DNA Technology: 150 Years of Research and Development

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The use of DNA identification methodologies has revolutionised crime scene investigation, but its use has often been the subject of controversy, and the use of forensic science in the courtroom has given rise to changes in the law and the interpretation of law. A series of three articles will look at how DNA interpretation has evolved and its implications for identification in criminal lawcourts

Deoxyribonucleic acid is a complex structure made up from relatively simple building blocks, and is generally found in the nucleus of cells. It carries the genetic instructions for the replication and function of all known organisms, excepting a small number of viruses. During sexual reproduction the gamete from each parent carries half the genetic information determining the physical characteristics to be inherited by the child.

The presence of DNA in living material was originally recognised in 1869 by a Swiss physician, Friedrich Miescher. By 1937, various components of DNA had been identified and x-ray diffraction had shown that DNA had a regular structure, and the link between DNA and hereditary function had been postulated. In 1953 Francis Crick and James Watson proposed the double-helix model of DNA structure. Two strands joined together by four distinct nitrogenous bases form a compact right-handed helix, allowing for a large amount of information to be encoded in a relatively small space. Crick and Watson's DNA helix discovery was enabled through the work of two other scientists; Maurice Wilkins, the pioneer of X-ray crystallography, and Rosalind Franklin who refined the technique for work with DNA. Together they identified the four bases which link the two strands of the helix: Adenine, Cytosine, Thymine and Guanine (A,C,T and G). These nitrogenous bases are attached to a ribose sugar on the phosphate-sugar backbone of each DNA strand.

Each molecule of DNA includes a pattern of these bases bonded together. Adenine forms hydrogen bonds with Thymine whilst Cytosine similarly engages with Guanine. This base pairing holds the two strands of the double helix in close proximity to each other. It is the sequence of these base pairs within genes that is the genetic "blueprint" for the organism, encoding sequential instructions for amino acids, which are the building blocks of proteins. The compact information encoded in DNA is held in structures called chromosomes, of which humans have a normal complement of 46; 23 of maternal and 23 of paternal origin. Humans share almost all of their DNA sequence with other humans, and much of the sequence information with other organisms. Only about one per cent is specific to humans when compared to a near relative such as a chimpanzee, and only about one tenth of that one percent of DNA differs from one human to the next (with the exception of identical twins). However, this small fraction still comprises some three million base pairs.

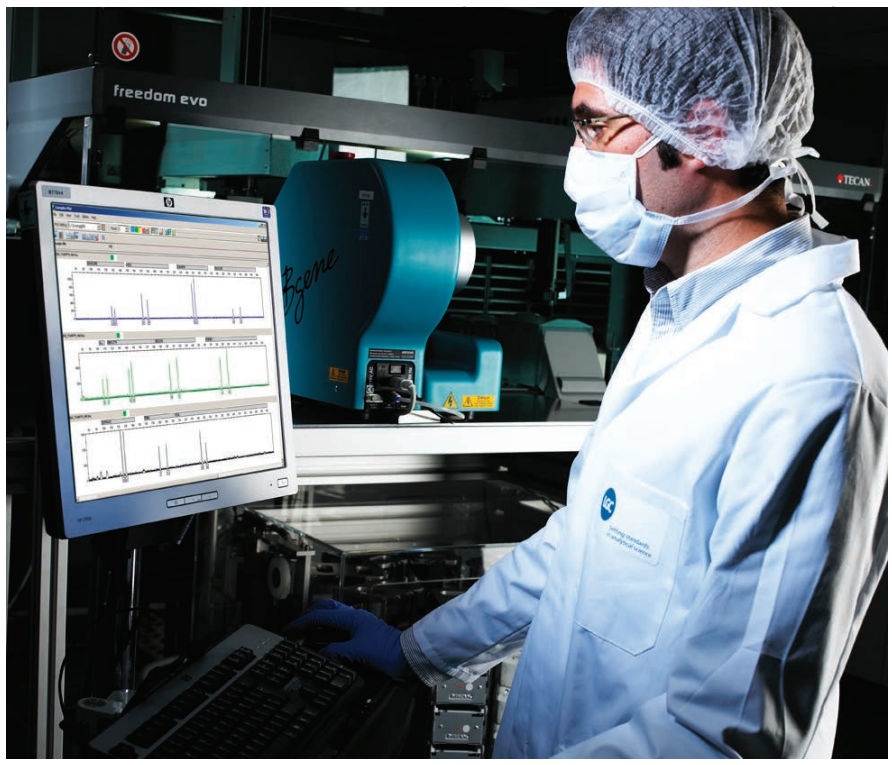
DNA Profiling Develops

The first paper reporting the use of DNA in a criminal context was published in 1985 by Alec Jeffreys, Professor of Genetics at Leicester University (Jeffreys, AJJ, 1985). Jeffreys was researching inherited variation in human DNA and he demonstrated how a DNA profile could be used to resolve issues of identity and kinship.

During the late 1980's and early 1990's DNA technology was the subject of research and development for the purposes of criminal investigation, primarily by the Forensic Science Service in the UK (FSS).

