to consult researchers with expertise in particular areas to ensure all the sections are up to date.

One of the points I find particularly interesting is the tremendous diversity between mosquito species, there are enormous differences in the size of their genomes, their behaviour and in the pathogens and parasites they transmit. It seems to me that one of the biggest hurdles to controlling these disease vectors at present is our lack of understanding of the basic biology of the insects. Bringing all the information together in this way should help researchers determine where the gaps are and act accordingly.

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Genome Analysis – Strategies for Physical Mapping. Vol. 4. Edited by KAY E. DAVIES and SHIRLEY M. TILGHMAN. Cold Spring Harbor Laboratory Press. 1992. 165 pages. Price $49. ISBN 0 87969 412 2.

You really need to have considerable background knowledge about the progress and status of gene mapping in different organisms to appreciate the work described in the five chapters of this slim but demanding volume. The first four chapters wriggle along the evolutionary ladder from *Escherichia coli* to the pig (*Sus scrofa*), pausing on an uneven plateau of *Drosophila melanogaster* and *Arabidopsis thaliana* along the way. The plateau refers to the fact that *Drosophila* and *Arabidopsis* have comparable estimated haploid genome sizes of 165 Mb and 100 Mb respectively. Every schoolchild knows that *Drosophila* is virtually synonymous with genetic analysis, but *Arabidopsis* will not ring many bells. The status of the genome maps in these two organisms reflects this unevenness. The clear-cut organized progress in *Drosophila* is not surprising, given the biological resources available. However, it is heartening to see that integrated analysis of the Thale cress (*Arabidopsis*) has produced a very respectable map using visible traits, cloned gene markers and anonymous genomic clones in the form of YACs from several carefully produced and available libraries. The emphasis throughout for both of these organisms is the need to integrate the maps produced with the aid of different markers and place these onto the YAC contig maps which are the immediate aim for the fruitfly and the cress as well as for the more notorious human map which manages to escape much mention in this volume. Among the differences which are clearly emphasized for *Drosophila* and *Arabidopsis*, is the fact that the Dipteran is uniquely endowed with the pinboard for the ultimate in cytogenetic maps – the giant polytene salivary gland chromosomes – while *Arabidopsis* has hopelessly small chromosomes not amenable to mapping for example by *in situ* hybridization even to the extent that mammalian chromosomes are. The pig map is in its earliest stages. Cytogenetic and contig mapping are possibilities shimmering on the horizon, but there is not yet a single marker assigned to three of the eighteen autosomes. However, although the possibility of genetic analysis is still being created by the systematic production of F2 hybrids between distant strains with a good number of allelic differences between them, it is clear to authors and readers alike that, given the necessary financial resources, the scientific tools are available for very rapid progress in creating a physical map onto which the genetic map can be superimposed and which will then permit direct selection of quantitative trait loci which are of major interest for a species whose main significance is commercial breeding.

In many ways the most disappointing chapter was the one describing the status of what should have been the best characterized organism: *E. coli* with a mere 4·6 Mb genome. The problems of computer representation for a five-enzyme restriction map of this well-known bug engender despair in those of us who look forward to having graphical representation available soon for the whole human genome, where the average size of a single chromosome is thirty times that of the *E. coli* circle. Even the integration of the well-studied physical and genetic conjugation maps has not been achieved satisfactorily for *E. coli*.

The final chapter is an optimistic attempt at analysing how much individual YAC clones, particularly in the context of their contiguous neighbours, will be able to contribute to the complete definition of complex genomes. This area is extremely fast-moving especially in human genome analysis. The next critical step at least for the human map will be the more or less exhaustive identification and isolation of genes (accounting for only about 5% of total genomic DNA) from large genomic fragments. The methods for this are still in the pipeline, and a chapter in a book like this cannot hope to be up-to-date with details of the improved efficiency of exon-trapping mechanisms which recently made a great contribution to the isolation of the gene for Huntington's Disease, or the claim, at a meeting I have just attended, that a US team of 100 people has sequenced at least a portion of about a quarter of all expressed RNA molecules from the human genome. European input (French in the shape of CEPH and Genethon) into such factory-scale genome research has nearly covered the whole human genome with contiguous, if frequently chimaeric, YAC clones. The next improved library is already replacing these clones with cleaner, larger ones. Perhaps we shall see a complete human map before *E. coli* is fully finished. Certainly no paper-bound book can keep up with progress in the fast lane of physical mapping.

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