1

Current and future trends in forensic molecular biology

Simon J. Walsh

1.1 Introduction

Forensic science is part of a process beginning at a crime scene and concluding in a court room. This means that as one of the key forensic disciplines, the field of forensic molecular biology resides within the complex and adversarial context of the criminal justice system (CJS). The key areas of the CJS that are relevant to the use of forensic molecular biology are the domains of law enforcement and the justice system (Figure 1.1). Due to the intersection of these three domains, changes and developments in one can have a resultant impact on the other adjacent areas. Therefore, when considering the current and future trends in forensic molecular biology it is important to do so not only from the perspective of their effect within the forensic field itself, but also from the perspective of their interaction with neighbouring areas of the system. After all, it is in these neighbouring areas that forensic outcomes are eventually put to use.

Forensic molecular biology has developed rapidly into a comprehensive discipline in its own right and, perhaps more so than any scientific advance before it, has had a profound impact across the CJS. Within the forensic science discipline, as expected, development has been science and/or technology driven. It has followed a trend towards achieving greater sophistication, throughput and informativeness for the DNA-based outcomes of scientific analysis. Developments in forensic molecular biology that have influenced law enforcement could be thought of as operational developments as they predominantly apply to the manner or degree that forensic molecular biology is utilized. As such, they typically have both a technical and policy-oriented basis. Progress in forensic biology

Molecular Forensics. Edited by Ralph Rapley and David Whitehouse

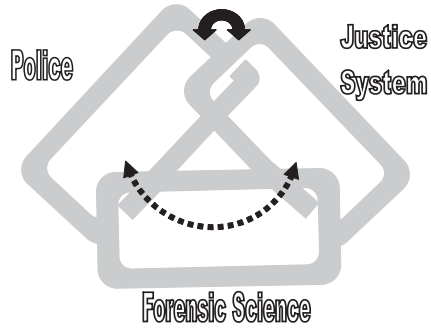

Figure 1.1 A simplified representation of the areas of the CJS that are relevant to forensic molecular biology. A large number of cases flow directly between the police and legal domains (solid arrow) whereas a reduced number of cases flow through the forensic domain (dashed arrow). Each of the three areas can be thought of as intersecting and, as such, each has the capacity to exercise some effect on the others

has also influenced the justice sector. This is characterized, for example, by the iterative response of both the legislature and the courts to changes in the volume and nature of forensic DNA tests. Throughout the history of the field there has also been associated debate and controversy accompanying these legal developments. This reflects the array of socio-legal and ethical issues associated with more widespread use of forensic molecular biology.

This chapter chiefly describes the process of development within the forensic molecular biology field. It also touches briefly on the way such developments intersect with the neighbouring fields of law enforcement and the justice system. By considering developmental trends in this way the overall impact of changes in forensic molecular biology can be appropriately placed in context, allowing reflection on their effect to date and foreshadowing their potential effect in the future.

1.2 Developments within the field of forensic molecular biology

From the time the field settled on a uniform technological platform (Gill, 2002), forensic molecular biologists have done a masterful job at extending the applicability of this testing regime as far as conceivably possible. The discriminating power of short tandem repeat (STR)-based tests has been increased by combining up to 16 (Collins *et al.*, 2000; Krenke *et al.*, 2002) STR loci into a single polymerase chain reaction (PCR; see Chapter 2). The sensitivity of the routine tests has also been driven downward so that successful analysis is now achieved from as little as 100 pg of starting template (Whitaker *et al.*, 2001).

Advancing the capabilities of the DNA methodology has also expanded the range of criminal cases and sample types able to be successfully analysed. For many years forensic molecular biology was limited to testing templates such as blood, semen, hair and saliva. However, the increased efficiency of the STR-based methods now means that DNA can be successfully analysed from discarded clothing or personal effects (Webb *et al*., 2001), skin cell debris from touched or handled surfaces (Van Oorschot and Jones, 1997; Wiegand and Kleiber, 1997; Zamir *et al*., 2000; Bright and Petricevic, 2004), dandruff (Lorente *et al*., 1998), drinking containers (Abaz *et al*., 2002), food (Sweet and Hildebrand, 1999) and fingernail clippings and scrapings (Harbison *et al*., 2003). Recent approaches such as reduced-amplicon STR analysis (Butler *et al*., 1998, 2003; Wiegand and Kleiber, 2001; Coble and Butler, 2005) and low copy number (LCN) profiling (Gill, 2001a; Whitaker *et al*., 2001) have enhanced reaction sensitivity even further and improved the ability to analyse the most troublesome and highly degraded samples.

Many of the routine techniques have been adapted onto automated platforms so as to facilitate high-throughput analysis and reduce the amount of sample handling (Gill, 2002; Varlaro and Duceman, 2002; Fregeau *et al*., 2003) (see Chapter 3). Computer-assisted data analysis has also further streamlined the analytical process and reduced some areas of subjectivity, such as mixture interpretation (Perlin and Szabady, 2001; Bill *et al*., 2005; Gill *et al*., 2005, 2006b) (see Chapter 11). The next generation of laboratory instrumentation includes micro-scale electrophoresis devices (Woolley *et al*., 1997; Mitnik *et al*., 2002) that not only promise rapid analysis times but also allow for the possibility of remote or portable laboratory platforms (Hopwood *et al*., 2006).

The observable trend in the development areas mentioned above is that they are all directed towards improving the ability to undertake routine DNA-based identity testing. Whilst this refinement of routine typing technologies is of vital importance, it has meant that for the most part the field has sought only one dimension of information from biological evidence samples. Through recent research into the physical and genetic properties of human DNA this is now changing, allowing the forensic field to diversify its capabilities and begin to address questions beyond the identification of source.

There are already several examples of forensic molecular biology applications that either apply different forms of typing technologies or address a different line of genetic inquiry via new polymorphisms or loci. One such area is non-autosomal DNA profiling, particularly the analysis of mitochondrial DNA (mtDNA) and Y chromosome markers (see Chapters 7, 8 and 9). Whilst mtDNA analysis has been widely used in human evolutionary biology for a number of years (Cann *et al*., 1987), its routine application to forensic work has been consistently evolving. In forensic science, mtDNA is most often analysed in circumstances where nuclear DNA fails to give a result, such as in the analysis of telogenic hairs (Wilson *et al*., 1995), nail material (Anderson *et al*., 1999) and bone (Bender *et al*., 2000; Edson *et al*., 2004) or when distant relatives

must be used as reference (Gill *et al*., 1994; Ivanov *et al*., 1996; Pfeiffer *et al*., 2003). Analysis typically involves direct sequencing of the hypervariable regions 1 and 2 (HV1 and HV2, respectively) (Tully *et al*., 2001) although SNP-based approaches offer the potential to complement or substitute the need for sequencing (Budowle *et al*., 2004; Coble *et al*., 2004; Quintans *et al*., 2004). Recent developmental progress in the forensic use of mtDNA has also been shaped by the context within which it has been required. In particular, the large-scale multi-national response to recent wars (Huffine *et al*., 2001; Andelinovic *et al*., 2005), refugee crises (Lorente *et al*., 2002) and mass fatalities (Roby, 2002; Vastag, 2002; Budjimila *et al*., 2003; Holland *et al*., 2003; Budowle *et al*., 2005) has seen a rapid evolution of these and other specialist identification sciences so as to respond to the unprecedented logistical and technical challenges presented by these circumstances.

