



(REVIEW ARTICLE)



Deciphering the Genetic Code: Mechanisms, Evolution, and Implications for Biotechnology

Mustapha Abdulsalam *, Fatima Zarah Yerima Ubah, Hasiya Ummi Ahmed, Ummulkhulthum Ahmed Tafida and Aisha Wada Nasir

Department of Microbiology, Skyline University Nigeria.

World Journal of Advanced Research and Reviews, 2024, 21(01), 858–868

Publication history: Received on 24 September 2023; revised on 06 January 2024; accepted on 09 January 2024

Article DOI: <https://doi.org/10.30574/wjarr.2024.21.1.2195>

Abstract

The study of the genetic code explores the foundational language of life, aiming to fathom how DNA orchestrates the synthesis of proteins. This study explores various facets of the genetic code, from the widespread use of the triplet codon system to the vital role of transfer RNA (tRNA) in translation. This study unravels the intricacies of interactions between codons and anticodons, as well as the orchestration of ribosomes, casting illumination on the initiation, elongation, and termination stages of protein synthesis. Furthermore, it delves into the regulatory factors and mechanisms for quality control that wield influence over the translation processes. In the exploration of the genetic code's evolution, the study meticulously examines its universal principles, exceptions, and the compelling conjectures enveloping its origins. The coevolution of tRNA and codons, along with adaptations in the code observed in diverse organisms and organelles, yields valuable insights. Notably, the research underscores the vast biotechnological applications encompassing genetic engineering, codon optimization, and protein design. This study not only addresses uncharted territories in genetic code research but also propounds future research directions. It highlights current challenges and opportunities within this domain, including code expansion and gene editing advancement. Ultimately, the study of the genetic code remains a dynamic, ever-evolving field with profound implications for science, technology, and our comprehension of life's fundamental processes. This research unravels the captivating narrative of the genetic code, revealing novel areas and applications that continue to captivate and inspire.

Keywords: Genetic code; Codon-anticodon interactions; Translation; Biotechnology; Evolution

1. Introduction

The deciphering of the genetic code, often referred to as the universal language of life, stands as a pivotal achievement in the annals of biological research [1]. This genetic code serves as the translator, seamlessly converting the intricate instructions encoded within DNA into the proteins that govern the orchestration of life's fundamental processes [2]. The significance of this study lies in its ability to shed light on the mechanisms, evolution, and implications of the genetic code, which span far beyond the boundaries of basic biology and extend into the realms of cutting-edge biotechnology. A journey through the genetic code commences with a global perspective, traversing through the annals of scientific history. The elucidation of the genetic code's mechanics began in the mid-20th century with groundbreaking contributions from Francis Crick and Sydney Brenner [3]. These early pioneers laid the foundation for a multitude of questions and the ongoing pursuit to decipher the genetic code. The broader landscape of genetic code research transcends borders, with scientific minds worldwide seeking to unlock the code's mysteries. While the global perspective provides a panoramic view of the genetic code's historical development, this study strategically zooms in on local contexts, specifically within the domain of secondary data sources. We delve into a comprehensive review of

* Corresponding author: Mustapha Abdulsalam

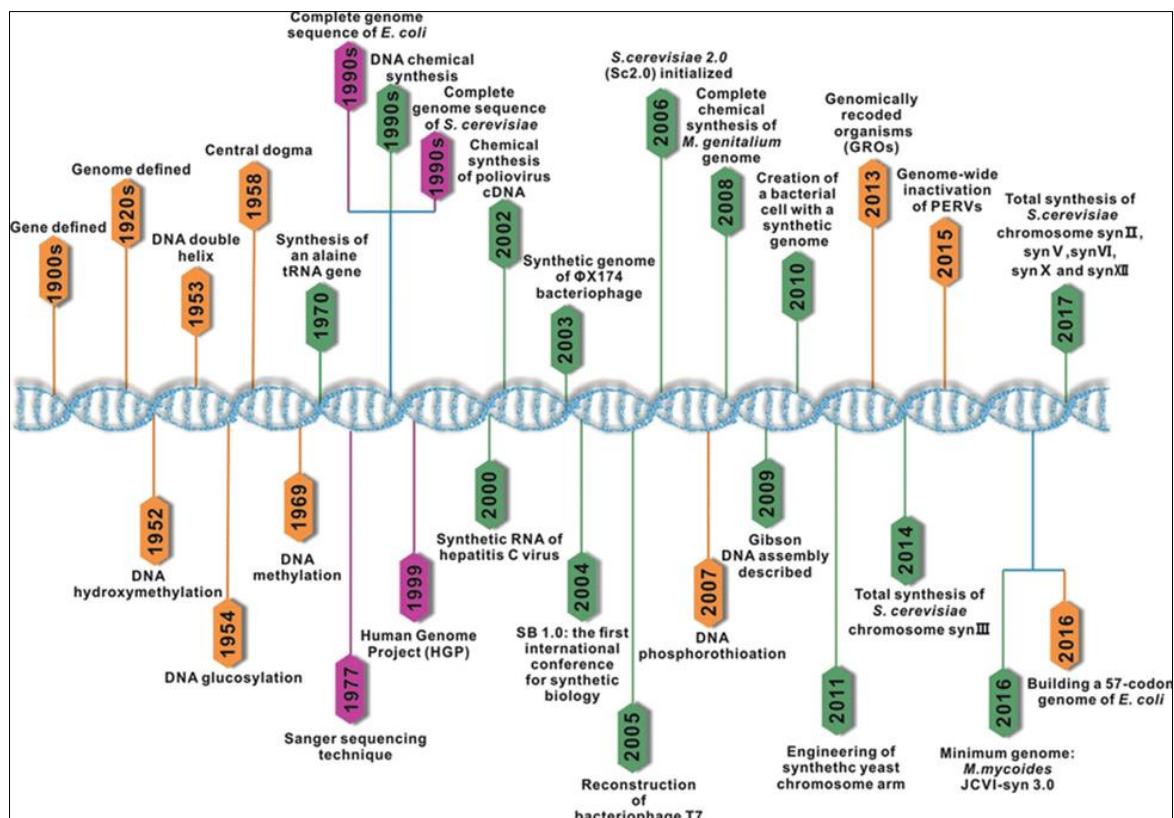
scientific literature, encompassing journals, books, and academic works. These local sources will be our compass, guiding us through the multifaceted aspects of the genetic code and its significance.

