

1 Introduction to forensic genetics

The development and application of genetics has revolutionized forensic science. In 1984, the analysis of polymorphic regions of DNA produced what was termed ‘a DNA fingerprint’ [1]. The following year, at the request of the United Kingdom Home Office, DNA profiling was successfully applied to casework when it was used to resolve an immigration dispute [2]. In 1986, DNA evidence was used for the first time in a criminal case involving the murder of two young women in Leicestershire, UK: DNA analysis exonerated one individual who had confessed to one of the murders, and following a mass screen of approximately 5000 individuals, identified Colin Pitchfork as the murderer. He was convicted in January 1988 [3].¹

Following on from early success in both civil and criminal cases, the use of genetics was rapidly adopted by the forensic community and now plays an important role worldwide in both the investigation of crime and in relationship testing. The scope and scale of DNA analysis in forensic science is set to continue expanding for the foreseeable future.

Forensic genetics

The work of the forensic geneticist will vary widely depending on the laboratory and country that they work in, and can involve the analysis of material recovered from a scene of crime, kinship testing and the identification of human remains. In some cases, it can even be used for the analysis of DNA from plants [6–18]; animals [19–36] including insects [37–60]; and microorganisms [61–67]. The focus of this book is the analysis of biological material that is recovered from the scene of crime – this is central to the work of most forensic laboratories. Kinship testing will be dealt with separately in Chapter 11 and a brief introduction is given to the testing of non-human material in Chapter 14.

Forensic laboratories receive material that has been recovered from scenes of crime, and reference samples from both suspects and victims. The role of forensic genetics within the investigative process is to compare samples recovered from crime

¹ Note: The first convictions in criminal cases came in 1987, when DNA evidence played an important role in the conviction of two rapists: Robert Melias in the UK and Tommy Lee Andrews in the USA [4, 5].

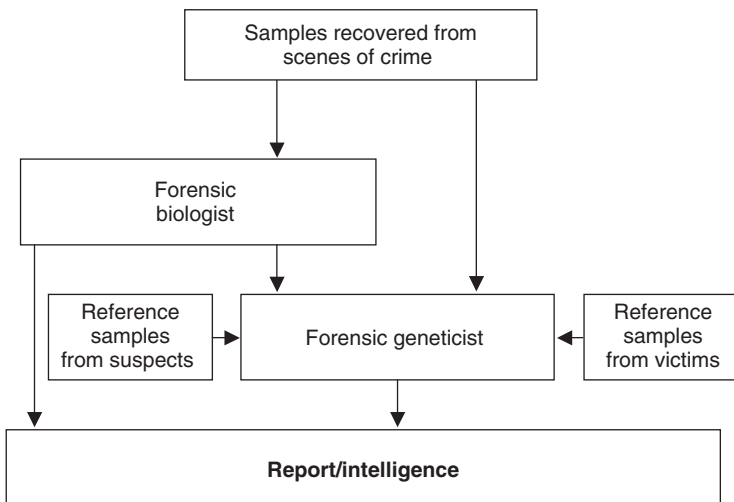


Figure 1.1 The role of the forensic geneticist is to assess whether samples recovered from a crime scene match to a suspect. Reference samples are provided from suspects and also victims of crime

scenes with suspects and possibly victims, resulting in a report that can be presented in court or intelligence that may inform an investigation (Figure 1.1).

Several stages are involved in the analysis of genetic evidence (Figure 1.2) and each of these is covered in detail in the following chapters. In some organizations one person will be responsible for collecting the evidence, the biological and genetic analysis of samples and ultimately presenting the results to a court of law. However, the trend in many larger organizations is for individuals to be responsible for only a very specific task within the process, such as the extraction of DNA from the evidential material or the analysis and interpretation of DNA profiles that have been generated by other scientists, or just reporting the findings.

A brief history of forensic genetics

In 1900 Karl Landsteiner described the ABO blood grouping system and observed that individuals could be placed into different groups based on their blood type. This was the first step in the development of forensic haemogenetics. Following on from this, numerous blood group markers and soluble blood serum protein markers were characterized and could be analysed in combination to produce highly discriminatory profiles. The serological techniques were a powerful tool but were limited in many forensic cases by the amount of biological material that was required to provide highly discriminating results. Proteins are also prone to degradation on exposure to the environment.

