

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

genes, except for the mouse, the rabbit (11 colour and fur genes out of 56), and *Peromyscus* (8 colour or pattern genes out of 23). No colour or coat characters are listed for the cow (60 genes), sheep (25 genes), dog (39 genes), rat (90 genes) or Chinese hamster (62 genes). Even the cat gets only two colour or fur genes (orange and albino) out of 57. This appears to be due to a very strong bias among the geneticists concerned in favour of biochemical/molecular markers, but details of all the colour, coat and morphological genes known would have been of interest.

Volume 3 gave details of the nucleic acid and protein sequence databases, but these are not mentioned in the current volume. So one cannot check how these sequences are progressing without turning to other sources. It is being suggested that the *E. coli* genome will have been completely sequenced within a few years and the human genome by the end of the century. But I am inclined to think that this will not make the further pursuit of bacterial and human genetics redundant.

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Germ Line – Soma Differentiation. Edited by W. HENNIG. Berlin, Heidelberg, New York, Tokyo: Springer-Verlag. 1986. 196 pages. Price DM 98. ISBN 3 540 16635 1.

This volume comprises four reviews on the problems posed by the segregation of the germ line from the somatic cell lines, which in different groups of metazoa occurs at the cleavage stage of their embryos. However this problem may also be studied outside the metazoa; e.g. the recent work by D. L. Kirk's group on *Volvox* (*Genes Dev.* 1, 573, 1987) shows that differential expression of a gene at the *regA* locus prevents somatic cells from redifferentiating as generative cells. These problems are among the oldest in developmental biology and were studied by A. Weismann (1885) for his germ-line theory and by T. Boveri (1887) in his classic observations on the cleavage stages of the nematode now known as *Parascaris equorum*. Here the segregation of the germ line from the somatic cells is accompanied by chromosome fragmentation and chromatin elimination in the somatic lines. It was subsequently found that in most animal species the differences between the germ line and the soma were not achieved by chromatin elimination, which then came to be regarded as a cytological curiosity peculiar to a limited number of species. However, these chromatin-elimination systems would seem to offer a fine opportunity to analyse the nature and the role of the eliminated DNA, but this opportunity seems to have been largely neglected. In well-studied embryos like *Caenorhabditis*, *Drosophila* and *Xenopus* for

instance, germ line determination seems to depend upon the presence of germinal granules localized at the posterior or vegetal pole of the egg. Yet we still do not understand what component of the granules is essential to the determination process or how it operates.

The first review by H. Tobler: 'The differentiation of germ and somatic cell lines in nematodes' is a detailed work with a considerable bibliography, which not only does full justice to the topic indicated by its title, but has a wider scope. Indeed it manages to introduce most of the principles that have guided embryology in the past century while still maintaining a clear and uniform account.

The second review by S. A. Gerbi entitled: 'Unusual chromosome movements in sciarid flies' is concerned with the fantastically complicated chromosomal cytology of *Sciara coprophila* which was first studied by the late Charles Metz and latterly by Helen Crouse. Here germ-line differentiation is accompanied by the elimination of whole chromosomes, rather than by elimination of the distal arms of chromosomes as occurs in *Parascaris*. Moreover in sciarids some chromosome elimination occurs in the germ line as well as in the soma and the meiosis in males takes a most unusual form.

The third review by G. Steinbruck: 'Molecular reorganisation during nuclear differentiation in ciliates' concerns a subject which is now being tackled by a number of laboratories using modern molecular techniques. In ciliates each transcriptionally active macronucleus develops from a germ-line micronucleus. It appears that in those ciliates, like *Tetrahymena* and *Oxytricha* where the problem has been properly investigated, the micronuclei contain germ-line specific DNA which is eliminated in the course of macronuclear development. Micronuclear chromosomes are fragmented to form linear subchromosomal macronuclear DNA molecules, stabilised at their ends by added telomere sequences. Each macronuclear DNA molecule is usually derived from several non-contiguous micronuclear chromosomal segments that become joined together. It seems clear that the idea of constant DNA composition throughout the life cycle of the organism is not even remotely true of ciliates.

Chromatin eliminated from the germ line in nematodes and sciarids is heterochromatic so that appropriately the final short review in the volume is by W. Hennig and entitled: 'Heterochromatin and germ-line restricted DNA'. Here the properties of heterochromatin are restated together with the author's speculations upon the biological role of these DNA sequences with no protein coding function.

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