Crucially, this background to the study addresses several pressing questions. What is known about the broad topic of genetic code deciphering? The historical development in this field has unearthed remarkable insights into the universal nature of the code and its role in the origins of life [4]. However, what becomes evident are the gaps, the mysteries that beckon further exploration. The intricacies of codon-anticodon interactions, the underlying mechanisms, and the implications for biotechnology continue to pose intriguing challenges. Addressing these gaps holds immense significance, not just for the advancement of biological knowledge but for potential breakthroughs in fields like genetic engineering, synthetic biology, and protein design.

In light of the vast potential and unanswered questions, this study aims to unravel the complex tapestry of the genetic code. By investigating the mechanisms, evolution, and biotechnological applications of the code, we seek to bridge these gaps and push the boundaries of our understanding. The rationale is clear: as we uncover the secrets of the genetic code, we open doors to transformative biotechnological advancements. Consequently, the significance of this study lies not only in enhancing our knowledge of biology but also in illuminating the path to future innovations driven by our comprehension of the genetic code. This study aims to provide a comprehensive understanding of the genetic code's mechanisms, its evolutionary history, and its significance for biotechnology. Specific objectives include elucidating codon-anticodon interactions, exploring the universality and variations of the code, and examining its applications in biotechnology.

The study delves into the genetic code's intricate mechanisms and evolutionary aspects, illuminating its vital role in life processes and adaptability across organisms. It aligns with a timeline of synthetic genomics milestones from the 1900s to 2017 as shown in Figure 1, where green represents genome synthesis achievements, purple denotes sequencing technology progress, and orange signifies theoretical support for synthetic biology biotechnology [5]. This connection underscores the profound synergy between our understanding of the genetic code and our capacity to engineer genomes, emphasizing its pivotal role in advancing.

2. Statement of the Problem



Source: [5]

Figure 1 A timeline depicting synthetic genomics milestones spanning from the 1900s to 2017

The study addresses several critical challenges within the realm of genetic code research. These encompass the imperative for a more profound understanding of the complex mechanisms orchestrating the transformation of genetic information into proteins. Furthermore, it seeks resolutions to persistent inquiries regarding the evolutionary genesis of this universally employed code and endeavors to bridge the existing gaps hindering the complete realization of its biotechnological capabilities. In addition, the study grapples with the multifaceted issues and prospects that emerge from interdisciplinary collaborations spanning the domains of biology, computer science, and artificial intelligence. Simultaneously, it contemplates the ever-evolving ethical and societal ramifications in an era marked by advanced genetic engineering and biotechnology. Addressing these problems is vital for advancing our understanding of the genetic code and unlocking its transformative potential.

3. Literature Review

3.1. Historical Context: Discovery of the Genetic Code

The genetic code, the fundamental language of life, has a rich historical context. Crick and Watson's elucidation of the DNA double helix structure in 1953 set the stage for understanding the code. This monumental discovery paved the way for the deciphering of the genetic code, as it revealed the physical carrier of hereditary information [6]. The work of Marshall Nirenberg and Har Gobind Khorana, in the 1960s, was groundbreaking in cracking the code. Nirenberg's use of synthetic RNA sequences to identify codons and Khorana's synthesis of the first artificial gene contributed significantly to this endeavor [7,8,9].

3.2. Mechanisms of Genetic Code Deciphering

3.2.1. Transcription and RNA

Transcription, the process by which DNA is transcribed into messenger RNA (mRNA), is a key step in genetic code deciphering. RNA polymerase catalyzes this process. The transcription process is finely regulated, ensuring accurate mRNA formation and, consequently, faithful translation [10].

3.2.2. Translation: Ribosomes and tRNA

Translation is the central process of protein synthesis, where mRNA is decoded into a protein. Ribosomes, complex cellular structures, act as the translation machinery. Transfer RNA (tRNA) molecules play a critical role by matching mRNA codons with the corresponding amino acids. The accuracy of translation is maintained by the interaction of tRNA with ribosomes [11].

