Forensic DNA

DNA typing is the analysis of DNA that is extracted from a biological sample obtained from an individual. The sequence of genetic markers in the genome, also known as minisatellites, is the same in almost every individual, but the number of repeats is different. The resulting pattern is a DNA profile, which is unique to every person aside from twins.

In the 1980's, Restriction Fragment Length Polymorphism (RFLP) became the first genetic test that used DNA. This procedure uses restriction enzymes to cut the DNA at specific sites, then the fragments of differing sizes are separated using gel electrophoresis. Radiolabeled probe molecules that are complementary to repeat sequences are added to the denatured DNA, which identifies the regions that contain Variable Number Tandem Repeats (VNTR). The probe molecules hybridize to the VNTRs and appear as fluorescent bands on the film. This process served as the scientific basis of paternity tests, considering its power of exclusion is greater than 99.99 percent. Alec Jeffreys first used this technique in 1985 during an immigration case. He proved that a boy from Ghana who was trying to enter England was in fact the son of the awaiting family. Shortly after, RFLP was used to solve a double homicide. The bodies of two 15-year-old girls, Lynda Mann and Dawn Ashworth, were found after being raped and strangled. Jeffreys tested the DNA from the semen that was present in the victims and confirmed that they were attacked by the same man, but not the suspect the police had in custody. Subsequently, a mass DNA screen was conducted where samples were collected from 5,000 local men, but no matches were found. One man, Colin Pitchfork, who had successfully avoided the dragnet was reported to the police and his DNA was later discovered to be a match to the samples recovered from the crimes. However, this test is rarely conducted nowadays because the amount of DNA required for testing requires a blood sample and there is a long turnaround time.

In the 1990's, the Polymerase Chain Reaction (PCR) method replaced RFLP analysis. This procedure amplifies specific portions of the DNA sample, mimicking the biological process of DNA replication. It requires less DNA and the results are generated faster. Further developments to it brought about the system of DNA typing used today. Some chromosomal regions contain repeating units of the same type of DNA molecule, also known as Short Tandem Repeats (STR). These STR markers may vary between individuals, so they are targeted with sequence-specific primers and undergo PCR amplification. The DNA fragments are separated using either capillary or gel electrophoresis before being statistically analyzed. The findings can be used for identification in forensic casework. This method was implemented in Joseph Castro's case. In 1987, 20-year-old Vilma Ponce and her 2-year-old daughter were stabbed to death in their Bronx apartment. The police found bloodstains on Castro's watch while questioning him, and STR amplification was carried out using the PCR technique to determine that it belonged to Ponce. However, DNA can also be found in the mitochondrion of the cell. Unlike nuclear DNA, which only has two copies per cell, there are multiple copies of mitochondrial DNA present in the cell. This makes it possible to analyze DNA from degraded or environmentally disturbed samples, as in the Romanov case. In 1991, nine skeletons were found in a shallow grave in Russia. STR analysis proved that of the remains, there was a family of two parents and three daughters. The mitochondrial DNA analysis revealed a sequence match between Tsarina Alexandra and the three children with a living maternal relative. Amplified mitochondrial DNA extracted from the remains of Tsar Nicholas had a sequence match with several of his living maternal relatives as well.

The incorporation of family relatedness in forensic genetics has taken DNA evidence in a new direction. Genetic genealogy is the process of identifying individuals from their relatives

based on DNA testing. It can be used to determine the level and type of genetic relationship that exists between people. This was implemented in the aforementioned Romanov case as well as in the Golden State Killer case. During the latter, DNA from the crime scene was uploaded to an ancestry website. A list of how much DNA each individual shared with the sample was returned; the more DNA they shared, the more closely they were related. Police explored the family trees of the closest matches in search of men who fit the profile of the Golden State Killer. This was how they were able to zero in on Joseph DeAngelo, whose DNA sample later proved to match that recovered from the crime scene. Furthermore, cases regarding immigration and the identification of remains have greatly benefited from this relatively new technique. However, its use in criminal cases has raised privacy concerns. Previously, police were limited to searching law enforcement databases, which only contain data from arrested for crimes. But with the increasing use of family relatedness in forensic testing, legal experts worry that this development will allow police to look into people's genetics without probable cause.

