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Relictual tRNAs Recognized not Chemically Inert Amino Acids, but Chemically Active Aminoacyl-Adenylates

Yuri Pivovarenko

Research and Training Center 'Physical and Chemical Materials Science' Under Kyiv Taras Shevchenko University and NAS of Ukraine, Kiev, Ukraine

Email address:
y.pivovarenko@gmail.com

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Abstract: Some authors believe that the genetic code originated due to the ability of amino acids to form complexes with the corresponding antikodons. We believe that it is wrong and hypothesize that the relic tRNAs did not form complexes with chemically inactive amino acids. The formation of such complexes was devoid of "biological meaning". Instead, they recognized of chemically active forms of amino acids, namely aminoacyl-adenylates. Thus, relict recognition of amino acids, which led to the formation of the genetic code do not occur through the formation of complexes, but through a chemical reaction between the corresponding aminoacyl-adenylates and tRNAs relic. All the necessary elements of the relic of the mechanism of recognition of aminoacyl-adenylates evolutionary entrenched in the structure of modern tRNAs. The main element of such mechanism is the uridine base, which is always before the anticodons of modern sense tRNAs. Thus, thanks to our hypothesis, we can answer two fundamental questions: 1. Why only ATP activates amino acids? 2. Why only U-bases are placed before the anticodons of modern sense tRNAs?

Keywords: Genetic Code Origin, Chemical Base of the Genetic Code, Amino Acid Recognition, Amino Acids Nucleotides Relationships

1. Introduction

Many authors have tried to explain the origin of genetic code [1-12]. However, recent articles on this topic indicate that an acceptable answer to this question is still not received [13-17].

Analyzing a proposed explanation, it is easily seen that usually they are variants of the model "key-lock". In our opinion, this model is unsatisfactory because it does not imply a further evolution of the recognized amino acids. Indeed, the formation of stable complexes between amino acids and nucleotides encoding is pointless. In any case, the formation of stable complexes has no biological meaning. This obviously complicates or makes impossible the further modification of the recognized amino acids.

It should be noted that most of the hypotheses seeking to explain the origin of the genetic code, have one thing in common: they do not imply the possibility of experimental verification. You can verify that the creation of hypotheses explaining the origin and structure of the genetic code has evolved over time into a competition of wit. This competition has demonstrated the wit of many authors, but it did not solve obviously the problem of the origin of the genetic code. Instead, it was necessary to better analyze structure and modalities of coding nucleotides.

2. Main Body

In the beginning we should say that we agree with those authors who believe that the structures of modern tRNAs preserved relictual mechanisms that allow knowing the amino acids in ancient times. For example, we are very impressed by the views of some modern authors [18-20]. However, we believe that such recognition was not accompanied by the formation of the complex between the anticodon and the corresponding amino acid. We fundamentally believe that free amino acids could not participate in this recognition, since they are chemically inert. We are convinced that the prehistoric recognition of amino acids (formally) was carried out by chemical interaction

between the corresponding tRNA and aminoacyl-adenylate, which is the chemically active form of recognizable amino acids. Thus, the relic of the mechanism of recognition of amino acids, which ensured the formation of the genetic code, was implemented through chemical interaction.

In our opinion, it is only natural that evolution has preserved not only the chemically active form of recognizable amino acids, but the fragments of tRNA. As these fragments we offer sequence antikodon loops modern tRNAs: 5'-U-anticodones. Thus, we assume that prehistoric recognition of amino acids based on the chemical interaction between 5'-U-anticodones and the corresponding reactive amino acids, namely aminoacyl-adenylates.

