

diversity and another on the evolution of ribosomal DNA (rDNA). The chapters are, however, of mixed quality and only a few would have fared well in good journals.

The papers are assembled in the style of a journal issue with a series of stand-alone papers. Unfortunately, there is insufficient editorial rigor in this book. There is no cross-referencing among chapters or removal of redundancy. This did lead to inconsistencies—e.g., in their chapter on evolution of repetitive DNA in *Aegilops*, Belyayev et al. indicate that homogenization of rDNA operates very strongly in the Triticeae. Cao's chapter on Triticeae evolution makes no mention of homogenization in a section devoted to rDNA. Both chapters contrast with Wissemann's discussion of rDNA evolution in general—here, Triticeae provide examples of rDNA divergence by “nonconcerted evolution.” In addition, this book is riddled with spelling and grammatical errors, which include ambiguities and invented words (e.g., the word “evolutive” appears in many articles and one chapter talks about plants being “primitive” and “advanced”). Errors of this type mean that the book cannot be recommended to students.

An enormous weight (one-quarter of the book) was given to Kondo et al.'s paper on phylogenetic relations in *Chrysanthemum*. It is unclear why it was given such prominence and the paper was unable to hold my attention. Apart from a few chapters (e.g., Ananthawat-Jönsson's presentation of the role of triploids in *Betula* evolution), there are few general insights to be gleaned. This is not a book to browse, and the stand-alone nature of the papers means that this volume is for research scientists with an interest in the taxonomic group mentioned in the title.

ANDREW LEITCH, *Biological Sciences, Queen Mary, University of London, London, United Kingdom*

ANNUAL REVIEW OF GENETICS. *Volume 37: 2003.*

Edited by Allan Campbell, Wyatt W Anderson, and Elizabeth W Jones. Palo Alto (California): Annual Reviews. \$70.00. x + 690 p + 31 pl; ill.; subject index and cumulative indexes (contributing authors and chapter titles, Volumes 33–37). ISBN: 0–8243–1237–6. 2003.

THE HOPE, HYPE, & REALITY OF GENETIC ENGINEERING: REMARKABLE STORIES FROM AGRICULTURE, INDUSTRY, MEDICINE, AND THE ENVIRONMENT.

By John C. Avise. Oxford and New York: Oxford University Press. \$35.00. xiii + 242 p; ill.; index. ISBN: 0–19–516950–6. 2004.

The history of biotechnology took a sharp turn around 1980. Congress failed to act on at least a dozen bills that were introduced to regulate recom-

binant DNA research, ending four years of intensive debate over whether the guidelines issued by the National Institutes of Health (NIH) should be enacted into law. In his memoir of that period, the late former NIH director Donald Fredrickson describes the intense lobbying by agency insiders and members of professional societies advocating flexible and relaxable guidelines and opposing refractory legislation. Also in 1980, the commercialization of molecular biology had ostensibly begun. Scientists, who retained their academic positions, incubated hundreds of new venture capital firms. The Bayh-Dole Act (1980) transferred to researchers and their commercial partners all intellectual property rights derived from federally funded research discoveries.

In that first decade, a flurry of new products and therapeutic applications of molecular genetics brought a second generation of concerns over the social, ethical, and ecological impacts of genetically modified organisms (GMOs). Among the developments, human insulin was derived from a genetically modified bacterium, field trials had been completed for dozens of GMOs, and the first human gene therapy trials were underway. Also, the Supreme Court gave its imprimatur to the first patent of a genetically modified oil-degrading bacterium. Popular science magazines and the news media rode the wave of hyperbole in discussing the benefits of new genetic discoveries, from promises of cancer cures to engineering perfect babies.

John Avise, a professor of genetics at the University of Georgia and member of the National Academy of Sciences, who views himself as a “scientific outsider peering into the genetic engineering industry” and “a genetically informed but relatively detached and objective perspective on the promises and pitfalls of GMOs” (p ix), has written a book to educate readers about what is realistic and virtuous in contrast to what is unrealistic and ethically problematic about biotechnology. The author provides 63 vignettes of new advances in biotechnology and gives his appraisal of the social merit of commercial and medical applications as well as their likelihood of success in the marketplace.

Avise creates his own biotechnology appraisal gauge he calls the “boonmeter,” where each product or process is given a rating from worst (boondoggle) to best (boon) on an analog scale. To cite some examples, the author ranks the Flavr Savr[™] tomato and the antimicrobial mosquito as boondoggles, while he ranks as boons the mass screening of alleles for Tay-Sachs and Huntington's disease in conjunction with programs that prevent these aberrant gene sequences from being transmitted to new generations of children.

