

SERIOUS DIFFICULTIES FOR ABIOGENESIS

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1. DEFINITION OF TERMS:

- 2LT- 2nd Law of Thermodynamics
- Ordered Arrangement- An arrangement with a periodic pattern; thus, only a relatively short algorithm which defines the repeating pattern is needed to completely define the arrangement.
- Complex arrangement- An arrangement with a no periodic pattern; thus, the smallest algorithm that can completely define this arrangement is close to the size of this arrangement.
- Complex random arrangement- A complex arrangement that serves no specific function.
- Complex specific arrangement- A complex arrangement that can perform a specific function.
- Biospace- A very complex many dimensional space. Each dimension represents some variable that defines the chemical structure of life forms. Positioned throughout this space are all the possible life forms.
- Fitness terrain- The fitness for survival of a certain life form is dependent upon its' ability to survive in its' environment and the variables which define its' position in biospace. This fitness for survival variable changes as the biospace or environmental variables change. These changes can be thought of as defining the slopes, valleys, peaks and plateaus of this terrain. Fundamentally, the claim of the evolutionists is that all life evolved through randomly meandering through this terrain.
- 10^X - 1 with X zeroes after it.
- Mole- 6.02×10^{23} molecules

2. INTRODUCTION

The astonishing order of life brings to mind the obvious questions, how in the world did it originate? The amazing thing about life that makes it unique in the known universe is it's ability to reproduce itself or self-replicate. The process by which the first replicators that led to nucleic acid based self-replicating cell is termed abiogenesis. This article discusses the probability of abiogenesis by natural processes. It also discusses natural processes that have been proposed for abiogenesis.

Ref. 31 explains the rational way to prove the supernatural intervention is by showing that there is no plausible natural explanation for abiogenesis. This means to dismiss purely natural evolution one must show that all possible natural evolutionary pathway from basic chemicals in a plausible prebiotic soup to a nucleic acid based self-replicating cell are implausible. This article attempts to make such a case.

3. THE NATURE OF 2LT & ENTROPY

Probabilistic analysis is an important part of determining if a proposed a natural process is realistically plausible. 2LT is often defined according to entropy, "The entropy of a closed system increases during any natural process that occurs spontaneously. (1)" A proper definition of entropy is related to the number of different ways that the system's mass or energy can be arranged. The more ways it can be arranged the more freedom it has to produce disorder; thus, it is assigned a higher entropy value. A logarithm of the probability associated with a certain state is used to define entropy so that the entropy value is directly proportional to the mass of the system rather than an exponential of the mass of the system. The standard formulation of entropy is $S=k \ln(\omega)$ where k is the boltzman constant and ω is the number of different ways that the system can be arranged for a given state. When comparing two different states of a system, ω should sufficiently measure the relative probability between the two different states which the change of the system is being considered. If the relative probability

between two possible states can be determined then it can be determined if the system will spontaneously change from one to the other if there are no other constraints.

Configuration entropy focuses on the arrangement of mass throughout that system; thus, the number of ways the mass in the system can be arranged and is related to the configuration entropy. Brillouin (22) has shown that $S = k \ln(\omega)$ not only defines the entropy for how the energy is arranged, but also how the mass is arranged (configurational entropy) such as in molecular sequences. The statistical evaluation explained in Ref. 22 to show the $S = k \ln(\omega)$ relationship for the entropy of the mass is essentially the same as for the configuration of the energy as derived in Ref. 1. This is because changes in either the mass or energy distributions follow the same fundamental principal, "The direction of spontaneous change is away from a state of lower intrinsic probability towards the one of greater intrinsic probability (1)".

The thermodynamic view of entropy focuses on the arrangement of energy throughout that system; thus, the number of ways the energy in the system can be arranged is related to the thermal entropy. Consideration of heat flow (dQ) determines the following relation for entropy, $dS = dQ / (\text{temperature})$. According to 2LT for any spontaneous change, the energy in the system always becomes more evenly distributed. This definition is often applied to engines to predict their efficiency which according to 2LT can never be perfect, "No process is possible in which the sole result is absorption of heat from a reservoir and its conversion to work.(1)"

4. THE NATURE OF LIFE

A key feature of life is the DNA which is contained in the cells which are the basic building blocks of life. The DNA sequence is basically a 4 letter language. 4 different nucleotides are used to form molecular chains that make up the DNA, which then form the information or blueprint that is used to define all the rest of the chemistry that builds a living animal or plant. DNA and RNA are nucleic acids. As shown in Figure 1, The first step in the copying process is the transcription process where RNA is formed from DNA which is accomplished with the help of a RNA polymerase enzyme. Then as shown in Figure 1 and Figure 2 this RNA is translated into protein molecules. These protein molecules make up the structure and perform the functions of the cell. 20 different amino acids are used to form molecular chains that make up protein molecules.