The versatility of DNA typing was strengthened when it was discovered that DNA tests could be applied to nonhuman samples. This was first implemented in the case of Douglas Beamish, where a bloodstained jacket covered in short, white hairs was recovered. The blood matched that of the victim and the police believed it was possible to link the hairs with Beamish's parents' cat, Snowball. Despite there being no precedence, a scientist from Maryland agreed to run DNA fingerprinting analyses on the hairs from the jacket, Snowball, and the blood of 19 other local cats. It was concluded that there was enough diversity among the cats and that the odds of any other cat besides Snowball having the same DNA as the sample were extremely small. This was sufficient evidence to establish a connection between Beamish and the jacket

and therefore the murder. The nonhuman DNA tests were not questioned by the defense in this case, paving the way for its acceptance in future cases.

When taken to trial, the admissibility of DNA evidence is determined by many principles. For DNA evidence to be presented in court, scientifically acceptable procedures must permit reliable analysis. This means that a scientific basis must exist to conclude that properly performed comparisons can distinguish potential sources. The general acceptance standard derived from the case of *Frye v United States*; it holds that the methodology must be generally accepted within the relevant scientific community. When the DNA evidence is deemed admissible, the jury is presented with the information that is essential to convey the reliability of the testing and the significance of the results. The courts require that experts demonstrate how DNA profiles vary from one person to the next, as well as produce undisputed, quantitative estimates of how rare the identifying characteristics are within particular groups. From this, the expert may share their opinion on whether they believe the DNA belongs to the defendant. However, succumbing to prosecutor's fallacy, where false assumptions stemming from probabilities of guilt are made, should be avoided.

Without supporting evidence, DNA analysis can only reveal who was involved in the case, but not when, where, why, or how. To address this, a hierarchy of propositions was established. It assists in deciding which level to address DNA casework. In the case of Amanda Knox, a hierarchy of propositions was used to analyze a knife that was found in one of the suspect's apartments. There was difficulty in identifying whether the knife that had Knox's DNA on the handle was used to kill Kercher. There was no blood found on the knife, so the prosecutors offered the hypothesis that it had been cleaned. With this mindset, there was a lack of source-level interpretation; the prosecution did not seek DNA to connect the suspect with the

victim, rather they attempted to explain why and how the knife was connected to the murder. Whereas, the inference in relation to the source of the DNA might be strong, these propositional inferences, which offer alternative relationships between evidence and identity, may be more tentative.

Developments in DNA typing have also allowed for the exoneration of those who were wrongfully convicted. To do so, DNA from crime scene evidence that was not tested at the time of trial is analyzed. It could prove conclusively that the prisoner did not commit the crime, or it would raise enough reasonable doubt to overturn the conviction. Additionally, newer technologies have aided the successful analysis of aged, degraded, or previously inconclusive samples. States across the nation have different laws that set the standard for post-conviction DNA analysis requests. Judges use these to determine whether the evidence will have enough of an impact on the prior ruling to justify reopening the case. Groups like the Innocence Project dedicate their work to the improvement of post-conviction DNA review.

Genetic testing helps to identify changes in chromosomes, genes, or proteins. The results can be used to confirm or deny genetic conditions. However, making this test universal has its pros and cons. It can be very beneficial to the police, who could turn the database into a valuable asset to be used when comparing DNA samples. In turn, this could lead to more efficient investigations. On the contrary, creating and storing a full profile of people based on their DNA could raise privacy concerns. Furthermore, if these profiles are not properly secured, they may find themselves in the hands of the wrong people. On another note, DNA information is not completely accurate, and maintaining inaccurate profiles for future use may lead to tainted conclusions.

Considering DNA testing is still a fairly new science in the field of forensic evidence, there are many obstacles it has yet to overcome. For instance, as genetic testing technology evolves, additional questions of ethics and social responsibility are inevitable. Additionally, standardization of guidelines as well as quality assurance methodology repeatedly establish themselves as points of conflict when debating DNA evidence, especially since there is always the chance of human error in the form of contamination or mishandling. Finally, science needs to develop at a pace that can keep up with modern activity. Once these issues are resolved, DNA evidence will prove to be a force to be reckoned with in a broad range of legal matters.

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