Our hypothesis is based on the following facts:

1. The anticodon loops of all modern sense tRNAs contain U-base before anticodon (Figure 1) [21, 22];

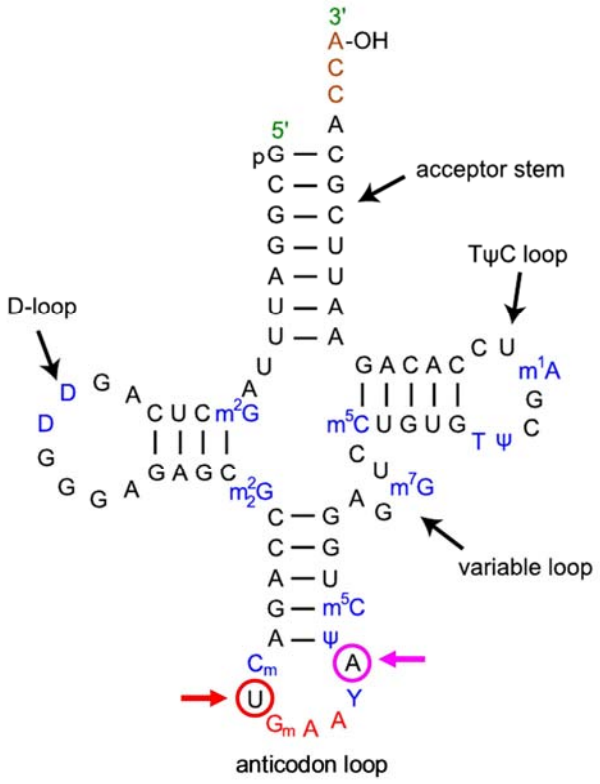

Figure 1. *tRNA secondary structure. Red arrow shows the conserved U-base, which is before the 5'-end of anticodon [21,22]. Violet arrow shows the conserved (or semi-conserved [22]) A-base, which has sixth position after conserved U-base [21].*

2. Anticodon loops of modern antisense tRNAs may not have such a U-base [21];
3. All amino acids form chemically active aminoacyl-adenylates, before attaching to tRNAs; not activated amino acids are not attached to tRNAs [21, 22];
4. Only ATP activates the amino acids [18], – other nucleoside triphosphates not activate amino acids.
5. The adenine is complementary to uridine [21, 22].

After analyzing these facts, we hypothesized that the tetra-nucleotides, namely 5'-U-anticodones, could recognize the corresponding aminoacyl-adenilates [23].

We believe that the proposed hypothesis is very promising. First, it answers two fundamental questions: 1. Why only ATP activates the amino acids? 2. Why is it always the U-base located in front of the anticodons of sense tRNAs? Second, it can receive the next evolution.

So, it is known, that the anticodon loop contains the conserved A-base, which has a sixth position after described conserved U-base (Figure 1) [21]; other authors think that it is semi-conserved A-base [22]. It is also known that the rings, which form hex-nucleotides with complementary end-bases, are most stable [21]. For this reason, it can be assumed that the relic tRNAs formed the stable rings: 5'-U-anticodon-A-3' (Figure 2).

One can also assume that the recognition of the aminoacyl-adenylates was accompanied by the release of amino acid radicals, which have a highly reactivity at the moment of release (in situ). Since destruction of the aminoacyl-adenylates leads to appearance of amino acids with high chemical activity, they can be attached to ribose OH-group of near 3'-A. This way, the adenine (Figure 2) was a prototype terminal adenosine of acceptor stem of modern tRNAs (Figure 1). Thus, the relic aminoacyl-tRNAs had the structure: 5'-U-anticodon-A-3'-O-aminoacyl.

Figure 2. *Arrow shows the hypothetical hydrogen bounds between the conserved U-base and semi-conserved A-base of hex nucleotides that contain the anticodon loops of modern tRNAs. As hex nucleotides with complementary end-bases form most stable rings [21], we offer them as a secondary structure of relic tRNAs.*

In fact, the primary tRNAs was comprised of sites that are only identified aminoacyl-adenylates and attached amino acids residues that were included it their composition. But, as we hypothesized, they should have a selective catalytic activity against aminoacyl-adenylate, they should have the properties of typical ribozymes [24, 25].