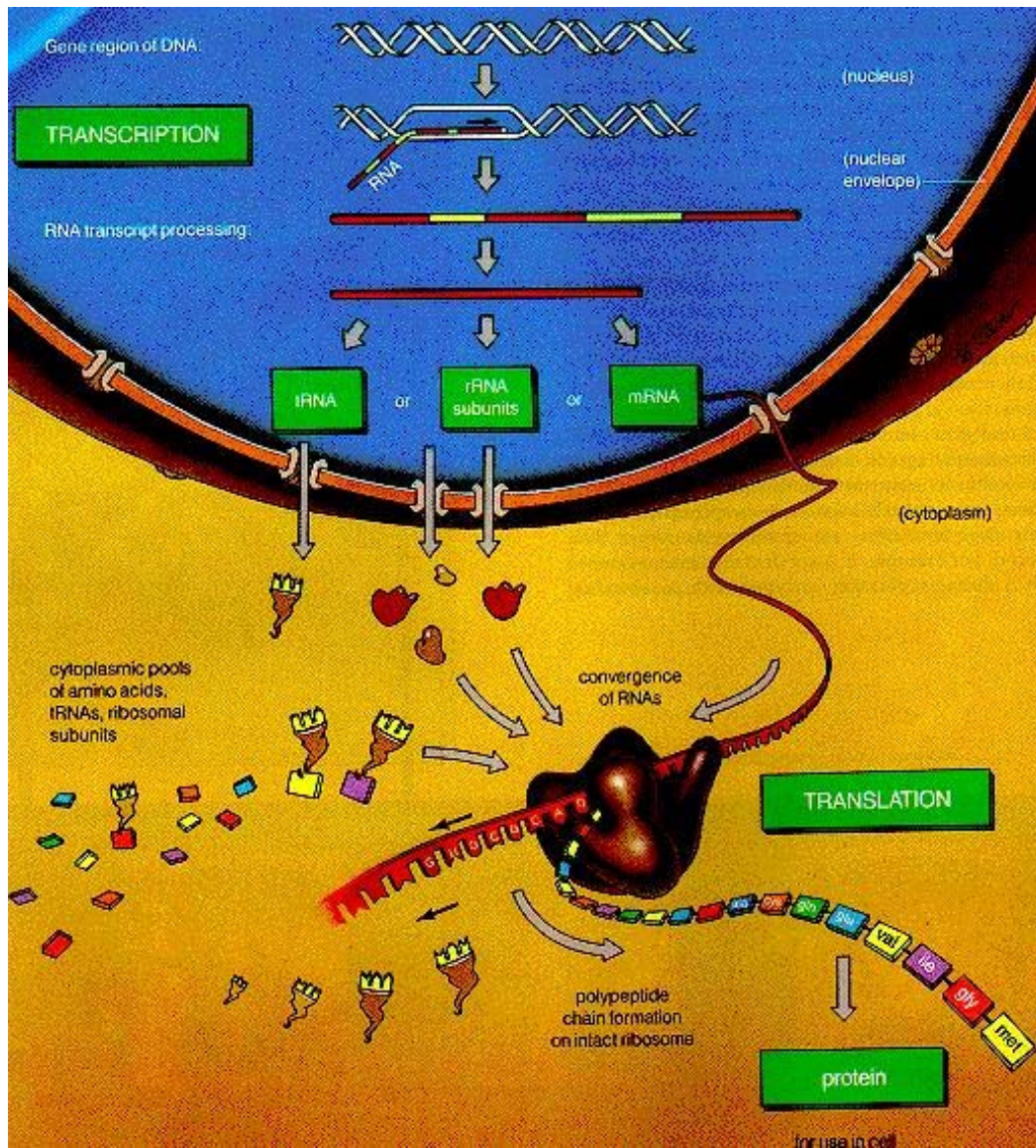


Figure 1 Flow of Genetic Information in Protein Synthesis of Eukaryotic Cells

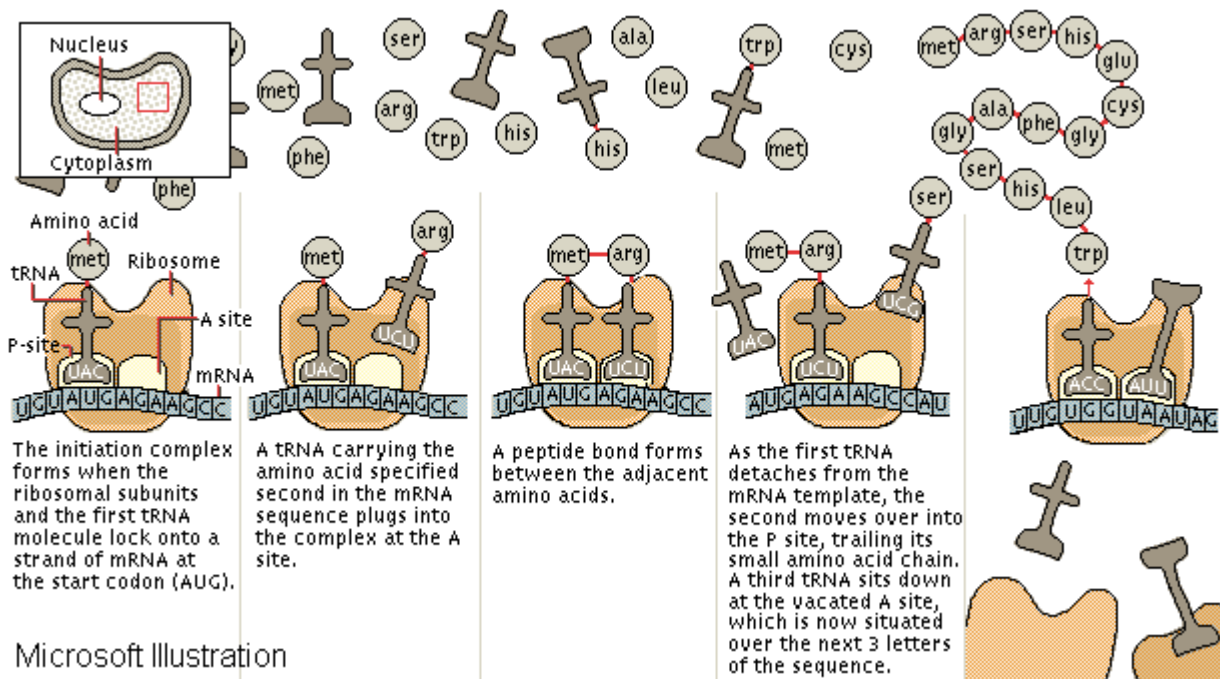


Figure 2 Translation Process of RNA to Proteins

The protein molecule spontaneously folds into a specific 3-D geometry that allows it to perform its specific chemical functions as shown in the example of a sperm whale myoglobin in Figure 3. The protein molecule is contained in gray. Figure 3 shows how the myoglobin acts on the heme. The 3-D shape matches well with other molecules that it acts on so it can hold them in proper position long enough to allow for electron transfer to occur; thus, it can perform its function as a catalyst or enzyme. This is accomplished by grooves or cavities in the 3-D structure. Certain amino acids strategically located within the 3-D structure react with other molecules in order to bring the proper change to their chemistry. The nucleic acids also naturally form a coiled-up 3-D chemical structure.

