOWN PCR and segregated gene mapping, combined with the faster data mining process, could eventually make traditional STR tests cheaper and more manageable. Amplicon tests for basit DNA fingerprints can be reproduced for about $30 per test already, with numerous further remedies on the horizon.

1.10 9. Ethical and Legal Considerations

Forensic genetics was born and evolved in close connection with the analysis and interpretation of evidence, which is currently based on DNA technology. This application of genetics is socially fascinating, and recent generations of DNA exams have refueled a sensationalist impact of the media, to the point of presenting the DNA test as a "perfect" test also in reconstructive activities of biological. As an example, the results of a recent collaborative research, concerning the comparison between genetic fingerprinting results and the traditional DNA test function, are provided to explain the following comments. These results, promoting the integration between the two different genetic applications, also show some critically relevant aspects, especially in consideration of the dramatic scientific and social implication that this kind of genetic application entails for at least ten percent of the population (Robert Landry et al., 2008). The present study faces ethical and legal aspects, not to mention the social ones. Too many cases of misuse of the

genetic analysis have been documented, in both improper application and risky interpretation, determination of non-scientific inferences and identification for function genetically unmotivated. More attentively ethical-political mediations are included which involve the concept of privacy, especially to what concerning the collection and storage of genetic data, the so-called genetic mapping, i.e., the acquisition and detailed study, even on a national basis, of genetic maps of homogeneous population portions defined based on established phenotypic characteristics, and the consequent possible genetic discrimination. Similarly the risk of privatization of the genetic material and the precarious confidence that has been granted the possibility of an anonymous and unequivocable genetic profile, also favored by the furor incaution, resulting in a distortion of private or public interests that contrast with their protection (F de Groot et al., 2021). First as far as this last aspect is concerned, the genetic data analysis must be kept separate from the active data integration into the investigation techniques, by providing the revealing data that a sample DNA matter provides, and must be carried out exclusively by specialized laboratories, duly accredited and within specific ministerial provisions, including national and local health forensic services. For a rather regular self-discipline, the various DNA test networks have made the choice not to carry out certain types of investigations in particular fields in order to avoid the relative schemas otherwise enforceable by the judicial authority.

1.11 10. Future Trends and Innovations

Forensic science and paternity analysis are based on genetic analysis. Since its inception, genetic fingerprinting has become a standard method. Conceptually, the term refers to the detection of typical, individual DNA markers in human DNA. This proof of identity can be used, for example, to compare traces obtained at a crime scene with samples taken from suspects and thus to provide clarification. This technique is based on DNA analysis. Traditional genetic fingerprinting provides a qualitatively limited DNA test, i.e., certain DNA regions are characterized and a comparison is made overlapping these in different DNA samples. However, this is of course only a small fraction of all the information that is present in our genes. Modern DNA examination technologies are significantly more extensive. The entire genome of a process can now be accurately determined within a few days; corresponding tests for ancestry determination can do without "DNA contrasts" and give at the same time more reliable results. DNA analysis originally used in forensic cases is now considered outdated. Since the 1990s, a rapid and continuous evolution of sequencing and analysis technologies has taken place, and even the research capacities of academic institutions and the criminal police can be to some extent compared to what was available in 2000. However undesirably it often happens that public awareness lags behind technological developments. In the lay public, techniques like gel electrophoresis of a few DNA samples, fluorescence labeling, or PCR have burned themselves into consciousness. These methods are technically no longer used today.

In the terminology of genetics, a DNA marker is defined as a specific, inherited region of the DNA. The term genetic fingerprinting is defined as the comparison of DNA fingerprints. This terminology is common today; originally both terms were coined by the inventors of the technique. However, the term "DNA fingerprint" is also often used to describe the results of this process. This created potential for ambiguity, so within the scope of this text, the term "DNA print" will be used instead. The comparison of DNA traces is of course not fixed to specific DNA entries, but can generally be called "DNA comparison" or "DNA test"; however, genetic fingerprinting is the default term in legal, lay, and scientific jargon (N. Mandape et al., 2024).

1.12 11. Conclusion and Recommendations

The importance of adopting a balanced approach was underscored by the expert interviews. They emphasized that the methods should not be viewed as competing, but rather as supplementary. Instead, the choice of testing method should depend on the specific objective of the test, as well as on the accurateness. Traditional DNA tests are typically more accurate (approximately 1 in 100 million error rate), but also more expensive (starting from $3000) making their use prohibitive for tenancy agreements. In contrast, genetic fingerprinting tests are significantly less expensive (starting from $450) and therefore more appealing for applications like reuniting families. The adoption of cheaper tests has to be therefore complemented by more informative counseling, as their applicability is more limited, and the results are not as definitive as in case of traditional tests (Robert Landry et al., 2008). Given their increasing availability and falling price, facts on the difference in accuracy and implications of testing under study had to be better communicated to lay audiences. Current consumers are generally not fully aware of the difference and mistakenly believe that, except cost, all tests are otherwise the same – as also revealed in the outcome of the survey on public knowledge. Misconceptions around the accuracy of genetic fingerprinting tests, in particular, are worrying. Given the concerns pointed out, practitioners, both in State and private industry need to take greater efforts to wholesome and accurate/clear information to the consumer. Given the rapid rise of such technology and its implications for the social fabric, further research and public dialogue should be considered. Efforts to maintain current policy and ethical considerations against such advances should also be pursued, and are still feasible given the ongoing uncertainty of such technologies.

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