In the 1960s and 1970s, developments in molecular biology, including restriction enzymes, Sanger sequencing [68] and Southern blotting [69], enabled scientists to examine DNA sequences. By 1978, DNA polymorphisms could be detected using

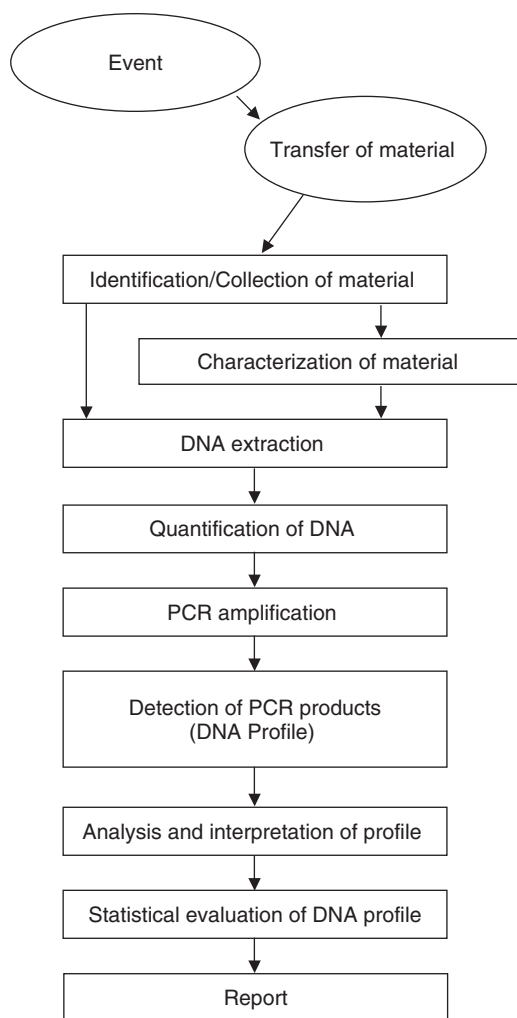


Figure 1.2 Processes involved in generating a DNA profile following a crime. Some types of material, in particular blood and semen, are often characterized before DNA is extracted, allowing the DNA evidence to be linked to a cell type and possible transfer mechanism

Southern blotting [70] and in 1980 the analysis of the first highly polymorphic locus was reported, where the polymorphism was caused by differences in the lengths of the alleles [71].

It was not until September 1984 that Alec Jeffreys realized the potential forensic application of the minisatellite loci [1, 72, 73]. The technique developed by Jeffreys entailed extracting DNA and cutting it with a restriction enzyme before carrying out agarose gel electrophoresis, Southern blotting and probe hybridization to detect the polymorphic loci. The end result was a series of black bands on X-ray film, which was called a DNA fingerprint (Figure 1.3).

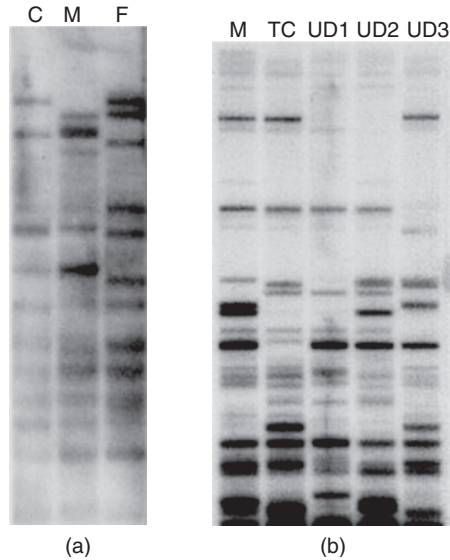


Figure 1.3 (a) The first ever DNA fingerprint, produced in Alec Jeffreys' laboratory on the 10th September 1984. It shows the banding pattern from a mother, child, and father: the bands in the child's profile can be attributed to either the mother or the father. (b) Profiles from a mother, a tested child (TC) (Immigration Officials in the UK did not believe that the boy was the biological son of the mother) and three of the mother's undisputed children (UD 1-3): the results demonstrated that the tested child was indeed the biological son of the woman and was therefore allowed to stay in the UK [2]. (Images provided by Sir Prof Alec Jeffreys, Department of Genetics, University of Leicester, UK)

With the first DNA fingerprints the multi-locus probes (MLPs) detected several minisatellite loci simultaneously, leading to the multiple band patterns. While the multi-banded fingerprints were highly informative they were difficult to interpret. New probes were designed that were specific to one locus (single locus probes, SLPs) and therefore produced only one or two bands for each individual [74] (Figure 1.4).

