

THE PRIMORDIAL PROTEIN SELF-GENERATION:
SELF-ORDERING, PERIODICITY, HOMOGENEITY,
PROTEOLYSIS

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An increasing set of protein sequences with various functions from organisms, representing different levels of evolutionary development were examined in our previous papers. A universal method was used, based on the analysis of distances between amino acid residues - both identical and very similar in structure-function-mutability sense (Ivanov, 1983). As a result the presence of the following regularities in the protein primary structure were established:

- Preference in bonding: each amino acid binds preferably the same or a very similar one (Ivanov and Ivanov, 1973).
- Periodicity: a repetition of identical or very similar residues along the chain. The phenomenon is more clearly expressed in more conservative proteins performing an old (in evolutionary sense) function. The same was found for the generated nodal ancestors (Ivanov and Ivanov, 1980).
- Homogeneity: The long protein chains retain a very close preference in bonding and periodicity after dividing into a small number of equally long parts (see Ivanov and Ivanov, 1973).

Our further studies of the whole set of proteins sequenced up to November 15, 1984 revealed the universal character of the above mentioned regularities (Ivanov and Förtsch, 1986).

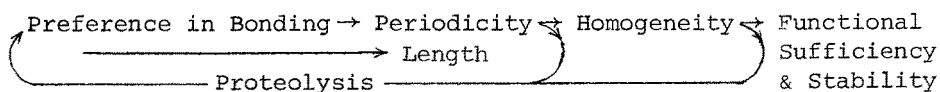
Taking into account the increased regularity in more conservative proteins and particularly in the proteinoids synthesized by Fox and co-workers (Fox and Harada, 1960; Fox, 1984) under simulated prebiotic conditions the following suggestions could be made. The primordial proteins must have been built on the principle of preference in bonding (not requiring the nucleic acid participation) from a relatively small number of amino acids (in view of the small periodicity established). The observed homogeneity appears to be a consequence of the periodicity. In our opinion the symbiosis between proteins and nucleic acids has occurred later and its major advantage is the

relatively conservative heredity. It is logical to expect that at the stage of protein self-synthesis the lack of above advantage has been compensated by a rapid generation of protein chains followed by a combination of parts of them up to a composition and sequence, corresponding to a functional sufficiency and relative stability, respectively.

Several years ago we paid attention to a number of cases when relatively short protein chains coincide with parts of longer ones, as well as to the cases of N- and C-terminal heterogeneity. We suggested that the protein chain shortening mechanism possesses a universal character (Ivanov and Ivanov, 1978a,b,c). Recently this abundance of cases became even more pronounced. There are no more doubts about the extremely broad distribution of the proteolytic processing (Kräusslich and Wimmer, 1988).

Is that not a relic from the above mentioned primordial mechanism, ensuring a rapid recombination of parts of the chains? An evidence for this is the broad distribution of limited proteolysis in proteins, performing very different functions in practically all organisms - even in viruses (see Kräusslich and Wimmer, 1988). The same holds for the most of the proteinases known, part of which have a common evolutionary origin (Ivanov and Genov, 1987a,b). Another evidence in favour of the primordial hierarchy of above mechanism is the considerable rate of protein synthesis in the course of embryonic development, decreasing after delivery (Remesar et al., 1987). This led us again to the Haeckel's biogenetic law for whose validity on molecular level, there is evidence (see Ivanov, 1987).

Thus, there are serious grounds to consider that the primordial proteins, a part of them being proteinases, have undergone a rapid evolution (self-generation) according to the scheme



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