Book review

Chater, K.F.; Cullis, C.A.; Hopwood, D.A; Johnston, A.W.B.; Woolhouse, H.W. (eds.): Genetic Rearrangement. London, Canberra: Croom Helm 1983. $ 16.95.

From Sept. 14–17, 1983, the 5th symposium entitled "Biological Consequences of DNA Structure" was held at the John Innes Institute, Norwich, England. The written record comprises this book of 17 self-contained, uniform and precise research articles written by authorities in their respective fields. Almost all these papers center around DNA, its genetic uptake, recombination, topology, transposition and amplification. Gene cloning, DNA sequencing and Southern hybridization techniques have provided a technical unity to many of these articles and indicate that while modern genetic engineering techniques using DNA technology are powerful and full of potential, they are also loaded with numerous ambiguities. Many of these are cleared up by new information presented in this book. For instance, the ability of recombination enzymes to interact with Chi is known to be conditioned by the polarity of either packaging or infection. Frank Stahl and his associates, however, through elegant experiments, have found similar Chi-activity when the enzymes are introduced through routes other than injection. Similarly, whereas for site-specific recombination of bacteriophage Lambda, supercoiled DNA substrate is normally required, Pollock and Nash demonstrated that even under certain optimal conditions, non-supercoiled DNA can also recombine. The recombination is low and slow due to topology of circular DNA as revealed through the use of the enzymes DNA topoisomerase I and II.

Major agents causing genetic-noise and genome-instability are specific DNA sequences – the transposable elements. Sherratt et al. detail the pathway and control of Tn_3 bacterial family transposons. Cloning and characterisation of Tam I transposable elements of *Antirrhinum majus* and Cini and Teol DNA inserts of *Zea mays* and *Z. mexicana* are described by Saedler et al. Burns et al. elucidate the structural aspects of retroviral long terminal repeats. Once integrated, the viral genome is stable and transpositions and excisions become rare. This implies that retroviruses represent a valuable vector system for gene transfer in eukaryotic systems. Systems that mediate DNA inversions in bacteriophages and the transposon associated recombinational mechanisms in *Salmonella* flagellin genes have been described by Szekely and her colleagues. Schrempf has found biological variation in the sequences involving plasmids or transposons that appears to be associated with a prevalence of reiterated sequences within several *Streptomyces.*

When cells are placed in an environment in which survival and/or growth advantage results from protein overproduction, gene amplification often occurs. Schmike describes various properties of amplified genes and mechanisms of gene amplification. Agents that inhibit replication or induce damage to replicating DNA, lead to amplification of large DNA lengths. But how and why this occurs is not known. Renaturation kinetics of flax genotrophs reveal DNA sequence differences ranging from highly repeated sequences to low-copy number. Cullis considers DNA amplications and deletions to be environmentally induced. However, integration of Simian Virus 40 DNA into chromosomal DNA of rodent cells is nonspecific and viral sequences are frequently tandemly duplicated. Rigby et al. have demonstrated that following the integration, a complex series of amplification and rearrangement events occur that involve viral sequences and flanking-cellular rodent-DNA. DNA transfection experiments reveal mutant T-antigens to be competent for transformation but defective in viral DNA replication initiation. Thus, it is suggested that replication function of large T-antigen is involved in genome amplification, which is deleterious to the cell.

In DNA, certain nucleotide sequences are conserved in sex chromosomes of snakes, birds and humans. Jones et al. show these sex specific transcripts to be detectable by Bkm probes. Hepburn et al. studied the fate of T-DNA introduced into the flax genome through *Agrobacterium tumefaciens* strain T37. The inserted genes remain silent and are probably switched off in the transformed cells. For switch-on, demethylation signals and promoter genes are required. On the other hand, Borst et al. found VSG genes to have a single expression site over which the genes move, or transpose for expression. Rabbitts et al. demonstrate the necessity of certain DNA S-segments for human immunoglobin gene expression and evolution. In maize segments, similiar DNA S_1, S_2 episomes integrate into the mt-DNA genome and these alterations are considered to be the cause male sterility. The genetic significance of these alterations S_1, S_2 and Ct DNA sequences are discussed by Lonsdale et al.

The overall organisation of the book is exceptionally tight, the format is excellent and the contents are revealing with enough new information. In a few papers the main theme is lost; in all of them summarized information is missing; some depend on theoretical models for developing a conclusion. Keeping in view the quality and contents of this book, which are broader than its title suggests, it is a valuable addition to the fast, ever expanding field of DNA-technology and molecular genetics.

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