of these accounted for more than 95% of the radioactivity and had a mobility identical with that of the maleyl-peptide obtained from the dimer. Less than 5nmol of these peptides was available, but a micro 'dansyl'-Edman technique for determining the sequence was developed by scaling down the standard technique (Gray, 1967) to permit the detection of 10pmol of DNS-amino acid. By using this procedure the peptides, after being unblocked, were shown to have the sequence Ala-Gly-Gly-Thr.

As only one *N*-terminal sequence was detected, it is highly probable that the subunits of methionyl-tRNA synthetase are identical. Also, since the *N*-terminal sequences of both the dimer and the tetramer are the same, the conversion of tetramer into dimer cannot involve proteolytic cleavage except from the *C*-terminus.

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Heat Inactivation of Lysyl-Transfer-Ribonucleic Acid Synthetase and Arginyl-Transfer-Ribonucleic Acid Synthetase from Yeast: Evidence for Substrate-Induced Conformational Changes

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A 400-fold-purified preparation of lysyl-tRNA synthetase [L-lysine-tRNA ligase (AMP), EC 6.1.1.6] from baker's yeast (Chlumecká, von Tigerstrom, D'Obrenan & Smith, 1969) was protected against heat inactivation by L-lysine alone but not by normal substrate-level concentrations of ATP and MgCl₂ or tRNA and MgCl₂. The heat stability of the enzyme in the presence of lower concentrations of L-lysine was increased considerably by addition of ATP and MgCl₂ or tRNA and MgCl₂. Studies of the rate of heat inactivation of the enzyme in the presence of different concentrations of L-lysine suggested that the characteristics of binding of the amino acid to the enzyme in the absence of other substrates were different from those found in the presence of ATP and MgCl₂ or tRNA and MgCl₂. The experiments also suggested that the binding of tRNA to the enzyme in the presence of L-lysine was stronger than that found in the absence of the amino acid.

Experiments carried out with a partially purified preparation of arginyl-tRNA synthetase [L-arginine-tRNA ligase (AMP), EC 6.1.1.-] from baker's yeast (Mitra & Smith, 1969) showed different patterns of protection by substrates against heat inactivation from those found with the lysine enzyme. For the arginyl-tRNA synthetase maximum protection was observed in the presence of L-arginine, tRNA and MgCl₂, whereas L-arginine, ATP and MgCl₂ gave little protection. These results, suggesting that the binding of L-arginine is rather weak in the absence of tRNA, are consistent with other results (S. K. Mitra, A. H. Mehler & K. Chakraborty, unpublished work) and with the observed absolute requirement for tRNA in the activation of arginine by arginyl-tRNA synthetase (Mitra & Mehler, 1967; Mitra & Smith, 1969).

The kinetics of inactivation of lysyl-tRNA synthetase and arginyl-tRNA synthetase may be interpreted in terms of conformational changes that are facilitated by the presence of tRNA and MgCl₂ or ATP and MgCl₂ and result in enhanced binding of amino acid.

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Possible Selective Genetic Controls in Synthesis of Messenger Ribonucleic Acid by Means of 'Paired' Histones along the Wide Groove of the Double Helix of Deoxyribonucleic Acid

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The original proposal of Stedman & Stedman (1950) that histones can act as genetic repressors has been extensively considered in terms requiring unmasking of the DNA genetic template by total removal of histones from their association with DNA (for extensive references see Busch, 1965; de Reuck & Knight, 1966; Bonner *et al.* 1968). I have proposed that unmasking of specific parts of the DNA template need not involve total separation of the histone from the DNA; instead a histone may be turned on its ionic linkage (of guanidinium or ammonium groups with the DNA phosphate group, in a manner similar to the opening of a door; Lewin, 1968, 1969).

As a result of construction of numerous correctly proportioned molecular models (Courtauld and

Corey-Pauling-Koltun atomic models) and in conformity with energy limitations, I found it possible to refine the thesis in that the wide groove of the B-form of the double helix of DNA can be covered by adjacent 'paired', i.e. placed in parallel, histones (respectively linked ionically to the phosphate groups of the parallel DNA chains, as well as by hydrogen bonds to suitably located hydrogen-bond-acceptor sites on the purines and pyrimidines), which may be partnered by interpolypeptide non-covalent linkages. Utilizing the previous conclusions that the amino groups of adenine and cytosine (and therefore the corresponding hydrogen-bond-acceptor ternary nitrogen atoms) and the methyl group of thymine are restricted to the wide groove (Lewin, 1967*a,b*), I have computed that the 64 possible trinucleotides can be differentiated from one another stereochemically as well as by their hydrogen-bond-acceptance potential and hydrophobic attachments. Assuming such differentials to determine the corresponding, specific, histone attachments by hydrogen-bond donation it follows that any two histone sections attached in parallel along the wide groove to particular base-paired trinucleotides cannot be equally bound sequentially to the two respective areas of the base-paired purines/pyrimidines that they cover. Hence a particular set of conditions may weaken the hydrogen-bonded coverage of one histone, thereby allowing it to turn on its ionic linkage, while the other histone, placed in parallel, remains attached. The unmasked DNA section would allow mRNA synthesis, but the corresponding area masked by the histone in parallel would be unable to participate in mRNA synthesis. This pattern can therefore encompass histone specificity with associated repression potential.

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Some Aspects of Phenylalanine Incorporation in Deuterium Oxide (D₂O) Substitution for Water (H₂O) in Polyuridylic Acid-Directed Ribosomal Protein Biosynthesis

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It has been effectively demonstrated that D₂O substitution for H₂O can result in significant effects on biological processes both *in vivo* (for extensive references see Kritchevsky, 1960; IUPAC, 1963; Hübner, 1967) and in enzymic activities *in vitro* (e.g. Henderson & Henderson, 1969; Belleau, 1967).

The finding that D₂O substitution for H₂O can favour the stabilities of polyribonucleotides, DNA and ribosomes (Lewin, 1966, 1967*a,b*, 1969; S. Lewin, B. A. Williams & D. Munroe, unpublished work) and the considerations favouring the thesis that at low ionic strength certain deuterium bonds are stronger than the corresponding hydrogen bonds (Lewin, 1967*a,b*) has prompted an overall investigation of the effect of D₂O on synthetic ribonucleotide-directed ribosomal protein biosynthesis (S. Lewin, unpublished work); the present communication is concerned with certain facets of the incorporation of phenylalanine in polyuridylic acid-directed ribosomal protein biosynthesis.

Ribosomes were prepared from *RNAase⁺ Escherichia coli* (strain B) by using somewhat modified techniques of Matthaei & Nirenberg (1961) or Godson & Sinsheimer (1967) followed by biosynthetic procedures and protein precipitations utilizing the techniques of Matthaei & Nirenberg (1961) or Bretscher & Jones (1967). The concentrations of polyuridylic acid and the magnesium salts were respectively 10 µg/ml and 15–20 µmol/ml.

In general increasing concentrations of D₂O up to 60% enhanced phenylalanine uptake. When, however, only freshly prepared (1–2 days old only) S-30 fractions were used a maximum enhancement of phenylalanine incorporation appeared in the region of 15–20% D₂O. Our results may be contrasted with those of Holland & Antoni (1968), who, using ribosomes from guinea-pig liver, concluded that D₂O did not enhance polyuridylic acid-directed incorporation of phenylalanine, but that increased incorporation of several amino acids results from the corresponding microsomes.

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