Although it may be useful to have summaries and assessments of five dozen applied projects of biotechnology in a single volume, these cases are primarily of value for investors or teachers. People who do not have the time to read about these developments in any depth may find it useful to have a simple and straightforward "up or down" view of what one scientific observer believes are the prospects of these biogenetic applications in the marketplace or when measured against the likelihood of social acceptance. Scientists will not find the book very useful beyond its instructional potential for engaging students by having them develop their own appraisal strategies and comparing them with the author's opinions.

Finally, it is worth noting that *Awise* reaches a conclusion about the societal impact of gene engineering: "Humankind's newly found capacity to purposefully manipulate genes is surely among the most extraordinary achievements in the history of our species" (p 177). Ironically, based on the vignettes discussed in the book, the collective innovations of gene technology thus far can hardly measure up, in their contributions to human well being, and to the discovery of penicillin. The greatest contribution of genetics to date is not found in all the drugs, crops, or prenatal tests, but rather the revolution in forensic science, which has provided exculpatory evidence for falsely convicted criminal suspects who were sent to death row. Perhaps the "boonmeter" could be applied to some of the author's own claims about genetic technology.

SHELDON KRIMSKY, *Urban & Environmental Policy & Planning, Tufts University, Medford, Massachusetts*

BIOTECHNOLOGY FROM A TO Z. *Third Edition.*

By William Bains. *Oxford and New York: Oxford University Press.* \$47.50 (paper). vii + 413 p; ill.; index. ISBN: 0-19-852498-6. 2004.

GENES IN THE ENVIRONMENT. *The 15th Special Symposium of the British Ecological Society held at St. Catherine's College, Oxford, 17-19 September 2001.*

Edited by Rosie S Hails, John E Beringer, and H Charles J Godfray. *Malden (Massachusetts): Blackwell Publishing.* \$99.50 (hardcover); \$64.95 (paper). xviii + 336 p + 1 pl; ill.; index. ISBN: 0-632-06507-9 (hc); 0-632-06508-7 (pb). 2003.

This edited volume contains the contributions to a special symposium of the British Ecological Society and highlights research that exploits molecular techniques to address ecological questions. The 17 chapters are assembled into three parts: gene flow and spatial dynamics; microbial com-

munity dynamics in soils and water; and host-pathogen interactions. Research presented depicts the work of scientists based in the United Kingdom, which is understandable given the symposium sponsorship and funding restrictions that organizers likely had to deal with. The scope of topics covered seems somewhat limited, however, and a more diverse contributor pool might have provided for a better representative perspective of the ever expanding field of molecular ecology. For example, only a small section of a single chapter is devoted to discussion of quantitative trait loci, which belies the extent of work on QTLs.

Part 1 (seven chapters) introduces the volume with an array of topics, theory, and ways in which molecular tools have been integrated into ecological research. Contributions cover *intraspecific* gene flow under a variety of spatial configurations, fitness advantages of *interspecific* genetic introgression, integrative analyses of quantitative and molecular genetic diversity, and a literature based analysis of the breadth of questions being investigated in plant evolutionary ecology using molecular approaches. A variety of theoretical models are described and employed, including the Galton-Watson branching process to study gene flow in metapopulations, spatial autocorrelation analysis to explore range expansion and invasion dynamics, clustering algorithms to identify interspecific hybridization events, and maximum likelihood approaches to model impacts of intermate distance distributions on reproductive success. Types of genetic data analyzed included allozymes, nucleotide sequences, quantitative trait loci, and microsatellites, and the systems studied cover viruses, fungi, plants, and insects.

Part 2 is much more restricted in focus, with significant overlap among the individual contributions with respect to questions being addressed, genetic regions analyzed, and techniques utilized. All four chapters in this section describe research that seeks to quantify bacterial community diversity with an aim toward linking metabolic activity, environmental modifiers, and taxonomic identity of either the methane or ammonia-oxidizing bacterial species groups. Although these chapters detail important research, highlight use of molecular techniques to characterize microbial communities (as opposed to culturing techniques) and, in some cases, emphasize different aspects (e.g., only the chapter by Chistoserdova and Lidstrom detail the genetic basis of methylotrophic metabolism), this section could have easily been reduced to allow for greater overall diversity of topics covered in the book. Of all the chapters in this section, the final one (by Prosser et al.) offers the greatest clarity and most successfully places the research into its