

Overall, the volume starts in a very logical fashion but then descends in a more fractured body of work where the connection among articles is difficult to ascertain. Thus, the papers become self-contained with a lack of continuity not unusual for a collection of short review articles/brief reports. However, most of them are interesting and well written. There are some excellent summaries that would be of value to both novices in the hemato-poiesis field as well as hematopoietic stem cell aficionados.

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GENETICS

GENETICS 101. *Science 101*.

By Michael Windelspecht. Westport (Connecticut): Greenwood Press. \$49.95. xvi + 195 p.; ill.; index. ISBN: 978-0-313-33381-1. 2007.

Volumes in the Science 101 series are intended for nonscience students and general public. Therefore, it is appropriate that *Genetics 101* is not considered a textbook of genetics, but rather "an accessible summary of . . . [genetic] ideas" (p. xi). This caveat does not excuse the scientific factual errors or organizational flaws that plague the volume. For those reasons, my overall assessment is negative.

Considering the target audience, organization takes on an additional role beyond clarity. The beginning of the book is problematic. The first taste of the science is a daunting list of abbreviations, including dsRNA, STS, and VNTR to mention a few of the questionable entries. For the most part, jargon is avoided in the text, but the Introduction contains an unacceptable amount of it! In the first six pages, "transgenic" is mentioned three times without definition and it is not in boldface as promised for entries that appear in the glossary. The boldfaced "transgenic" comes on page 31. To the extent that anyone can put themselves in another's shoes, I would have already felt lost by page 6.

How is a reader supposed to feel comfortable with genetics if several of the infrequent figures are not fully explained or are just wrong? Figure 1.7 (p. 23) misrepresents the gametes produced by the F1 generation. So the crisscross pattern of sex-linked inheritance in the F2 is not a Eureka moment. In Chapter 3, the text states that AUG in the start codon in translation, however, it is not

seen in Figure 3.6 (p. 69) and methionine is not the first amino acid of the growing polypeptide chain.

The good news is that the text (195 pages and seven chapters) is well written. The historical timeline is well developed, with an occasional sidebar that is refreshing. A reward comes from the penultimate chapter, Manipulating the Gene and the Genome. Topics such as GMO, GT, knockouts, and RNA interference are presented. The final chapter, Applications of Genetics, is more of a collection of leftovers than a conclusion and is somewhat anticlimactic.

Editing and proofreading of galley were lax in the production of *Genetics 101*, but it does have a nice cover. This is a sad commentary for a volume that could help overcome science illiteracy but, as printed, I cannot recommend it.

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GENETIC VARIATION: A LABORATORY MANUAL.

Edited by Michael P. Weiner, Stacey B. Gabriel, and J. Claiborne Stephens. Cold Spring Harbor (New York): Cold Spring Harbor Laboratory Press. \$240.00 (hardcover); \$165.00 (paper). xxi + 472 p.; ill.; index. ISBN: 978-0-87969-779-2 (hc); 978-0-87969-780-8 (pb). 2007.

This is an edited volume that seeks to provide specialists with a guide to the study of genetic variation in the age of genomics. It will be most appealing to anyone studying human genetic variation since this is the primary area of coverage, although other model systems are touched upon. A strength of the book is its conciseness, which is achieved by limiting the contents to basic introductions of the issues and citing more comprehensive references.

The volume is separated into five sections consisting of 34 chapters, plus an introductory stand-alone chapter on current ethical guidelines for human genetic research. The first section concerns study design and includes chapters on choosing populations (bottlenecked, inbred, or admixed) for mapping human genetic diseases, power analysis, usage of linkage versus association analysis, and introductions to the NCBI dbSNP and HapMap databases on human genetic variation. Section 2, on laboratory protocols, is the longest in the book. The protocols are primarily geared toward isolation of DNA from different mammalian and plant sources, but include other protocols (e.g., preparation of RNA from plant tissues and whole-genome amplification). Later chapters in this section provide overviews of a series of intermediate to high-throughput genotyping approaches using both SNPs and copy number

variation and constitute a particularly valuable resource. The third section is broadly on data analysis, with the final two chapters in this section on assessing significance in genetic association studies and detecting natural selection having especially broad appeal. Section 4 summarizes current knowledge of eight model systems (three plants and five mammals) with emphasis on the genetic resources available. The final section consists of three chapters on insights into human genetic variation, including uses of mtDNA and Y chromosomes as well as forensic DNA testing.