3.2.3. Codon-Anticodon Interactions

The specificity of the genetic code lies in codon-anticodon interactions. Codons on mRNA are recognized by complementary anticodons on tRNA molecules. The Watson-Crick base pairing rules govern these interactions, ensuring the correct amino acid is incorporated into the growing polypeptide chain [12].

3.3. Evolution of the Genetic Code

3.3.1. Universality of the Genetic Code

The genetic code exhibits a remarkable degree of universality across life forms. Despite the diversity of species, the same codons specify the same amino acids. It accentuates the highlights of the common genetic heritage of all life on earth and has been used as evidence in the study of evolution [13].

3.3.2. Variations and Adaptations

Although the genetic code is predominantly universal, subtle variations and adaptations exist. These differences, such as codon reassignments, provide insights into evolutionary mechanisms and adjustments to specific environments. Notably, in certain species, the codon UGA, conventionally a stop codon, serves the distinctive function of encoding the amino acid selenocysteine [14].

3.3.3. Implications for the Origins of Life

The genetic code holds significance in theories regarding the origins of life. Unraveling the code's emergence and determining whether it resulted from chance or necessity remains a subject of scientific investigation. The evolutionary aspects of the genetic code offer valuable insights into the mechanisms that gave rise to life [13].

3.4. Biotechnological Applications

3.4.1. Genetic Engineering

The genetic code plays a vital role in genetic engineering, affording scientists the means to manipulate organisms through modifications in their DNA sequences. Methods such as site-directed mutagenesis and CRISPR-Cas9 are employed to precisely introduce alterations in genes. Genetic engineering serves as the cornerstone of diverse biotechnological applications [15].

3.4.2. Synthetic Biology

Synthetic biology harnesses the genetic code to engineer artificial biological systems and organisms tailored to specific functionalities. By designing DNA sequences with desired codons, researchers engineer organisms for various purposes, including the production of biofuels, bioplastics, and pharmaceuticals [16].

3.4.3. Protein Design

Understanding the genetic code facilitates protein design. By encoding specific amino acids with synonymous codons, researchers can engineer proteins with tailored properties, such as increased stability or modified functionality. This has applications in biotechnology, medicine, and materials science [17].

3.5. Interdisciplinary Insights: Genetic Code and Beyond

3.5.1. Computer Science and Bioinformatics

The genetic code and its deciphering have inspired computer science and bioinformatics. Algorithms for sequence alignment, gene prediction, and molecular modeling draw parallels to the code's mechanisms. Computational tools aid in studying genomics and proteomics [18].

3.5.2. Artificial Intelligence and Machine Learning

Artificial intelligence and machine learning have become indispensable for genetic code analysis. These technologies predict gene function, identify regulatory elements, and offer insights into the relationships between codon usage and protein expression [19].

4. Conceptual Framework

4.1. Theoretical Foundations in Genetic Code Research

Understanding the genetic code is supported by various theoretical foundations that have fashioned the field of genetic code research.

4.1.1. The Central Dogma of Molecular Biology

The Central Dogma, proposed by Francis Crick in 1958, is a foundational theory in molecular biology. It outlines the flow of genetic information within a biological system: DNA is transcribed into RNA, and RNA is translated into proteins. This theory imparts a framework for understanding how the genetic code is transcribed and translated [20].

4.1.2. Information Theory and Genetics

Information theory, developed by Claude Shannon in the 1940s, has reflective implications for genetics. It offers a quantitative framework for measuring information content in DNA sequences, codon usage, and the redundancy of the genetic code. Information theory principles are instrumental in evaluating the efficiency of information transfer in biological systems [21].

4.2. Examples of Theoretical Frameworks

Several theoretical frameworks have been pragmatic to conceptualize the genetic code, shedding light on its properties and implications.

4.2.1. The Genetic Code as a Language

Considering the genetic code as a language is a potent analogy that accentuates the structured communication between nucleic acids and proteins. Codons, resembling three-letter genetic "words," serve to specify amino acids, much like words convey meaning in human language. This language analogy enhances our conception of the mechanisms through which information is transmitted within the genetic code [22].

4.2.2. Information Transfer in Biological Systems

Information transfer in biological systems is a key theoretical framework. This perspective explores the efficiency, accuracy, and reliability of genetic information transmission. It cogitates how mutations can alter the information transfer process, leading to variations in codon usage and their effects on protein expression [23].

