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The Forensic Institute

The Forensic Institute is a network of experts and facilities developed to deliver high quality scientific and medical services and training relevant to civil or criminal justice. The Institute is based in Glasgow and provides specialist forensic scientific, medical, and managerial consultancy services, and training in civil or criminal investigations and legal proceedings.

An extensive network of experts provides the expanding knowledge upon which The Institute is founded. Our extensive expertise is drawn from across the world and includes public and private forensic science laboratories, plus academic establishments. A group of distinguished experts form the College of The Forensic Institute.

Through The Forensic Institute Research Network (FIRN), an international association of Higher Education Institutions, we encourage and enable research and teaching excellence. FIRN's activities include a Journal, conferences, and an online discussion forum.

The Institute will express opinion only on matters of science and not social policy.

1. The interpretation of bioinformation

There are two aspects to the reliability of the SGM+ kit; the reliability of the profiles (i.e. the allelic designations) and the reliability of those profiles to identify an individual.

Although the SGM+ system has been validated for amounts of DNA between 1 and 2.5ng, there are a number of circumstances where the allelic designations may be open to question. For example, the discovery of partial profiles can be accounted for by degradation of DNA, by the presence of low amounts of DNA, or a combination of both. There are attempts within the UK to increase the sensitivity of the technique to sub-100pg amounts. This has been called Low Copy Number DNA (LCN – although there is debate about what this actually means). It has been used by the FSS (and ONLY the FSS) in circumstances where they suspect that the level of DNA is so low (pgs) that quantitation is not possible. In our opinion this is a scientifically unvalidated procedure with an unknown reliability. This is especially so when the profile has multiple contributors.

This technique has been eschewed even by the FBI, yet the lack of proper scientific challenge in court, until recently, has enabled the FSS to continue to present it as reliable evidence.

The public perception, judged by a wholesale acceptance of the National DNA Database (NDNAB) as 'A Good Thing', underlines the need to educate people, and especially those involved in the investigation and prosecution of crime, of the potential dangers that accompany the undoubted benefits of this technology.

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DNA analysis is one of the most scientifically robust techniques to be placed before a court. A series of legal and scientific challenges has honed the collection, processing, analysis and evaluation of DNA evidence to reduce the possibilities for erroneous results.

Two features of DNA evidence that can be viewed as its major benefits also produce its greatest potential dangers; specificity and sensitivity. Specificity can be considered as being similar to what used to be called discriminating power, in effect how useful it is in telling two people apart. In DNA this is usually expressed as the match probability; the probability that the DNA profile would be obtained by choosing a person at random from the population. This number is now routinely in excess of 1 in a billion (1 thousand million). Unfortunately this is usually wrongly perceived as meaning that the odds are 1 billion to 1 that the accused is the perpetrator. This even has a name; the Prosecutor's Fallacy. (The defence have their very own, different, fallacy too).

Sensitivity is a measure of how little DNA we need to perform analyses and produce a profile. Until recently DNA was recovered from visible stains like blood splashes or semen stains. Then we started to collect samples, usually by swabbing, from areas where we may expect to find DNA from body fluids e.g. cigarette ends, cutlery, spectacle frames. The introduction of LCN has seen us now enter an era where single pieces of DNA may produce profiles; that is, less than 100 picograms (0.0000000001g) of DNA.

To understand why that may be a problem it is useful to consider that each of us have about 10^{14} cells in our body, each with a full DNA profile packed inside them. We lose a number of these cells every minute of every day (and night, that's what keeps a family of bed bugs in food). Everywhere you go you leave your DNA. And here's the problem; your DNA goes places you've never been. This is probably one of the main differences between DNA and fingerprints. A correct fingerprint identification, on a fixed object, can establish that you were at a particular point, but DNA can be transferred from you to someone else and from that someone to somewhere else where you may have never been. When we had blood or semen stains that could be seen we were perhaps a little more confident that this established a link between the source of the stain and the location of the donor. But if you can walk through the supermarket and one of your cells blow into a vehicle or onto a surface a distance away then it has literally distanced itself from you. Combine the compelling *specificity* with molecular level *sensitivity*, and a population DNA database, and you have a potential scenario where your DNA is found at a crime scene that you have never been near. Your name and address are obtained from the database and the police informed that there is a 1 in a billion match probability. Inevitably, you become a suspect. Is it just possible that this apparently compelling evidence will be placed alongside some other circumstantial evidence (can YOU account for, and prove, where you are every hour of every day?) to gain a conviction. A key scientific practice is the control sample. This is an experimental

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technique used to establish that the effect that you observe is caused by the material under test and not some other component of the system. In forensic science the fact to be established is that the DNA profile originated from the material recovered from a crime scene or a suspect; not the investigator, the laboratory, packaging, or analytical instruments. There are now some who argue that this principle cannot be applied to LCN DNA analysis because even in a tightly controlled analytical procedure a significant number of supposedly negative controls give a positive result i.e. they indicate the presence of DNA.

