

THE INFORMATION ARTEFACT OF THE GENETIC CODE

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As the current view point on the local code self-assembly has not been objectively confirmed, opposite variant of the directional panspermy (Crick and Orgel, 1973) should not be disregarded. The artefact of the code allows an intellectual message to be included in its structure (Marx, 1979). The genome spacer and intronic regions may be material carriers of the main part of message.

The formal systematization principle established heuristically, reveals an unknown regularity of cooperative base symmetry of the universal eukaryotic (TGA codes Cys - Marshal *et al.*, 1967) genetic code: "Series of synonymic triplet codons are united in groups of code degeneracies established separately for each series with the same 5'-base doublet, the codons compressed at the 3'-base position to the scale of 1: "The group code degeneracy" are arranged within each group in the order of monotonically changing nucleon numbers in the atoms of the coded neutral amino acid molecules (zero nucleon numbers correspond to termination codons), each codon being positioned so that its three bases are aligned only with the bases of the same position of other codons, and the groups following the order of monotonically changing degeneracies of the united series and being divided into two parts so that the central symmetry axis of the degeneracy IV group and the central common symmetry axis of other groups, both of which are perpendicular to the lines, are coaxial, within the groups with the common axis the direction of changing nucleon numbers being the same" (Shcherbak, 1988).

The discovered base sequences are interpreted

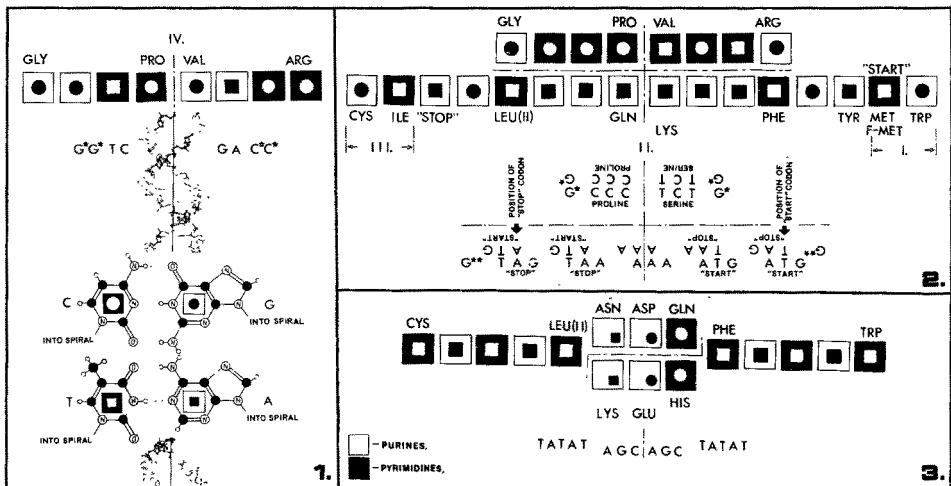
within the code symbolism as an intellectual message. Syntactic division is ascribed by purine-pyrimidine composition.

(1) 5'-base position, group IV: "DNA symbol - rules of canonical pairing", "Significance of double pair $G \equiv C$ " (fig. 1).

(2) Central position, groups III, II, I and IV: "Palindrome with the symbol of genome spacer region", "Significance of base G and poly-A background for the spacers", "Pro and Ser parameters decisive for the inner organization of the spacer and/or their positions in the genome" (fig. 2).

(3) 5'-position, groups III, II, I: "The Hogness box-symbol of a transcription unit with intrones" (the semantics of the codons RRY RRY or AGC AGC is not clear) (fig. 3).

(4) 5'- and 3'-position, group II: "Instructive substantiation of the Gln and Lys position" *etc.*



A subjective understanding, as the only way of stating the semantic load of a sign sequence, is collectively verifiable and the predicting conclusions are refutable by the "Human genome" programme data.

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 Marshal, R.E., Cascey, T.C. and Nirenberg, M.: 1967,
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