1 *Genet Res., Camb.* (1989), **53**, *pp.* 237–242 *Printed in Great Britain*

Book reviews

Carcinogen Risk Assessment: New Directions in the Qualitative and Quantitative Aspects. Banbury Report 31. Edited by RONALD W. HART AND FRED D. HOERGER. New York: Cold Spring Harbor Laboratory. 1988. 308 pages. Cloth $85.00 ISBN 0 87969 231 6.

The reports of meetings held at the Banbury Centre have now covered an extensive range of topics relating to human health and the impact of exposure to environmental agents in particular. A feature of these volumes is the space devoted to reporting the panel discussions of the various experts brought together to review a particular topic. These discussions are often more illuminating than the individual papers themselves and the contents of this volume are no exception.

At a time when the magnitude of the problem of regulating the use and disposal of chemicals can sometimes look overwhelming with current resources, the topic of Risk Assessment has become of paramount importance if only in helping us define research priorities. At the present time there are more than 60000 'manmade' chemicals produced at levels of more than 1 ton/annum, with a rate of increase in new products of at least 10% per annum. Current estimates would suggest that in the USA alone, there are more than 50000 dump sites with at least 2000 containing some hazardous chemicals. There is also increasing information to suggest that numerous 'natural' materials such as various components of the diet represent some toxicological hazard that requires assessment.

This volume is divided into five sections: *Structure/activity relationships*, *Pharmacokinetic and Metabolic Activity*, *Molecular Biology*, *Integration* and *Policy and Research*. Each section contains a number of keynote papers followed by detailed discussions which fortunately in some cases go beyond the specific topics covered by the formal presentations. Undoubtedly for the specialist the discussions provide a major incentive to the purchase of this volume.

The section on *Structure/Activity Relationship Data* outlines some of the current attempts to predict toxicological hazard of chemicals using our knowledge of the activity of related structures and most importantly illustrates the limitations of such applications. Individual and species variation in the metabolism of potentially toxic chemicals is well illustrated in the *Pharmacokinetic* section. Models of the rates of such factors as partition coefficients between air, blood and various tissues, blood flow rates, respiratory rates etc. are becoming of increasing importance in regulatory decisions upon such chemicals as methylene chloride, where man and the experimental models may show substantial differences which influence the quantitative aspects of the chemical's toxic action.

The section on *Molecular Biology* is rather limited in scope, in that it includes only two presentations; namely a brief review of 'The interactions of some carcinogens with DNA' by Singer and a discussion of 'Non-genotoxic mechanisms in carcinogenesis' by Trosko and Chang. Both papers provoked some lively discussion but this section would have been better balanced if it had included some presentations on present developments such as the role of identifying specific oncogene activation in future hazard assessment.

Overall, the book makes a valuable contribution in presenting the problems that face us in the whole area of assessing the risks of toxic chemicals and the publishers are to be commended on producing the volume in a relatively short interval after the meeting. However, in view of the overwhelming importance of the discussions in these volumes I wonder if they would not be better produced as tapes for more rapid communication to the scientific community.

JAMES M. PARRY
School of Biological Sciences,
University College of Swansea,
Swansea, Wales, UK

Mutation, Developmental Selection and Plant Evolution. By EDWARD J. KLEKOWSKI, JR. New York: Columbia University Press. 1988. 373 pages. $55.00. ISBN 0 231 06528 0.

It has been argued that biological systems have been fashioned by adaptive response to extrinsic conditions of life and intrinsic hazards of genetic instability and error. This book investigates the latter, less familiar of the two categories. Mutation is treated as a destabilizing influence which can be mitigated by particular forms of development and reproductive behaviour, as well as the way the genome is ordered. Plants lack a germline and therefore somatic mutation is an important, potential contributor to mutation frequency in the gametes. But the chances that a somatic mutation will be transmitted to the gametes will be greatly influenced by the position of the affected cell in relation to meristem organization and the rules about which cell layers contribute to

sporogenesis. The general thesis is developed in a well-documented, comparative survey of relevant evidence from angiosperms, gymnosperms and pteridophytes.

Possible sources of mutational change in plants add up to quite an impressive tally. Whether it be misalignment mutagenesis associated with particular nucleotide sequence 'hot spots', DNA slippage and mispairing, errors in protein, especially DNA polymerase synthesis, the disputed origins and status of repeated sequences, unequal crossing-over, gene conversion, the possible consequences of RNA reverse transcriptase activity, transposable elements, the results of interaction between microbes and plant genomes etc., there are enough demons of genetic disarray to justify the reference to van Valen's Red Queen Effect.

