polyacrylamide-gel electrophoresis has shown these proteins to be heterogeneous and similar in all tissues studied. However, tissue specificity in this group of proteins cannot be eliminated, as the complexity of the gel patterns makes it difficult to observe differences. The phosphorylation of nuclear proteins has been correlated with changes in the rate of DNA transcription (Frenster, 1965; Gershey & Kleinsmith, 1969; Kamiyama & Dastugue, 1971), and therefore it may be that in any tissue the species of nuclear proteins that are phosphorylated are characteristic of that tissue.

Nuclei from mouse brain, kidney, liver and Landschütz ascites cells were incubated with [γ - ^{32}P]-ATP, and the non-histone proteins were separated on hydroxyapatite columns. Measurement of the radioactivity associated with proteins after sodium dodecyl sulphate-polyacrylamide-gel electrophoresis showed that some species were phosphorylated and that the pattern of phosphorylation was tissue-specific. It appeared that the more highly phosphorylated proteins were eluted from the column after the bulk of the non-histone protein.

Addition of mouse liver non-histone proteins to an RNA-synthesizing system containing *Escherichia coli* RNA polymerase and mouse liver DNA as template stimulated the rate of RNA synthesis. No such effect was observed if the mouse liver proteins were added to calf thymus DNA or *E. coli* DNA under the same conditions. Bovine serum albumin had no effect on the template activity of any of these DNA preparations. Preliminary observations on the mechanism of this stimulation suggest an increase in the number of initiation sites for RNA synthesis on the DNA template in the presence of homologous non-histone proteins. It is not clear whether the effect is due to the phosphoproteins alone, and work is now in progress to fractionate the non-histone proteins into components with different effects on the rate of transcription.

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Homopolymer Sequences in Mammalian Deoxyribonucleic Acid

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It has recently been speculated that deoxyribonucleotide homopolymer sequences in mammalian-cell DNA might serve as specific signals for RNA polymerases with different functions (Becker, 1972). Utilization of [^3H]poly(U) and [^3H]poly(C) has allowed the detection and quantitative determination of complementary sequences in DNA by the standard techniques of nucleic acid hybridization (Shenkin & Burdon, 1972).

Hybridization of [^3H]poly(U) to hamster DNA is optimal at 18–22°C and is complete by 4h. Approx. 0.42% of the genome is complementary to [^3H]poly(U), the deoxyadenylate-rich sequences being randomly distributed throughout the DNA molecules, whatever their adenine + thymine content, as judged by CsCl equilibrium centrifugation. The 'melting' profile of the hamster DNA·[^3H]poly(U) hybrid suggests some heterogeneity in size of the sequences hybridized and approx. 10% mismatching of base pairs in the hybrids.

On the other hand, hybridization of [^3H]poly(C) to hamster DNA takes place optimally at 54–62°C, the reaction being complete in 5 min at 62°C. There does, however, appear to be considerable mismatching of base pairs within this hybrid. Approx. 0.04% of the hamster DNA hybridizes to [^3H]poly(C), the complementary sequences being found only to a slightly greater extent in those DNA molecules with a high guanine + cytosine content. Shearing of the DNA to an average molecular weight of 2×10^5 before centrifugation in CsCl does not alter the patterns of hybridization with either [^3H]poly(C) or [^3H]poly(U).

The polydeoxyadenylate-rich and polydeoxyguanylate-rich sequences, thus detected, are found to a much greater extent in the mammalian DNA species than in the bacterial or bacteriophage DNA species so far tested. Although the significance of this finding is not clear, it may be related to the presence of adenylate-rich sequences detected in mammalian mRNA species (Lim & Canellakis, 1970; Darnell *et al.*, 1971) and in heterogeneous rRNA species (Edmonds & Caramela, 1969).

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