An Introduction to Forensic Genetics (2nd Edition) is written by William Goodwin, Adrian Linacre and Sibte Hadi and is published by Wiley-Blackwell. Two of the authors are from a UK university, and the other author is from an Australian university. An Introduction to Forensic Genetics (2nd Edition) is aimed at readers who are undergraduate students studying courses or modules in Forensic Genetics. This book mainly describes the underlying principles and applications of genetics in forensic use, the application of DNA technologies and its use in the legal system.

The introductory chapter is a relatively small chapter which introduces the history of forensic genetics, including; the ABO blood grouping system (Landsteiner, 1900), the use of restriction enzymes, Sanger sequencing (Sanger, 1977), Southern Blotting (Southern, 1975, Kan, 1978) and the first DNA finger print produced (Jefferys, 1985a), giving as an example, a criminal case in 1986, when DNA evidence was used to identify a murderer for the first time (Jefferys, 1985b).

The second chapter provides a basic understanding of DNA and chromosomal structure, essential knowledge such as short tandem repeats (STRs) (Watson, 1953) and single nucleotide polymorphisms (SNPs), in order to make sense of the later chapters.

From the third chapter onwards, the chapters are organised in a step-by-step sequence, from biological evidence collection and confirmation of specimen with mRNA analysis (Alvarez, 2004, Juusloa, 2005, 2007, Setzer, 2008, Juusloa, 2003), to presenting the evidence in court (Cook, 1998, Evett, 2000). In addition, the remaining chapters described the operation and legislation of data bases (INTERPOL, 2008), parentage testing (Szibor, 2003, Hatsch, 2007), the use of mitochondria DNA (mtDNA) (Giles, 1980) and DNA typing of non-human materials (Hsieh, 2001, Irwin, 1991) (e.g for crimes which involve animals and plants, either as victims or as a part of the evidence).
To analyse DNA for forensic use is not easy and it requires time and skill. In essence, the biological materials are either visible or invisible to the naked eye when reagents can be used to locate the samples for collection (Grodsky, 1951). The samples need to be stored in certain conditions. Cell lysis and protein denaturing (Walsh, 1991) allow the DNA to be separated and replicated. Incidental samples are difficult to avoid, but the PCR laboratory operates a workflow system (Goodwin, 2011) which prevents the samples being contaminated by post-PCR samples. A suitable amount of samples are required, and any incidental or contaminated DNA will be detected and influence the findings. Decomposing material can cause DNA slippage (Schlotterer and Tautz, 1992, Hauge and Litt, 1993) and can be benefited by using mtDNA profiling due to the high copy number (Melton, 2005, Melton and Nelson, 2001, Szibor, 2006). Sometimes the sample collected could contain cells from the victim as well as the suspect (e.g. in a sexual assault case), Y STR analysis (Prinz, 1997) is useful for identifying the samples and it is a valuable tool.

The language used in this book is straightforward and easy to understand. Although two of the authors are from a British University and the publisher is in the UK, the language used in this book is American English. The book provides a list of abbreviations, as well as the words in full appeared in text for their first use. The photos and figures in this book are illustrated in colour, and are therefore clear. The book provides a list of references at the end of each chapter, further reading and world-wide web resources at the end of some chapters. This book is a good resource for students who need an introduction to forensic genetics. Should any more in depth information is required; it can be found via the references. However, basic knowledge in sciences is somehow essential in order to have good grasp of the information in this book.

References