The analysis of polymorphisms on the non-recombining portion of the human Y chromosome (NRY) (Jobling *et al*., 1997; Kayser *et al*., 1997) has also steadily developed into a valuable forensic technique (Gill *et al*., 2001; Gusmao and Carracedo, 2003; Gusmao *et al*., 2006). The male specificity of the Y chromosome makes it particularly suitable for the resolution of problematic situations such as complex mixtures. In a casework setting Y chromosome analysis is especially useful for typing mixed male–female stains that commonly occur as a result of sexual assaults (Dettlaff-Kakol and Pawlowski, 2002; Dziegelewski *et al*., 2002; Sibille *et al*., 2002). As with autosomal markers, microsatellites are favoured for forensic Y chromosome analysis and a number of suitable Y-STRs have been identified and validated for forensic use (Bosch *et al*., 2002; Butler *et al*., 2002; Redd *et al*., 2002; Hall and Ballantyne, 2003; Johnson *et al*., 2003; Hanson and Ballantyne, 2004; Schoske *et al*., 2004) and a selection of them included into commercially available multiplexes (Shewale *et al*., 2004; Krenke *et al*., 2005; Mulero *et al*., 2006).

Potentially the most valuable target markers for a diverse range of novel forensic molecular biology applications are single nucleotide polymorphisms (SNPs; see Chapter 6). These offer a range of forensic applications in traditional and novel areas and confer some particular advantages in comparison to STRs, including a low mutation rate (making SNPs highly suitable for kinship and/or pedigree analysis), amenability to high-throughput processing and automated data analysis, a shorter PCR amplicon size (assisting their ability to be multiplexed and making them good target loci for highly degraded samples), a vast abundance in the genome, and in some cases simplified interpretation (due to the absence of certain STR artifacts such as stutter). Single nucleotide polymorphisms are being investigated for use in forensics in both the identity testing and intelligence areas.

By virtue of the fact that there is greater allelic diversity at STR loci compared with SNPs, STRs have a profound advantage over SNPs in forensic identity testing. As a crude estimate, one would be required to type three to five SNP loci to discriminate between individuals at the same level as a single STR. This

means that to approach the degree of certainty of the current STR kits up to 50 SNP loci would be needed, which presents a formidable technical challenge. In addition, changing routine target loci is undesirable, due largely to the significant investment in databases that has already occurred. In combination, these reasons make a universal change of DNA typing platform unlikely (Gill, 2001b; Gill *et al*., 2004). Nonetheless, the recent development of more advanced SNP genotyping technologies, and the desirable properties of SNP loci, has seen a continued focus on developing highly informative SNP-based multiplexes for forensic identity testing (Inagaki *et al*., 2004; Dixon *et al*., 2006; Kidd *et al*., 2006; Sanchez *et al*., 2006).

Single nucleotide polymorphism markers in coding regions linked to physical or behavioural (personality-related) traits are also being researched for forensic purposes. This research aims to provide investigators with an inferred description of an offender, based on biological evidence recovered from a particular crime and subsequent DNA analysis. In one example researchers have described approaches for screening genetic mutations associated with the red-hair phenotype (Grimes *et al*., 2001; Branicki *et al*., 2006). A comprehensive candidate gene study for variable eye colour has also been conducted by an American company DNAPrint Genomics (Sarasota, FL, http://www.dnaprint.com) (Frudakis *et al*., 2003a). On the basis of this research (Sturm and Frudakis, 2004) DNAPrint Genomics have developed and validated RETINOME™, a high-throughput genetic test for predicting human iris colour from DNA. A blind validation test of RETINOME™ on 65 individuals of greater than 80% European ancestry revealed that the test was 97% accurate in its predictions.

Other SNP-based techniques potentially enable the inference of biogeographical ancestry from a DNA sample. As SNPs can be found in areas of the genome subject to evolutionary-selective pressures, such as coding and regulatory regions of DNA, they can exhibit far greater allele and genotype frequency differences between different populations than other forensic loci. In 2003, Frudakis *et al.* developed a classifier for the SNP-based inference of ancestry (Frudakis *et al*., 2003b). This research found that allele frequencies from 56 of the screened SNPs were notably different between groups of unrelated donors of Asian, African and European descent. Using this panel of 56 autosomal SNPs, Frudakis *et al.* report successful designation of the ancestral background of European, African and Asian donors with 99%, 98% and 100% accuracy, respectively. Applying a reduced panel of the 15 most informative SNPs the level of accuracy reduces to 98%, 91% and 97%, respectively (Frudakis *et al*., 2003b). This work represents the most significant step towards the development of a DNA-based test for the inference of ancestry in a forensic setting and has led to the generation of a commercially available tool known as DNA Witness™ (DNA-Print Genomics, Sarasota, FL).

A significant amount of research effort has also been invested in the study of non-autosomal SNPs. This approach is commonplace in human migration studies, with a large body of work examining SNP haplotype diversity on the

Y chromosome (Underhill *et al*., 2000, 2001; Jobling and Tyler-Smith, 2003) or mtDNA genome (Budowle *et al*., 2004; Jobling *et al*., 2004; Wilson and Allard, 2004). In the forensic context Y- or mtDNA-SNPs are also potential markers of biogeographical ancestry. They have often been preferred in this capacity as they can be locally customized and applied also to understand local population substructure, which in turn can support statistical interpretation models. Large-scale non-autosomal SNP multiplexes already exist (Sanchez *et al*., 2003; Brion *et al*., 2004, 2005; Coble *et al*., 2004; Quintans *et al*., 2004; Sanchez *et al*., 2005) and population data and supporting information are readily available (YCC, 2002).

Commensurate with the advances in the molecular tools available to forensic scientists, the interpretation of DNA evidence has also had to develop considerably over recent years. Early in the history of forensic molecular biology this was an area of heated dispute (Lander, 1989; Lewontin and Hartl, 1991) requiring concerted efforts to address concerns of the scientific and legal community (National Academy of Sciences, 1996). Now there is a far greater depth of understanding and an important sub-discipline of the field has developed (Robertson and Vignaux, 1995; Evett and Weir, 1998; Aitken and Taroni, 2004; Balding, 2005; Buckleton *et al*., 2005a). Nonetheless, each new molecular adaptation brings an associated requirement to reassess the weight or meaning of the outcomes statistically. Approaches are continually being refined to deal with routine complexities such as mixed profiles (Weir *et al*., 1997; Curran *et al*., 1999; Fukshansky and Bar, 2000; Bill *et al*., 2005; Wolf *et al*., 2005; Gill *et al*., 2006a), partial profiles (Buckleton and Triggs, 2006) and relatedness (Ayres, 2000; Buckleton and Triggs, 2005). In addition, novel theory has been needed to assess results obtained from LCN approaches (Gill *et al*., 2000), non-autosomal markers (Krawczak, 2001; Buckleton *et al*., 2005b; Fukshansky and Bar, 2005; Wolf *et al*., 2005), DNA database searches (Balding, 2002; Walsh and Buckleton, 2005), multi-trace cases (Aitken *et al*., 2003), mass disasters (Brenner and Weir, 2003; Brenner, 2006) and so on.