The ways in which the effects of mutation can be restricted are grouped into two general categories, namely those which arise from the way the genome is organized and replicated and those which are determined by the particular style of development and/or reproduction. As to the former there are the obvious effects of diploidy and dominance in reducing the immediate effects of somatic mutation, the possible buffering effects of redundant DNA, the possible non-random distribution of transposons, the general advantages of partitioning the genome among a number of chromosomes, thereby diminishing the hazards of acentic fragments produced by chromosome breaks, the short-term advantages of diffuse centromeres in a few groups etc. But with respect to DNA synthesis and repair, including the discrimination against insertion of the wrong nucleotides, correction during replication at the DNA growing point, mismatch repair and the like, the author is cautious, given current ignorance about exactly what happens in plants and recognition that simple extrapolation from mammalian systems may be risky. Also at present it is a matter of speculation how far the relations between the nuclear, mitochondrial and chloroplast genomes might contribute to genetic stasis.

The ground appears firmer when we turn to the consequences of alternative patterns of development and reproduction, and it is these aspects which take up most of the discussion. The chance of a somatic mutation being transmitted to the gametes will differ according to whether the primary event occurs in what the author terms a structured or a stochastic meristem. In a structured meristem the division of an initial cell always results in a daughter cell which acts as the next initial, while the other cell may divide and contribute to the soma. In a stochastic meristem the initials divide to give rise to a population of cells from which subsequent initials are selected. Structured meristems with more than one initial favour the establishment of sectorial and mericlinal chimeras and diminish the scope for competition between mutant and non-mutant initials. In stochastic meristems mutations may be lost by chance, resulting in transient chimeras and maximum scope for competition between genetically different cells and tissues, although random loss is considered likely to be more important.

These basic ideas are developed in considerable detail, with reference to comparisons of the scope for intra-plant cellular competition according to the often disputed interpretations of the way apical meristems behave. Stratified meristems, with a corpus surrounded by one or two tunica layers, have revealed how different kinds of chimera arise and whether or not a particular somatic mutation is likely to be transmitted to the gametes. In dicots sporogenous tissue is generally derived from the inner of usually two tunica layers (L11), while in monocots both tunica layers contribute. But periclinal divisions leading to cell displacement between layers confuse the picture since ontogenetic fate is determined by the layer in which a cell finds itself. The likelihood of such divisions varies widely for both genetic and environmental reasons. Interpretation becomes more difficult in component meristems, given the uncertainty about the permanence or otherwise of apical initials. The author gives a balanced account of the alternative possibilities and concludes that most somatic mutations are selectively neutral within the apical meristem. In somatic tissues ramet competition, the main cause of selective loss of mutations, is supplemented by random loss.

Restriction of the phenotypic effects of somatic mutation may operate at two levels. There may be primary, genomic tolerance to mutation, inherent in the properties of the genetic code, the incidence of DNA methylation, the occurrence of nucleotide sequences which minimize the adverse effects on reading frames of adding or deleting a base etc. There are also the properties of developmental homeostasis, which allow plants to form functional organs from mixtures of mutant and normal cells. Hence the major significance of somatic mutations lies in their chance of transmission to the gametes. In this context more important than tissue competition will be developmental selection during early embryonic or gametophytic stages, e.g. inter-ovular selection within ovaries, selection between embryos, selection among male or female gametophytes or selection between gametes. The significance of these alternatives is discussed for different classes of plant.

From the effects of mutation at the level of the individual the author turns to consequences at the population level. There is a critical discussion of genetic load, including a summary of the author's comparative studies on ferns, whose gametophytic generation is singularly convenient for the estimation of genetic loads. The wide differences between species in genetic load are accounted for by differences in clone longevity and frequency of sexual reproduction.

Research workers, graduate students, indeed anyone interested in plant evolution, will find this book a stimulating exploration of ideas, which enrich the

texture of evolutionary debate. At this stage it is impossible to come up with confident estimates of the relative significance of the different ways in which genetic stasis may be threatened or secured. That must wait until there is better understanding of how the plant genome is organized, the practical importance of the different ways in which it may be altered, as well as in what ways the consequences of somatic mutation are subject to the vagaries of development and reproduction. In the interim the author is content to alert us to the manifold possiblities and engage our sympathy for his point of view.

