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

technique has permitted elegant EM studies of the synaptonemal complex in carriers of structural chromosome rearrangements in man; these studies and their bearing on classical ideas of chromosome pairing are reviewed. Similar work on female meiosis in mice trisomic due to parental Robertsonian translocation is also reported. Lastly in this section observations on spindle structure and chromosome alignment in freshly ovulated and in post-ovulatory aged mouse oocytes are discussed in relation to the increase of aneuploid offspring associated with maternal age.

The section on Nucleolar Organisers is introduced by a comprehensive review of studies on the molecular organization of the human 18S and 28S ribosomal genes. EM studies on the ultrastructure of nucleoli in several different types of cell are then described. The nucleolar organizer region of the chromosome is present within the nucleolus, and there is some disagreement between studies based on immunocytochemical localization of RNA polymerase I and studies employing [$^3$H]-uridine incorporation as to where within the structure transcription takes place. A combination of NOR-silver staining and EM has previously shown that the NOR's of several chromosomes are associated at pachytene within the fibrillar centre of nucleolus. This work has been extended by using *in situ* hybridization to localize the ribosomal genes in human oocytes and the results are discussed with reference to the involvment of human acrocentric chromosomes in numerical and structural anomalies.

Marsupials are one of the three living lines of mammalian evolution. Australian marsupials are thought to have reached there about 50 million years ago and were the only mammals present in Australia until comparatively recent times. There is a comprehensive discussion of chromosome evolution in this group, and comparison is made with evolution of marsupials in South America. Also in the section on evolution, the various types of chromosomal change observed are discussed with particular reference to their effect on genetic recombination. Chromosome homology in mammals deduced from G-banded karyotypes must be confirmed by comparative gene mapping studies. There is an account here of such work in three key species in the study of primate evolution, i.e. gibbon, capuchin monkey and mouse lemur. Finally from many observations in many species a model is presented here in another important aspect namely the evolution of c-band patterns.

Under the heading of *Drosophila* chromosomes a study is described which aims to build up a complete genetic map of two regions of *Drosophila* chromosome each containing several genes, and to relate this map to other levels of chromosome organization. Another study in this section is of three exceptional sequences which are under-replicated and whose cytogenetic locations had previously been described as intercalary heterochromatin. This study leads to the hypothesis that polyteny occurs through loss of functions normally used in the diploid cycle rather than by gain of specialized functions. The final contribution to this section is a discussion of the structure and function of *Y* chromosome genes in *Drosophila* which leads the authors to the conclusion that the biological function of the *Y* chromosomal genes is to accumulate nuclear proteins with the aid of the *Y* chromosomal transcripts.

Finally the collection of three papers under the heading of Molecular Cytogenetics contains first a discussion of new cytogenetic data on heterochromatin of *Drosophila* and maize. Unfortunately the ordering of the text in this contribution was rather confusing. An interesting study on the integration of foreign DNA shows that this may be accompanied by changes in the chromosome recognizable at the cytogenetic level. The last paper in this section is a comprehensive report on Bkm sequences and the possibility is raised that hypervariable Bkm RFLP's might be used to monitor for chromosome changes in oncogenesis.

It is not possible to do justice to the contributions to this conference in a short review; the book is full of useful information. As with all volumes of this nature there is the occasional error of grammar and spelling, but overall the production is excellent, and at a cost of £40 the book represents very good value.

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*Beyond the Gene: Cytoplasmic Inheritance and the Struggle for Authority in Genetics*. By JAN SAPP. Oxford University Press. 1988. 266 pages. £32.00. ISBN 0 19 504206 9.

In times past there has been much argument about the relative importance of nuclei and cytoplasm in the control of heredity. In the 20s and 30s of this century the *Drosophila* and maize workers were very busy establishing the chromosome theory and most geneticists of that period, especially in the USA, came to accept the then rather crude mechanistic ideas of genes on chromosomes arranged like strings of beads, even though the material nature of genes was then completely unknown. In 1926 Morgan felt able to announce that 'cytoplasm may be ignored genetically'. However, some German geneticists were studying various plant characters which were inherited through the cytoplasm. Some biologists, especially those concerned with embryology, even thought that the role of the genes was quite trivial, and that control of the development of living organisms was directed by some kind of cytoplasmic system, the details of which were, needless to say, never specified.

In the years immediately following World War II, the nucleus *vs* cytoplasm controversy flared up again.