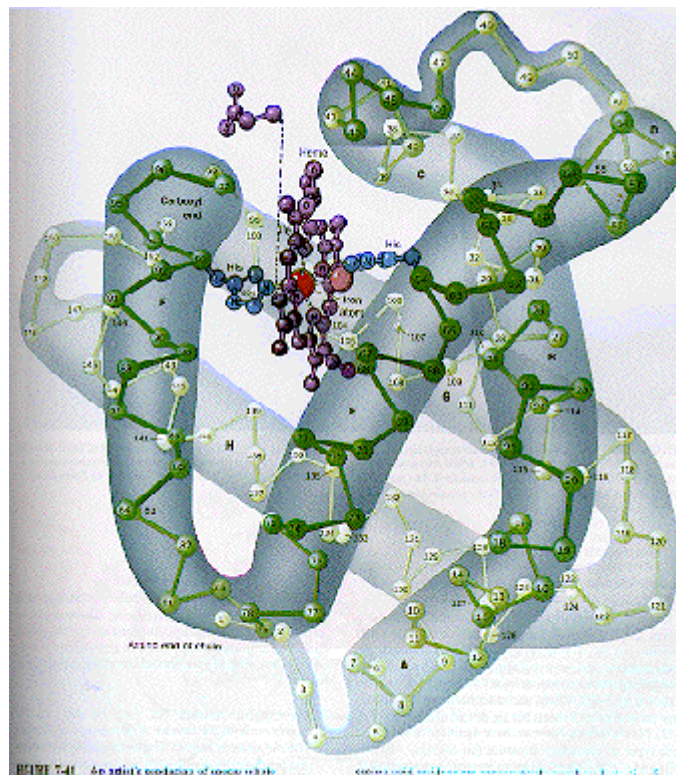


Figure 3 3-D Geometric Shape of Sperm Whale Myoglobin Protein (17)

5. REDUNDANT ORDERED ARRANGEMENTS COMPARED TO SPECIFIC COMPLEX ARRANGEMENTS

Evolutionists claim that developing the level of complexity in life is not an improbable event. Some claim examples of redundant order that spontaneously forms imply that the specific complexity of life could just as well form. Some have compared the complexity of life to the redundant ordered arrangement of atoms in a crystal. For instance, in Ref. 2 and 3 the snowflake is compared to the order of life. The snowflake is a crystal structure. Crystal structures are made up of many repetitive units (atoms) which is similar to DNA; however, crystal structures are different in that these repetitive units are related to one another in constant fashion. The geometrical arrangement of crystals is repetitive so that they form an essentially constant lattice structure. There are only fourteen ways to arrange lattice points which can be defined by only seven different crystal systems (triclinic, monoclinic, orthorhombic, tetragonal, cubic, hexagonal and rhombohedral). Atoms are repeating units with symmetry; thus, when packed together they form symmetrical structure. The unique feature about snowflakes is that their crystal structure (hexagonal) is formed in the air. This gives them the freedom to form their unusual and beautiful shapes. Still the fundamental structure is a redundant arrangement of atoms. Sometimes an atom will not pack in properly or a different size atom will get packed in which will produce a local aberration or dislocation in the crystal structure. Thus, every real crystal and snowflake is different depending upon the defect. Even though every snowflake is different, the fundamental structure is still a redundant arrangement of atoms. Due to the symmetry of many of the basic building blocks in nature, it is not surprising nor is it improbable that often redundant order is spontaneously produced.

DNA and proteins certainly have their redundancy, respectively, they are made up of 4 or 20 repeated units; however, they are not repeated in any sort of constant fashions as in crystal structure. This allows DNA or proteins to form many different possible sequences; thus, it can be very informational intensive where the crystal structure is not. Granted not every site in the sequence is crucial, approximately 10% percent of the sites in proteins are chemically active sites. The other sites are still important for they specify the series of steps comprising the folding pathway which ultimately determine the important 3 dimensional structure of the molecule (17).

The proper positioning of crucial amino acids is key to the development of life. For example, the sickle cell mutation in humans is caused by only a single amino acid substitution (valine, where glutamic acid should be) in a long-chained protein. A single amino acid represents only one of the billions of amino acids that make up the unique protein sequences of a human. The sickle cell state has a significant effect on the whole human body. It causes the four-chained hemoglobin molecule to form incorrectly when oxygen is low. Defective hemoglobins bind together, forming long rods that stretch the red blood cell into a crescent. These "sickled" red blood cells cannot fit through small blood vessels causing blood circulation problems which can cause serious medical problems and sometimes death. Thus, this state can have a dramatic effect on the survival or the continuation of the existence of that certain individual. This is quite different than analogies of nonredundant order that have been used to attempt to dismiss the relevance of probability. Would a change in just one molecule per billion affect the very continuation of the existence of a certain snowflake, tornado, graded river bed, stalactite, sand dune or water swirl? (examples that evolutionist gives in Ref. 2&3) Definitely not. This shows the stark contrast between the nonredundant complex information intensive characteristics of biological molecules of life and redundant order.

Systems far from equilibrium do produce order as explained by Prigogine in Ref. 18. Water forming a swirl while going down a drain is an example of this phenomenon. The intermediate states that these systems pass through on their way to equilibrium have a high level of redundant order such as the symmetrical shape of the water swirl. However, the important feature of biological molecules is that they have a specific high complexity which is a completely different kind of arrangement of molecules than the redundant order that is produced in certain systems far from equilibrium. There is no apparent connection between the kind of spontaneous ordering that occurs from energy flow in such systems and the work required to build specific information intensive macromolecules such as DNA and protein.

