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The Model for Genetic Code Origin Study Based on the Dipeptide Yields Variation with the nucleosides

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Introduction: Genetic code origin is one of the most essential issues of origin of life. How the "primitive code" derived from the very beginning? The genetic code recognition system in modern ribosome is a very complicated system and it is not easy to touch the core of the problem.

Some previous reports have focused on potential importance of weak direct interactions between amino acids and triplet codon nucleotides[1,2]. In order to uncover the possible origin of the genetic code, the influence of nucleotide on peptide synthesis should also be considered. Therefore, we build up a simplified chemical model for the origin of genetic code studies. This system consists of phosphorous compounds, amino acids and nucleosides. From aqueous phase to organic phase, six representative amino acids (Phe, Trp, Tyr, Val, Leu and His) were tested in this chemical model. It was found that the "translation products" dipeptide yields for each of the five amino acids (Phe, Trp, Tyr, Val and Leu) showed some positive correlation with their 2nd position on their codon/anticodon nucleosides, respectively. For some amino acids, such as Val and Leu, the 1st position of the triplet code also provides some profound effect. That means the codon/anticodon nucleosides of the 2nd and 1st position both have the helpful effect on the translation products, but the 2nd position is more important.

The chemical model we raised here is the first model that can be used in experimental tests, and could be considered as the core of the genetic code translation mechanism. It may provide some new strategies to understand the origin of genetic code that confounded people for years.

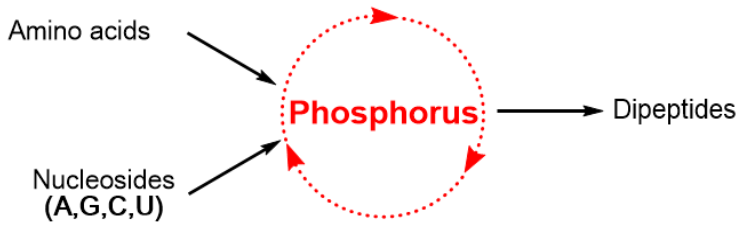

Figure 1. Chemical model for the origin of genetic code studies

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