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Book reviews

The Eukaryote Genome in Development and Evolution. By B. JOHN and G. MIKLOS. London: Allen and Unwin. 1988. 416 pages. Hardback £40, paperback £14.95. ISBN 0 04 575033 5

This book sets out to evaluate the impact of modern genetic and molecular studies on our understanding of embryonic development and evolutionary problems. The reader is given an outline description of some of these molecular techniques and the operation of natural selection, neutral drift and molecular drive in the spread and fixation of germ-line variants in natural populations. The authors then review our present understanding of embryonic development. Molecular studies of *Drosophila* development predominate here, although other systems such as those of *Caenorhabditis*, *Xenopus*, mammals and even yeast and the ciliates occasionally enter into the discussion. The *Drosophila* maternal-effect genes control polarity and the spatial coordinates of the egg: there are three distinct classes of segmentation gene; the homeotic selector genes determine appropriate patterns of differentiation in each segment of the fly; other genes regulate sexual differentiation and dosage compensation, while another considerable group of genes controls development of the nervous system. Most of these genes show tissue-specific patterns of expression. They are transcribed at particular stages of development and gene expression is usually regulated by the activity of other genes expressed at an earlier stage, so that a hierarchical network of gene expression becomes apparent. The genome can be divided into genes which are involved in major developmental decision-making and those genes necessary for carrying into effect the developmental decisions but not involved in making them. These matters have of course been recently reviewed elsewhere but they form an essential part of the present book and have obviously influenced the ideas of the authors to a considerable extent.

In nature, the genomes of eukaryotic organisms have undergone almost every conceivable permutation and combination of genomic size, composition and organization. In the central sections of their book the authors make extensive use of comparisons between observations made on different species. Thus the highly repeated DNA sequences in heterochromatin are shown to have no known direct influence on the phenotype in spite of the many speculative hypotheses that have been advanced in efforts to assign some function to them. Mobile elements which are widely dispersed in the genome of *Drosophila melanogaster*, where they comprise about 20% of it, are equally unlikely to play any important role in the gross organization of the genome. The so-called C-value paradox (that the genomes of organisms with similar morphology and anatomical complexity often possess widely-different amounts of DNA) is no longer considered a problem at the level of metabolism and development, for when similar tissues from related organisms with diverse C-values are compared, they are found to have similar polysomal RNA complexities – so the excess DNA has no functional significance. Speciation has evidently often been accompanied by the accumulation of various types of chromosomal rearrangement. For example the Indian and Chinese muntjac have completely different karyotypes but morphologically they and their diploid hybrids show close similarity. There is no evidence that chromosomal rearrangement has played a significant part in speciation or any accompanying morphological changes in the organism. Induced chromosome rearrangements can be associated with mutation at either breakpoint, but in *Drosophila* at least 50% of all such breakpoints have no overt effects of any kind. Work with P-element vectors has indicated that, given the presence of a few thousand bases of flanking sequence to either side of the coding sequence, most genes seem to function quite normally when inserted almost anywhere in the euchromatic portion of the *Drosophila* genome. There is an interesting section on the evolution of gene families where the evidence suggests that duplication of an ancestral gene has been followed by diversification in the functions of the individual genes and the occurrence of pseudogenes. Examples of gene-amplification are also described.

In a final section the authors try to consider the

possible origins of evolutionary novelty. This is difficult because the major metazoan phyla originated in the Cambrian under uncertain genetic and environmental circumstances. The authors think that increasing complexity may have resulted not so much from increasing numbers of novel genes but from altered regulatory interactions between relatively stable sets of genes. This idea receives some support from the finding of stretches of homologous base sequence (such as the homeobox) within genes expressed at embryonic stages of organisms with widely different patterns of development. Somewhat surprising in view of the designation of one of the authors, Bernard John, as Professor in a Population Genetics Group, is the final statement that they should abandon neo-Darwinian theory, the construction of phylogenetic trees, estimates of divergence times between species etc., so as to put their main effort into the study of molecular embryology where the quintessence of morphological novelty must obviously lie!

I find this substantial book both scholarly and easy to read. It would suit anybody wanting to find out what has been happening in the field during the past ten years or so. There is a subject index and a reference list with over 900 references but the text is most usefully accompanied by 187 figures and tables in which the essential findings of the original works under discussion are clearly presented and illustrated. There is a clear logical thread throughout the book, although this thread tends to wander in some places. However, many of the side issues are well worth reading about. For instance, I was interested to learn that the elaborate post-natal development of the mammalian brain is accompanied by a substantial increase, over time, in the complexity of poly $(A)^-$ mRNA.

Some of the terminology I thought was rather odd. References to 'developmental circuits' and 'gene circuits' are made throughout the book, but the use of the term circuit in this connection is never explained. In my youth I was taught to think of genes acting, in an epigenetic landscape, to switch development between alternative pathways – an idea I still find serviceable, but closed circuits are no part of the picture. I also find the term 'genomic landscape' inappropriate because a landscape is essentially three-dimensional, whereas a genomic sequence is linear.

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Chromosomes today, Vol. 9, Edited by A. STAHL, J. M. LUCIANI and A.-M. VAGNER-CAPODANO. London: Allen & Unwin. 1987. 317 pages. £40.00. ISBN 0 04 575031 9.

The series *Chromosomes Today* publishes the papers presented at the International Chromosome Conferences which have been held every two to three years since 1964. The ninth volume is the record of the most recent of these meetings, which was held in Marseille in June 1986. As it is thus nearly two years since the conference there is naturally nothing immediately new in these pages, in fact in some areas, as for example, the search for the testis determining factor, there have been considerable developments since this time. Nevertheless, the material contained here – 29 papers grouped under 7 headings – will be of value to readers with a wide range of interests as it contains both reviews and original work in areas of current research.

The section on chromosomes and malignant change contains two excellent reviews on the molecular analysis of the breakpoints involved in the specific chromosome rearrangements associated with certain malignancies. The first deals with malignant lymphoid cell proliferations, particularly the breakpoints involving genes of the immunoglobin superfamily, while the second concerns the Philadelphia chromosome. Typically found in chronic myeloid leukaemia the Ph′ is also sometimes present in other leukaemias where it is indistinguishable at the cytogenetic level from that found in CML but appears heterogeneous when examined by molecular methods. Also in this section is a description of the discovery and characterization of three retroviruses each containing two oncogenes – their value in studies on the co-operation of genes in normal and pathological cell growth stimulation is discussed.

The section on sex chromosomes begins with an interesting discussion of why, in the course of evolution, the particular chromosome chosen as the sex chromosome was selected. The section continues with a review of the isolation and characterization of human *Y* specific DNA sequences. There is now evidence for the presence of such sequences from the short arm of the *Y* in the DNA of males with *XX* chromosome constitution; these studies and the possible mechanisms of *Y*: *Y* interchange are discussed together with the molecular basis of clinical symptoms in *XX* males.

A comparison of homologous regions of *X* and *Y* chromosomes in man and the higher primates based on visualization of regions of early replication and on *in situ* hybridization studies using DNA probes for the pseudoautosomal region completes this section and leads into the following one on aspects of meiosis. There is a detailed comparison of information on the meiotic behaviour of the *X* and *Y* chromosomes obtained from cytogenetic observations with the molecular data on these chromosomes now available. The use of sensitivity to DNAse I digestion as an indicator for active genes – previously described in mitotic chromosomes – is here extended to a meiotic study of *X* and *Y* where it is shown that active genes are confined to the terminal regions of the long arms and the pairing region of the short arms of both chromosomes. The use of the surface spreading