

clone the $\Delta 12$ desaturase gene in the hope that successful transfer would initiate the conversion of oleic acid to polyunsaturated linoleic acid. Another would go for intervention in milk production with a view to reducing the lactose content, or suppressing β -lactoglobulin in bovine milk, to the advantage of infants, or increasing the casein and organic phosphate content. The lactose idea is appealing. Some 90% of human beings are lactose intolerant, while the high lactose content in milk poses problems for industrial processing. Inhibition of the α -lactalbumin gene by anti-sense RNA or secreting an active β -galactosidase into milk are suggested ways to encompass the objective. Merely to mention them is to point to the stony path that lies ahead.

In a slightly different context we find a report from an Edinburgh group who are investigating the use of transgenic livestock to secrete valuable human proteins in their milk. The preferred animal is the lactating ewe, cast in the improbable role of surrogate bacterium. Since some 20 animals could meet the annual requirement of some of the proteins they have in mind, the advantages of this project will accrue to medicine not agriculture.

Although injecting DNA into single cells occupies the centre of the transgenic stage a more sophisticated medium of delivery may be hatching in the wings. This refers to the use of C-type retroviruses which appear to have several potential advantages in ease of introduction, integration at low copy number as well as ability to enter the germ line and carry foreign DNA. It may be possible to tailor such vectors for better control of insertion. There are many difficulties to be overcome and so much has yet to be learnt about mammalian retroviruses. But it would be in keeping with the development of molecular biology if simple presentation gave way to controlled insertion. It will be interesting to see how well the rival horses run.

In the remaining contributions we are carried back to the problems of polygenic variation. One of them demonstrates a correlation between the presence of transposable P elements in *Drosophila* and response to selection for abdominal bristle number. There is no direct message for animal breeding since transposable elements are apparently absent in mammals. But if the properties of polygenic variation can be clarified by making use of P elements and the mutations they induce, then breeders of livestock should take note, especially since mammalian retroviruses may be relevant in this context.

A theoretical contribution takes up the theme of detecting sufficient restriction fragment length polymorphisms, scattered across the genome, to provide markers for genes which determine quantitative variation and thereby give selection a sharper cutting edge. The limiting factor here is the proportion of quantitative variation associated with variation in the markers. Given the cost and effort required, the counter attractions of transgenic animals, analysing

single gene effects and manipulating embryos are likely to take precedence.

Many of the projects discussed in this Symposium are already in train in research centres in Europe and the U.S.A. Scientific animal breeding is breaking away from the douce life-style dominated so long by calculating machine and, more recently, computer and is making for the turbulent, high ground of experimental biology. New kinds of scientist are entering the arena. This is exciting and not without risk. Who can reckon the tally of dashed hopes two decades hence? But that is the price of innovation. The happiest outcome would be one in which the alternative approaches, old and new, would be seen as complementary.

A further reflection might occur to a thoughtful observer. All the new technology of embryo manipulation is likely, sooner or later, to settle down to rather mundane laboratory routine, practised by a large number of expert technicians. But the whole bag of tricks is potentially applicable to our own species. Is it conceivable that widespread familiarity with them could erode the general concern to keep them beyond the pale of humankind? Who can doubt the need for global agreement about where to set the boundary fence?

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Molecular Evolution of Life. Edited by HERRICK BALTSCHJEFFSKY, HANS JORNVALL and RUDOLF RIGLER. Cambridge University Press, 1986. 375 pp. £40. ISBN 0 521 33642 2.

The collection of papers in *Molecular Evolution of Life* represent the proceedings of a conference organized by the Swedish Academy of Sciences and held in September 1985. The list of participants is impressive, and the quality of the papers correspondingly high. The contributions are a sample of current research activity in what the editors describe in the preface as 'fundamental molecular aspects of the prebiological and biological evolution of life'.

It is often a problem with meetings of this kind (perhaps especially so in meetings concerned with evolution, where research in all areas of biology have some importance) that contributors largely ignore the theme of the meeting, simply presenting the latest instalment of their research and letting the audience (perhaps with the help of a token sentence or two) make its own connections. This is not the case in the present volume where only a few papers fail to tackle the evolutionary significance of their subject matter. Although most of the contents are written by researchers reporting their own research, there are a number of short reviews also.

Perhaps the major omission among the papers is in population genetics, where a review, if not one or two

theoretical contributions, on models of, for example, gene families, 'selfish DNA' and concerted evolution, would have been useful. Although populational aspects are not addressed, these issues have not been ignored, and biochemical and molecular biological perspectives relating to them are to be found within the volume.