5. Empirical Study

5.1. Extensive Review of Related Studies

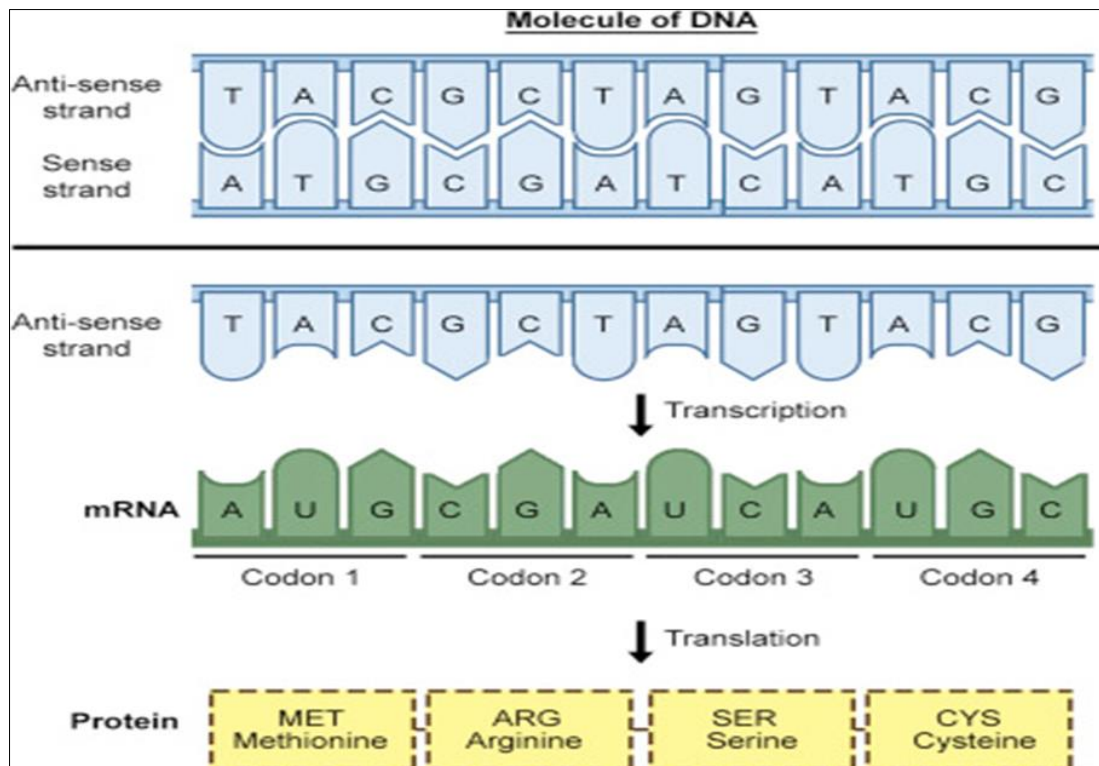
A systematic review of recent research in the field of genetic code studies serves as the basis for the empirical study.

5.2. Research Gap: The Uncharted Territory

The empirical study ascertains an uncharted research territory, including in-depth analyses of codon reassignments and regulatory mechanisms and mapping the role of tRNA modifications in codon decoding. This research gap offers avenues for further exploration.

5.3. Key Findings and Insights

5.3.1. Mechanisms of the Genetic Code



Source: [26].

Figure 2 Data flow, from DNA to protein, involves the antisense DNA strand guiding mRNA transcription. The ribosome reads mRNA in codons, starting with AUG for methionine. Codon base sequences dictate amino acid additions in protein synthesis

The Triplet Codon System and its Universality

The triplet codon system is an inherent mechanism of the genetic code. It involves a sequence of three nucleotides in mRNA, referred to as a codon, which links to a specific amino acid during the process of protein synthesis. This system exhibits near universality across all domains of life, spanning from bacteria to humans, underscoring its fundamental role in the transfer of genetic information [13].

The Role of Transfer RNA (tRNA) Molecules in Translation

Transfer RNA (tRNA) molecules are universal in the genetic code, carrying amino acids to the ribosome during translation, forming bonds with mRNA codons through their anticodons. This interaction ensures that the correct amino acid is added to the growing polypeptide chain. tRNA molecules are highly conserved and essential for accurate translation [24, 25]. These molecules transport amino acids to the ribosome, where they engage with mRNA codons through anticodons, ensuring precise amino acid addition to the growing protein chain. This conservation and necessity for translation accuracy underscore their significance as shown in Figure 2.

Codon-Anticodon Interactions and Ribosome Function

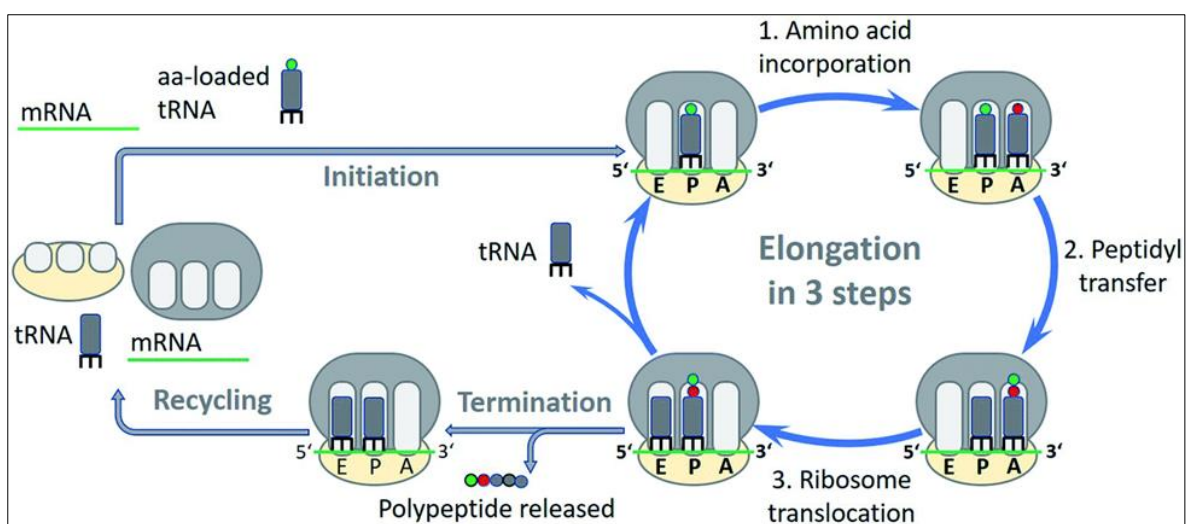
Codon-anticodon interactions between mRNA and tRNA are key to deciphering the genetic code. Ribosomes, the molecular machines responsible for translation, facilitate these interactions. The ribosome ensures accurate codon-anticodon pairing and catalyzes peptide bond formation, enabling the synthesis of proteins [27].