Minisatellite analysis was a powerful tool but suffered from several limitations: a relatively large amount of DNA was required; it would not work with degraded DNA; comparison between laboratories was difficult; and the analysis was time consuming. Even so, the use of minisatellite analysis, using SLPs, was common for several years [75] until it was replaced by polymerase chain reaction (PCR)-based systems.

A critical development in the history of forensic genetics came with the advent of a process that can amplify specific regions of DNA – the PCR (see Chapter 5). The PCR process was conceptualized in 1983 by Kary Mullis, a chemist working for the Cetus Corporation in the USA [76]. The development of PCR has had a profound effect on all aspects of molecular biology including forensic genetics, and in recognition of the significance of the development of the technique Kary Mullis was awarded the Nobel Prize for Chemistry in 1993.

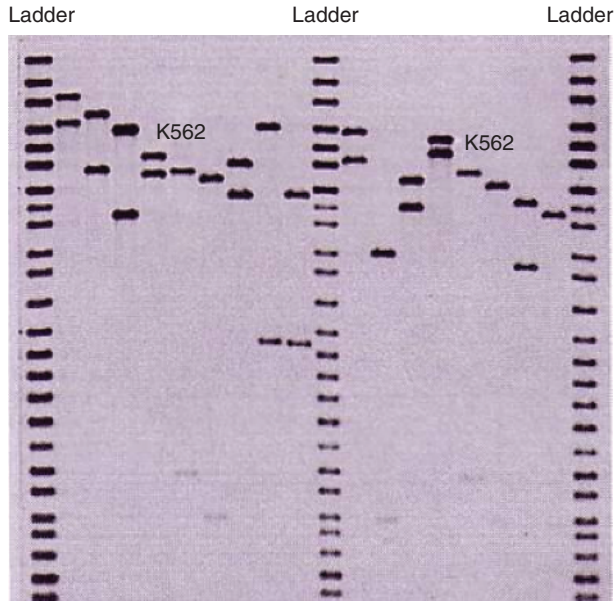


Figure 1.4 Minisatellite analysis using a single locus probe: ladders were run alongside the tested samples that allowed the size of the DNA fragments to be estimated. A control sample labelled K562 was analysed along with the tested samples

The PCR increases the sensitivity of DNA analysis to the point where DNA profiles can be generated from just a few cells, reduces the time required to produce a profile, can be used with degraded DNA and allows just about any polymorphism in the genome to be analysed.

The first application of PCR in a forensic case involved the analysis of single nucleotide polymorphisms in the human leukocyte antigen (HLA)-DQ α locus (part of the major histocompatibility complex (MHC)) [77] (see Chapter 12). This was soon followed by the analysis of short tandem repeats (STRs), which are currently the most commonly used genetic markers in forensic science (see Chapters 6–8). The rapid development of technology for analysing DNA includes advances in DNA extraction and quantification methodology, the development of commercial PCR-based typing kits and equipment for detecting DNA polymorphisms.

In addition to technical advances, another important part of the development of DNA profiling that has had an impact on the whole field of forensic science is quality assurance. The admissibility of DNA evidence was seriously challenged in the USA in 1989 – *People v. Castro* [78]; this and subsequent cases in many countries have resulted in increased levels of standardization and quality assurance in forensic genetics and other areas of forensic science. As a result, the accreditation of both laboratories and individuals is an increasingly important issue in forensic science. The combination of technical advances, high levels of standardization and quality

assurance have led to forensic DNA analysis being recognized as a robust and reliable forensic tool.