The book is divided into four sections, respectively entitled: Prebiotic Systems and Evolutionary Pathways, Nucleic Acids and Informational Systems, Proteins and Enzymatic Functions, Complex Systems and Organization. The first section, which begins with a review by Stanley Miller of experiments in the prebiotic synthesis of small molecules, is a little incestuous, with four of the seven contributions coming from Manfred Eigen and his colleagues at the Max Planck Institute for Biophysical Chemistry, and a fifth from Peter Schuster (who collaborated closely with Eigen in the development of the 'kinetic theory of molecular evolution' in the late 1970s). Together, however, these papers give a good feel for the philosophy of the model, and the kind of directions research informed by it can take. The other contribution to the section is by Ohno and Jabara, which is certainly original in containing three pages of musical notation (almost half the paper) illustrating short recurring themes in coding sequences with the 'transformation' of a mouse C57 immunoglobulin-G variable heavy chain.

The section on nucleic acids and informational systems is not simply a collection of reports of new gene sequences. Although sequence data are central in many of the papers, more than half of the contributions are mainly concerned with higher levels of structure. DNA as well as RNA structure is examined. The section also covers other components of the genetic machinery: in particular, ribosome structure (the contribution by Lake *et al.*) and elongation factors (Liljas *et al.*) are used to make inferences about the evolutionary relationships between archaeobacteria, eubacteria, organelles, and eukaryotes. These relationships are difficult to disentangle because of the antiquity of the events and have important implications for models of early cellular evolution.

The review by Dickerson *et al.* on 'Pathways of information readout in DNA' addresses the nature of the primitive translation apparatus in the light of how DNA in modern systems functions in the roles of coding and control. The different structural features of DNA exploited in these areas may well hold the key to our understanding of this nature, and this is clearly argued in the paper. Contributions by Shepherd and by Lagerkvist examine aspects of genetic code evolution from the comparative sequence data and unorthodox codon reading respectively, elaborating on previous published work by the authors. With so many diverse strands now bearing on the problem, one begins to feel some hope that a synthetic model of the evolution of the genetic code is not far away.

The third section of the book, on protein and enzyme evolution, contains three reviews on evolutionary aspects of protein structure (Tom Blundell on the evolutionary stability of tertiary structure in proteins, Hans Neurath on domains, and a contribution by Brennan, Weaver and Matthews on inferring distant evolutionary relationships in proteins). The other contributions address particular groups of proteins, with emphasis on hormones, blood clotting proteins, and proteins of the photosynthetic and respiratory systems. Gilbert's ideas of exon-shuffling are given further support in a review by Branden which examines the relationship of domain boundaries in α/β proteins and the exon-intron boundaries of their genes.

The book would have benefited from an editorial review for each section, outlining the issues each section addresses, and relating the papers to each other. Of course, this raises practical difficulties, as it arguably cannot begin till all the papers are in, and then the time required to produce the editorial overviews conflicts with the requirement to publish as quickly as possible. The final section, particularly, which contains many interesting papers, would certainly have been improved by a discussion of the problems that complex systems present to evolutionary theory, so that the particular instances supplied could be compared and contrasted in the way that the problems are raised and addressed.

Three of the contributions in the section deal with viruses. Two of these are concerned with viral (adenoviruses and rhinoviruses) structure and evolutionary relationships. (Should these have been in the section on nucleic acids? After all, ribosomes have more complex organization.) The third is by Robert Gallo, and looks at the role of human t-lymphotropic retroviruses in malignancy and immune suppression. Gallo's classification of the AIDS virus as 'HTLV-III', related to the leukaemia viruses (HTLV-I and HTLV-II, which form the subject of the first half of the paper), has not gained wide acceptance in the AIDS research community in the intervening period. The controversy surrounding this work is not material to the subject of the book, however, and I shall not step outside my area of competence to comment further.

There is a short contribution in this section by Schimke and co-workers pursuing their suggestion that 'over-replication' of DNA is the mechanism of dihydrofolate reductase gene amplification in methotrexate resistant CHO cells, and suggesting that these kinds of amplification events occur during mitotic division in germ-line cells and contribute to rapid genomic changes of evolutionary significance. (Again, I might quibble that this paper is in the wrong section!)

Other contributions look at the immune system, and at bacterial metabolic systems, and of course at development. The final paper by Gerald Edelman on

molecular mechanisms of morphologic evolution nicely rounds off a volume that will sit nicely in every university and college library.

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Genetic Maps/1987, vol. 4: *A compilation of Linkage and Restriction Maps of Genetically Studied Organisms*. Edited by STEPHEN J. O'BRIEN. New York: Cold Spring Harbor Laboratory. 1987. 755 pages. US\$55.00. ISBN 0 87969 303-7.