6. Decoding the Genetic Message

6.1. Initiation, Elongation, and Termination of Protein Synthesis

Translation is a multi-step process that includes initiation, elongation, and termination. During initiation, the ribosome assembles on the mRNA, recognizing the start codon. Elongation involves the stepwise addition of amino acids to the growing polypeptide chain, guided by codon-anticodon interactions. Termination takes place upon encountering a stop codon, resulting in the liberation of the freshly synthesized protein [28].

The key processes of peptidyl transfer and ribosome translocation coincide with the initiation, elongation, and termination phases of protein synthesis in eukaryotic protein synthesis, where amino acids are integrated using tRNA (EPA) and mRNA traverses in a 3' to 5' direction. As seen in Figure 3, the ribosome assembles on the mRNA and detects the start codon during the initiation phase. During elongation, amino acids are introduced to the growing polypeptide chain in a methodical manner directed by codon-anticodon interactions. When a stop codon is encountered, the process is terminated, resulting in the release of the newly synthesized protein. This complex mechanism is essential for protein synthesis in eukaryotic cells [29].



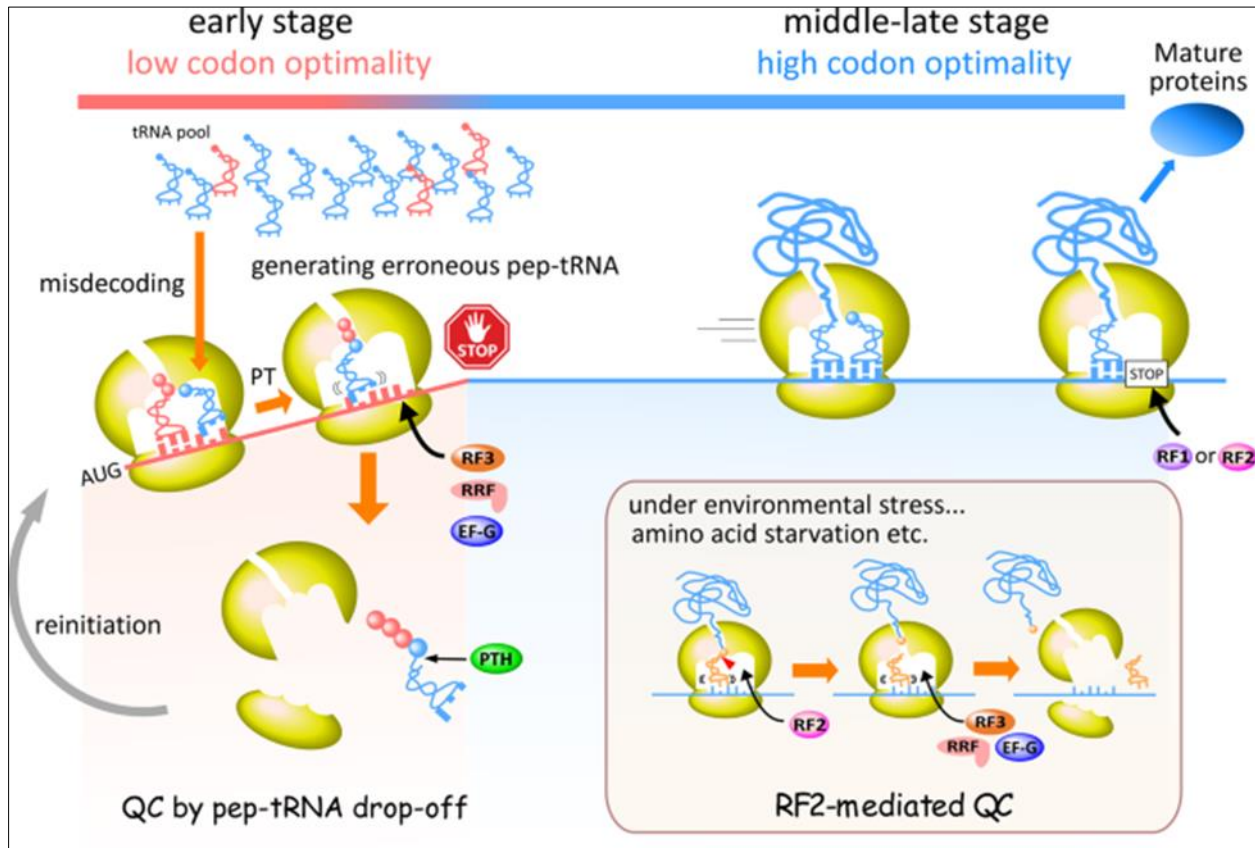
Source: [30]

Figure 3 Protein synthesis in eukaryotic organisms

6.2. Regulatory Elements Influencing Translation

Translation is intricately regulated by a range of factors, such as riboswitches, microRNAs, and translation factors. These components exert control over the pace and precision of translation, enabling cells to adjust to shifting circumstances and react to external cues [30].