FORBES W. ROBERTSON
41 Braid Farm Road,
Edinburgh EH10 6LE

Proceedings of the Second International Conference on Quantitative Genetics. Edited by BRUCE S. WEIR, EUGENE J. EISEN, MAJOR M. GOODMAN and GENE NAMKOONG. Sunderland, Mass., U.S.A.: Sinauer Associates. 1988. 763 pages. $38.50 (paper), ISBN 0 87893 901 6. $60.00 (cloth), ISBN 0 87893 900 8.

The so-called quantitative characters tend to be given a wide berth by most geneticists, in spite of the very important part they must play in evolution and the fact that they form the main raw material for food plant and livestock improvement programmes. Such characters are generally assumed to be under the influence of many genes of small individual effect, whose interplay is obscured in practice by the large amount of environmental variation, though an occasional major gene may be caught segregating.

Study of these genetic systems is frustratingly slow to yield significant results, and this doubtless explains why the first and second international conferences on quantitative genetics were held eleven years apart (in 1976 and 1987), and attracted only a modest 250 and 500 participants, respectively. The proceedings of the second conference, under review here, might under these circumstances have been organized more with the potential newcomer to the field in view. This could have been achieved by starting with some review articles designed to give us a clear picture of progress over the years made with crop plants, livestock and 'model' laboratory animals, followed by a not too difficult review of the progress made in mathematical theory which can be applied in these areas. But we do not get assistance of this kind, and the newcomer or tenderfoot will have to pick his way among the 55 chapters (the editors' name for the individual contributions, which range from 2 to 28 pages in length) looking for the background picture. There is often only a limited connexion between neighbouring chapters (e.g. the Booroola sheep's F gene is sandwiched between two papers on human genetics); and the large amount of mathematics distributed liberally among the papers may also cause him to run for his Hardy. However, a detailed subject index is invaluable in tracing topics, and all references are collected at the end of the book to form an excellent bibliography. A few notes from scanning both chapter headings and index will give the reader a rough idea of what the book contains and omits.

Seven papers deal specifically with human quantitative genetics, and include Smouse & Long on the population structure of two tribes of slash and burn horticulturalists, Sing *et al.* on disease-associated traits, Eaves *et al.* on human developmental change (a model), Cloninger on alcoholism, Fulker on genetic and cultural transmission in human behaviour and Iselius on genetic epidemiology of common diseases. A number of papers consider livestock quantitative genetics and its applications: the Booroola sheep in which the F gene has a marked effect on ovulation rate (Piper & Bindon), finding genes which affect quantitative traits (Pirchner), inserting retroviruses – specifically the avian leucosis virus – into the avian germ line (Crittenden & Salter – this would certainly frighten the British egg-consumer), selection response for egg production in inbred lines (Abplanalp), genetic technology and its potential in animal breeding (articles by Bechard and by Smith), and selection in farm animals (articles by Van Vleck and by Ollivier).

Molecular genetics has yet to make a major impact on livestock, regardless of the well-known transgenic mice. In plant breeding, however, major progress seems closer, following the many years of work on *Agrobacterium tumifaciens* and its T plasmid, the new methods such as shooting microprojectiles coated with DNA into plant cells, and linkage analysis with RFLPs to locate useful quantitative genes. Several papers discuss some of these possibilities in a rather general way: these include Soller & Beckmann, who invent the horrible term 'Genomic Genetics' for RFLP analysis in this context and give us a mathematical run-down on how to treat the data when we get some, Sozonov on the use of biochemical markers (gliadins, glutenins etc.) to distinguish valuable wheat and barley genotypes, Shillito on the fate of DNA introduced into plants, Dudley on identifying lines useful for improving elite single crosses in corn, and Vencovsky *et al.* on corn breeding studies in Brazil.

Experiments on laboratory animals get less than their fair share of attention, being only represented by Mukai on genotype–environment interaction and the maintenance of variability in *Drosophila melanogaster* populations, Mackay on the novel study of transposable element-induced quantiative genetic variation in *Drosophila*, and Frankham on exchanges in the rDNA multigene family as a source of quantitative genetic variation in *Drosophila*. The mouse gets hardly mentioned, as do the important long-term selection experiments on tribolium by Enfield and *Drosophila* by Yoo and others – these focused attention on mutation as an important source of quantitative variation (see article by Hill & Keightley).

This by no means exhausts the range of topics