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The Evolution of Living Biomolecule of Organism based on its Relationship between Virons and Pirons

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Abstract: ***Aim**: The evolution of living organism based on its relationship between virons and pirons. The origin and evolution of life remain one of the most profound unsolved mysteries in science. This study explores the relationship between biomolecules, virions, and prions in shaping the evolution of living organisms. A theoretical model is proposed, suggesting that the evolution of living organisms (ELO) is directly proportional to virions (V) and inversely proportional to prions (P), with an amino acid constant (K) providing a molecular framework to quantify this relationship. The hypothesis is grounded in key prebiotic and molecular evolution theories, including the Miller–Urey experiment, the RNA world hypothesis, and ribonucleoprotein (RNP) formation. Prions, as misfolded proteins, might have played a role in stabilizing early RNA molecules, while viroids, as non - coding RNA replicators, could be remnants of an ancestral RNA world. Experimental data from protein and nucleotide sequence analysis supports the potential role of amino acid sequences in understanding evolutionary patterns. By applying bioinformatics approaches, this model could help decode the evolutionary impact of virions and prions, providing new insights into the emergence of life. Furthermore, future advancements in AI - ML applications could utilize this model to predict potential life - supporting conditions on Mars and other planets, enhancing Astro biological research.*

Keywords: Biomolecules, Virons, Pirons, Evolution and Amino acids

1. Introduction

The next few decades AI will capture all over the world and still the mystery evolution of living organisms and origin of life on the earth unsolved. The key questions like (1) How biomolecules like DNA, RNA and Proteins evolve? (2) The pirons only protein coated living organisms without the source of genetic machinery, how this living microorganism replicates. (3) As we know, virons only possess either RNA/DNA, but absence of protein coat which protects the virus's genetic material. Then how these organisms survive on the earth even though nature has harsh conditions. (4) And the last question is, is there a relationship between biomolecules and virons - pirons? To answer these questions first we have to understand the relationship between biomolecules of living organisms and Viron - Piron.

The Miller–Urey experiment, conducted in 1959, demonstrated the laboratory synthesis of organic compounds from simple inorganic precursors, including water (H_2O), methane (CH_4), ammonia (NH_3), and hydrogen (H_2), under conditions that mimicked early Earth. Using artificial lightning as an energy source, the experiment successfully produced several biomolecules, including five different amino acids [1]. Protein is a fundamental subsystem of life, and it plays a vital role in life's functioning [2].

Stanley Prusiner discovered 'prions, ' which are infectious particles composed of proteins, specifically the prion protein known as PrP. This protein predominantly exists in a natively folded cellular form referred to as PrPC. However, it can occasionally adopt a beta - sheet rich structure called the 'scrapie' form (PrPSc). This altered conformation effectively induces PrPC to transform into PrPSc, leading to the polymerization into amyloid fibers. The conformational change of this single polypeptide is linked to a variety of prion diseases [3 - 4]. Furthermore, prion proteins demonstrate functional preservation alongside structural interchangeability, while also exhibiting functional diversity despite having identical or similar molecular building blocks. It is very probable that in the context of life's chemical evolution, prion - like proteins offered essential protection to the emerging RNA polymers in the Earth's primitive and hostile environment. This period was significant for the establishment of a connection between proteins and RNAs, culminating in the formation of ribonucleoproteins (RNPs). This connection is clearly illustrated by the fact that ribosomes, which are RNPs, are crucial for all cellular life forms, including both RNA and DNA viruses [5].

Viroids represent a distinct class of pathogens affecting plants, composed of diminutive circular RNA molecules ranging from 220 to 450 nucleotides in length [6]. Naturally occurring viroid's can be enzymatically active, i. e. act as ribozymes, and catalyze the cleavage of RNA [7]. Both ribozymes and viroids possess numerous structural characteristics in common. They are circular RNA molecules that do not encode proteins; however, viroid's are larger, with sizes ranging from 246 to 434 nucleotides and a conserved central region referred to as CCR. Ribozymes, on the other hand, are smaller, consisting of a core and three helices, totalling between 50 and 150 nucleotides [8]. Viroids and viroid - like RNAs represent the simplest forms of replicators, being the only known entities that do not code for proteins and likely do not significantly surpass the theoretical minimum size for replicators. Consequently, the notion that these RNA replicators are remnants of the proposed primordial RNA world is both compelling and appealing [6].

The RNA world hypothesis, in its most basic explanation, proposes that life originated from a self - replicating system of RNA molecules, which acted as both the carriers of genetic information and the functional entities produced by that genetic information [9].