6.3. Quality Control Mechanisms and Proofreading During Translation



Source: [32]

Figure 4 Quality control during initial translation elongation through pep-tRNA dissociation

During translation, quality control mechanisms are in operation to avert errors in protein synthesis. These include the surveillance of accurate codon-anticodon pairing, amino acid attachment to tRNA, and proper polypeptide folding. Proofreading mechanisms, such as the "tRNA selection" process, ensure high fidelity during translation [31]. This study uncovers a new quality control mechanism in protein synthesis. At the start of open reading frames (ORFs), non-cognate aminoacyl-tRNA (aa-tRNA) enters the ribosome due to suboptimal codon usage. This leads to the presence of non-cognate peptidyl-tRNA (pep-tRNA) at the P-site. The ribosome is then efficiently disassembled by RF3 and RRF/EF-G, releasing the non-cognate pep-tRNA for recycling by PTH, with the disassembled ribosome participating in the next translation round. In regions of the mRNA where codon usage bias decreases, protein synthesis proceeds smoothly as shown in Figure 4. Under stress conditions, such as amino-acid starvation, RF2 detects miscoding, triggers peptide release, and mediates ribosome disassembly, following the same recycling mechanism [32].

7. Evolution of the Genetic Code

7.1. Universality and Exceptions in the Genetic Code

While the genetic code is largely universal, exceptions and variations exist. For example, in some organisms, the stop codon UGA codes for selenocysteine instead of terminating translation. The existence of these exceptions highlights the code's adaptability [33].

7.2. Hypotheses on the Origin and Early Evolution of the Code

The origin of the genetic code is a subject of scientific inquiry. Hypotheses include the coevolution of tRNA and codons, early protein synthesis through small peptides, and the gradual emergence of the modern genetic code through genetic code expansion [34].

7.3. Coevolution of tRNA and Codons

The genetic code is thought to have coevolved with tRNA molecules, shaping codon-anticodon interactions and ensuring translation accuracy. Coevolutionary processes are pivotal in comprehending the stability and adaptability of the genetic code [35, 36].

8. Variations and Adaptations

8.1. Alternative Genetic Codes in Mitochondria and Other Organelles

The genetic coding within mitochondria and other organelles displays variations. These distinctions, including the utilization of non-standard codons, signify adaptations rooted in the unique evolutionary history of these organelles. For instance, the mitochondrial code differs from the conventional code, shedding light on the coevolutionary dynamics between mitochondria and host cells [37].

8.2. Non-Standard Codons and Their Significance

Non-standard codons, also referred to as sense codons, serve the purpose of incorporating non-standard amino acids. These codons broaden the functional scope of the genetic code, facilitating the creation of proteins endowed with distinctive attributes, including modified structures and heightened stability [38].

8.3. Recoding Events and Their Implications

Recoding events encompass the reassignment of codons to alternate amino acids in the course of translation. These occurrences bear significance for how organisms adapt to particular environments and can exert influence over the regulation of gene expression [39].

9. Recommendations for Future Research

9.1. Bridging the Research Gap

To explore the uncharted realms in genetic code research, forthcoming investigations should concentrate on unveiling the functional implications of codon reassignments, delving into the functions of modified tRNAs, and unraveling the molecular mechanisms underpinning codon optimization.

9.1.1. Biotechnological Applications

Genetic Engineering and Synthetic Biology

The genetic code strengthens genetic engineering and synthetic biology. Researchers utilize the code's principles to design and engineer organisms with tailored genetic sequences, enabling the production of biofuels, pharmaceuticals, and other biotechnological products [40,41].

Codon Optimization for Heterologous Protein Expression

Codon optimization is a biotechnological strategy that enhances heterologous protein expression. By selecting codons preferred by the host organism, researchers maximize protein production. This approach is essential in biopharmaceutical and industrial applications [42].

Protein Design and Novel Genetic Codes

The genetic code guides protein design by specifying amino acid sequences. Researchers can design novel genetic codes to create proteins with desired properties, such as increased stability, altered functions, or entirely novel structures [43].

10. Future Perspectives

10.1. Current Challenges and Unresolved Questions in Genetic Code Research

Genetic code research confronts persistent challenges, such as unraveling the code's origin, comprehending codon reassignments, and uncovering the complete scope of codon interpretations. Exploring these analyses offers promising avenues for future research [44].

10.2. Prospects for Expanding the Genetic Code and its Applications

Broadening the genetic code to encompass extra amino acids and functions presents substantial potential in biotechnology and medicine. Furthermore, advancements in gene editing techniques, such as CRISPR-Cas9, offer new pathways for genetic code manipulation [45].

