

SELF-SEQUENCING OF AMINO ACIDS AND ORIGINS OF POLYFUNCTIONAL PROTOCELLS

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Abstract. The primal role of the origins of proteins in molecular evolution is discussed. On the basis of this premise, the significance of the experimentally established self-sequencing of amino acids under simulated geological conditions is explained as due to the fact that the products are highly nonrandom and accordingly contain many kinds of information. When such thermal proteins are aggregated into laboratory protocells, an action that occurs readily, the resultant protocells also contain many kinds of information. Residue-by-residue order, enzymic activities, and lipid quality accordingly occur within each preparation of proteinoid (thermal protein).

In this paper are reviewed briefly the phenomenon of self-sequencing of amino acids, its relationship to evolutionary processes, other significance of such self-ordering, and the experimental evidence for original polyfunctional protocells.

PROTEIN SYNTHESIS AS AN EVOLUTIONARY LIFELINE

The two main approaches to the origin of life have been built on the premises of proteins (cells)-first or nucleic acids (genes)-first (1). Our choice of the former context in which to do experiments was based on the functional diversity, versatility, and specificity of the proteins (2). The choice was based also on the fact that at the time there existed methodology for study of sequences of monomers in proteins (3,4) but not yet for nucleic acids (5). Although the role of specific proteins in

the formation of nucleic acids was to be much more fully appreciated only later (6,7), it was evident to some of us in the 1950s that nucleic acids do not, strictly speaking, replicate themselves. They are replicated. The replication is managed by enzymes, which transfer energy from phosphates. Since all enzymes are specific, it was not apparent that polymerases would not contribute to the specificity of nucleic acids. It is still not clear how and how much they do that, but we do know that there are DNA polymerases and there are RNA polymerases. The specificity imparted by multiple types of enzyme, or multiple polymerase factors, is theoretically greater than that from a single enzyme (8).

THE SELF-SEQUENCING OF AMINO ACIDS

The finding that amino acids sequence themselves during thermal polycondensation (9) supplies an explanation for the origins of biological information. The information, in this view, is latent in the mixed amino acids, in fact in the special interactions of the sidechains of the various types of α -amino acid (10). The evidence is from many laboratories and is of many kinds. The degree of self-ordering is remarkably high, and in those cases in which sequence has been studied it is residue-by-residue or singular (11-14).

The fact that the amino acids are self-sequencing is equivalent to stating that the corresponding step in evolution would have been responsible for an endogenously self-limiting evolution.

EVOLUTIONARY SIGNIFICANCE

Thermal proteins that are ordered products of self-sequencing of reactant amino acids are informational, as already indicated. The presence of informational macromolecules initially at the polymer level is thus explained by an emergent property from the hierarchically lower monomer level.

This relationship is uniquely evolutionary. Information is fed in at the monomer level, to emerge in a different form at the polymer level. Since the process is one of self-ordering, there result multiple copies of each type of macromolecule formed. This multiplicity results in greater power for any protoenzymic molecule than would accrue from a single one of each type, as in a hypothetical random synthesis.

The number of catalytic activities can however, in this situation, cover a wide range. It is undoubtedly rooted in the

reactive groups of amino acid sidechains: carboxylic, amino, benzenoid, aliphatic, etc., and the innumerable configurations and interactions that are possible from those amino acid sidechains within polymers (10).

The uncoded information that has thus been generated is endogenous, specific, and varied within a self-limited range. The variety is not only by type of group, but their interaction configurations and the variable distance between groups that can accrue in polymers.

It is in this way that we can understand that biological information originated in thermal proteins. The sequence of molecular evolution thus stemmed from proteins-first, actually amino acids-through-proteins-first. This is understandable because the monomeric reactants react specifically with each other, and yield polymers that interact specifically with substrates, including with nucleotides that are thereby polymerized. We have no evidence for an origin of polynucleotide without prior enzyme, template, or primer, as Chairman Dose has emphasized.

The specificity of the coded genetic process thus resides in a product, the gene, but its evolutionary precursor was a process, the self-ordering of amino acids.

POLYFUNCTIONAL PROTOCELLS

The thermal proteins easily and abundantly yield the proteinoid microsphere, which is the model for the protocell (15). The functions that have been catalogued in these bodies are now numerous (16).

As a kind of capstone property, the continuing study of the properties of the prenucleic acid protocell has established the potential for a remarkable degree of excitability in these units (17). The significance of protein-based properties of this general kind has been explained by Szent-Györgyi (18).

One remarkable composite feature of the proteinoid cell is that it predated modern (a) membrane (17), (b) metabolism (10), and (c) ordered nucleic acid separately. This equivalence, as indicated, is supported by extensive experiments. For such functions to exist simultaneously in a protocell composed of a single type of polymer, proteinoid, having all such properties obviates the need for the highly improbable events of protein, nucleic acid, and phospholipid arising separately and somehow joining together (19). It is also noteworthy that proteinoid

microspheres have such a roster of biomimetic properties despite the absence of DNA/RNA in their history.

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