References

1. Jeffreys, A.J., Wilson, V. and Thein, S.L. (1985) Individual-specific fingerprints of human DNA. *Nature*, **316**, 76–79.
2. Jeffreys, A.J., Brookfield, J.F.Y. and Semenov, R. (1985) Positive identification of an immigration test-case using human DNA fingerprints. *Nature*, **317**, 818–819.
3. Seton, C. (1988) Life for Sex Killer who Sent Decoy to Take Genetic Test. *The Times* (London).
4. McCarthy, M. (1987) Rapist in Genetic Fingerprint Case Jailed for 8 Years. *The Times* (London).
5. Andrews, T.L. (1987) State v. Andrews. 9th Cir. Ct, Orange Co., Fla, Div 15.
6. Kress, W.J., Wurdack, K.J., Zimmer, E.A., Weigt, L.A. and Janzen, D.H. (2005) Use of DNA barcodes to identify flowering plants. *Proceedings of the National Academy of Sciences of the United States of America*, **102**, 8369–8374.
7. Linacre, A. and Thorpe, J. (1998) Detection and identification of cannabis by DNA. *Forensic Science International*, **91**, 71–76.
8. Bless, C., Palmeter, H. and Wallace, M.M. (2006) Identification of *Acer rubrum* using amplified fragment length polymorphism. *Journal of Forensic Sciences*, **51**, 31–38.
9. Cowan, R.S., Chase, M.W., Kress, W.J. and Savolainen, V. (2006) 300,000 species to identify: problems, progress, and prospects in DNA barcoding of land plants. *Taxon*, **55**, 611–616.
10. Craft, K.J., Owens, J.D. and Ashley, M.V. (2007) Application of plant DNA markers in forensic botany: genetic comparison of *Quercus* evidence leaves to crime scene trees using microsatellites. *Forensic Science International*, **165**, 64–70.
11. Datwyler, S.L. and Weiblen, G.D. (2006) Genetic variation in hemp and marijuana (*Cannabis sativa* L.) according to amplified fragment length polymorphisms. *Journal of Forensic Sciences*, **51**, 371–375.
12. Ferri, G., Alu, M., Corradini, B. and Beduschi, G. (2009) Forensic botany: species identification of botanical trace evidence using a multigene barcoding approach. *International Journal of Legal Medicine*, **123**, 395–401.
13. Finkeldey, R., Leinemann, L. and Gailing, O. (2010) Molecular genetic tools to infer the origin of forest plants and wood. *Applied Microbiology and Biotechnology*, **85**, 1251–1258.
14. Howard, C., Gilmore, S., Robertson, J. and Peakall, R. (2008) Developmental validation of a *Cannabis sativa* STIR multiplex system for forensic analysis. *Journal of Forensic Sciences*, **53**, 1061–1067.
15. Howard, C., Gilmore, S., Robertson, J. and Peakall, R. (2009) A *Cannabis sativa* STR genotype database for Australian seizures: forensic applications and limitations. *Journal of Forensic Sciences*, **54**, 556–563.
16. Kojima, M., Seki, H., Yoshida, S. and Muranaka, T. (2006) DNA polymorphisms in the tetrahydrocannabinolic acid (THCA) synthase gene in “drug-type” and “fiber-type” *Cannabis sativa* L. *Forensic Science International*, **159**, 132–140.
17. Kress, W.J., Erickson, D.L., Jones, F.A., Swenson, N.G., Perez, R., Sanjurjo, O. *et al.* (2009) Plant DNA barcodes and a community phylogeny of a tropical forest dynamics plot in Panama. *Proceedings of the National Academy of Sciences of the United States of America*, **106**, 18621–18626.
18. Tsai, L.C., Yu, Y.C., Hsieh, H.M., Wang, J.C., Linacre, A. and Lee, J.C.I. (2006) Species identification using sequences of the trnL intron and the trnL-trnF IGS of chloroplast genome among popular plants in Taiwan. *Forensic Science International*, **164**, 193–200.
19. Hebert, P.D.N., Ratnasingham, S., deWaard, J.R. (2003) Barcoding animal life: cytochrome c oxidase subunit 1 divergences among closely related species. *Proceedings of the Royal Society of London Series B: Biological Sciences*, **270**, S96–S99.

