IRON-SULPHUR PROTEINS: THEIR POSSIBLE PLACE IN THE ORIGIN OF LIFE AND THE DEVELOPMENT OF EARLY METABOLIC SYSTEMS

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Abstract. A review is made of certain features of the biology and chemistry of the iron-sulphur proteins which suggests that these proteins may be descended from an ancestral form or forms which arose very early in the development of biological metabolic systems (the origin of life). If this hypothesis is correct it would suggest that this class of proteins developed during the epoch in which the Earth's atmosphere was reducing in nature and that the relative facility with which the active site of certain contemporary iron-sulphur proteins is experimentally reconstituted may have played a part in their evolutionary development.

1. Introduction

Remarkable advances have been made in recent years towards understanding the processes by which the earliest steps in the evolution of life may have taken place. It is possible that progress in these studies may yield evidence as to the presence of living matter in extraterrestrial environments as well and we are now preparing to examine the planet Mars for evidence of the presence now or in the past of living matter (Ponnamperuma and Klein, 1970). It is feasible that the chemical events which took place on our planet in prebiological times also occurred in one or more of the other bodies distant from us in time and space. Some recent laboratory investigations have therefore set out to examine the possibility of synthesis of organic compounds under conditions which are thought to have existed on the primitive earth. It has now been repeatedly shown that simple carbon compounds such as cyanides and hydrocarbons are formed in small amounts by electric discharges under such conditions and that these substances combine by condensation and polymerisation reactions to form more complex organic molecules (see Ponnamperuma, 1972). The organic, inorganic and gaseous composition of many present day extraterrestrial environments have been investigated (see Buhl and Ponnamperuma, 1971; Michaux, 1967) and the presence of materials such as ammonia, methane and hydrogen unequivocally established. Furthermore it has been found that most of the amino acids which constitute living proteins can be produced abiologically from these simpler organic materials (see Harada and Fox, 1964) and it is also possible to polymerise these amino acids to form polypeptides with many properties similar to proteins. These proteinoids can have mo-

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molecular weights (3000–25000) which are higher than those of certain natural proteins (Fox et al., 1962).

In view of the current state of knowledge of chemical evolution it appears to be of interest to try to identify any present day proteins or classes of proteins whose ancestors may have been constituents of primitive enzymatic metabolising systems. In view of the immense number and diversity of enzymes found in present day organisms a task of randomly or nonselectively surveying all known proteins could be laborious. Useful criteria for selection of a protein for examination could be smallness in size of the protein molecule and relative simplicity in the structural organisation of the molecule and of its active site. It could also be postulated that an enzyme or class of enzymes which is indispensable (directly or indirectly) for the optimal functioning of a variety of metabolic reactions or which is widely distributed through the microbial, plant and animal kingdoms may well qualify for further investigation. This possibility would be in keeping with suggestions that since coenzymes are very widely distributed catalysts in living processes they are likely to have risen early in the evolutionary development of living processes (see Oparin, 1972). A third possible guiding characteristic could be that the enzyme or enzymes concerned use as substrates elements or relatively simple compounds or such molecules as may have been present in the ‘primordial soup’ as a consequence of abiogenic synthetic activity. The purpose of the present paper is to set forth arguments that the iron-sulphur proteins (ISPs) are a class of proteins which meet these indications and have many other properties to suggest strongly that one of their ancestors was a constituent of early enzymatic metabolising systems.

2. Iron-Sulphur Proteins (ISPs)

The ISPs are small proteins containing iron atoms linked to a polypeptide moiety by means of acid-labile sulphur bonds. At low pH the sulphur bonds are disrupted to yield hydrogen sulphide and an iron-free apoprotein with the concomitant loss of functional activity. The function of ISPs appears to be the electron transfer brought about by the alternate reduction and reoxidation of the iron atoms at low potentials. The generic term is used here to include proteins such as the ferredoxins, rubredoxins, putidaredoxin, high potential iron proteins, azoferrredoxin, molybdoferredoxin, hydrogenase, adrenodoxin, testodoxin and other iron-sulphur proteins participating in steroid hydroxylations in ovarian and placental mitochondria. Proteins such as succinic dehydrogenase, NADH dehydrogenase, and xanthine and aldehyde oxidases (which have flavin moieties in addition to other differences) are not usually considered typical members of the class.

3. Distribution in Living Organisms

The typical ISPs are today found to be widely dispersed among both unicellular and multicellular living organisms. Listings of various living species in which these proteins have been identified have appeared elsewhere (Malkin and Rabinowitz, 1967; Wick-