Initially, scientists believed that early life relied on both RNA (for storing information) and proteins (for enzymatic functions). However, discoveries of RNA molecules with enzymatic properties—such as ribozymes that catalyse reactions—suggested that early life could have been RNA - based. In this RNA world, RNA molecules not only stored genetic information but also catalysed their own replication and biochemical reactions. Over time, RNA likely evolved to produce proteins, which performed similar enzymatic functions more efficiently. Eventually, DNA emerged as a more stable information storage system, relegating RNA to intermediary roles in modern biology. The exon - intron structure of genes today may be a remnant of this ancient RNA - driven evolution [9 - 10].

The **bottom - up** approach to understanding the origin of life examines how life may have developed from basic molecules through the process of chemical evolution. It starts with the prebiotic chemistry present on early Earth and explores the formation of small organic molecules, their assembly into larger macromolecules, and the eventual emergence of self - replicating systems such as RNA. Laboratory experiments, including in vitro selection of RNA molecules, lend support to the notion that RNA could have acquired the catalytic functions essential for primitive biochemistry. Furthermore, studies on non - enzymatic RNA polymerization and the influence of molecular crowding and encapsulation offer valuable insights into the potential emergence of early self - replicating RNA systems. This methodology investigates how simple prebiotic reactions could evolve into more intricate systems, ultimately resulting in the first self - sustaining biochemical cycles, cellular compartments, and the initial living cells [9 - 12].

The **top - down** approach to the origin of life reconstructs early evolution by analysing modern organisms, tracing life back to LUCA through conserved genes, proteins, and metabolic pathways. Evidence suggests LUCA had a translation system, metabolic networks, a DNA genome, and a cell membrane, though uncertainties remain due to Bacteria - Archaea differences. Ancestral sequence reconstruction, which revives ancient proteins for lab testing, provides key insights into early biochemical functions, environmental conditions, and evolutionary changes that shaped modern life [13 - 14].

The structure of a protein serves as a bridge connecting its genotype and phenotype (function). Nonetheless, it seems that protein structure is conserved to a greater extent than both the coding sequence and the function of the protein. For instance, when examining the divergence in amino acid sequences alongside the divergence in structures of the same protein sets, it typically takes a significant amount of variation in sequence to result in a noticeable change in structure [15 - 16]. Several non - Mendelian traits in fungi have been linked to heritable changes in protein conformation, which may occasionally be advantageous. This finding has expanded the prion hypothesis. The precise function of cellular cofactors is still largely unknown, but mechanistic similarities between the Prion phenomena in yeast and mammals suggest that conformation - based infection and inheritance, which involve the spread of ordered beta - sheet - rich protein aggregates known as amyloid, have universal characteristics [18].

The relationship between the evolution of living organisms and the roles of virions (viral particles) and prions (misfolded proteins) is still not fully understood. Viruses are acknowledged as significant contributors to evolutionary processes due to their capacity to transfer genetic material between species. In contrast, the influence of prions on evolution is less well - defined. Prions, which are infectious proteins responsible for neurodegenerative diseases by causing normal proteins to misfold, lack genetic material unlike viruses. Nevertheless, emerging research indicates that prion - like mechanisms may be involved in adaptive responses, protein - based inheritance, and even the evolution of living organisms. The interplay between virions and prions in influencing biological systems remains largely uncharted.

Hypothesis and Theoretical Model

The relationship between living organisms' evolution and viron - pirons. My principle of the evolution of living organisms is directly proportional to virons and inversely proportional to pirons whereas K as amino acid constant. The amino acid constant K have amino acid sequences which help to understand the evolution of particular living organisms.
$ELO \ \alpha \ V$
$ELO \ \alpha \ 1/P$
$ELO = K \ V/P$
ELO = Evolution Living Organisms
P = Piron
V = Virons. K = Amino Acid constant
NOTE: Following is random example not a sequence of organisms.

Example:
Viron sequence –
AAAUUUUGGGGGCCCCUUUAAAAACCCGGAGGAGCCAUGGGAACCCCAAAAGGGAGAGAGAGAGAUUUUUUUUAAAAGGGGUAAAAUGAUG

Piron Sequence - MMFRNIGTKNIRNIILLL

X organism to check value of K sequence - ATCATATTAGGAGAGAGAGAGAGATATGTTCGGAATATATAATTA TAGGCTTTAAATATTAGGCTAC

Viron sequence into protein sequence using BLAST - MGT P KGRERDF
X organism into protein sequence using BLAST and Expasy - MFRNI
K = EOL × Pirons /Virons
Result - K = NINIMMNIRNIILLL / PGD

The amino acid constant may be in division form or in one line sequence form which depends on amino acid sequences of predicting ELO. Its help to understand the relationship between virons and prions. This sequence hypothetically showing direct and indirect relationships of viron and prions to evolution of particular living organism.