11. Conclusion

This study not only spotlights recent genetic code advancements but also uncovers ongoing challenges and controversies, revealing uncharted research domains. It signifies progress in understanding the genetic code, offering fresh insights into its evolution and applications in biotechnology. This research fosters optimism in genetic code studies, impacting biology, industry, and our comprehension of life's core language. Our exploration unveils rich knowledge, delving into the code's mechanisms, evolution, variations, and broad scientific implications. The genetic code, with its triplet codons and tRNA control in translation, is life's language foundation, nearly universal, and pivotal for protein synthesis. Our journey through translation complexities provides profound insights into the code's evolution, universality, exceptions, and intriguing hypotheses. The coevolution of tRNAs and codons, along with adaptations in various organisms and organelles, illuminates life's remarkable adaptability. Genetic code research significantly advances biotechnology and healthcare, fostering personalized treatments and innovative medications. Serving as a versatile platform in synthetic biology, the code shapes innovative materials, enzymes, and even new life forms. The dynamic nature of genetic code research constantly ventures into uncharted territory and tackles challenging questions. From expanding the code to utilizing cutting-edge gene editing, the genetic code's future looks promising. In summary, we're at the threshold of remarkable discoveries, ready to write the next chapter in the captivating genetic code research narrative—a journey that never ends, with mysteries inviting us to unveil and reap endless rewards.

Compliance with ethical standards

Disclosure of conflict of interest

The authors acknowledged no conflicts of interest.

References

- [1] Koonin EV, Novozhilov AS. Origin and evolution of the universal genetic code. *Annu Rev Genet.* 2017; 51:45-62.
- [2] Wills PR. Origins of Genetic Coding: Self-Guided Molecular Self-Organisation. *Entropy.* 2023; 25(9):1281.
- [3] Turnpenny PD, Ellard S, Cleaver R. Emery's Elements of Medical Genetics E-Book. Elsevier Health Sciences. 2020.
- [4] Muchowska KB, Varma SJ, Moran J. Nonenzymatic metabolic reactions and life's origins. *Chem Rev.* 2020; 120(15):7708-7744.
- [5] Wang L, Jiang S, Chen C, He W, Wu X, Wang F, Chen S. Synthetic genomics: from DNA synthesis to genome design. *Angew Chem Int Ed.* 2018; 57(7):1748-1756.
- [6] Watson JD, Crick FH. Molecular structure of nucleic acids: a structure for deoxyribose nucleic acid. *Nature.* 1953; 171(4356):737-738.
- [7] Nirenberg MW, Matthaei JH. The dependence of cell-free protein synthesis in *E. coli* upon naturally occurring or synthetic polyribonucleotides. *Proc Natl Acad Sci.* 1961; 47(10):1588-1602.
- [8] Schürle K. History, current state, and emerging applications of industrial biotechnology. In: *Sustainability and Life Cycle Assessment in Industrial Biotechnology.* 2020:13-51.

