evolution to positive natural selection for improvements in the function of hemoglobin and the slow evolution to stabilising natural selection after the improvements were fixed", following which "natural selection would then be able to shape the finer adaptations of the protein". It is possible to propose, however, various interpretations to account for such observations, and Goodman acknowledges this point.

Fitch, in discussing molecular evolutionary clocks, says that "we have several sloppy clocks", which may be an example of sloppy diction. He states that "the tRNAs are mostly paralogous", which was news to me, because there are many examples of homologous tRNAs for the same amino acid occurring in related species of organisms. Obviously, many thousands of such tRNAs have not yet been sequenced. Fitch tells us it came as something of a shock to him that Δ haemoglobin has never been sequenced, which leads me to comment that those who accept the sequences in the *Atlas of Protein Sequence and Structure*, instead of referring to the original literature from which the sequences are derived (sometimes by presuming the sequences of unordered peptides), should expect such shocks. Fitch gives a good discussion of the rates of 'silent' nucleotide substitutions. He challenges comparisons of snake, bird and turtle cytochromes *c* by suggesting that "either one or more of its sequences is incorrect", which is an easy out of the argument.

The review by Galau and co-workers is a valuable compilation of recent results on the rate of re-association of various types of DNA. Wilson presents an excellent summary of the differences in rates of evolution between frogs and placental mammals in support of his thesis that contrasts the rates of organismal change and structural gene evolution. The apparent similarities of different species of frogs to each other conceals the fact that they may be widely separated in terms of ancestral history, and also in terms of amino acid differences between their homologous proteins. Hinegardner discusses the wide variations in haploid DNA contents per cell in various groups of organisms. The DNA content per cell has increased during the history of life on Earth, but mammals do not lead the parade.

I wish that the term "nonsense" for polypeptide chain-terminating codons, and the non-word "missense" for mutations that produce single amino acid changes (as used and defined by Ayala) could be relegated to the graveyard of discarded and superseded neologisms. But new words never seem to die, or even fade away. □

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# Somatic cell hybrids

**R. T. Johnson**

*Cell Hybrids.* By N. R. Ringertz and R. E. Savage. Pp. 366. (Academic: New York and London, 1976). $29.50; £20.95.

THERE are relatively few events in the recent history of biology which have so fired and re-directed the imagination as somatic cell fusion. Suddenly, in the mid-1960s, the unexpected and unnatural seemed commonplace in cell biology. Somatic cells of diverse origin and nature could be brought together within a single cell, their interactions studied and their hybrid progeny cultured for subsequent analysis. The revolution that Sendai virus-promoted fusion brought to the embryonic subject of cell hybridisation not only permitted the achievement of a greater number of fusion events by a greater number of people but also generated the enthusiasm to develop hybrids between seemingly impossible combinations of cells. The search for agents that promote fusion between unlikely partners remains an area of continuing interest, with the recent demonstration of polyethylene glycol-induced fusion of human and plant cells.

The unusual attraction and usefulness of cell hybrids to biologists soon became evident from the growing number of publications covering a very wide area of contemporary biology. Cell fusion rapidly became one of the most attractive ways of detecting differences between cells. By combining two cells it is possible to monitor some of their differences by following interplay with respect to such general genetic activities as the initiation of RNA and DNA synthesis, and more specifically, to the extinction, re-expression and activation of single genes. Although fraught with difficulties, the analysis of the differentiated state by means of cell hybrids has now progressed to a stage where general rules for the expression of facultative functions can be expected before long. Similarly, the usefulness of somatic cell hybrids in gene complementation and mapping is in no doubt, and advances here and in the study of differentiated expression in hybrid cells are fortunate to have coincided with a revolution in methods for chromosome identification. Cell fusion has also provided an opportunity to study the nucleocytoplasmic interactions in mammalian cells in ways which are similar to the investigations so elegantly carried out using the technique of nuclear transplantation in large cells like Protozoa or amphibian oocytes.

In this well illustrated volume the authors have gathered together, for the first time, the accumulated work up to the end of 1975 on somatic cell fusion and cell hybrids. This is a large, complex, controversial and expanding field and we are therefore indebted to Drs Ringertz and Savage for this timely compilation and review of the subject, reduced to manageable proportions and written with clarity.

The aim of *Cell Hybrids* is to provide an up-to-date account of the contributions made by cell fusion and cell hybrid studies to major areas of somatic cell investigation including cell cycle control, the expression of differentiated functions and malignancy, and the mapping of constitutive genes. It is also intended that the volume should serve as an introduction to students and to workers in other areas. A useful background is therefore included in each chapter providing sufficient information for critical appraisal of results obtained.

Because of their limited lifespan animal cell heterokaryons are less frequently investigated than their hybrid progeny. As the authors stress, however, heterokaryons permit analysis of regulatory phenomena in the presence of complete genomes and should be included whenever possible in any full description of gene expression in hybrid cells which usually contain a reduced and occasionally modified complement of chromosomes. Possibly the most famous heterokaryons contain chick erythrocyte nuclei which, as Henry Harris showed 12 years ago, are reactivated from the quiescent state. Much of the elegant work on erythrocyte activation has emerged from the Karolinska Institute and this is well represented in *Cell Hybrids*.

The very great problems that attend the unravelling of genetic interplay in somatic cell hybrids may to some extent be reduced by the use of reconstructed cells, and a full description of this new area of cell manipulation is included. For example, the production of hybrids by the fusion of whole cells with microcells containing very small quantities of DNA not only predetermines the segregation pattern but may speed up and ultimately simplify the analysis of gene localisation and regulation.

The advent of cell hybridisation has permitted many new experimental approaches to major and seemingly intractable biological problems. A number of the problems have now been reduced in stature and others re-defined because of cell hybrids. We should be grateful to the authors for this comprehensive and readable work on the subject.

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