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BOOK REVIEW

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Review of: *An Introduction to Forensic Genetics, 2nd edn.*

REFERENCE: Goodwin W, Linacre A, Hadi S. An introduction to forensic genetics, 2nd edn. West Sussex, UK: Wiley-Blackwell, 2011, 191 pp.

The authors of this text, William Goodwin, Adrian Linacre, and Sibte Hadi, each have extensive experience as forensic science educators as well as knowledge and expertise in the research and practice of forensic DNA analysis. This experience is apparent in their careful, straightforward descriptions of complex subjects. While the very basic level of this text may prevent it from being widely adopted in more advanced or scientifically rigorous courses, the Preface indicates the target audience for this text as "undergraduate students studying courses or modules in Forensic Genetics." The introduction of the field of forensic science as a stand-alone scientific discipline, and the recent associated advances in foundational forensic research, has led to an explosion in the number of university-related courses and curricula. This growth has fueled a need for textbooks of this nature. This text seeks to provide undergraduate students with a basic overview of the process of forensic DNA profiling. After a brief introduction, the book takes the reader sequentially through the steps of traditional short tandem repeat (STR) typing for human identification. The authors also offer very rudimentary reviews of several specialized applications, including databasing, kinship testing, single nucleotide polymorphisms (SNPs), lineage markers, and non-human typing.

The introductory material includes three chapters, which briefly introduces the reader to the field and its history, reviews the key elements of DNA structure and function, and outlines the basics of collection and characterization of biological evidence material. Chapter 1 orients the reader to the application of DNA testing of crime scene material and touches briefly on historical methods (VNTR testing by RFLP, PM-DQα by reverse dot blot testing). Likewise, the illustrated review of DNA structure and genetic diversity provided in Chapter 2 is sufficient to prepare the reader for the remainder of the text. Chapter 3 provides a brief overview of the most common sources of biological evidence material, as well as an overview of traditional chemical and microscopic tests for presumptive and confirmatory biological fluid testing. However, this discussion is limited to testing for blood, saliva, and semen, and focuses only on traditional procedures (Kastle–Meyer, crystal tests, acid phosphatase testing, sperm microscopic staining, and immunochromatographic methods). Traditional methods for species identification testing are not covered in this chapter, and the species-specific nature of the monoclonal antibodies used in some of the referenced tests is not mentioned. The authors review the importance of epithelial cells as potential sources of evidence; however, they may underestimate the sensitivity of modern testing methods when stating "In most cases the number of cells is very low and the success rate of DNA profiling is limited" (p. 29).

The primary focus of the midsection of this text is to step the reader through the technical steps of the analytical processes used in DNA profiling. Chapter 4 reviews several chemistries for purification and quantification of DNA, including Chelex®, silica-based column methods (Qiagen, Valencia, CA), traditional organic extraction (phenol–chloroform), and FTA® paper (Whatman Inc., Clifton, NJ). For quantification, both historical methods (agarose gel visualization, UV- and fluorescence-spectrophotometry, Quantiblot®; Applied Biosystems, Foster City, CA) and currently utilized methods (TaqMan® based real-time PCR; Applied Biosystems) are discussed. More recently developed techniques such as magnetic-bead extractions and Plexor chemistries for qPCR are not mentioned. Chapter 5 includes an excellent review of PCR components, the amplification process, and contamination prevention (including laboratory design) which may serve as a useful review even for seasoned professionals or advanced students. Chapters 6 through 9 focus exclusively on the major aspects of STR testing, including structure of STR loci, assessment of common amplification artifacts, statistical interpretation of STR profiles, and the presentation of that information to a lay audience. The discussion is very basic and often includes outdated terms (e.g., "matrix" to describe the algorithms used for spectral calibration of capillary electrophoresis instruments) and overly simplistic explanations of STR artifact development without any information on resolution of or interpretation of those products. The brief discussion of methods for low-template DNA testing is heavily skewed toward the methods employed in the U.K. (LCN-PCR testing). The authors leave a significant gap in material by leaping from assessment of STR profiles (Chapter 7) to basic population genetics and statistics (Chapter 8) without any discussion of data review procedures, the growing importance of automated systems for STR data analysis, mixture deconvolution, or how "matches" are concluded and reported. While the authors provide an excellent, elegant description of the use and role of Bayesian calculations for evaluation of forensic DNA evidence, their description of random match probabilities also favors the U.K. approach ("ceiling principle").

The third and final section of this text includes bonus material covering related topics or specialized applications of forensic DNA testing methods. Chapter 10 includes an excellent and informative review of U.K. legislation and the current status of their database (National DNA Database [NDNAD]) as well as a brief update on other major DNA databases worldwide. Chapter 11 provides a

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comprehensive review of paternity testing calculations which is more thorough than what is provided on this topic in other introductory textbooks. However, the reader should be warned that the title of the chapter (“Kinship testing”) is somewhat misleading given that the focus is strictly on parentage testing. Chapters 12 and 13 provide basic overviews of SNPs and lineage markers (mitochondrial DNA and Y-STRs), respectively. This includes a clear description of Sanger sequencing and a very brief explanation of how statistics are applied to these data. The final chapter (Chapter 14, Non-human typing) is the most prominent update from the previous edition of the text. In this chapter, the authors provide tangible examples of cases that exploit molecular testing for identification of non-human materials (illegally traded species, poached species, domestic species ID, microbial ID) and clearly discern the basic questions of this application (what is the species?, what individual within the species contributed the sample?).

In conclusion, this text nicely highlights the most important areas of forensic genetics and serves as an excellent starting point for those interested in the topic. The authors should be applauded for their efforts to bring complex analytical processes to the level of introductory science students. These topics, when introduced early in the academic career of a student, may improve our ability to capture and retain the best young scientific minds. While many mechanistic details are not fully explored in this text, the simple, candid descriptions provided in this text are perfectly suited for those who seek a basic overview of the field. The authors offer many useful original graphics, including several color figures, which enhance the overall value of the book. The referencing is not comprehensive, but does include the most significant published sources for each topic and the authors offer “further reading” as an added bonus for those who seek a more advanced textbook for the individual topics addressed. This book will serve as a valuable asset for introductory-level science students, non–science students in related majors (criminal justice), and for professionals that have a peripheral interest in the field.