When analysing person-specific DNA variations for forensic purposes, the sections of DNA examined are called Short Tandem Repeats (STRs). As the name suggests these are short sequences of DNA normally just four bases long repeated as adjacent blocks. It is predominantly the number of repeats of the core sequence that varies within individuals. STRs are, fortuitously, found in the non-coding regions of the genome (i.e. not within the genes) but the position (locus) of these on the chromosomes does not usually change from one person to the next. For crime scene investigation in the UK, a DNA profile is produced by measuring the physical length of the DNA at 10 STR loci simultaneously, and the DNA analyser displays the results as a series of peaks on a graph known as an electropherogram (EPG). The information to be inferred from the EPG is statistically very powerful, and the probability of a match being from someone other than the suspect and unrelated to them is given a numerical value. Assessments of match probabilities are made with reference to STR profiles separated into different racial groups in order that the most conservative figure is given.

The Multi Locus Probe was introduced to routine casework in 1987, but required a large amount of sample material to produce a profile, although a full profile could give a likelihood ratio of one in a million. This was followed by the Single Locus Probe (SLP) in 1989 which allowed smaller samples to be tested and could produce statistics of one in 20-30 million.



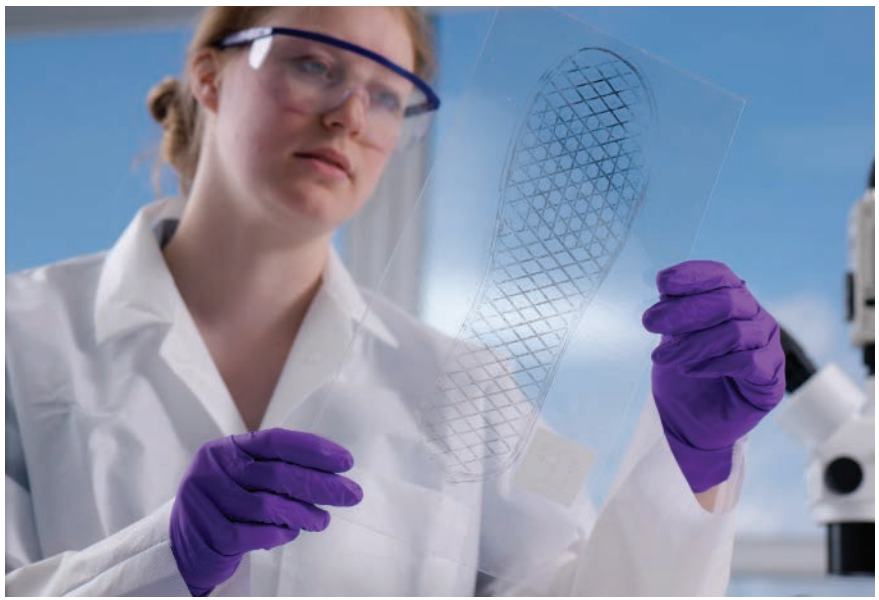
DNA profiling

In some cases, the possibility of extracting DNA from crime scene samples will be reduced if the sample is old, degraded or otherwise small in quantity. These can be subjected to more specialised techniques depending on the severity of the crime. All high sensitivity work is performed in ultra-sterile conditions. The FSS developed Low Copy Number (LCN) to deal with samples containing insufficient good quality DNA for standard profiling. The sample is subjected to 34 cycles of PCR to give more copies from which to draw a profile, but challenges in the courts in the last decade have lead to the belief that profiles thus obtained are not capable of robust and reliable interpretation.

Enhanced Results Through DNASenCe

Further developments include DNASenCe (sensitive capillary electrophoresis) which removes the impurities which interfere with the PCR process, enhancing the resulting profile by a factor of thirteen. Other procedures can further enhance profiles with the added advantage of leaving the original sample available for analysis using alternative techniques, whereas the LCN procedure used up all the original material.

DNA is also used for identification of the deceased. Samples from the newly dead may be treated in the same way as from the living, but other strategies, such as Minifiler STR analysis, are particularly useful in 'cold-case' investigations. Where a corpse is badly burned or heavily decomposed samples may be sought in deep muscle tissue where nuclear DNA has not been exposed to degradation, or if there is none remaining DNA may be obtained from bones or teeth. The eight mini-STRs examined are smaller versions of eight of the regions looked at in standard SGM+ profiling.



Footprint marks under examination

The smaller size means they are more robust and less prone to degradation but resulting profiles are still compatible with database searching.

Currently, Next Generation Multiplexes (NGMs) examine an increased number of sites comprising those presently used for SGM+ profiling plus additional sites.

Of course, in some cases it is not possible to obtain a viable sample for analysis. When there is insufficient good quality DNA to produce a full profile a partial profile may still be possible. The match probability of such a profile can be significantly reduced to the point where it is not possible to reach any conclusion as to evidential or even intelligence value. In order to calculate the probability of a partial match, reference databases are used to estimate the proportion of the STR profile in the corresponding populations. The rarity of certain characteristics is also taken into account.

Further problems arise when the sample is mixed. The profile derived from the electropherogram from a single source will have two peaks at each locus, one from each parent. Were, for example, samples from a crime scene to contain blood from two people, the EPG would show four peaks at each locus. The more contributors to the mix, the more difficult interpretation becomes. Without being able to subtract known profiles, such as from a victim or others known to have had the potential to contribute, the mixture has too many variables to interpret with certainty.

Contrary to the impression given in "CSI" type media, even a standard crime scene sample can still take 48 hours to process, with further time taken for interpretation, depending on the complexity of the result. Under exceptional circumstances this time can be reduced, but only with greatly increased demands on equipment time and personnel therefore incurring greatly increased costs. Obviously, the more complex the profiling method used, the longer it will take to interpret the findings, and inevitably the more the technology advances the greater the demand will be for DNA to be the key to the presentation of evidence to the Courts in criminal trials.