20. Parson, W., Pegoraro, K., Niederstatter, H., Foger, M. and Steinlechner, M. (2000) Species identification by means of the cytochrome b gene. *International Journal of Legal Medicine*, **114**, 23–28.
21. Eichmann, C. and Parson, W. (2007) Molecular characterization of the canine mitochondrial DNA control region for forensic applications. *International Journal of Legal Medicine*, **121**, 411–416.
22. Fernandes, C.A., Ginja, C., Pereira, I., Tenreiro, R., Bruford, M.W. and Santos-Reis, M. (2008) Species-specific mitochondrial DNA markers for identification of non-invasive samples from sympatric carnivores in the Iberian Peninsula. *Conservation Genetics*, **9**, 681–690.
23. Halverson, J.L. and Basten, C. (2005) Forensic DNA identification of animal-derived trace evidence: tools for linking victims and suspects. *Croatian Medical Journal*, **46**, 598–605.
24. Hellmann, A.P., Rohleder, U., Eichmann, C., Pfeiffer, I., Parson, W. and Schleenbecker, U. (2006) A proposal for standardization in forensic canine DNA typing: allele nomenclature of six canine-specific STR loci. *Journal of Forensic Sciences*, **51**, 274–281.
25. Hsieh, H.M., Huang, L.H., Tsaim L.C., Liu, C.L., Kuo, Y.C., Hsiao, C.T. *et al.* (2006) Species identification of *Kachuga tecta* using the cytochrome b gene. *Journal of Forensic Sciences*, **51**, 52–56.
26. Imaizumi, K., Akutsu, T., Miyasaka, S. and Yoshino, M. (2007) Development of species identification tests targeting the 16S ribosomal RNA coding region in mitochondrial DNA. *International Journal of Legal Medicine*, **121**, 184–191.
27. Lee, J.C.I., Tsai, L.C., Yang, C.Y., Liu, C.L., Huang, L.H., Linacre, A. *et al.* (2006) DNA profiling of shahtoosh. *Electrophoresis*, **27**, 3359–3362.
28. Magnussen, J.E., Pkitch, E.K., Clarke, S.C., Nicholson, C., Hoelzel, A.R., Shivji, M.S. (2007) Genetic tracking of basking shark products in international trade. *Animal Conservation*, **10**, 199–207.
29. Meganathan, P.R., Dubey, B., Haque, I. (2009) Molecular identification of crocodile species using novel primers for forensic analysis. *Conservation Genetics*, **10**, 767–770.
30. Melton, T. and Holland, C. (2007) Routine forensic use of the mitochondrial 12S ribosomal RNA gene for species identification. *Journal of Forensic Sciences*, **52**, 1305–1307.
31. Menotti-Raymond, M.A., Dubey, B. and Haque, I. (2005) An STIR forensic typing system for genetic individualization of domestic cat (*Felis catus*) samples. *Journal of Forensic Sciences*, **50**, 1061–1070.
32. Nakaki, S., Hino, D., Miyoshi, M., Nakayama, H., Moriyoshi, H., Morikawa, T. *et al.* (2007) Study of animal species (human, dog and cat) identification using a multiplex single-base primer extension reaction in the cytochrome b gene. *Forensic Science International*, **173**, 97–102.
33. van Asch, B., Alves, C., Gusmao, L., Pereira, V., Pereira, F. and Amorim, A. (2009) A new autosomal STR nineplex for canine identification and parentage testing. *Electrophoresis*, **30**, 417–423.
34. van Asch, B., Pinheiro, R., Pereira, R., Alves, C., Pereira, V., Pereira, F. *et al.* (2010) A framework for the development of STR genotyping in domestic animal species: Characterization and population study of 12 canine X-chromosome loci. *Electrophoresis*, **31**, 303–308.
35. Wan, Q.H. and Fang, S.G. (2003) Application of species-specific polymerase chain reaction in the forensic identification of tiger species. *Forensic Science International*, **131**, 75–78.
36. Webb, K.M. and Allard, M.W. (2009) Mitochondrial genome DNA analysis of the domestic dog: identifying informative SNPs outside of the control region. *Journal of Forensic Sciences*, **54**, 275–288.
37. Mazzanti, M., Alessandrini, F., Tagliabracci, A., Wells, J.D. and Campobasso, C.P. (2010) DNA degradation and genetic analysis of empty puparia: genetic identification limits in forensic entomology. *Forensic Science International*, **195**, 99–102.
38. Chen, W.Y., Hung, T.H. and Shiao, S.F. (2004) Molecular identification of forensically important blow fly species (Diptera: Calliphoridae) in Taiwan. *Journal of Medical Entomology*, **41**, 47–57.
39. Desmyter, S. and Gosselin, M. (2009) COI sequence variability between Chrysomyinae of forensic interest. *Forensic Science International-Genetics*, **3**, 89–95.