A properly arranged chain of amino acids does not have any special symmetry that causes it to form spontaneously out of basic non-replicating constituents. Thus, the flawed analogies of redundant order do not have any significant relevance when comparing to the nonredundant order of DNA or proteins in biological molecules.

6. OPEN SYSTEMS

Planet earth is an open system with the sun as a constant source for energy input. The sun does provide the energy which allows for life forms to continue their existence by maintaining their highly complex specific arrangement at the expense of creating more disorder through their waste products. But the Origin of life involves not just the maintaining of this specific complexity but also the origination of this specific complexity.

Energy flow through a certain system can decrease the entropy of a specific part of a system at the expense of another part of the system increase in entropy. This is often observed when intelligently designed engines flow heat through their system to convert it into mechanical work. Thus, if there is a mechanism or process in place to properly use the flow of energy, useful arrangement of mass or energy that represents a local decrease in entropy can occur. However, just because energy is flowing through a system, does not mean that any kind of order or complexity will be spontaneously produced. For instance, there is a certain entropy decrease in the chemical formation of 100 complete human males out of a prebiotic soup in just a few minutes. There is certainly enough

mass in the rest of the earth that can increase in entropy during the same time as this formation in order to make that total system of the earth still have a total increase in entropy. However, just because energy was flowing through the prebiotic soup does not mean the above scenario is plausible. There needs to be some sort of mechanism or process to use the flow of energy to produce the proper arrangement of molecules or local decrease in entropy. This is just what a typically factory does, it uses the flow of energy through the factory to create an increase in order or specific complexity in a piece of material which is their product. A intelligent factory has all the tools and devices in place which efficiently use the energy to convert the disordered material into a highly organized product. The challenge for originating useful DNA through energy flow is finding a suitable mechanism for using the energy flow to produce the proper nucleic acid sequences. Ref. 5 criticizes the different mechanisms which evolutionists propose could produce the proper arrangement of either nucleic or amino acids. They question how the decrease in thermal entropy from energy flow through the system could be coupled to do the proper configurational entropy work required.

“There is no apparent connection between the kind of spontaneous ordering that occurs from energy flow through systems and the work required to build aperiodic informational intensive macromolecules like DNA. Apparently a very special apparatus (or factory) would be necessary to play the crucial role of a template, metabolic motor, etc..., that would direct the flow of energy in such a way as to create the unique information that defines life.”

In order for this apparatus to properly define the DNA, it would have to at least the same level of information of the DNA. Thus, the question of how did this apparatus originate would be just as challenging as the question of how did the DNA originate.

7. DIFFICULTIES FOR ABIOGENESIS

The previous discussions has shown that there is no special symmetry about life forming DNA or protein that causes that proper DNA or protein sequences to form spontaneously. In addition, there is apparently no special feature in nature that causes DNA or protein structures suited for self-replication to form spontaneously, even in an environment which has energy flowing through it. Thus, it appears that the only natural mechanism left for naturally producing the proper DNA or protein sequences for the 1st replicator is just the pure chance of them forming through random intermingling in a prebiotic soup. This section discusses some of the major difficulties in developing a nucleic acid based cell.

7.1 Consideration of Constant Stereochemistry of a Simple Cell

All reproducing organisms are made of cells which contain both nucleic acids and proteins. A simple cell is the least complicated of all modern life form; thus, it's fitness terrain region is where the fewest variables are involved. Therefore, the region of the fitness terrain involving abiogenesis is the one which has the most potential to be thoroughly understood. However, on the other hand if life completely evolved, then the life forms involved abiogenesis would produce the most sparse geological record. A crucial step for abiogenesis is obviously developing this fundamental building block, the cell. Ref. 19 estimates that the simplest cell would have at least 300 proteins. This appears reasonable since the simplest known cell, *Mycoplasma hominis* H39, has around 600 different kinds of proteins (4).

In order for a molecule to directly replicate itself or pass on information to other molecules in an efficient manner it has to have certain geometrical features at the instant it replicates or passes on information. In order to efficiently transfer it's sequence, the units of the sequence being copied must be exposed for bonding to the new molecule being formed and aligned in a manner so that the complementary pairing relationships can be made from the template being copied. In the case of direct replication the pairing relationships are self-complimentary. The bonding locations must be on the same side of the chain so that the new chain can be continuously arranged from one side of the template. This is analogous to the requirement for all letters on a piece of paper being copied in a Xerox machine to be on one side of that piece of paper being copied. Otherwise a much more complicated copy machine is needed in order to make the copy in a continuous fashion. In biological molecules this fundamental requirement is met by all the amino acids being left handed and all the nucleic acids being right handed. This makes all the pairing molecules line up on the same side of the chain as in the replication of DNA shown in Figure 4. In addition, if the molecule does not have constant stereochemistry (constant left or right handed) it does not fold properly to it's 3-D shape. This creates a challenge for origins scenarios because naturally in chemical soups the percentage of left and right handed nucleotides is always essentially 50% (racemic).

“The probability of the formation of one antipode or the other is therefore the same. As the law of averages applies to chemical reactions the appearance of an excess of one antipode is very improbable, and, in fact, we never encounter it under the conditions of non-living nature and in laboratory synthesis. (Ref. 6, pg. 59)”

