

The talk at Sant Feliu, ppt with brief linking texts between (under) the pictures.

(For more details and references - see Trifonov, E. N., Tracing Life back to elements, Physics of Life Reviews 5, 121-132, 2008)

2. The reconstructions indicate that the repeating GCY triplets are special in several ways. Especially their high ability to expand, observed today in triplet expansion diseases. These sequences should have won in the earliest competition with other sequences.

3. There are over 100 different expert opinions on the possible temporal order of appearance of various amino acids in evolution. It would be impossible to derive consensus by the way of arguments, as it is not clear which of suggestions (authors) should be given higher weight. The consensus shown is derived by, essentially, principal component analysis, that does not leave much room for arguments. Still, the consensus remains a speculation.

4. It turned out that the codons corresponding to the amino acids in the chronology follow fundamental rule of thermostability: The earlier amino acids are encoded by codons for which melting enthalpy (codon-anticodon pairs) is higher. Correspondingly, complementary codons come simultaneously, as a pair. This allows to build evolutionary table of codons as, essentially, unique solution.

5. Since in the process of consecutive formation of new codons the purines in the middle stay purines, and pyrimidines stay pyrimidines, one can predict that, probably, this rule would be still recognizable in modern amino acid substitutions.

6. Indeed, modern substitution matrices do split in two distinct boxes, for Ala- and Gly-families of amino acids (with Y and, respectively, R in the middle of their codons).

7. The ancient miniproteins AlaAlaAla... and GlyGlyGly... could not be very long because of insolubility. Fusion of respective genes would generate preferentially alternating mosaics of AAA... and GGG... segments. This mosaics is still detectable in modern protein sequences, and the segment size is 7 amino acid residues.

8. Writing modern sequences in binary alphabet offers their ancestral form. Because of accumulated mutations only occasionally one may find them in, indeed, mosaic form, as in the picture.

9. These sequences are found to have maximal numbers of relatives in modern proteins. Presumably, these are the early prototypes. But the real earliest sequences can be detected today as omnipresent motifs, i. e. present in every proteome, including, presumably, the proteome of Last Universal Common Ancestor.

10. The omnipresent sequences belong either to Aleph prototype, or to Beth prototype. Few of them do not resemble anything.

11. They turned out to be actually, all relatives, as they all belong to the same network of closely related fragments. The networks in the formatted sequence space is a new discovery (by Z. M. Frenkel and the author), that allows to trace the kinship via chains of relatives. The fragments belonging to the same network have often not even single common letter. Yet, they are well traceable relatives.

12. The sequence space allows to build evolutionary tree of the omnipresent elements. They all originate from some common ancestor at the bottom of the tree, that corresponds to 60% match between connected fragments of the common network.

13. The common origin is confirmed by presentation of the omnipresent elements in binary form. They all fit to a common binary consensus.

14. The consensus can be split in three identical "duplex" elements, that differ from the ancient heptamers by only one G to A mutation (A to G in opposite strand). Thus, two reconstructions, from "zero time" up and from modern sequences down, meet.

15. Ancient Aleph and Beth in binary form are complementary. That means they both have been encoded by the same duplex RNA.

16. The modern representatives of Aleph and Beth are involved in functions related to energy, as well as, presumably, their ancestors. Indeed, Life required energy from the very beginning.

17. The Darwin's definition of Natural Selection can be considered as definition of Life, as it has two major attributes of Life - self-reproduction and variations.

18. The above definition, when applied to the codon evolution chart, reveals the transition between mere self-reproduction and Life proper - the very point of Life origin.

19. This allows to formulate the "product definition" of Life - the set of molecules for the exploration of the predicted No-Life - Life transition.