40. DiZinno, J.A., Lord, W.D., Collins-Morton, M.B., Wilson, M.R. and Goff, M.L. (2002) Mitochondrial DNA sequencing of beetle larvae (Nitidulidae: Omosita) recovered from human bone. *Journal of Forensic Sciences*, **47**, 1337–1339.
41. Draber-Monko, A., Malewski, T., Pomorski, J., Los, M. and Slipinski, P. (2009) On the morphology and mitochondrial DNA barcoding of the flesh fly sarcophaga (*Liopygia*) *argyrostoma* (Robineau-Desvoidy, 1830) (Diptera: Sarcophagidae) – an important species in forensic entomology. *Annales Zoologici*, **59**, 465–493.
42. Garipey, T.D., Kuhlmann, U., Gillott, C. and Erlandson, M. (2007) Parasitoids, predators and PCR: the use of diagnostic molecular markers in biological control of Arthropods. *Journal of Applied Entomology*, **131**, 225–240.
43. Harvey, M.L., Dadour, I.R. and Gaudieri, S. (2003) Mitochondrial DNA cytochrome oxidase I gene: potential for distinction between immature stages of some forensically important fly species (Diptera) in western Australia. *Forensic Science International*, **131**, 134–139.
44. Harvey, M.L., Gaudieri, S., Villet, M.H. and Dadour, I.R. (2008) A global study of forensically significant calliphorids: implications for identification. *Forensic Science International*, **177**, 66–76.
45. Harvey, M.L., Mansell, M.W., Villet, M.H. and Dadour, I.R. (2003) Molecular identification of some forensically important blowflies of southern Africa and Australia. *Medical and Veterinary Entomology*, **17**, 363–369.
46. Malgorn, Y. and Coquoz, R. (1999) DNA typing for identification of some species of Calliphoridae – an interest in forensic entomology. *Forensic Science International*, **102**, 111–119.
47. Nelson, L.A., Wallman, J.F. and Downton, M. (2007) Using COI barcodes to identify forensically and medically important blowflies. *Medical and Veterinary Entomology*, **21**, 44–52.
48. Nelson, L.A., Wallman, J.F. and Downton, M. (2008) Identification of forensically important *Chrysomya* (Diptera: Calliphoridae) species using the second ribosomal internal transcribed spacer (ITS2). *Forensic Science International*, **177**, 238–247.
49. Park, S.H., Zhang, Y., Piao, H., Yu, D.H., Jeong, H.J. and Yoo, G.Y. (2009) Use of Cytochrome c Oxidase Subunit I (COI) nucleotide sequences for identification of the Korean *Luciliinae* fly species (Diptera: Calliphoridae) in forensic investigations. *Journal of Korean Medical Science*, **24**, 1058–1063.
50. Park, S.H., Zhang, Y., Piao, H., Yu, D.H., Jeong, H.J., Yoo, G.Y. *et al.* (2009) Sequences of the Cytochrome C Oxidase Subunit I (COI) gene are suitable for species identification of Korean *Calliphorinae* flies of forensic importance (Diptera: Calliphoridae). *Journal of Forensic Sciences*, **54**, 1131–1134.
51. Reibe, S., Schmitz, J. and Madea, B. (2009) Molecular identification of forensically important blowfly species (Diptera: Calliphoridae) from Germany. *Parasitology Research*, **106**, 257–261.
52. Rodrigues, R.A., de Azeredo-Espin, A.M.L. and Torres, T.T. (2009) Microsatellite markers for population genetic studies of the blowfly *Chrysomya putoria* (Diptera: Calliphoridae). *Memorias Do Instituto Oswaldo Cruz*, **104**, 1047–1050.
53. Schroeder, H., Klotzbach, H., Elias, S., Augustin, C. and Pueschel, K. (2003) Use of PCR-RFLP for differentiation of calliphorid larvae (Diptera, Calliphoridae) on human corpses. *Forensic Science International*, **132**, 76–81.
54. Thyssen, P.J., Lessinger, A.C., Azeredo-Espin, A.M.L. and Linhares, A.X. (2005) The value of PCR-RFLP molecular markers for the differentiation of immature stages of two necrophagous flies (Diptera: Calliphoridae) of potential forensic importance. *Neotropical Entomology*, **34**, 777–783.
55. Wallman, J.F. and Adams, M. (2001) The forensic application of allozyme electrophoresis to the identification of blowfly larvae (Diptera: Calliphoridae) in southern Australia. *Journal of Forensic Sciences*, **46**, 681–684.
56. Wallman, J.F. and Donnellan, S.C. (2001) The utility of mitochondrial DNA sequences for the identification of forensically important blowflies (Diptera: Calliphoridae) in southeastern Australia. *Forensic Science International*, **120**, 60–67.