From this summary we can distil the following trends that appear set to characterize future years. The addition of more routine markers, and the wider use of known ones, appears likely to continue. Testing platforms will increase in their overall efficiency and move closer to the goal of rapid, portable micro-devices. Taking the DNA science out of the laboratory is a move that could bring considerable advantage to many investigations but is also one with associated challenges. Progress will continue towards answering more diverse questions than 'who is the source of this DNA sample?'. There is almost limitless potential as to where this approach may lead as we unravel the full potential of information accessible via genetic testing. Of course we must observe that with this increased capability comes an associated increase in complexity. Scientists have the potential to step beyond the routinely applied testing regimes, but to do so they must understand the strengths and weaknesses of new approaches and, importantly, be equipped to deal with associated complexities

such as the statistical assessment of outcomes. The forensic community must take ownership of this challenge and continue to ensure that proper validation, training and independent research occur. This will at times be awkward given the growing demands for all forms of DNA analysis and an increasingly commercialized operational environment. It will also be important to ensure appropriate management of expectations regarding emerging capabilities on the part of police, legal professionals and the general public.

1.3 Developments influencing law enforcement – operational impacts

The current environment where forensic molecular biology operates as a tool of the law enforcement community is starkly different to the mid-1980s, when its role in this context first began. This is unsurprising given the rapid evolution of the techniques, as described above. The most notable operational difference is the frequency of use of DNA evidence in criminal casework. Across the world the overall number of cases submitted annually for DNA analysis has increased by many fold. In the UK the average annual inclusion of crime samples onto the national DNA database (NDNAD™) increased from 14 644 for the period 1995–2000 to 59 323 for the period 2000–2005. In Canada, 7052 crime samples were added to the national DNA databank in 2005 compared with 816 in 2000. In NSW (the most populous State of Australia) the annual DNA case submissions have risen from 1107 in 1998 to 10 146 in 2005.

The major driver of this change in case volume has been the global implementation of forensic DNA databases. Forensic DNA databases have altered the landscape of the criminal justice system and irrevocably re-shaped the field of forensic science. Their growth has been rapid with millions of STR profiles now held from convicted offenders, suspects and unsolved crimes (Table 1.1). Links provided through DNA database searches have contributed valuable

Table 1.1 Size and effectiveness of major national DNA databases

	Database and date				
	UK Feb. 2006	Europe Dec. 2005	USA Apr. 2006	Canada May 2006	New Zealand Apr. 2005
Total profiles	3 693 494	987 671	3 275 710	123 603	63 678
Offender profiles	3 406 488	772 355	3 139 038	94 999	54 159
Crime scene profiles	287 006	215 316	136 672	28 604	9 419
Investigations aided	721 495	116 057	34 193	5 963	2 451

Source: Publicly available figures on the Internet.

intelligence to hundreds of thousands of police investigations. Often links are provided for crimes that are notoriously difficult to resolve, such as burglary and vehicle theft.

Along with the increase in case volume that has been catalysed in part by the introduction of DNA databases, there has also been an alteration to the types of crimes and evidence submitted for biological analysis (see Chapter 11). In the 1980s and 1990s DNA profiling was primarily applied to serious crimes. Nowadays, however, forensic molecular biology contributes to the investigation of a broader spectrum of crimes. Data from the NSW State Forensic DNA Laboratory over the period 1998–2005 show a clear pattern of decrease in the proportion of cases from serious crime categories and an increase in the proportion of cases submitted from volume crime categories (Figure 1.2). The change in the case submission profile, that is, the proportions of different case types submitted for analysis, occurred from 2001 forward. This was the beginning of DNA database operations.

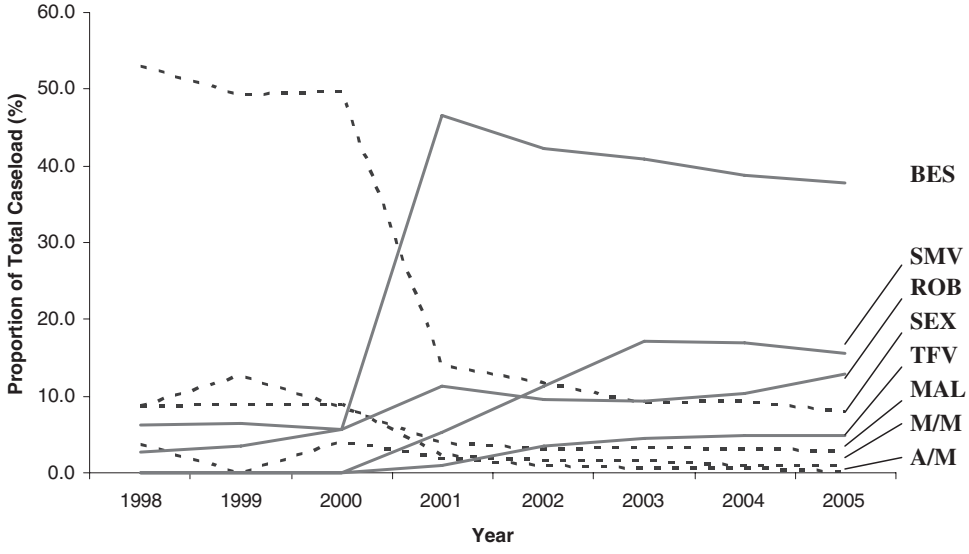

Figure 1.2 Changing case submission trends at a State Forensic DNA Laboratory in Australia. Case categories where there was a decrease in proportional submissions are represented by the dashed lines. The actual categories are Sexual Assault (SEX; 53.0% to 8.0%), Murder & Manslaughter (M/M; 8.7% to 1.0%), Malicious Wounding (MAL; 8.9% to 2.9%) and Attempt Murder (A/M; 3.6% to 0.3%). The case categories where there was an increase in proportional submissions are represented by the solid lines. These include Break, Enter and Steal (BES; 2.7% to 37.8%), Stolen Vehicle (SMV; 0.0% to 15.6%), Robbery (ROB; 6.3% to 12.8%) and Theft from Vehicle (TFV; 0.0% to 4.9%)

Table 1.2 Changing evidence types analysed by the NSW State Forensic DNA Laboratory between 2001 and 2005

	Proportion of total (%)				
Sample type	2001	2002	2003	2004	2005
Blood	44.7	49.1	38.4	33.8	26.5
Bone	0.0	0.1	0.2	0.1	0.1
Cigarette butt	4.5	8.0	10.9	8.4	9.1
Hair	10.0	3.1	2.2	2.0	1.3
Miscellaneous[a]	30.9	33.4	41.1	50.4	57.3
Semen	8.3	4.6	5.7	3.9	4.4
Fingernail scrapings	1.7	1.8	1.5	1.3	1.2

[a] Includes mostly trace DNA samples.

The changing nature of the case submission profile in forensic molecular biology laboratories has been accompanied by a changing evidence type away from traditional templates such as blood and semen to more discrete evidence types such as trace DNA and discarded items (including drinking containers and cigarette butts). This is again illustrated in data from the NSW State Forensic DNA Laboratory from between 2001 and 2005 (Table 1.2).