Although I would have liked to have seen a taxonomically (e.g., fish, microbes) and conceptually (e.g., evolutionary origin and significance of genetic variation) broader treatment, this book addresses topics spanning all stages of applied genetic research, from design to interpretation, and is thus quite useful as a quick reference to research methods on genetic variation, especially in humans.

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FUNCTIONAL PLANT GENOMICS.

*Edited by J.-F. Morot-Gaudry, P. Lea, and J.-F. Briat. Enfield (New Hampshire): Science Publishers. \$119.50. xiii + 699 p.; ill.; index. ISBN: 978-1-57808-506-4. [Originally published as *La Génomique en Biologie Végétale*, by INRA, Paris, France, 2004.] 2007.*

Whole-genome sequencing is a critical milestone for the global molecular and biochemical analysis of every organism. Nevertheless, harnessing the power of large-scale genome sequencing projects requires not only the annotation and assignment of putative functions to various genes, but also the deployment of functional tools to analyze the expression patterns and functions of these genes throughout the life cycle and development of the organism. In this book, the editors bring together an impressive collection of chapters dedicated to functional plant genomics.

Organized into five sections, the topics in this volume range from general chapters that discuss *in silico* analysis and structural genomics to those that describe the use of genomics and genetic variability for plant breeding. A special section describes the concepts and methods used in determining gene functions in plants. Readers will find this section to be something of a guided tour through many of the basic tools used in functional genomics, including gene transfer to plants, mutant analysis, DNA microarray, proteomic tools, metabolomics, gene expression analysis, and more. In another section, the editors go beyond *Arabidopsis* and dedicate several chapters to the description of scientifically and

economically important plant models in genomics (such as rice, *Medicago truncatula*, and tomato). One interesting chapter in this section is dedicated to grapevine: it describes the current state of grapevine genomic research and the vision of using the acquired genomic information and functional genomic tools to improve this economically important crop plant.

Other distinctive features worth mentioning are the extensive glossary provided at the end of the book as well as the impressive number of authors who contributed to this volume. By broadening the discussion to a wide range of genomics topics and extending it beyond *Arabidopsis*, the editors have created a book that can serve as a blueprint for scientists who wish to apply genomic tools in their research, as well as for educators who may find it to be an excellent reference for graduate and advanced undergraduate students.

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AVIAN GENOMICS IN EVOLUTION, AGRICULTURE, AND HEALTH.

*Edited by Jacqueline Smith and Indrajit Nanda. Basel (Switzerland) and New York: Karger Publishers. \$172.00. 404 p.; ill.; author index. ISBN: 978-3-8055-8338-1. [Reprint of *Cytogenetic and Genome Research 2007*, Volume 117, Numbers 1–4.] 2007.*

Avian genomics is finally reaching the lightning pace that researchers studying mammals have known for years. This volume, a special issue of *Cytogenetic and Genome Research*, captures the excitement of this field, particularly as it applies to the chicken. Through a collection of over 40 articles, the entire canvas of avian genomics is covered in extensive detail, from chromosome evolution and cytogenetics, to multigene families, alternative splicing, and QTL mapping, to the latest advances in chicken bioinformatics, small RNAs, and the molecular bases of development and disease resistance. The result is a publication that is absolutely essential for anyone interested in the evolution of birds and their genomes, as well as for poultry scientists interested in improving chicken stocks for human welfare.

A wide array of topics are presented in 11 sections: Resources; Cytogenetics; Evolution; Gene Expression; Immunology; Development; Sequence Analysis; Quantitative Trait Loci and Single Nucleotide Polymorphism; Genes and Longevity; Proteomics; and Avian Viruses. The volume is introduced in a forward-looking essay by Burt and White in which they celebrate the successes of the chicken genome project, but also argue for additional avian genome projects—such as the mallard duck (*Anas platyrhyn-*