57. Wells, J.D., Pape, T. and Sperling, F.A.H. (2001) DNA-based identification and molecular systematics of forensically important sarcophagidae (diptera). *Journal of Forensic Sciences*, **46**, 1098–1102.
58. Wells, J.D. and Sperling, F.A.H. (2001) DNA-based identification of forensically important Chrysomyinae (Diptera: Calliphoridae). *Forensic Science International*, **120**, 110–115.
59. Wells, J.D. and Stevens, J.R. (2008) Application of DNA-based methods in forensic entomology. *Annual Review of Entomology*, **53**, 103–120.
60. Zehner, R., Amendt, J., Schutt, S., Sauer, J., Krettek, R. and Povolny, D. (2004) Genetic identification of forensically important flesh flies (Diptera: Sarcophagidae). *International Journal of Legal Medicine*, **118**, 245–247.
61. Hoffmaster, A.R., Fitzgerald, C.C., Ribot, E., Mayer, L.W. and Popovic, T. (2002) Molecular subtyping of Bacillus anthracis and the 2001 bioterrorism-associated anthrax outbreak, United States. *Emerging Infectious Diseases*, **8**, 1111–1116.
62. Bhattacharjee, Y. and Enserink, M. (2008) Anthrax investigation – FBI discusses microbial forensics – but key questions remain unanswered. *Science*, **321**, 1026–1027.
63. Budowle, B., Schutzer, S.E., Einseln, A., Kelley, L.C., Walsh, A.C., Smith, J.A.L., et al. (2003) Building microbial forensics as a response to bioterrorism. *Science*, **301**, 1852–1853.
64. Cummings, C.A. and Relman, D.A. (2002) Genomics and microbiology – microbial forensics – “Cross-examining pathogens”. *Science*, **296**, 1976–1979.
65. Enserink, M. (2008) Anthrax investigation – full-genome sequencing paved the way from spores to a suspect. *Science*, **321**, 898–899.
66. Keim, P., Pearson, T. and Okinaka, R. (2008) Microbial forensics: DNA fingerprinting of Bacillus anthracis (Anthrax). *Analytical Chemistry*, **80**, 4791–4799.
67. Pattnaik, P. and Jana, A.M. (2005) Microbial forensics: applications in bioterrorism. *Environmental Forensics*, **6**, 197–204.
68. Sanger, F., Nicklen, S. and Coulson, A.R. (1977) DNA sequencing with chain-terminating inhibitors. *Proceedings of the National Academy of Sciences of the United States of America*, **74**, 5463–5467.
69. Southern, E.M. (1975) Detection of specific sequences among DNA fragments separated by gel electrophoresis. *Journal of Molecular Biology*, **98**, 503–517.
70. Kan, Y.W. and Dozy, A.M. (1978) Polymorphism of DNA sequence adjacent to human B-globin structural gene: relationship to sickle mutation. *Proceedings of the National Academy of Science of the United States of America*, **75**, 5631–5635.
71. Wyman, A.R. and White, R. (1980) A highly polymorphic locus in human DNA. *Proceedings of the National Academy of Science of the United States of America*, **77**, 6754–6758.
72. Jeffreys, A.J. and Wilson, V. (1985) Hypervariable regions in human DNA. *Genetical Research*, **45**, 213–213.
73. Gill, P., Jeffreys, A.J. and Werrett, D.J. (1985) Forensic application of DNA ‘fingerprints’. *Nature*, **318**, 577–579.
74. Wong, Z., Wilson, V., Patel, I., Povey, S., Jeffreys, A.J. (1987) Characterization of a panel of highly variable minisatellites cloned from human DNA. *Annals of Human Genetics*, **51**, 269–288.
75. Hallenberg, C. and Morling, N. (2002) A report of the 2000 and 2001 paternity testing workshops of the English speaking working group of the international society for forensic genetics. *Forensic Science International*, **129**, 43–50.
76. Saiki, R.K., Scharf, S., Faloona, F., Mullis, K.B., Horn, G.T., Erlich, H.A. et al. (1985) Enzymatic amplification of beta-globin genomic sequences and restriction site analysis for diagnosis of sickle-cell anemia. *Science*, **230**, 1350–1354.
77. Stoneking, M., Hedgecock, D., Higuchi, R.G., Vigilant, L. and Erlich, H.A. (1991) Population variation of human mtDNA control region sequences detected by enzymatic amplification and sequence-specific oligonucleotide probes. *American Journal of Human Genetics*, **48**, 370–382.
78. Patton, S.M. (1990) DNA fingerprinting: the Castro case. *Harvard Journal of Law and Technology*, **3**, 223–240.