As well as having a profound effect on the number and types of cases submitted for DNA analysis, forensic DNA databases have also catalysed a re-think of the role that forensic evidence can play in the investigative process. Traditionally forensic DNA evidence has been thought of as information for the use of the court. This focus sees the scientist retrospectively attempting to obtain results for a given case to assist in the resolution of a single crime. The primary focus, therefore, is towards crime-solving rather than crime reduction or prevention. For some years now, policing strategy has evolved from a traditional focus on capturing or incarcerating offenders towards a more holistic understanding of crimes and criminals and a prevention-based approach to law enforcement. Forensic science has not contributed greatly to changes in policing and crime management strategies, although lately there has been a move to embrace scientific advances under the concept of intelligence-led policing (Smith, 1997; Thompson and Gunn, 1998; Gunn, 2003; Tilley, 2003). Forensic molecular biology clearly has a role to play in the generation of law enforcement intelligence products (Walsh *et al.*, 2002), particularly when one considers the potential of combining rapid, portable DNA typing with the use of DNA databases or phenotypic inferences about an offender. As such it has the potential to play a more proactive role in broader-scale crime investigation.

Achieving this requires shifting the philosophical mind-set of forensic practitioners, understanding where, when and how forensic science data can be useful in an intelligence context, and designing systems capable of relaying findings in 'real-time'. A number of approaches have begun to emerge that embrace this operational strategy. Some remain ill-informed and are based around centralized

database creation. Other more successful examples create meaningful forensic intelligence and combine it with investigative and crime analysis tools (Ribaux and Margot, 1999, 2003).

In summary there has been a trend towards greater use of DNA, across a more diverse range of cases and in a more intelligence-based context or framework. It is important to note, however, that these developments (and the DNA databases that have predominantly catalysed them) remain at a preliminary stage. Standards and approaches still vary enormously between jurisdictions and in future there may be continued moves towards greater harmonization. Undoubtedly there will be progress towards greater cross-jurisdictional exchange of DNA information, possibly facilitated at the level of organizations such as Interpol. Managing this era of wider national and international use of forensic DNA profile information will be challenging as, through these developments, the science we apply moves increasingly into the public and political realm.

1.4 Developments influencing the justice system – socio-legal impacts

Practical and philosophical aspects of the legal system have been impacted by developments in the field of forensic molecular biology. Practical issues emanate from the construction of laws that regulate the collection of DNA material from persons associated with the justice system, and the subsequent use of any DNA-related evidence in our courts. These are flanked by important philosophical considerations in areas such as social justice, ethics and privacy.

From the time of its first introduction the courts have had mixed experiences with the presentation of forensic DNA evidence. Scientists, lawyers, judges and jurors have battled to come to terms with this new forensic application of a complex scientific technique. Initially complicating matters further was the public fanfare that accompanied early DNA successes, creating an aura of scientific certainty around the technology. Whilst forensic molecular biology is a powerful means of identification, this sort of misrepresentation in the public arena can create unrealistic perceptions of its capability. At a relatively early stage, the admissibility of DNA evidence in criminal trials was successfully challenged in the United States (*People v Castro*, 1989, 545 NYS 2d 985) and elsewhere (*R v Tran*, 1990, 50 A Crim R 233; *R v Lucas*, 1992, 2 VR 109; *R v Pengelly*, 1992, 1 NZLR 545). Many of the issues upon which early challenges were mounted were the subject of conflict in the scientific community at the time (Lander, 1989; Chakraborty and Kidd, 1991; Lewontin and Hartl, 1991). The scrutiny of the legal system in these instances must be seen to have been strongly positive as it brought about further refinement and validation of the forensic DNA methodology and the implementation of structures to regulate quality assurance. In recent times challenges to DNA admissibility are rarely

successful, as, in general terms, the science has reached the important point of being accepted practice. This is not to say that legal scrutiny has abated entirely, rather, if anything, legal challenges have evolved in their complexity along with the evolution of the technology itself. Instead of focusing on general issues, it is now specialized components of the analytical or interpretative process that have become the subject of questioning.

Widening the use of forensic DNA evidence and implementing forensic DNA databases have required the formulation of specific statutes. The enactment of the DNA-based laws has generated considerable commentary in the legal literature regarding the process of enactment and the final constitution of the laws themselves. In most cases the legal discussion is critical, suggesting that the passage of legislation was hurried and justified under the populist appeal of 'law and order' politics. Others fear that compulsory acquisition of genetic material by the state represents an encroachment into previously sacred territory of criminal law and a diminution of basic rights such as the right to silence and the right against self-incrimination. Many commentators express concern over the mass storage of human genetic information and the associated potential risk of future misuse.

Overall, the practical developments at the intersection of forensic molecular biology and the legal system have progressed from general issues (such as whether DNA testing has a place in the CJS at all) to specific refinements (such as how DNA evidence was obtained and tested). Again it is important to note that this period of interplay between the science of DNA testing and the regulation of legal sector is a relatively recent phenomenon and is bound to evolve considerably, even in the short term. The balance that is sought relates to attempting to achieve maximal effectiveness from the use of DNA, whilst minimizing the incursion into a person's basic civil and legal rights. In different cases, different countries and at different times striking this balance can be influenced by external pressures. Recently, for example, heightened anxiety around terrorism has seen governments override individual rights in favor of more expansive investigative powers. The use of forensic molecular biology is linked to many of these broad socio-legal issues.

1.5 Summary

The field of forensic molecular biology has entered a period of development where more genetically diverse applications are emerging and are able to be delivered by a more responsive and technically advanced platform. There is also an emphasis for forensic DNA outcomes to be delivered as intelligence products as well as evidence for the court. This allows it to take on a more purposeful role in the investigative phase of the process alongside other items of forensic or non-forensic intelligence. Understandably, these enhancements in capability are continuing to drive a great demand to access and utilize this technology. So

far this demand has, in many cases, outstripped the ability of forensic laboratories to cope, and case backlogs are commonplace in many jurisdictions.

These trends signal the beginning of an exciting era for forensic molecular biology. As forensic professionals, however, we must remember that adding these dimensions to our capability also adds to our overall onus of responsibility. Such changes require a continual broadening of our outlook and expertise. Also, due to the emotional and social stakes that exist in the criminal justice system, many developments in our field are somewhat double-edged: able to be viewed either positively as strengthening our ability to fight against crime or terrorism or negatively as examples of an increasing loss of civil liberties and greater surveillance by the state on her citizens. Whilst forensic scientists remain impartial players in this environment, it is important that we do not extricate ourselves from this debate that essentially defines how and to what end our scientific endeavour is applied. Of paramount importance is that, across all techniques within our field, we continue to ensure the quality of our scientific outcomes. By doing this our work will remain an objective and reliable component of the criminal justice system.

1.6 References

Abaz, J., Walsh, S.J., Curran, J.M., Moss, D.S., Cullen, J.R., Bright, J., Crowe, G.A., Cockerton, S.L. and Power, T.E.B. (2002) Comparison of variables affecting the recovery of DNA from common drinking containers. *Forensic Sci. Int.* **126**: 233–240.