The first three volumes of *Genetic Maps* appeared biennially, in 1980, 1982 and 1984, and this new volume is only a year 'late'. When I reviewed the 1984 volume (*Genetical Research* 45, 232, 1985), I wrote that the authors put me in mind of the Spanish nobles who drove the Moors out of Seville in 1401. Having determined to build a Christian cathedral on the ruins of the Great Mosque, they said 'Let us build such a great Edifice as all men who see it shall think us mad.' Given the continuing rapid expansion of genetic knowledge, I thought volume 3 would be the last genetic edifice of this kind, but here is volume 4, only a year 'late', with much updating of the previous record and with the same intention as before, of rendering the previous volume obsolete. Dr O'Brien, the continuing editor, is like his compilers still imbued with the 'Seville' spirit, and looks forward to new editions which are bound to exceed 800 or 1000 pages, and may have to be printed in more than one volume. This volume contains more than 100 genetic maps in its 752 pages plus index, and I can only praise the editor and compilers for a remarkable achievement, and say firmly that this new volume simply must get onto the shelves of every library haunted by any kind of geneticist or related animal. It will be an essential element in their education.

To give an indication of the changes in the new volume, one can look first at the new organisms which make their entry. There are no new bacteriophages, and I am sorry to see no T-odd phages to compare with T4, although T7 has been completely sequenced; phage Mu is still missing, as is P22, and other phages ought to be queuing up for acceptance. A good example is set by Animal Viruses, now divided into DNA and RNA types: new (to this volume) DNA viruses include Epstein-Barr virus, a number of Papillomaviruses and Vaccinia virus; for RNA viruses, the human T-lymphotropic retroviruses are brought up to date as at October 1986, including HTLV-I (isolated on numerous occasions), HTLV-II (isolated on nine occasions, but with no clear disease association), the AIDS-associated virus HTLV-III (also designated LAV, ARV and HIV), isolated on hundreds of occasions, and HTLV-IV (isolated repeatedly from individuals in West Africa). References to the published nucleotide sequences of these viruses

are given, and data on restriction sites, genes, ORF's and proteins are included here. The remaining viruses introduced for the first time in this volume are the Ungulate lentiviruses of sheep, goats and horses.

There are no new genera of Bacteria, Protozoa or Algae added, but the fungi have grown from five to eight, and now include *Sordaria macrospora*, *Coprinus cinereus*, *Ustilago maydis* and *U. violacea*. *Drosophila pseudoobscura*, *Anopheles albimanus* and *Aedes triseriatus* have been added to the Insects. *Saguinus oedipus*, the cotton-topped marmoset has been added to the Primates, and the sheep, *Mustela vison* (American mink) and some still fragmentary information on Marsupials and Monotremes to the group of Other Mammals. Finally, we now have gene maps of the soybean (*Glycine max*), *Arabidopsis thaliana* and *Petunia hybrida*. These are simply the species which have appeared for the first time in *Genetic Maps*. Most of the other maps have been updated, often with a great deal of new information, including chloroplast and mitochondrial maps, and restriction site maps. As an example, for the tomato we have not only the classical gene map but also a molecular map containing 125 RFLP's.

The human gene map includes over 4000 loci identified mainly by mendelizing phenotypes (of which half are not fully identified or validated). Nearly 400 RFLP's are listed, and there is also a new table entitled 'The morbid anatomy of the human genome' giving an alphabetical list of about 300 disorders for which the mutation has been mapped to a specific site. Among these disorders, a few that strike the eye are Dyslexia-1 (presumably a clearly inherited form of word-blindness), Diphtheria-toxin sensitivity, African pygmy (probably associated with mutation in the gene for insulin-like growth factor I), and Leprechaunism. This last intrigues me because my dictionary defines a leprechaun as 'a little brownie who helps Irish housewives'. Ragweed sensitivity is also listed, but I could not find any mention of a mutation causing either sensitivity to grass pollen (hay fever), which in my case included sensitivity to dust from the old Tottenham Court Road (London) cinema, or causing asthma. These genes are surely due for verification in time for inclusion in *Genetic Maps* 5. Volume 4 contains 136 pages on the human genome compared with 48 in volume 3, which indicates the speed of progress.

Progress in mouse genetics has also been dramatic: there are now 1550 genes listed, together with 139 RFLP's, compared with 1068 genes in 1984. So the mouse is doubtless moving further ahead of *E. coli* in gene count, which is a remarkable achievement. The *E. coli* map has not been updated in this volume, so I cannot check this forecast. Counting genes soon becomes an obsession when one starts making comparisons of this kind, so I am tempted to add a few more details. In the mammals listed there is an almost complete absence of colour and coat character