DIRECT INTERACTIONS BETWEEN HOMOCODONIC AMINO ACIDS AND NUCLEOTIDES : A POSSIBLE PHYSIOCHEMICAL BASIS FOR THE ORIGIN OF THE GENETIC CODE

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The origin of nucleic acid-directed protein synthesis system is a critical circumstance in the history of living organisms. Despite the fact that molecular mechanisms of the modern protein synthesis system have been known in increasingly detailed terms, our understanding of the history of the genetic code remains poor.

A study of the associations of homocodonic amino acids (Phe, Lys, Pro, Gly) and nucleotides was undertaken with a view to establish a possible physical basis for the origin of the codon assignment. The associations of L-Phenylalanine, L-Lysine, L-Proline and Glysine with various nucleotide sequences (Nucleoside-2'-, nucleoside-3', nucleoside-5'- monophosphates; dinucleoside-(2'5')-, dinucleoside-(3'-5')- monophosphates; and trinucleoside-(3'-5')-diphosphate) were studied using ^{1}H NMR spectroscopy. Association constants for various interactions were determined by following the changes in the chemical shifts of the anomeric and ring protons of the nucleotide as a function of amino acid concentration and fitting experimental data to a binding curve.

The strongest associations of all the homocodonic amino acids were with their respective anticodonic nucleotide sequences. The strength of association was seen to increase significantly with increase in the chain length of the anti-codonic nucleotide from monomer dimer, through trimer The association of amino acids with different phosphate esters of nucleosides suggest that a definite isomeric structure is required for association with an amino acid; the 5'-mono-nucleosides and (3'-5') linked dinucleotides are the favoured geometries for strong associations. The conclusion reached as a result of these studies is that there is a possible anticodonic basis for the origin of the genetic code.