Aitken, C.G.G. and Taroni, F. (2004) *Statistics and the Evaluation of Evidence for Forensic Scientists* (2nd edn), John Wiley & Sons, Chichester.

Aitken, C.G.G., Taroni, F. and Garbolino, P. (2003) A graphical model for the evaluation of cross-transfer evidence in DNA profiles. *Theor. Pop. Biol.* **63**: 179–190.

Andelinovic, S., Sutlovic, D., Erceg Ivkosic, I., Skaro, V., Ivkosic, A., Paic, F., Rezic, B., Definis-Gojanovic, M. and Primorac, D. (2005) Twelve-year experience in identification of skeletal remains from mass graves. *Croat. Med. J.* **46**: 530–539.

Anderson, T.D., Ross, J.P., Roby, R.K., Lee, D.A. and Holland, M.M. (1999) A validation study for the extraction and analysis of DNA from human nail material and its application to forensic casework. *J. Forensic Sci.* **44**: 1053–1056.

Ayres, K.L. (2000) Relatedness testing in subdivided populations. *Forensic Sci. Int.* **114**: 107–115.

Balding, D.J. (2002) The DNA database search controversy. *Biometrics* **58**: 241–244.

Balding, D.J. (2005) *Weight-of-Evidence for Forensic DNA Profiles*, John Wiley & Sons, Hoboken, New Jersey.

Bender, K., Schneider, P.M. and Rittner, C. (2000) Application of mtDNA sequence analysis in forensic casework for the identification of human remains. *Forensic Sci. Int.* **113**: 103–107.

Bill, M., Gill, P., Curran, J.M., Clayton, T., Pinchin, R., Healy, M. and Buckleton, J.S. (2005) PENDULUM – a guideline-based approach to the interpretation of STR mixtures. *Forensic Sci. Int.* **148**: 181–189.

Bosch, E., Lee, A.C., Calafell, F., Arroyo, E., Henneman, P., de Knijff, P. and Jobling, M.A. (2002) High resolution Y chromsome typing: 19 STRs amplified in three multiplex reactions. *Forensic Sci. Int.* **125**: 42–51.

Branicki, W., Kupiec, T., Wolanska-Nowak, P. and Brudnik, U. (2006) Determination of forensically relevant SNPs in the MC1R gene. *Int. Congr. Ser.* **1288**: 816–818.

Brenner, C.H. (2006) Some mathematical problems in the DNA identification of victims in the 2004 tsunami and similar mass fatalities. *Forensic Sci. Int.* **157**: 172–180.

Brenner, C.H. and Weir, B.S. (2003) Issues and strategies in the DNA identification of World Trade Center victims. *Theor. Pop. Biol.* **63**: 173–178.

Bright, J.A. and Petricevic, S.F. (2004) Recovery of trace DNA and its application to DNA profiling of shoe insoles. *Forensic Sci. Int.* **145**: 7–12.

Brion, M., Sanchez, J.J., Balogh, K., Thacker, C., Blanco-Verea, A., Borsting, C., Stradmann-Bellinghausen, B., Bogus, M., Syndercombe-Court, D., Schneider, P.M., Carracedo, A. and Morling, N. (2005) Introduction of an single nucleodite polymorphism-based 'Major Y-chromosome haplogroup typing kit' suitable for predicting the geographical origin of male lineages. *Electrophoresis* **26**: 4411–4420.

Brion, M., Sobrino, B., Blanco-Verea, A., Lareu, M.V. and Carracedo, A. (2004) Hierachical analysis of 30 Y-chromosome SNPs in European populations. *Int. J. Legal Med.* **119**: 10–15.

Buckleton, J.S. and Triggs, C.M. (2005) Relatedness and DNA: are we taking it seriously enough? *Forensic Sci. Int.* **152**: 115–119.

Buckleton, J.S. and Triggs, C.M. (2006) Is the 2p rule always conservative? *Forensic Sci. Int.* **159**: 206–209.

Buckleton, J.S., Triggs, C.M. and Walsh, S.J. (2005a) *Forensic DNA Evidence Interpretation*, CRC Press, Boca Raton, FL.

Buckleton, J.S., Walsh, S.J. and Harbison, S.A. (2005b) Nonautosomal forensic markers. In: *Forensic DNA Evidence Interpretation* (J.S. Buckleton, C.M. Triggs and S.J. Walsh, eds), CRC Press, Boca Raton, FL, pp. 299–339.

Budjimila, Z.M., Prinz, M.K., Zelson-Mundorff, A., Wiersema, J., Bartelink, E., MacKinnon, G., Nazzaruolo, B.L., Estacio, S.M., Hennessey, M.J. and Shaler, R.C. (2003) World Trade Center human identification project: experiences with individual body identification cases. *Croat. Med. J.* **44**: 259–263.

Budowle, B., Bieber, F.R. and Eisenberg, A.J. (2005) Forensic aspects of mass disasters: strategic considerations for DNA-based human identification. *Legal Med.* **7**: 230–245.

Budowle, B., Planz, J.V., Campbell, R.S. and Eisenberg, A.J. (2004) Single nucleotide polymorphisms and microarray technology in forensic genetics – development and application to mitochondrial DNA. *Forensic Sci. Rev.* **16**: 21–36.

Butler, J.M., Li, J., Shaler, T.A., Monforte, J.A. and Becker, C.H. (1998) Reliable genotyping of short tandem repeat loci without an alleleic ladder using time-of-flight mass spectrometry. *Int. J. Legal Med.* **112**: 45–49.

Butler, J.M., Schoske, R., Vallone, P.M., Kline, M.C., Redd, A.J. and Hammer, M.F. (2002) A novel multiplex for simultaneous amplification of 20 Y chromosome STR markers. *Forensic Sci. Int.* **129**: 10–24.

Butler, J.M., Shen, Y. and McCord, B.R. (2003) The development of reduced size STR amplicons as tools for analysis of degraded DNA. *J. Forensic Sci.* **48**: 1054–1064.

Cann, R.L., Stoneking, M. and Wilson, A.C. (1987) Mitochondrial DNA and human evolution. *Nature* **325**: 31–36.

Chakraborty, R. and Kidd, K.K. (1991) The utility of DNA typing in forensic work. *Science* **254**: 1735–1744.

Coble, M.D. and Butler, J.M. (2005) Characterization of new miniSTR loci to aid analysis of degraded DNA. *J. Forensic Sci.* **50**: 43–53.

Coble, M.D., Just, R.S., O'Callaghan, J.E., Letmanyi, I.H., Peterson, C.T., Irwin, J.A. and Parsons, T.J. (2004) Single nucleotide polymorphisms over the entire mtDNA genome that increase the power of forensic testing in Caucasians. *Int. J. Legal Med.* **118**: 137–146.

Collins, P., Roby, R.K., Lori, H., Leibelt, C., Shadravan, F., Bozzini, M.L. and Reeder, D. (2000) Validation of the AmpFlSTR Identifiler PCR amplification kit. In *Proceedings of 11th International Symposium on Human Identification*, Billoxi, Missouri, September 2000. Available at http://www.promega.com/geneticidproc/ussymp11proc/content/collins.pdf

Curran, J.M., Triggs, C.M., Buckleton, J.S. and Weir, B.S. (1999) Interpreting DNA mixtures in structured populations. *J. Forensic Sci.* **44**: 987–995.