2. Conclusion & Future Work

This hypothesis delves into the complex relationship between the evolution of living organisms and the functions of virions (particles that carry genetic material) and prions (infectious proteins that have misfolded). It proposes that evolution is positively related to virions and negatively related to prions, with an amino acid constant (K) being a significant factor in

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understanding evolutionary dynamics. Foundational concepts such as the Miller - Urey experiment and the RNA world hypothesis support the idea that early biomolecules were vital for the emergence of life. Prions, despite their lack of genetic material, may have influenced early molecular evolution by providing stability to RNA structures. In contrast, viroid's, which are simple RNA entities, may be remnants of an ancient RNA world that played a role in the formation of early life.

- The model suggests that analyzing amino acid sequences can reveal the evolutionary impact of virions and prions on organisms.
- This equation in future perspectives help to develop AI - ML model for predicting life possible on Mars and other planet.
- The amino acid sequence obtained from the equation will help to illustrates the primitive biomolecular structure of a specific organism from the moment it emerged on Earth. This sequence represents the organism's initial molecular identity at the dawn of life, acting as a fundamental model prior to its evolutionary changes.

References

[1] Miller, S. L.; Urey, H. C. Organic Compound Synthes on Primitive Earth: Several questions about the origin of life have been answered, but much remains to be studied. Science 1959, 130, 245–251.

[2] Chatterjee, S., & Yadav, S. (2022). The coevolution of biomolecules and prebiotic information systems in the origin of life: a visualization model for assembling the first gene. Life, 12 (6), 834.

[3] Prusiner SB, Groth DF, Bolton DC, Kent SB, Hood LE. Purification and structural studies of a major scrapie prion protein. Cell.1984; 38: 127–34.

[4] Prusiner SB, McKinley MP, Bowman KA, Bolton DC, Bendheim PE, Growth DF, et al. Scrapie prions aggregate to form amyloid - like birefringent rods. Cell.1983; 35: 349–58.

[5] Jheeta, S., Chatzitheodoridis, E., Devine, K., & Block, J. (2021). The way forward for the origin of life: prions and prion - like molecules first hypothesis. Life, 11 (9), 872.

[6] Lee, B. D., & Koonin, E. V. (2022). Viroids and viroid - like circular RNAs: do they descend from primordial replicators?. Life, 12 (1), 103.

[7] Flores, R.; Gago - Zachert, S.; Serra, P.; Sanjuán, R.; Elena, S. F. Viroids: Survivors from the RNA world? Annu. Rev. Microbiol.2014, 68, 395–414.

[8] Diener, T. Potato spindle tuber "virus. " IV. A replicating, low molecular weight RNA. Virology 1971, 45, 411–428.

[9] Gilbert, W. (1986). Origin of life: The RNA world. nature, 319 (6055), 618 - 618.

[10] Liberles, D. A., Chang, B., Geiler - Samerotte, K., Goldman, A., Hey, J., Kaçar, B.,. . . & Storfer, A. (2020). Emerging frontiers in the study of molecular evolution. Journal of molecular evolution, 88, 211 - 226.

[11] Popović M, Fliss PS, Ditzler MA (2015) In vitro evolution of distinct self - cleaving ribozymes in diverse environments. Nucleic Acids Res 43: 7070–7082.

[12] Poole AM, Jeffares DC, Hoeppner MP, Penny D (2015) Does the ribosome challenge our understanding of the RNA world? J Mol Evol 82: 1–4.

[13] Becerra, A., Delaye, L., Islas, S., & Lazcano, A. (2007). The very early stages of biological evolution and the nature of the last common ancestor of the three major cell domains. Annu. Rev. Ecol. Evol. Syst., 38 (1), 361 - 379.

[14] Pross A, Pascal R (2013) The origin of life: what we know, what we can know and what we will never know. Open Biol 3: 120190 10.1098/rsob.12019.

[15] Chothia, C., & Lesk, A. M. (1986). The relation between the divergence of sequence and structure in proteins. The EMBO journal, 5 (4), 823 - 826.

[16] Illergård, K., Ardell, D. H., & Elofsson, A. (2009). Structure is three to ten times more conserved than sequence—a study of structural response in protein cores. Proteins: Structure, Function, and Bioinformatics, 77 (3), 499 - 508.

[17] Furnham N, Sillitoe I, Holliday GL, Cuff AL, Laskowski RA et al. (2012) Exploring the evolution of novel enzyme functions within structurally defined protein superfamilies. PLoS Compu Biol 8: e1002403.10.1371/journal. pcbi.100240.

[18] Lupi, O., Damali, P., Cruz, E., Sanberg, P. R., & for Prion, T. C. T. F. (2006). Are prions related to the emergence of early life?. *Medical hypotheses*, *67* (5), 1027 - 1033.