- [9] Gupta NK, Ohtsuka E, Sgaramella V, Buchi H, Kumar A, Weber H, Khorana HG. Studies on polynucleotides, 88. The enzymatic joining of chemically synthesized segments corresponding to the gene for alanine-tRNA. *Proc Natl Acad Sci.* 1968; 60(4):1338-1344.
- [10] Werner F, Grohmann D. Evolution of multisubunit RNA polymerases in the three domains of life. *Nat Rev Microbiol.* 2011; 9(2):85-98.
- [11] Voorhees RM, Schmeing TM, Kelley AC, Ramakrishnan V. The mechanism for activation of GTP hydrolysis on the ribosome. *Science.* 2010; 330(6005):835-838.
- [12] Duechler M, Leszczyńska G, Sochacka E, Nawrot B. Nucleoside modifications in the regulation of gene expression: focus on tRNA. *Cell Mol Life Sci.* 2016; 73:3075-3095.
- [13] Crick FH. The origin of the genetic code. *J Mol Biol.* 1968; 38(3):367-379.
- [14] Rosandić M, Paar V. The Evolution of Life Is a Road Paved with the DNA Quadruplet Symmetry and the Supersymmetry Genetic Code. *Int J Mol Sci.* 2023; 24(15):12029.
- [15] Jinek M, Chylinski K, Fonfara I, Hauer M, Doudna JA, Charpentier E. A programmable dual-RNA-guided DNA endonuclease in adaptive bacterial immunity. *Science.* 2012; 337(6096):816-821.
- [16] Gibson DG, Benders GA, Andrews-Pfannkoch C, Denisova EA, Baden-Tillson H, Zaveri J, Smith HO. Complete chemical synthesis, assembly, and cloning of a *Mycoplasma genitalium* genome. *Science.* 2008; 319(5867):1215-1220.
- [17] Ferruz N, Höcker B. Controllable protein design with language models. *Nat Mach Intell.* 2022; 4(6):521-532.
- [18] Ferreira R, Amado F, Vitorino R. Empowering peptidomics: utilizing computational tools and approaches. *Bioanalysis.* 2023; 0.
- [19] Angermueller C, Clark SJ, Lee HJ, Macaulay IC, Teng MJ, Hu TX, Reik W. Parallel single-cell sequencing links transcriptional and epigenetic heterogeneity. *Nat Methods.* 2016; 13(3):229-232.
- [20] Crick F. The central dogma of molecular biology. *Nature.* 1970; 227(5258):561-563.
- [21] Shannon CE. A mathematical theory of communication. *Bell Syst Tech J.* 1948; 27(3):379-423.
- [22] Zolyan S. On the minimal elements of the genetic code and their semiotic functions (degeneracy, complementarity, wobbling). *Biosystems.* 2023; 231:104962.
- [23] Stoletzki N, Eyre-Walker A. Synonymous codon usage in *Escherichia coli*: selection for translational accuracy. *Mol Biol Evol.* 2007; 24(2):374-381.
- [24] Holley RW. Structure of an alanine transfer ribonucleic acid. *JAMA.* 1965; 194(8):868-871.
- [25] Smith TJ, Giles RN, Koutmou KS. Anticodon stem-loop tRNA modifications influence codon decoding and frame maintenance during translation. In: *Seminars in Cell & Developmental Biology.* Academic Press. 2023.
- [26] Weed Population Genetics. In: *Fundamentals of Weed Science (Fifth Edition).* 2018:179-208.
- [27] Rodnina MV. Translation in prokaryotes. *Cold Spring Harb Perspect Biol.* 2018; 10(9):a032664.
- [28] Klein U, Tu Y, Stolovitzky GA, Mattioli M, Cattoretti G, Husson H, Dalla-Favera R. Gene expression profiling of B cell chronic lymphocytic leukemia reveals a homogeneous phenotype related to memory B cells. *J Exp Med.* 2001; 194(11):1625-1638.
- [29] Brönstrup M, Sasse F. Natural products targeting the elongation phase of eukaryotic protein biosynthesis. *Nat Prod Rep.* 2020; 37(6):752-762.
- [30] Winkler WC, Cohen-Chalamish S, Breaker RR. An mRNA structure that controls gene expression by binding FMN. *Proc Natl Acad Sci.* 2002; 99(25):15908-15913.
- [31] Blanchard SC, Gonzalez Jr RL, Kim HD, Chu S, Puglisi JD. tRNA selection and kinetic proofreading in translation. *Nat Struct Mol Biol.* 2004; 11(10):1008-1014.
- [32] Nagao A, Nakanishi Y, Yamaguchi Y, Mishina Y, Karoji M, Toya T, Suzuki T. Quality control of protein synthesis in the early elongation stage. *Nat Commun.* 2023; 14(1):2704.
- [33] Labunskyy VM, Hatfield DL, Gladyshev VN. Selenoproteins: molecular pathways and physiological roles. *Physiol Rev.* 2014; 94(3):739-777.

- [34] Di Giulio M. The extension was reached by the minimization of the polarity distances during the evolution of the genetic code. *J Mol Evol.* 1989; 29:288-293.
- [35] Groll M, Heinemeyer W, Jäger S, Ullrich T, Bochtler M, Wolf DH, Huber R. The catalytic sites of 20s proteasomes and their role in subunit maturation: a mutational and crystallographic study. *Proc Natl Acad Sci.* 1999; 96(20):10976-10983.
- [36] Lei L, Burton ZF. Evolution of life on earth: tRNA, aminoacyl-tRNA synthetases, and the genetic code. *Life.* 2020; 10(3):21.
- [37] Sengupta S, Yang X, Higgs PG. The mechanisms of codon reassignments in mitochondrial genetic codes. *J Mol Evol.* 2007; 64:662-688.
- [38] Jin X, Park OJ, Hong SH. Incorporation of non-standard amino acids into proteins: challenges, recent achievements, and emerging applications. *Appl Microbiol Biotechnol.* 2019; 103:2947-2958.
- [39] Bekaert M, Rousset JP. An extended signal involved in eukaryotic-1 frameshifting operates through modification of the E site tRNA. *Mol Cell.* 2005; 17(1):61-68.
- [40] Xian FU, Tao LI, Fan ZHANG, HZ, Wenwei ZHANG, HY, Shida ZHU, Xun XU, Yue SHEN. Progress in the study of genetic code expansion-related methods, principles, and applications. *Synth Biol J.* 2020; 1(1):103.
- [41] Abdulsalam M, Fari HI, Tihamiyu BB, Salam OL. Optimizing α -amylase production from locally Isolated *Aspergillus* sp. Using selected Agro waste as substrate. *Biosci Biotechnol Res Commun.* 2022; 15(3):424-430.
- [42] Gustafsson C, Govindarajan S, Minshull J. Codon bias and heterologous protein expression. *Trends Biotechnol.* 2004; 22(7):346-353.
- [43] Rovner AJ, Haimovich AD, Katz SR, Li Z, Grome MW, Gassaway BM, Isaacs FJ. Recoded organisms are engineered to depend on synthetic amino acids. *Nature.* 2015; 518(7537):89-93.
- [44] Knight RD, Freeland SJ, Landweber LF. Rewiring the keyboard: evolvability of the genetic code. *Nat Rev Genet.* 2001; 2(1):49-58.
- [45] Montecillo JA V, Chu LL, Bae H. CRISPR-Cas9 system for plant genome editing: Current approaches and emerging developments. *Agronomy.* 2020; 10(7):1033.