Dettlaff-Kakol, A. and Pawlowski, R. (2002) The first Polish DNA 'manhumnt' – an application of Y-chromosome STR's. *Int. J. Legal Med.* **116**: 289–291.

Dixon, L.A., Koumi, P. and Gill, P. (2006) Development of an autosomal SNP multiplex containing 20 SNP loci plus amelogenin. *Int. Congr. Ser.* **1288**: 31–33.

Dziegelewski, M., Simich, J.P. and Rittenhouse-Olsen, K. (2002) Use of a Y chromosome probe as an aid in the forensic proof of sexual assault. *J. Forensic Sci.* **47**: 601–604.

Edson, S.M., Ross, J.P., Coble, M.D., Parsons, T.J. and Barritt, S.M. (2004) Naming the dead – confronting the realities of rapid identification of degraded skeletal remains. *Forensic Sci. Rev.* **16**: 63–90.

Evett, I.W. and Weir, B.S. (1998) *Interpreting DNA Evidence*, Sinauer Associates, Sunderland, MA.

Fregeau, C.J., Leclair, B., Bowen, K., Porelle, F. and Fourney, R.M. (2003) The National DNA Data Bank of Canada – a laboratory bench retrospective on the first year of operation. *Int. Congr. Ser.* **1239**: 621–625.

Frudakis, T., Thomas, M., Gaskin, Z., Venkateswarlu, K., Chandra, K., Ginjupalli, S., Gunturi, S., Natrajan, S., Ponnuswamy, V. and Ponnuswamy, K. (2003a) Sequences associated with human iris pigmentation. *Genetics* **165**: 2071–2083.

Frudakis, T., Venkateswarlu, K., Thomas, M.J., Gaskin, Z., Ginjupalli, S., Gunturi, S., Ponnuswamy, V., Natarajan, S. and Nachimuthu, P.K. (2003b) A classifier for the SNP-based inference of ancestry. *J. Forensic Sci.* **48**: 771–782.

Fukshansky, N. and Bar, W. (2000) Biostatisitcs for mixed stains: the case of tested relatives of a non-tested suspect. *Int. J. Legal Med.* **114**: 78–82.

Fukshansky, N. and Bar, W. (2005) DNA mixtures: biostatistics for mixed stains with haplotypic genetic markers. *Int. J. Legal Med.* **119**: 285–290.

Gill, P. (2001a) Application of low copy number DNA profiling. *Croat. Med. J.* **42**: 229–232.

Gill, P. (2001b) An assessment of the utility of single nucleotide polymorphisms (SNPs) for forensic purposes. *Int. J. Legal Med.* **114**: 204–210.

Gill, P. (2002) Role of short tandem repeat DNA in forensic casework in the UK – past, present and future perspectives. *BioTechniques* **32**: 366–385.

Gill, P., Brenner, C., Brinkmann, B., Budowle, B., Carracedo, A., Jobling, M.A., de Knijff, P., Kayser, M., Krawczak, M., Mayr, W.R., Morling, N., Olaisen, B.,

Pascali, V., Prinz, M., Roewer, L., Schneider, P.M., Sajantila, A. and Tyler-Smith, C. (2001) DNA Commission of the International Society of Forensic Genetics: recommendations on forensic analysis using Y-chromosome STRs. *Forensic Sci. Int.* **124**: 5–10.

Gill, P., Brenner, C.H., Buckleton, J.S., Carracedo, A., Krawczak, M., Mayr, W.R., Morling, N., Prinz, M., Schneider, P.M. and Weir, B.S. (2006a) DNA Commission of the International Society of Forensic Genetics: Recommendations on the interpretation of mixtures. *Forensic Sci. Int.* **160**: 90–101.

Gill, P., Curran, J.M. and Elliot, K. (2005) A graphical simulation model of the entire DNA process associated with the analysis of short tandem repeat loci. *Nucleic Acids Res.* **33**: 632–643.

Gill, P., Ivanov, P.L., Kimpton, C., Piercy, R., Benson, N., Tully, G., Evett, I.W., Hagelberg, E. and Sullivan, K. (1994) Identification of the remains of the Romanov family by DNA analysis. *Nature Genet.* **6**: 130–135.

Gill, P., Kirkham, A. and Curran, J.M. (2006b) *LoComatioN*: A software tool for the analysis of low copy number profiles. *Forensic Sci. Int.* [Epub ahead of print] doi: 10.1016/j.forsciint.2006.04.016.

Gill, P., Werrett, D.J., Budowle, B. and Guerrieri, R.A. (2004) An assessment of whether SNPs will replace STRs in national DNA databases – Joint considerations of the DNA working group of the European Network of Forensic Science Institutes (ENFSI) and the Scientific Working Group on DNA Analysis Methods (SWGDAM). *Sci. Justice* **44**: 51–53.

Gill, P., Whitaker, J.P., Flaxman, C., Brown, N. and Buckleton, J.S. (2000) An investigation of the rigor of interpretation rules for STR's derived from less than 100 pg of DNA. *Forensic Sci. Int.* **112**: 17–40.

Grimes, E.A., Noakes, P.J., Dixon, L. and Urquhart, A. (2001) Sequence polymorphism in the human melanocortin 1 receptor gene as an indicator of the red hair phenotype. *Forensic Sci. Int.* **122**: 124–129.

Gunn, B. (2003) An intelligence-led approach to policing in England and Wales and the impact of developments in forensic science. *Aust. J. Forensic Sci.* **35**: 149–160.

Gusmao, L., Butler, J.M., Carracedo, A., Gill, P., Kayser, M., Mayr, W.R., Morling, N., Prinz, M., Roewer, L., Tyler-Smith, C. and Schneider, P.M. (2006) DNA Commission of the International Society of Forensic Genetics (ISFG): An update of the recommendations on the use of Y-STRs in forensic analysis. *Forensic Sci. Int.* **157**: 187–197.

Gusmao, L. and Carracedo, A. (2003) Y chromosome-specific STRs. *Profiles DNA* **5**: 3–6.

Hall, A. and Ballantyne, J. (2003) The development of an 18-locus Y-STR system for forensic casework. *Anal. Bioanal. Chem.* **376**: 1234–1246.

Hanson, E.K. and Ballantyne, J. (2004) A highly discriminating 21 locus 'megaplex' system designed to augment the minimal haplotype loci for forensic casework. *J. Forensic Sci.* **49**: 40–51.

Harbison, S.A., Petricevic, S.F. and Vintiner, S.K. (2003) The persistence of DNA under fingernails following submersion in water. *Int. Congr. Ser.* **1239**: 809–813.

Holland, M.M., Cave, C.A., Holland, C.A. and Bille, T.W. (2003) Development of a quality, high throughput DNA analysis procedure for skeletal samples to assist with the identification of victims from the world trade center attacks. *Croat. Med. J.* **44**: 264–272.