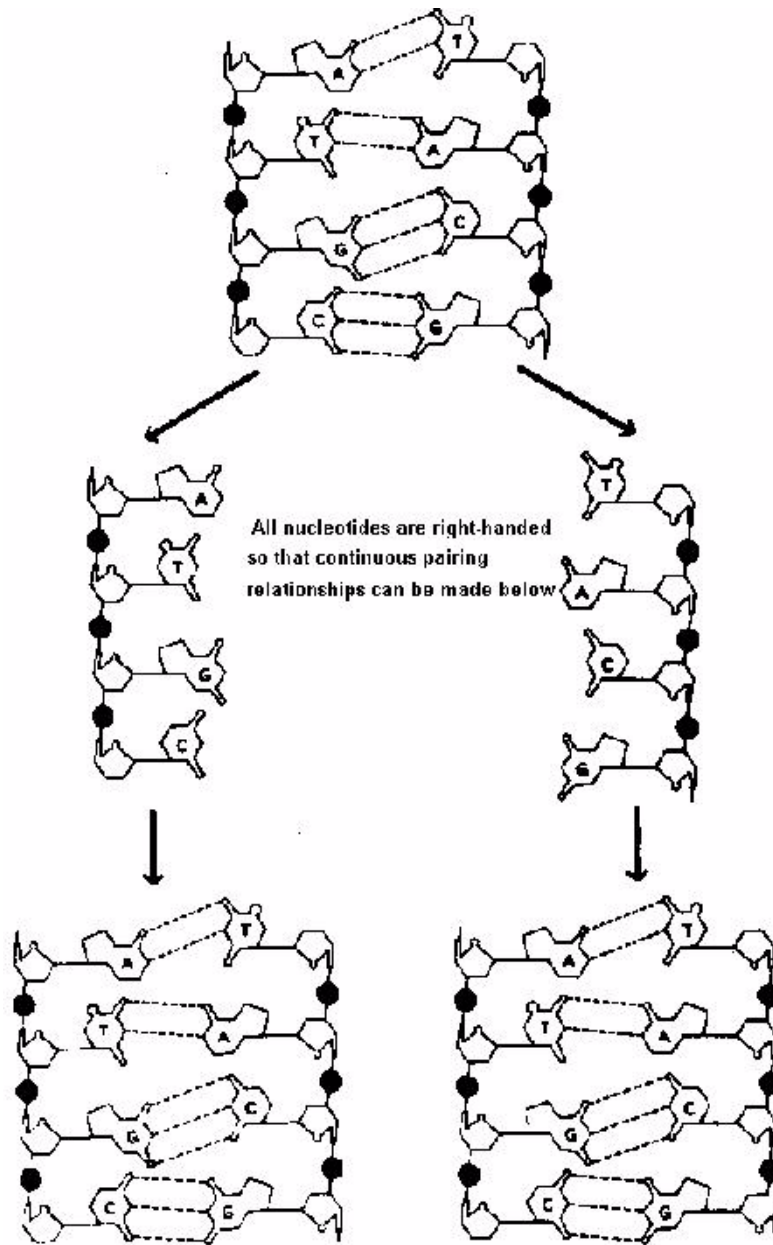


Figure 4 DNA Replication

The requirement of constant stereochemistry for just the simplest hypothetical simple cell of just 300 proteins can be simply determined by assuming that the formation of a left or right handed molecule is 1/2 just a coin toss. A conservatively small protein length of 100 units will be assumed. The chance of getting constant left or right handed stereochemistry is $(1/2)^{(300 \times 100)} \approx 1/10^{9031}$. This calculated odds are so small compared to the life (10^{17} seconds) and size (approx. 10^{83} total atoms and 10^{44} amino acids conservatively assumed in primeval soup, Ref. 19) of the observable universe. An conservative assumption that all the amino acids on earth reacted perfectly efficiently since the big bang give $10^{44} \times 10^{17} = 10^{61}$ attempts which is trivially small compared to 1 in 10^{9031} . Thus, it appears extremely unlikely that the most simplest cell would form by chance.

Conservative assumptions:

1. Only alpha-links occur between amino acids making polypeptides or only correct linking at the 3,5 position of sugar occurring in polynucleotides in nucleic acids. A quantification of these problems of specificity is addressed in Ref. 20.
2. No bonding or side reactions occur with the myriad of all the other types of molecules the would exist in the prebiotic soup.
3. The proper amino acids and nucleic acids did form naturally.
4. Formed chains are protected from ultraviolet light
5. Consider that if all the proper proteins or nucleic acids did form, they would all be in the same place at the same time and then form something like a cell which had a wall to hold things together.

6. Every unusable chain is immediately dismantled so another try can be made.

7.2 Consideration of Configurational Entropy

The 2nd Law of Thermodynamics which governs the way the energy in a system is distributed does not necessarily constrain the natural development of life. For example, Thomas Cech discovered that RNA does have some modest catalytic abilities; thus, energy flow could be solved by this feature for at least some initial stages of the evolution process. However, as pointed out in Section 3, probabilistic evaluation applies just as well to the way the mass is configured. Biological molecules are sequences of basic units so it is appropriate to consider the probability of certain sequences forming.

Ref. 5 presents an evaluation of the probability of just one specific protein sequence 100 amino acids long forming by chance. They make their assessment by determining the configurational entropy which they appropriately distinguish from thermal entropy so that the Gibbs free energy equation can be properly solved. Based upon the assumption of a 1 mole/liter (M) concentration of each amino acid they determine for one specific protein sequence a 10^{-338} M concentration. This is again trivially small compared to the life and size of the observable universe. The 1 M assumption is conservative because amino acids give up a water molecule when joined; thus, in a water solution their concentration would be minimized. Ref. 5 also points out that the configurational entropy for obtaining a typical DNA molecule for a protein is approximately twelve times greater than the protein they use in their example; thus, achieving the corresponding DNA is even more unlikely. In addition, current research implies that primordial atmosphere was neutral. Such an environment would also greatly minimize the amount of nucleic or amino acids in the hypothetical prebiotic soup. Granted there are many protein chains that are functional which is a nonconservative point in regard to the calculation just presented. However, it is questionable if this nonconservative assumption makes up for the significant conservative assumptions just mentioned and 1-5 listed in Section 7.1.