Lastly, the very small amounts of DNA and the vagaries of the method mean that it is frequently the case that replicate samples, that should produce the same results, don't. The process gets around this difficulty, it is claimed, by simply taking a vote of three replicates. DNA types found in 2 of the three are regarded as real and counted in the 'consensus' profile. So, for example, if a stain is extracted and divided into three parts (we call them aliquots), and subject to the same analytical procedure the results could be;

1. AA
2. AAB
3. AC

The consensus result would be AA. B and C would be regarded as "inconsequential".

From these results, how confident can we be that AA is the accurate or true result? Given this data, we must at least concede the possibility that after 5 replicates we may find more B's or C's (or fewer A's), so we are not 100% confident that AA is the true result. We use the consensus result as the basis of the statistical calculation of how rare this combination is in the population at large; in effect the probative value of the DNA evidence.

Now imagine that we take ten of these consensus results for different areas of DNA to calculate the match probability. This process will yield a statement of the form, "the probability of this profile coming from X rather than some unknown, unrelated person is …" and then a number that is frequently of the order of billions, but with no statement of the confidence that we can place in that result despite the clear, and probably measurable, uncertainty that must exist.

If even one of these is wrong then the opinion, as well as eliminating the real perpetrator, will be wrong by a factor determined by how rare the wrongly ascribed DNA type is. So if the profile includes a type that is present in $1/10^{th}$ of the population the match probability will be wrong by a factor of 10. So a match probability of a million to one will become 100,000 to 1; a significant difference.

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This is not an argument for the abandonment of any or all DNA methods. It is a warning of the dangers of not understanding the potential for honest error and margins of error. These new techniques are undoubtedly of tremendous value as intelligence in criminal investigation. In cold cases the requirement for other corroborative evidence must reflect the increased uncertainty in the LCN results.

In terms of identifying an individual; the random match probability (RMP) method has been well documented, studied, and used worldwide. However, there remain unresolved issues in the treatment of mixtures and partial profiles that affect the reliability of the technique even to provide RMPs.

Reliability, here and in the response to other questions, is therefore a matter that can and should be measured. The degree of reliability required of either the technique to produce an accurate result, or the result to produce an accurate identification, are probably socio-legal decisions that can be informed, but not dictated by, science.

2. Sampling powers

a.

The use of DNA for 'intelligence' purposes cannot, at the moment, be sensibly separated from its use as evidence. In criminal investigations, it is frequently the case that there is little or no information available to assist the investigating officers. In such circumstances, it is reasonable that any small piece of information that could generate a reasoned investigative avenue should be used. The difficulty is that this inconclusive fragment is then used with others to generate an apparently compelling circumstantial case against an innocent person.

Until the evidential implications of data with a low probative value are explored and resolved, then there remains a great danger of wrong judicial decisions.

b.

This is a topic for police.

c.

It is not clear why samples, in contrast to profiles, need to be retained if the only data that the police require is the SGM+ profile.

There is no doubt that the retention of a whole population DNA database would reduce crime and improve detection rates. Similarly, however, if every person was required to wear an electronic tag and be subject to 24 hour CCTV observation, this would further reduce crime. The issue is again socio-legal and not scientific.

d.

See c.

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3. The management of the NDNAD

n/a

4. Ethical issues

n/a

5. The evidential value of bioinformation

a.

We have previously submitted, to the Committee on the Public Understanding of Science, a request for funding to prepare a video presentation of the concepts of DNA evidence and its interpretation to be available for all juries about to hear such evidence; this was not granted. It is this type of initiative that should provide agreed background information to all groups involved in the CJ system. The Forensic Institute provides free seminars for lawyers, but are aware that most other groups (including public bodies) routinely seek funding for even small education projects. Information should be available to jurors, and forensic science education included in legal and law enforcement training – especially CPD to maintain a contemporary knowledge of the processes and their capabilities.

b.

The probative value, and sufficiency, of DNA evidence is wholly dependent on the circumstances of the case. Given the argument presented above regarding the transfer and persistence of DNA it may seem clearly and completely unacceptable that DNA alone should be accepted as sufficient evidence for a conviction. However, the case is posited of DNA being found on several items, all associated in some way with a crime scene, but with no visible staining. Is this sufficient when compared to the same scene with only one item with DNA? What if the DNA is found in association with a semen stain?

The question, in its current form, is incapable of a categorical answer.