Hopwood, A., Fox, R., Round, C., Tsang, C., Watson, S., Rowlands, E., Titmus, A., Lee-Edghill, J., Cursiter, L., Proudlock, J., McTernan, C., Grigg, K., Thornton, L. and Kimpton, C. (2006) Forensic response vehicle: Rapid analysis of evidence at the crime scene. *Int. Congr. Ser.* **1288**: 639–641.

Huffine, E., Crews, J., Kennedy, B., Bomberger, K. and Zinbo, A. (2001) Mass identification of persons missing from the break-up of the former Yugoslavia: structure, function, and role of International Commission on Missing Persons. *Croat. Med. J.* **42**: 271–275.

Inagaki, S., Yamamoto, Y., Doi, Y., Takata, T., Ishikawa, T., Imabayashi, K., Yoshitome, K., Miyaishi, S. and Ishizu, H. (2004) A new 39-plex analysis method for SNPs including 15 blood group loci. *Forensic Sci. Int.* **144**: 45–57.

Ivanov, P.L., Wadhams, M.J., Roby, R.K., Holland, M.M., Weedn, V.W. and Parsons, T.J. (1996) Mitochondrial DNA sequence heteroplasmy in the Grand Duke of Russia Georgij Romanov establishes the authenticity of the remains of Tsar Nicholas II. *Nature Genet.* **12**: 417–420.

Jobling, M.A., Hurles, M.E. and Tyler-Smith, C. (2004) *Human Evolutionary Genetics*, Garland Science, New York.

Jobling, M.A., Pandya, A. and Tyler-Smith, C. (1997) The Y chromosome in forensic analysis and paternity testing. *Int. J. Legal Med.* **110**: 118–124.

Jobling, M.A. and Tyler-Smith, C. (2003) The human Y chromosome: an evolutionary marker comes of age. *Nature Rev. Genet.* **4**: 598–612.

Johnson, C.L., Warren, J.H., Giles, R.C. and Staub, R.W. (2003) Validation and uses of a Y-chromosome STR 10-plex for forensic and paternity laboratories. *J. Forensic Sci.* **48**: 1260–1268.

Kayser, M., Caglia, A., Corach, D., Fretwell, N., Gehrig, C., Graziosi, G., Heidorn, F., Herrmann, S., Herzog, B., Hidding, M., Honda, K., Jobling, M.A., Krawczak, M., Leim, K., Meuser, S., Meyer, E., Oesterreich, W., Pandya, A., Parson, W., Penacino, G., Perez-Lezaun, A., Piccinini, A., Prinz, M., Schmitt, C., Schneider, P.M., Szibor, R., Teifel-Greding, J., Weichhold, G., de Knijff, P. and Roewer, L. (1997) Evaluation of Y-chromosomal STRs: a multicenter study. *Int. J. Legal Med.* **110**: 125–133.

Kidd, K.K., Pakstis, A.J., Speed, W.C., Grigorenko, E.L., Kajuna, S.L.B., Karoma, N.J., Kungulilo, S., Kim, J.-J., Lu, R.-B., Odunsi, A., Okonofua, F., Parnas, J., Schulz, L.O., Zhukova, O.V. and Kidd, J.R. (2006) Developing a SNP panel for forensic identification of individuals. *Forensic Sci. Int.* [Epub ahead of print] doi: 10.1016/j.forscient.2006.04.016.

Krawczak, M. (2001) Forensic evaluation of Y-STR haplotype matches: a comment. *Forensic Sci. Int.* **118**: 114–115.

Krenke, B., Tereba, A., Anderson, S.J., Buel, E., Culhane, S., Finis, C.J., Tomsey, C.S., Zachetti, J.M., Masibay, A., Rabbach, D.R., Amiott, E.A. and Sprecher, C.J. (2002) Validation of a 16-locus fluorescent multiplex system. *J. Forensic Sci.* **47**: 773–785.

Krenke, B.E., Viculis, L., Richard, M.L., Prinz, M., Milne, S.C., Ladd, C., Gross, A.M., Gornall, T., Frappier, J.R., Eisenberg, A.J., Barna, C., Aranda, X.G., Adamowicz, M.S. and Budowle, B. (2005) Validation of male-specific, 12-locus fluorescent short tandem repeat (STR) multiplex. *Forensic Sci. Int.* **151**: 111–124.

Lander, E.S. (1989) DNA fingerprinting on trial. *Nature* **339**: 501.

Lewontin, R.C. and Hartl, D.L. (1991) Population genetics in forensic DNA typing. *Science* **254**: 1745–1750.

Lorente, J.A., Entrala, C., Alvarez, J.C., Lorente, M., Arce, B., Heinrich, B., Carrasco, F., Budowle, B. and Villanueva, E. (2002) Social benefits on non-criminal genetic databases: missing persons and human remains identification. *Int. J. Legal Med.* **116**: 187–190.

Lorente, M., Entrala, C., Lorente, J., Alvarez, J.C., Villanueva, E. and Budowle, B. (1998) Dandruff as a potential source of DNA in forensic casework. *J. Forensic Sci.* **43**: 648–656.

Mitnik, L., Carey, L., Burger, R., Desmarais, S., Koutny, L., Wernet, O., Matsudaira, P. and Ehrlich, D. (2002) High-speed analysis of multiplexed short tandem repeats with and electrophoretic microdevice. *Electrophoresis* **23**: 719–726.

Mulero, J.J., Chang, C.W., Calandro, L.M., Green, R.L., Li, Y., Johnson, C.L. and Hennessy, L.K. (2006) Development and validation of the AmpFlSTR Yfiler PCR amplification kit: a male specific, single amplification 17 Y-STR multiplex system. *J. Forensic Sci.* **51**: 64–75.

National Academy of Sciences (1996) *National Research Council Report: The Evaluation of Forensic DNA Evidence*, United States National Academy of Sciences, Washington, DC.

Perlin, M.W. and Szabady, B. (2001) Linear mixture analysis: a mathematical approach to resolving mixed DNA samples. *J. Forensic Sci.* **46**: 1372–1378.

Pfeiffer, H., Benthaus, S., Rolf, B. and Brinkmann, B. (2003) The Kaiser's tooth. *Int. J. Legal Med.* **117**: 118–120.

Quintans, B., Alvarez-Iglesias, V., Salas, A., Phillips, C., Lareu, M.V. and Carracedo, A. (2004) Typing of mitochondrial DNA coding region SNPs of forensic and anthropological interest using SNaPshot minisequencing. *Forensic Sci. Int.* **140**: 251–257.

Redd, A.J., Agellon, A.B., Kearney, V.A., Contreras, V.A., Karafet, T., Park, H., de Knijff, P., Butler, J.M. and Hammer, M.F. (2002) Forensic value of 14 novel STRs on the human Y chromosome. *Forensic Sci. Int.* **130**: 97–111.

Ribaux, O. and Margot, P. (1999) Inference structures for crime analysis and intelligence: the example of burglary using forensic science data. *Forensic Sci. Int.* **100**: 193–210.

Ribaux, O. and Margot, P. (2003) Case based reasoning in criminal intelligence using forensic case data. *Sci. Justice* **43**: 135–143.

Robertson, B. and Vignaux, G.A. (1995) *Interpreting Evidence: Evaluating Forensic Science in the Courtroom*, John Wiley & Sons, Chichester.