However, no matter how attractive the proposed hypothesis, it needs experimental testing. It is also clear that a full validation of the hypothesis requires a large experimental work. First, such a test needs a large amount of

synthetic work. Second, such validation requires analytical work.

Not being able to perform a complete test of this hypothesis, we undertook some experiments. According to our knowledge, these simple experiments could confirm or refute proposed ideas. For this reason, it was such experiments that do not require a lot of effort. In addition, these experiments were cheap. (It should be recalled that the authors of the various hypotheses explaining the appearance and structure of the genetic code, offered no way to experimentally test such hypotheses.)

Starting to test our hypothesis, we decided to test the stability of some aminoacyl-adenilates in aqueous solutions of 0.01M $MgCl_2$ containing poly-U. According to our view, this polynucleotide is the fragment of anticodon loop of a lysine tRNA: 5'-U-UUU-3', where the terminal 5'-U- is a conserved uridine, part of the anticodon loops of all sense tRNAs (Figure 1), and UUU is the anticodon of a lysine [22]).

Studying the works devoted to the formation of the genetic code, we noticed one peculiarity: the authors of these papers did not discuss the composition of the environment in which implemented the alleged interaction (between amino acids and nucleotides). One gets the impression that in ancient times these interactions occurred in a vacuum. In our opinion, this approach is incorrect. We can confidently assert that the postulated interaction could occur in water-salt solutions. Moreover, we believe that the ionic composition of the solution was fixed in the course of evolution. We want to draw your attention: as working solutions we used only aqueous solutions containing magnesium ions Mg^{2+}. Because the processes of translation and transcription always involves magnesium ions [21, 22], we used as working solutions 0,01 – 0,1M solutions of magnesium chloride.

For our experiments, we synthesized adenylates, derivatives of some amino acids: L-Ala, L-Met, L-Ser, L-Phe, L-Trp, also L-Lysine and D-Lysine. Adenylates were synthesized in accordance with [26]. We determined concentrations of adenylate synthesized as in [26]. All working solutions had a temperature of: 0 – 4 C.

We have found that under such conditions L-Lys-adenylate completely hydrolyzed within 1 – 4 hours. We also found that the concentration of the other adenylates (including D-Lysine!) decreased by 10 – 20% over the same period. Thus, we have seen that poly-U selectively increases the speed of hydrolysis of the adenylate L-Lysine. So, we saw that poly-U can initiate the hydrolysis of l-Lysyl-adenylate, which is accompanied by the formation of chemically active L-Lysyl radicals. According to our hypothesis, these radicals could join the sixth A-base (Figure 2), forming relict L-Lysyl-tRNAs. Very convincingly, in our opinion that poly-U distinguishes between L - and D-amino acid derivatives. Also we have seen that our hypothesis is not without reason.

3. Conclusions

Relic tRNAs recognized not chemically inert amino acids, but chemically active aminoacyl-adenylates. In the process of recognition of this relic of tRNAs did not form complexes with chemically inert amino acids. With this recognition they reacted with the chemically active adenylates of amino acids. Thus, the relic of the mechanism of recognition of amino acids, which ensured the formation of the genetic code, was implemented through chemical interaction. All the elements necessary for the realization of the relic of the mechanism of recognition, evolutionary enshrined in the structures of modern sense tRNAs.

Proposed hypothesis helps to explain many features of the structure of modern sense tRNAs.

Also, this hypothesis allows to answer two basic questions: 1. Why only ATP activates amino acids? 2. Why only U-bases are placed before the anticodons of modern sense tRNAs?

References

[1] Welton M. G. E., and Pelc S. R. (1966) Stereochemical relationship between coding triplets and amino acids. Nature 210, 1265-1267.

[2] Woese C. R., Dugre D. H., Saxinger W. C., and Dugre S. A. (1966) The molecular basis for the genetic code. PNAS USA, 55, 966-974.

[3] Pelc S. R., and Welton M. G. E. (1966) Stereochemical relationship between coding triplets and amino acids. Nature, 209, 868-870.

