

## Book Reviews

*Mitochondrial Genes*. Edited by PIOTR SLONIMSKI, PIET BORST and GIUSEPPE ATTARDI. Cold Spring Harbor Laboratory, Cold Spring Harbor, New York, 1982.

This book contains a number of articles based on papers delivered at the Cold Spring Harbor meeting on 'Mitochondrial Genes' in May 1981.

The meeting was intended as a tribute to the memory of Boris Ephrussi and the book appropriately starts with an article by H. Roman summarizing the discovery of the mutation 'petite colonie'. The book is edited by three leading scientists in mitochondrial genetics and biogenesis, one of them a former student of Ephrussi. The ordering of the chapters is taxonomic, with sections on Mammalian (plus some *Drosophila* work), yeast, filamentous fungi, protozoan and plant mitochondrial genomes. This rather unnatural taxonomy reflects the emphasis on mitochondrial molecular genetics of specific model systems.

Some of the papers are up-to-date reviews of a section of studies on mitochondrial genetics (for example, Anderson *et al.* on The Human and Bovine Mitochondrial Genomes, and Jacq *et al.* on The Role of Introns) while others are preliminary research reports (e.g. Lansman *et al.*, where the words 'preliminary report' are actually in the title) while some others fall somewhere in between (our own paper on the *A. nidulans* mitochondrial genome).

Both approaches are indeed useful as it is important for the advanced student or research worker to have a summary of known facts as much as an indication of future trends. I would have found preferable, as someone involved in teaching advanced students, if the editors had followed the pattern of older Cold Spring Harbor books (*The Lactose Operon*, *The Bacteriophage Lambda*) in which review articles were separated rather than interspersed with research reports.

From reports of colleagues attending the meeting, this was quite exciting. New mutations in regions essential for RNA splicing, the identification of human URFs in fungal genomes, the presence of a silent gene for ATPase subunit 9 in fungal mitochondria, the presence of a gene not coding for a protein but necessary for tRNA synthesis or processing were all reported for the first time at the meeting and are summarized in the book. There is a cautionary note here. The student wishing to understand how the *var* peptide is coded for should remember that the article by Butow's group was written before they finally solved the apparent paradox of a genetic determinant that is not a gene and jump to the note added in proof where the paradox dissolves.

The book necessarily lost some of the flavour of discovery by the time it was published. Nevertheless, it provides an indispensable guide for both advanced students and research workers of the state of the art in the most important model systems of mitochondrial biogenesis and genetics.

In more than one way the book (and the meeting) reflects its timing. The emphasis is on 'mitochondrial genes', with little emphasis on the role of nuclear genes on mitochondrial biogenesis. (Exceptions are found in the articles of Kruszewska and of Garriga *et al.*). Several articles provide confirmatory evidence to the maturase model and are required penitential reading for those non-mitochondrial molecular biologists who doubted or ignored through prejudice the initial genetical evidence. The tone of the book is in some way set by the first research article of Anderson *et al.*, comparing the sequences of the human and bovine mitochondrial genomes. DNA or RNA sequences are presented almost everywhere. There are a few papers that mention results obtained using classical

genetics, e.g. some of the yeast papers where both approaches are combined and used to their full potential, and only one purely genetical paper (Birky *et al.*). The articles in the book indicate that an extremely stimulating and unexpected result can be derived by just looking at the structure of genomes, and almost marks the high point of this approach. Perhaps a new Cold Spring Harbor book in a few years' time will not be organized taxonomically but around central problems like: Do mitochondrial introns transpose? Is there more than one mechanism of intron excision? What are the URFs doing? How do sequences move between the nuclear and the mitochondrial (and the chloroplast) genomes? How are proteins imported into the mitochondria and put in their right place? How is stoichiometry between nuclearly coded and mitochondrially coded components maintained? What is the mechanism of recombination in organelle genomes?

The attentive reader might find pointers to all these problems in the present book.

CLAUDIO SCAZZOCCHIO

*Department of Biology*  
*University of Essex*  
*Wivenhoe Park*  
*Colchester CO4 3SQ*  
*Essex, U.K.*

*Structures of DNA*. Cold Spring Harbor Symposia on Quantitative Biology. Volume 47. Cold Spring Harbor Laboratory, Fulfillment Department, P.O. Box 100, Cold Spring Harbor, New York 11724. April 1983. \$140 (\$168 outside U.S.). ISBN 0 87969 046 1.

This extra-special Cold Spring Harbor Symposium, which appears in print in the thirtieth anniversary year of the discovery of the double helix, deals both with structure and with all aspects of DNA function that can be directly related to structure. Some idea of its scope and balance will be conveyed by the titles of its fourteen sections: handedness (19 papers), conformation (12), chemical modification (10), chemical synthesis (4), interactions with proteins (10), nucleosomes (9), methylation (9), replication (10), gyrases and topoisomerases (5), recombination and mutation (7), transcription and its control (15), gene organization (11), repetition and pseudogenes (7), and chromosomal replication origins, centromeres and telomeres (5). Almost everybody who is anybody in the DNA field is represented among the authors; this makes for a certain degree of repetition but not, I think, an excessive amount. The quality of the work presented is high, as one would expect in this company, and the standard of illustration is excellent. Indeed, some of the computer graphics showing DNA conformations are things of beauty.

My main criticism of the individual contributions (and it is more a criticism of editorial policy) is that, although they are not very different in complexity and density of content from the average research paper in, say, *Cell*, almost none of them has a summary. This makes needless difficulty for that great majority of readers who will not have time to read every one of the 1223 large double-column pages.

From a symposium of this quality it is not easy to pick out high spots for special discussion but two of its aspects may be especially noteworthy as signs of the times. Firstly, it is evident that the fascination with comparative structure and the urge to describe as fully and accurately as possible, often regarded as characteristics of an earlier generation, are still alive and well among the molecular biologists. Some of the fruits of the happy conjunction of rapid DNA sequencing and computerized information storage and retrieval are here on display, albeit in schematic form. The complete sequences of the bacteriophage lambda and T7 and the adenovirus-2 genomes stand as most impressive monuments, but information from selected regions of eukaryotic chromosomes –