It will certainly guide researchers to areas where sufficient understanding is lacking and provide the overview necessary for the integration of new research findings into the broader understanding of the fungi.

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Nonhistone Proteins

Acidic Proteins of the Nucleus. IVAN L. CAMERON and JAMES R. JETER, JR., Eds. Academic Press, New York, 1974. xvi, 346 pp., illus. $28.50. Cell Biology.

Stimulated by discoveries that histones are phylogenetically very stable proteins lacking both the specificity and the heterogeneity expected from gene regulatory macromolecules, the attention of many investigators turned to another family of nuclear proteins—the acidic proteins, or perhaps more correctly, the nonhistone protein components of chromatin and chromosomes. This poorly defined group seems to hold answers to the paramount questions of cell growth, proliferation, and differentiation. Although many of the nonhistone proteins may serve only simple functions and, like the histones, fail the crucial tests of specificity required for the sophisticated game of selective gene activation and restriction, it can be expected that at least some of the proteinaceous components of chromatin and the cell nucleus will prove to be true regulators of genetic activity. This optimistic expectation runs like the thread of Ariadne through *Acidic Proteins of the Nucleus.*

With minor exceptions, the individual chapters cover their topics clearly and comprehensively. The presentation flows logically from accounts of the methods for isolation and characterization of chromosomal nonhistone proteins through discussion of their in vivo modifications and biosynthesis to a more speculative finale concerning their roles in selective regulation of the eukaryotic genome and gene activation via hormonal interactions.

In the opening chapter, V. G. Allfrey presents a skillful discussion of the biochemical mechanisms by which individual genes may be regulated in higher organisms. He draws attention to gene regulatory proteins in prokaryotes as indicating a promising direction for research into the existence of functionally specific proteins with affinity for DNA in eukaryotic chromosomes. In the next chapter, G. L. Patel presents an extensive account of the isolation and fractionation procedures used by various investigators to characterize nuclear proteins. A logical extension of this chapter is a detailed critique of nuclear protein extraction procedures, especially of those using buffered aqueous phenol solutions. Subsequent authors (W. M. LeStourgeon and W. Wray) present evidence that phenol extraction procedures may be no more detrimental to numerous proteins than is exposure to more conventional solvents, such as high salt and urea solutions.

The next two chapters deal with the phosphorylation of nuclear nonhistone proteins in vivo. L. J. Kleinsmith, who, with several of his colleagues at the Rockefeller University, first pointed out the importance of nuclear phosphorylation, describes the many interesting features of these macromolecules, together with the properties of the enzymes (phosphoprotein kinases) responsible for their phosphorylation in vivo. An analysis of nuclear phosphoproteins in *Physarum polycephalum* is presented by B. E. Magun.

The third group of papers deals with chromosomal nonhistone proteins during cellular growth and differentiation. Drawing on their experience with *Physarum* and other cells, W. M. LeStourgeon, R. Totten, and A. Foer describe their discovery of contractile proteins in isolated nuclei and chromatin and aptly tie this description into more general discussion of nonhistone protein changes in differentiating cells. Special advantages that polytene chromosomes offer for structural and functional studies on chromosomal proteins are reviewed in detail by H. D. Berendes and P. J. Helmsing. The last chapter in this group is an excellent discussion of nuclear nonhistone proteins during the temporal flow of the cell cycle by Jeter and Cameron, the editors of the book.

The last two articles attempt the difficult task of implicating chromosomal nonhistone proteins in specific gene regulatory functions. T. C. Spelsberg lends his expertise in steroid hormones and chromatin biochemistry to guide the reader through the difficult and sometimes controversial experiments of various investigators who have attempted to unravel the mechanisms by which steroid hormones activate the transcription of selected genes in target cells. Although definite answers are still wanting, the experiments discussed point to the chromosomal nonhistone proteins as mediators of the biological actions of steroid hormones. The book ends with a discussion of some special properties of the nonhistone proteins by R. S. Gilmour. He shows that these macromolecules are essential for the ordered expression of genes and for the transcriptional specificity of chromatin.

This is a well-written, lucid book summarizing the knowledge of chromosomal nonhistone proteins up to about the end of 1972. Although *Physarum* receives perhaps more than its share of attention, other model systems are discussed, and students of the cell nucleus and its proteins will find this book a valuable if not essential addition to their libraries.

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RESEARCH NEWS

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tween real and randomly generated systems. He discovered that real clades of shallow water marine invertebrates that originated in the Cambrian and Ordovician periods differ from randomly generated clades. These clades fill up more quickly with species and die out more slowly than the random clades. However, during these periods, which occurred early in geological history, the earth was filling up with species. After the Ordovician, during the Silurian period, all major taxonomic groups were established and no new phyla originated. At this time, presumably, species diversity could have reached equilibrium. Gould found that the clade shapes for shallow water marine invertebrates during and after the Silurian resembled those of the randomly generated clades.

Not all investigators accept the models and conclusions drawn by Raup, Gould, Schopf, and Simberloff. Arthur Boucot of Oregon State University, for example, thinks the models are too simple. They are "clever, polished, but of limited use," he says. Randomness in evolution is not unexpected, Boucot points out. And major geological events, such as climactic changes, are correlated with major evolutionary events, such as massive species diversifications and extinctions. However, such correlations are not considered in the models that treat all species and all geological times alike.

Another criticism of the stochastic models of evolution is voiced by Karl Flessa and Jeffrey Levinton of the State University of New York at Stony Brook. These investigators used the independent statistical techniques of factor analysis and the runs test to argue that the originations of various taxa in the real world did not occur at random and that there are nonrandom patterns of taxonomic diversity in the fossil record. In other words, they believe that many of the patterns in the fossil record could not have been randomly generated. Gould and Schopf, however, are not convinced that Flessa and Levinton have demonstrated patterns above and beyond those that could be derived from random processes.

Although equilibrium models in paleobiology are still a new concept, Schopf believes that they are leading to a revitalization of that field. Investigators devoted the past century to studying the histories of individual species, but were unable to solve some major problems. Now that a new conceptual framework has been introduced, says Schopf, "it will be fun to see where things go."—GINA BARI KOLATA

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(Continued from page 630)

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