Roby, R.K. (2002) Automation for forensic mitochondrial DNA analysis. In *Proceedings of 5th Annual DNA Forensics Conference*, Washington, DC.

Sanchez, J.J., Borsting, C., Hallenberg, C., Buchard, A., Hernandez, A. and Morling, N. (2003) Multiplex PCR and minisequencing of SNPs – a model with 35 Y chromosome SNPs. *Forensic Sci. Int.* **137**: 74–84.

Sanchez, J.J., Borsting, C. and Morling, N. (2005) Typing of Y chromosome SNPs with multiplex PCR methods. *Methods Mol. Biol.* **297**: 209–228.

Sanchez, J.J., Phillips, C., Borsting, C., Balogh, K., Bogus, M., Fondevila, M., Harrison, C.D., Musgrave-Brown, E., Salas, A., Syndercombe-Court, D., Schneider, P.M., Carracedo, A. and Morling, N. (2006) A multiplex assay with 52 single nucleotide polymorphisms for human identification. *Electrophoresis* **27**: 1713–1724.

Schoske, R., Vallone, P.M., Kline, M.C., Redman, J.W. and Butler, J.M. (2004) High-throughput Y-STR typing of U.S. populations with 27 regions of the Y chromosome using two multiplex PCR assays. *Forensic Sci. Int.* **139**: 107–121.

Shewale, J.G., Nasir, H., Schneida, E., Gross, A.M., Budowle, B. and Sinha, S.K. (2004) Y-chromosome STR system, Y-PLEX™ 12, for forensic casework: development and validation. *J. Forensic Sci.* **49**: 1278–1290.

Sibille, I., Duverneuil, C., Lorin de la Grandmaison, G., Guerrouache, K., Teisiere, F., Durigon, M. and de Mazancourt, P. (2002) Y-STR DNA amplification as biological evidence in sexually assaulted female victims with no cytological detection of spermatozoa. *Forensic Sci. Int.* **125**: 212–216.

Smith, A. (1997) *Intelligence Led Policing; International Perspectives on Policing in the 21st Century*, International Association of Law Enforcement Intelligence Analysts, Lawrenceville, CA.

Sturm, R. and Frudakis, T. (2004) Eye colour: portals into pigmentation genes and ancestry. *Trends Genet.* **20**: 327–332.

Sweet, D. and Hildebrand, D. (1999) Saliva from cheese bite yields DNA profile of a burglar: a case report. *Int. J. Legal Med.* **112**: 201–203.

Thompson, J. and Gunn, B. (1998) Tomorrow's world. *Policing Today* **4**: 12–13.

Tilley, N. (2003) *Problem-Oriented Policing, Intelligence-Led Policing and the National Intelligence Model*, Report of the Jill Dando Institute of Crime Science, Crime Science: Short Report Series, University College London, UK.

Tully, G., Bär, W., Brinkmann, B., Carracedo, A., Gill, P., Morling, N., Parson, W. and Schneider, P.M. (2001) Considerations of the European DNA Profiling (EDNAP) group on the working practices, nomenclature and interpretation of mitochondrial DNA profiles. *Forensic Sci. Int.* **124**: 83–91.

Underhill, P.A., Passarino, G., Lin, A.A., Shen, P., Mirazon Lahr, M., Foley, R.A., Oefner, P.J. and Cavalli-Sforza, L.L. (2001) The phylogeography of Y chromosome binary haplotypes and the origins of modern human populations. *Ann. Hum. Genet.* **65**: 43–62.

Underhill, P.A., Shen, P., Lin, A.A., Jin, L., Passarino, G., Yang, W.-H., Kauffman, E., Bonne-Tamir, B., Bertranpetit, J., Francalacci, P., Ibrahim, M., Jenkins, T., Kidd, J.R., Medhi, S.Q., Seielstad, M.T., Wells, R.S., Piazza, A., Feldman, M.W., Cavalli-Sforza, L.L. and Oefner, P.J. (2000) Y chromosome sequence variation and the history of human populations. *Nature Genet.* **26**: 358–361.

Van Oorschot, R.A. and Jones, M. (1997) DNA fingerprints from fingerprints. *Nature* **387**: 767.

Varlaro, J. and Duceman, B. (2002) Dealing with increasing casework demands for DNA analysis. *Profiles DNA* **5**: 3–6.

Vastag, B. (2002) Out of tragedy, identification innovation. *J. Am. Med. Assoc.* **288**: 1221–1223.

Walsh, S.J. and Buckleton, J.S. (2005) DNA intelligence databases. In: *Forensic DNA Evidence Interpretation*, (J.S. Buckleton, C.M. Triggs, and S.J. Walsh, eds). CRC Press, Boca Raton, FL, pp. 439–469.

Walsh, S.J., Moss, D.S., Kleim, C. and Vintiner, G.M. (2002) The collation of forensic DNA case data into a multi-dimensional intelligence database. *Sci. Justice* **42**: 205–214.

Webb, L.G., Egan, S.E. and Turbett, G.R. (2001) Recovery of DNA for forensic analysis from lip cosmetics. *J. Forensic Sci.* **46**: 1474–1479.

Weir, B.S., Triggs, C.M., Starling, L., Stowell, L.I., Walsh, K.A.J. and Buckleton, J.S. (1997) Interpreting DNA mixtures. *J. Forensic Sci.* **42**: 213–222.

Whitaker, J.P., Cotton, E.A. and Gill, P. (2001) A comparison of the characteristics of profiles produced with the AMPFlSTR®SGM Plus™ multiplex system for both standard and low copy number (LCN) STR DNA analysis. *Forensic Sci. Int.* **123**: 215–223.

Wiegand, P. and Kleiber, M. (1997) DNA typing of epithelial cells after strangulation. *Int. J. Legal Med.* **110**: 181–183.

Wiegand, P. and Kleiber, M. (2001) Less is more – length reduction of STR amplicons using redesigned primers. *Int. J. Legal Med.* **114**: 285–287.

Wilson, M.R. and Allard, M.W. (2004) Phylogentics and mitochondrial DNA. *Forensic Sci. Rev.* **16**: 37–62.

Wilson, M.R., Polanskey, D., Butler, J.M., DiZinno, J.A., Replogle, J. and Budowle, B. (1995) Extraction, PCR amplification and sequencing of mitochondrial DNA from human hair shafts. *BioTechniques* **18**: 662–669.

Wolf, A., Caliebe, A., Junge, O. and Krawczak, M. (2005) Forensic interpretation of Y-chromosomal DNA mixtures. *Forensic Sci. Int.* **152**: 209–213.

Woolley, A.T., Sensabaugh, G.F. and Mathies, R.A. (1997) High-speed DNA genotyping using microfabricated capillary array electrophoresis chips. *Anal. Chem.* **69**: 2181–2186.

YCC. (2002) A nomenclature system for the tree of human Y chromosomal binary haplogroups. *Genome Res.* **12**: 339–348.

Zamir, A., Springer, E. and Glattstein, B. (2000) Fingerprints and DNA: STR typing of DNA extracted from adhesive tape after processing for fingerprints. *J. Forensic Sci.* **45**: 687–688.