7.3 Consideration of Information Content (Shannon Entropy)

Entropy can be defined in terms of the information content of the molecule. This is termed Shannon entropy and is defined in Ref. 19. Ref. 19 uses the protein iso-1-cytochrome c as an example for determining the information content of a protein. The only known function of the cytochrome c protein is electron transport involved with oxidative phosphorylation. Many of the sites in a protein chain, especially those that are not chemically active, can be replaced by other functionally equivalent amino acids. However, there are limitations for these sites because they do determine the folding sequence of the protein; thus, ultimately it's 3-D geometrical shape. Ref. 19 considers this by using an effective number of amino acids at each site. Ref. 19 also relates sequence of the amino acids to nucleic acids by considering the triplet relationship. Thus, Ref. 19 makes an accurate assessment of the fundamental information content of the system. Based upon this evaluation Ref. 19 determines that of all possible sequences (1.0×10^{168}), 2.3×10^{93} of them are functionally equivalent which represent a very small fraction (2.3×10^{-75}) of the total. The same conservative assumption mentioned in Section 7.1 (1-5) and 7.2 apply. Thus, it is not realistic to expect to get by chance out of a prebiotic soup a protein that performs the function of the iso-1-cytochrome c protein.

The above calculation was based upon a prebiotic soup that would contain essentially equal numbers of right and left handed nucleic and amino acids. Once life got started and developed the ability to screen out left from right handed it would be more appropriate to consider a calculation based upon constant stereochemistry. Under this case the total number of possible sequences is reduced to 1.15×10^{137} which changes the fraction to 2.00×10^{-44} .

Granted, replication does not necessarily need the function provided by iso-1-cytochrome C. There are many other protein functions that could be part of a replication process. However, there are other constraints, for example, all proteins perform specific functions on other molecules so they must be properly configured to accomplish this specific function on the molecules that are available in the prebiotic soup. Different functioning proteins that would be part of the replication system, must work together as a whole to achieve a higher level function which applies further constraints because there would be specific requirements to fit and react with these other molecules. Also, most all biological enzymes catalyze degradative processes; for example Ref. 24 states, "Nucleases and proteases catalyze the breakdown of nucleic acids and proteins, respectively. Deaminases and decarboxylases catalyze the deamination of amines and decarboxylation of carboxylic acids, respectively - and on and on." Thus, most enzymes involved with the self-replication process in life, in isolation perform degradative processes. Thus, it appears difficult to explain through molecular evolution how small individual molecules developed individually and then came together to work together as a complete replicating unit.

8. ANALOGIES AND HYPOTHETICAL SCENARIOS FOR ABIOGENESIS

The previous discussion has shown that obtaining anything like a cell appears unrealistic considering the life and size of the observable universe. Thus, naturally evolutionists have proposed that more simple forms different than cells such as single RNA strands were the first reproducers. However, it is questionable if such simple forms would lead to a cell. One of the key features unique to a cell is its membrane wall that keeps the contents of the cell together so all of the many proteins can work together to accomplish their tasks. There is no reason for

independent single RNA or protein strands to be suited for working together until they form a working unit as in the case of the cell.

8.1 Analogies to Abstract Mathematical and Geometrical Concepts

Analogies to geometrical shapes that develop from the repetition of some algorithm are often made such as the Sierpinski Gasket. Ref. 23 points out a wide variety of order that develops spontaneously; however, ref. 23 does not evaluate these systems to see if the important features of the concept relate to the crucial features of the chemistry in biology that allow it to self-replicate in order to determine if the analogy has any relevance at all.

Section 8.2 does give a good example of a geometrical analogy that is accurate and indeed replication did occur. However, once the analogy is applied to the molecules we find in life today, it breaks down because all biomolecules involved with the self-replication process fold over so there is no plane over which the self-complementary pairing relationships can be made as discussed in Section 8.2. Thus, in order for analogies to be relevant it is evident that the crucial features involved must be properly represented. Complexity theory is an abstract concept whose relevance to self-replication cannot be determined unless it is applied to real chemical scenarios.

8.2 Small Single Molecule Self-Replicators

This section discusses the two cases that I am aware of where single molecules self-replicated. This was achieved by these molecules drawing from a supply of non replicating basic constituents. In these cases the replication system has just one component, a single molecule.

8.2.1 Naphthalene Backbone

According to Ref. 13, self-replication was obtained by creating a small rigid self-complementary molecule that can pair up with basic constituents to form another one of itself. At first they tried to make longer less rigid molecules that better simulate proteins or nucleic acids. They discovered serious chemical problems.

"The chain was so long and flexible that the self-replicating structure doubled over on itself, rather like a jackknife folding shut."

These chains folded over like the protein and nucleic acid do in all known life forms. Then they tried shortened more rigid molecules which do not fold; thus, poorly simulate proteins or nucleic acids which do fold.

"The remedy called for inserting a larger and more rigid molecule in place of the single chain to prevent folding. Our choice was a larger stacking surface, a naphthalene, bolstered by a less flexible link between the two components, a cyclic ribose group"

These self replicating molecules were made up of the combination of just two small rigid molecules from a solution that was specifically designed to contain just their components. Thus, a self-replication of two units formed as shown schematically in Figure 5. Figure 6 shows a diagram of the chemical structure that Figure 5 is an analogy for. The ringed structure in Figure 6 represents the naphthalene group. The geometrical concept in Figure 5 well simulates the crucial features of an self-replicating molecule that these scientist helped develop. The positive and negative region in Figure 6 relate to the hydrogen and oxygen molecules that allow for the weak hydrogen bond that allows the molecule to assemble a replication and then come apart to possibly do more replication. Figure 6 shows the condition of the first step in Figure 5 where one AB molecule is bringing together an A and B molecule not yet covalently bonded together. The asymmetry plane in Figure 5 identifies the actual geometry which allows the self-complementary pairing to occur. Since the crucial features that allow the molecules to self-replicate are properly present in this geometrical diagram the analogy is accurate and indeed molecular self-replication did occur in the experiment. Molecule AB did replicate by drawing constituents from a soup of non self-replicating units, molecule A and molecule B.