[4] Dunnill P. (1966) Triplet nucleotide-amino acid pairing a stereochemical basis for the division between protein and non-protein amino acids. Nature, 210, 1265-1267.

[5] Wong J. T.-F. (1975) A Co-Evolution Theory of the Genetic Code. PNAS USA, 72, 1909-1912.

[6] Hopfield J. J. (1978) Origin of the genetic code: a testable hypothesis based on tRNA structure, sequence, and kinetic proofreading. PNAS USA, 75, 4334-4338.

[7] Balasubramanian R., Seetharamulu P.,and Raghunathan G.. (1980) A conformational rationale for the origin of the mechanism of nucleic acid-directed protein synthesis of "living" organisms. Orig. Life, 10, 15-30.

[8] Hendry L. B., and Bransome E. D. (1981) Are there structural analogies between amino acids and nucleic acids? Orig. Life, 11, 203-221.

[9] Shimizu M. (1982) Molecular basis for the genetic code. Journal of Molecular Evolution, 18, 297-303.

[10] Di Giulio M. (1997) On the origin of the genetic code. J. Theor. Biol., 187, 573-581.

[11] Schnitzer W., and Ahsen U. (1997) Identification of specific Rp-phosphate oxygens in the tRNA anticodon loop required for ribosomal P-site-binding. PNAS USA, 94, 12823-12828.

[12] Knight R. D., Freeland S. J., and Landweber L. F. (1999) Selection, history and chemistry: the three faces of the genetic code. Trends Biochem. Sci., 24, 241-247.

[13] Niu D. K., Lin K., and Zhang D. Y. (2003) Strand compositional asymmetries of nuclear DNA in eukaryotes. J. Mol. Evol., 57, 325-334

[14] Di Giulio M. (2005) The ocean abysses witnessed the origin of the genetic code. Gene, 346, 7-12

[15] Yarus M., Caporaso G., Knight R. (2005) Origins of the genetic code: the escaped triplet theory. Annu. Rev. Biochem. 74, 179-198.

[16] Mackiewicz P., Biecek P., Mackiewicz D. at al. (2008) Optimisation of Asymmetric Mutational Pressure and Selection Pressure Around the Universal Genetic Code. Lecture Notes in Computer Science (LNCS). 5103, 100-109.

[17] Hanyang Y., Zhang S., and Chaput C. (2012) Darvinian evolution of an alternative genetic system provides support for TNA as an RNA progenitor. Nature Chemistry 4, 183-187.

[18] Seligmann H (2010) Dypoot haensisticodons of misacylated tRNAs preferentially mismatch codons coding for the misloaded amino acid? Molecular Biology, 11 (41), 1-5.

[19] Erives A. (2011) A Model of Proto-Anti-Codon RNA Enzymes Requiring L-Amino Acid Homochirality. J Mol. Evol., 73, 10-22.

[20] Rodin A. S., Szathmáry E. and Rodin S. N. (2011) Biology Direct, 6, 1-24.

[21] Cantor, C. and Shimmel P. (1985) Biophysical chemistry 1, Moscow: Mir Saenger W. (1984) Principles of nucleic acid structure. New York: Springer-Verlag.

[22] Pyvovarenko Y. V. (1998) About the possible stereo chemical relationships between olygonucleotides and aminoacyl-adenylates as the basis of genetic code appearance (hypothesis). Journal of Evol. Biochemistry and Physiology, 34, 611-614.

[23] Doherty E. A., and Doudna J. A. (2001) Ribozyme structures and mechanisms. Annu. Rev. Biophys. Biomol. Struct., 30, 447-457.

[24] Joyce G. F. (2004) Directed evolution of nucleic acid enzymes. Annu. Rev. Biochem., 73, 791-836.

[25] Berg P. (1958) The Chemical Synthesis of Amino Acyl Adenylates. J. Biol. Chem., 233, 608-611.