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Book Reviews

Cold Spring Harbor Symposium on Quantitative Biology. Volume XLIX. *Recombination at the DNA level.* Cold Spring Harbor Laboratory. 1985. 854 pages. Cloth $130 ($156 elsewhere). ISBN 0-87969-049-6

After a gap of six years the Cold Spring Harbor Symposium on Quantitative Biology returned, in 1984, to the subject of Genetic Recombination. Volume 49 records the proceedings in 93 articles divided between 16 sections, and it is obvious that, in the intervening years, there has been a great deal of progress. Originally, studies into the mechanisms of recombination were confined to events associated with the recombination of homologous DNA molecules, but the discovery of several biologically important phenomena in which DNA molecules sharing little or no homology are rearranged has resulted in a greatly enlarged scope in recombination studies. There is now intensive interest in the processes involved in the so-called 'illegitimate recombination'. These symposium proceedings record in detail not only the progress but also the extended scope of research into recombination.

Perhaps the greatest strides have been made in understanding the enzymology of recombination. This has been facilitated by the development of methods for studying recombination *in vitro* – there is a section devoted to *in vitro* systems – which has led to the realization of the importance of 'protein factories' in recombination. The central role that factories – large multifunctional complexes of proteins acting as units – play is one of the recurrent themes of the symposium. In homologous recombination the characteristics of some enzymes and their likely *in vivo* role have been worked out in detail. For example, Rec A protein, in association with single strand binding protein, is known to be important in the initiation of recombination; promoting pairing, D-loop formation and unidirectional branch migration. One section comprising nine articles is devoted entirely to studies of this protein. Studies on proteins with equivalent properties in other organisms are reported by Holliday *et al.* for Rec I protein in *Ustilago* and Formosa and Alberts for UVS X protein in T4. Other proteins have been studied less extensively but are thought to play an important role in the resolution of recombination intermediates. Kemper *et al.* and de Massy *et al.* report studies on endonucleases in T4 and T7 respectively which cleave Holliday structures. Similar impressive strides have been made in studies into non-homologous recombination. The importance of type 1 topoisomerase in catalysing the breakage and reunion of DNA has been estabished in lambda integration and Tn 3 transposition. Type 1 topoisomerases are also known for other organisms although in these cases their *in vivo* role is not yet firmly established. Other articles also report work on enzymes with an unknown *in vivo* function. For example, Ferro *et al.* have studied poly(ADP-ribose) synthetase, an enzyme which adds polyADP-ribose chains to proteins. Topoisomerase I is a good substrate for this enzyme, being the best exogenous acceptor of polyADP-ribose yet discovered. As a result of the activity of the synthetase its substrate becomes progressively more negatively charged until the point is reached where the topoisomerase is effectively inactivated because it can no longer attach to DNA.

The availability of *in vitro* methods of studying recombination has resulted in the development of efficient methods for detecting and isolating proteins which interact with DNA. As a result it is very likely that, in the near future, there will be a considerably increase in the body of data on proteins involved in recombination. The progress that has been made is very well documented in this volume.

The structure of DNA intermediates and the nature of the interaction between DNA molecules during recombination also receives attention in several articles. There are papers on presynaptic alignment of DNA (although disappointingly not much on the mechanism of chromosome pairing), D-loop formation, branch migration, mismatch repair and chi-sequences.

The role of traditional genetic analysis receives less attention but is not entirely neglected. There is a section – curiously entitled 'Chromosomal mechanics' – which contains papers devoted to this method of analysing recombination. The article by Rossignol *et al.* illustrates that ascus analysis remains a powerful tool in discriminating between different models of recombination. In this respect two models which are currently receiving widespread attention are the double-strand break model (proposed originally by Resnick in the context of DNA repair and extended to recombination by Orr-Weaver *et al.*) and the Aviemore model of Meselson and Radding. Distinguishing these will depend on the analysis of the nature of the initiating steps and might be best achieved using the techniques of molecular biology rather than genetics.

This volume then gives a comprehensive coverage of the 'nuts and bolts' of the recombination process. With one or two exceptions it lacks articles giving an overview. The paper by Carpenter is an exception and considers the meiotic role of crossing-over and conversion. She speculates, in a very interesting way, on the evolutionary significance of recombinational pathways. Amongst the detailed analyses there is little room for speculation on the role of illegitimate recombination in the evolution of novel genomes or the evolutionary relationship (if any) between the mechanisms of homologous and non-homologous recombination (although the relationship of the various non-homologous systems is considered).

Those aspects of genetic recombination in which there is little progress towards a molecular explanation are also largely neglected. For example, there is no mention of interference between crossovers, although it did occur to me, when reading about the modification of topoisomerases by the addition of ADP-ribose moieties, that the progressive modification of a molecule involved in resolving recombinational intermediates might form the basis of an explanation for interference.

These are, however, minor criticisms of a symposium volume which provides a thorough analysis of current knowledge of recombination. The proceedings will take their place alongside others in the series as an indispensable addition to a genetics library.

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