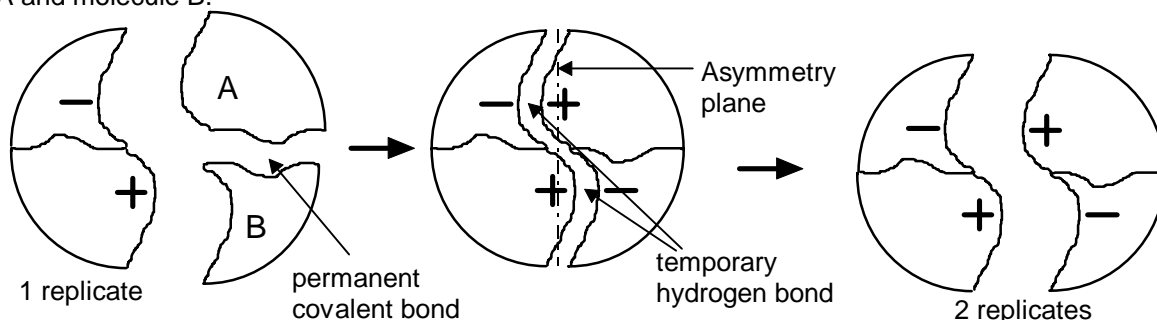


Figure 5 Schematic of Self-Replicating Molecule

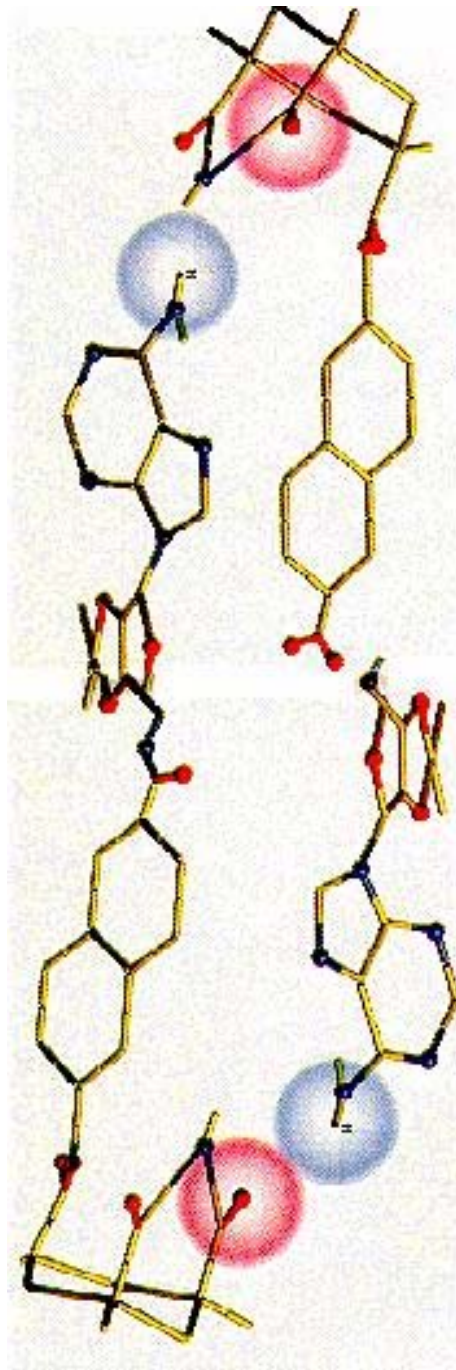


Figure 6 Schematic of Chemical Structure of Self-Replicating Molecule

Protein molecules are made up of a sequence of 50-3000 units of amino acids which have a backbone structure that allows them to fold over. These large molecules are not stable in a straightened out shape. Rather, they form a coiled up shape as shown in Figure 3 that keeps the molecule closed up so that it cannot form self-complimentary relationships as in the above examples. Proteins molecules start to fold over once they are 6 amino acid in length or longer. Nucleic acids are also not stable in a straightened out structure. They too will fold over like proteins do. As shown in Figure 2, the RNA ribosome properly exposes and lines up the proper amino acids so that proper amino acid sequence can form. In the transcription process which converts DNA to RNA, the RNA polymerase performs a similar function as the RNA ribosome. Just like a folded up and crumpled piece of paper cannot be copied by a Xerox machine, folded up molecules cannot be copied. The paper or molecules need to be laid out flat or bonding sites need to be exposed so that the pairing relationships can be made of the original template. This is what is done by the RNA shown in Figure 2. Thus, at least two different complex components are needed to replicate biological molecules that are soecifically tailored for the molculas being copied. One to unfold the molecule, then another to ensure the proper pairing relationships are made. Without such an interdependent system coiled-up molecules could not form the complimentary relationships which are crucial for self-replication.

There is no symmetry plane in the folded protein molecule shown in Figure 3 over which complementary pairing relationships could be made.

If life evolved, first single self-replicating molecules must have formed and then somehow evolved into something that resembles a cell. In order to resemble the molecules in a cell, these small uncoiled self-replicating molecules would eventually have to increase in size which would then create a problem because they would start folding over then they would not be able to self replicate. They would have the same folding problems that the intelligent Ref. 13 designers initially had in their experiment. The three dimensional folded shape is a common and important characteristic of biological molecules. The specific three dimensional shape determines important properties of a protein molecule as explained in Section 4. Thus, if anything the results in Ref. 13 emphasize that formation of RNA or protein self-replicators of the size we find in biology has serious fundamental problems. Scientific America titled Ref. 13, "Re-creating the origin of life" because the editors wanted to give the impression of achieving success for evolution. However, even the leading evolutionist, John Maynard Smith at least admitted that these specific results have limited relevance "Although by their nature are not immediately relevant to the origin of life" (Pg. 43, Ref. 30).

8.2.2 Peptide Backbone

According to Ref. 7, a alpha-helical peptide molecule actually self-replicated which is of special interest because protein molecules are peptides. Figure 7 shows a diagram of the self-replication. The purple and green molecules are the non-replicating basic constituents which the gray replicating molecule assembles on itself to form another copy of itself which can then disassemble to go onto to form even more replicates of itself. Notice that the gray self-replicating molecule is short enough so that it's backbone does not fold over but remains straighten which is important so that the proper sites remain exposed. The molecule does coil into an alpha-helix shape along the essentially straight line defined by the backbone of the molecule. This straight backbone allows the purple and green molecules to form the complementary pairing relationships resulting in them assembling in a geometry that is identical to the gray molecule.

