INTERACTIONS BETWEEN AMINO ACIDS AND NUCLEOTIDES IN THE PREBIOTIC MILIEU

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Abstract. In the study of chemical evolution we are interested in the path by which nucleic acids and proteins may have arisen under prebiotic conditions giving rise to those interactions which are generally postulated for the threshold of life. Although laboratory experiments have demonstrated that most of the building blocks of life can be generated from the raw material of the primitive atmosphere, in the genesis of polymers, however, the efforts have been less conclusive. It is reasonable to suppose that small peptides and small oligonucleotides may have interacted in the 'primordial soup' giving rise to the earliest association between nucleic acids and proteins. The beginnings of these processes could be related to the properties of individual amino acids and nucleotides. The interaction of oligomers with amino acids has been studied by the use of ion exchange and NMR spectroscopy. The observed affinities appear to depend on the given amino acid and the oligonucleotide chain length. The results so far suggest that direct amino-acid nucleotide interactions could have made a contribution to the early evolution of the Genetic Code.

Perhaps the major problem we face in elucidating the origin of living systems is the origin of nucleic acid directed protein synthesis. At present there exists no compelling hypothesis for how such a system might have arisen.

The nucleic acid double-helical structure and the function of DNA in the cell provide a strong suggestion for how, in principle, polynucleotides might have replicated under primitive abiotic or prebiotic conditions (Howard et al., 1966; Huang and Tso, 1966; Schweizer et al., 1965; van Holde, 1967). The relationship of gene to protein however is far more complex and does not readily suggest the evolutionary steps through which it came into being. In the gene-dependent mechanism for protein synthesis known as translation, information encoded in the primary sequence of nucleotide bases is transferred to the primary sequence of amino acids and consequently to the more or less exact structure of an enzyme capable of specifically interacting with its environment. The coding relationship, or genetic code is manifested by the assignment of one or more specific trinucleotide sequences to each of the 20 amino acids found in protein. In order to achieve this unique and thus accurate highly structured set of amino acid-codon correspondences the cell has evolved in a complex hierarchy of relationships and recognition processes between polypeptides and polynucleotides. It is obvious that such a system could not be the spontaneous product of simple random chemical combinations and so must be the result of a long and complex evolution.

There is no direct experimental evidence at present bearing on the identity of the primitive precursors of the present translation system. It is conceivable that primitive
forms of 'translation' could have been rather different from the present one. Speculations as to the nature of protein synthesis in that early evolutionary period before the establishment of the genetic code have taken the following lines (Rich, 1965; Woese, 1967; Crick, 1968). Early translation seems likely to have been quite inaccurate i.e., the gene-protein relationships in a primitive translation system must have been either imprecisely or ambiguously defined. This should follow from the fact that the accuracy and precision of the present translation system depends on the precise function of many if not all of its highly evolved and sophisticated protein components, e.g. activating enzymes and some ribosomal proteins. Since the accuracy and precision of at least some of these proteins are final products of the evolution of the entire system, it is conceivable that the precursors to the present protein synthetic system could have been ones in which precise functional roles of proteins would be of less importance and the role of the nucleic acids corresponding of more importance than seen today. Hypotheses for the origin of the genetic code have, then, to assign importance to the function of nucleic acid in determining codon assignments and the ordered arrangement of the present code.

One of the possibilities that must be explored is that the structure of the set of codon assignments and of the protein synthetic machinery somehow reflects 'recognition' or some other form of catalytic interaction between (some form of) nucleotides and (some form of) amino acids – perhaps only during a primitive stage in the evolutionary history of the cell. To examine this possibility, detailed studies of amino acid – oligonucleotide interactions are required.

Our purpose is thus threefold. First, to establish what types of interactions are possible between these two classes of molecules and how to characterize them. Second, to learn how to use the information from simple interpretable systems to interpret increasingly more complex systems. Third, to determine the degrees of selectivity attainable in systems of increasing chemical complexity.

Previous studies have shown that a variety of interactions can occur between nucleic acids and amino acids depending upon composition, conformation, state of polymerization and environment of the reacting species (see references in Saxinger and Ponnamperuma, 1971). These studies have led to the conclusion that a degree of specificity does exist although its origin has not yet been elucidated.

When the two reacting species are simple (i.e., neither is polymeric) one cannot expect to observe 'specificity' of the sort implied in the biological use of the term. What one can look for on this simplest level is evidence for 'selectivity' of some sort, e.g., cases where the strength of binding of an amino acid to a nucleotide under given conditions, is to some extent a function of the composition of both interaction species. While results of this sort from simple systems would not be spectacular from a biological viewpoint, they are nevertheless a necessary first step to any systematic study of a role for amino acid-nucleic acid interactions in the evolution of living systems. Working with monomeric species in aqueous media readily permits the effects of individual factors to be assessed, and so provides the basic information necessary to interpret more complicated polynucleotide-amino acid interactions. It would be surprising if