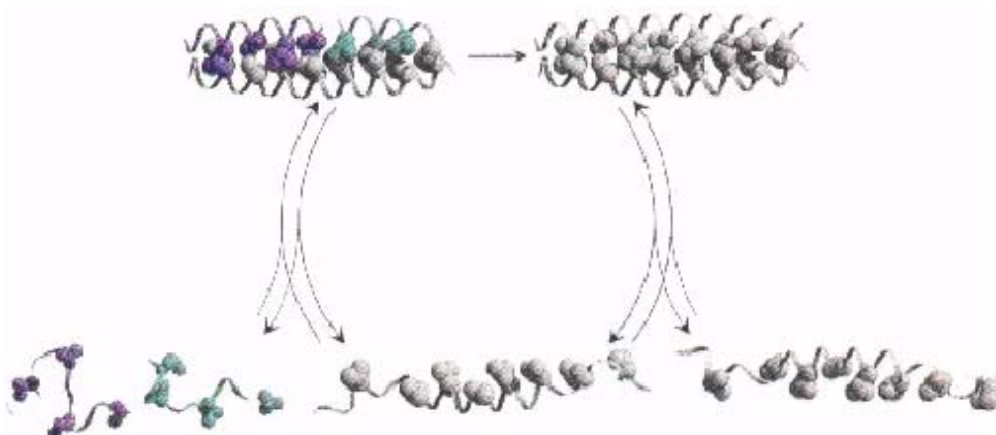


Figure 7 Diagram of Peptide Self Replication

The Ref. 7 intelligent designer selected a molecule with a straight structure just like the Ref. 13 ones did so that fundamental problem of self-replicating a folded over molecule would be avoided. The progression towards a nucleic acid based cell, requires the development of folded over molecules that would be part of a replication system. This result does not provide a solution to these fundamental problems. In addition, this self-replication occurred in an equal mixture of just the green and purple molecules. This provided an artificial constraint so that no other side reactions occurred; thus, minimum efficiency levels required for self-replication to continue to grow could be maintained. A realistic prebiotic soup would not contain equal mixtures of just these molecules; thus, side reaction would occur so that the proper level of efficiency for self-replication would not be obtained. In 8/97 I did ask the author of Ref. 7 if the amino acids which made up this molecule all had the same stereochemistry?; how could this replicator continue to reproduce at a sufficient efficiency level to grow more replicators in a realistic prebiotic soup?; and how would this molecule type replicate if it was folded over?. The author was gracious enough to send me a copy of the article and did say he was going look into these question when he had the time but has not yet responded.

8.2.3 Summary of Problems for Self-Replicating with a Folded over 3-D structure.

It appears impossible to get longer chains that represent biological molecules to self-replicate on an individual basis. A look at the 3-D coiled structure shown in Figure 2 shows the great difficulty in getting biological molecules to self-replicate on their own with out the interdependent system of nucleic acids and proteins in all modern life. 1) The 3-D structure does not have geometrical properties that would allow it to act as a template off which a

replication of itself could form because some of the chain would not be accessible to forming the complementary pairing relationships.. 2) Many of the angles are too tight and the density of the molecule so great that an attempt at replication would cause interference problems known to chemists as steric effects. 3) If a self replicator did form it could not get out because it would be all tangled up in this 3-D structure. Thus, it would have to break up in order to get out then it would not be a replication anymore.

Key functions in a DNA based cell appear to definitely require large 3-D folded molecules such as polymerase for DNA transcription and ribosome for protein formation. In any plausible origin of life scenario eventually 3-D replicating molecules will have to form, but when they initially form it seems they couldn't self-replicate on an individual basis so there will have to be already some more complex system in place to replicate them. This system would have to at least unfold the molecule and hold it into a position that would allow for replication of the folded molecule. This system I suspect would have to include 3-D folded molecules. These 3-D molecules would also have to self-replicate; thus, additional 3-D molecules would be required for their self-replication. Thus, there would have to be a system of interdependent 3-D molecules that compliment each other to function as a whole to self replicate.

All pathways leading to a nucleic cell will require the replication of folded molecules. However, it appears to require other folded over molecules to replicate any folded over molecule. Thus it appears several complimentary components are required for replication of folded over molecules. Since it appears that folded over molecules cannot self-replicate individually it appears any replicating system involving folded over molecules has irreducible complexity. Also, it appears quite improbable that folded over molecules that work together for a replication system would come together independently. Thus, consideration of the replication requirements for a replication system involving folded over molecules appears to indicate that all pathways cross a naturally insurmountable terrain.

Since these molecules have to compliment each other they must have the right sequence that performs the right function. Section 7.3 shows that out of all possible 110 site amino acid sequences for the cytochrome c protein 2.3×10^{93} of them are functionally equivalent which represent a very small fraction (2.00×10^{-44}) of the total 1.15×10^{137} . The chance of getting two molecules with the right functions is the multiplication the chances of getting the individual molecules. Thus, Ref. 3 concludes, "Since the probability of a mutational event is a number much smaller than unity, simultaneous events are of the second order". Since the scenario being considered is the evolution of the first replicator involving 3-D molecules; there appears no basis for natural selection to help select out the fitter 3-D molecules. Thus, it appears difficult to avoid these small probabilities that imply the natural development of 3-D replicator as implausible. This difficulty is further emphasized by estimates of the minimum number of proteins of molecular functions required for a minimum self-replicating cell. Ref. 3 reports an estimate of at least 300 proteins.

8.3 RNA-World Hypothesis

RNA is very similar to DNA and is the key molecule that allows DNA to make proteins. Apparently, the best proposal for abiogenesis is the RNA-world hypothesis. According to this theory self-replicating RNA molecules were the first self-replicators that began the replication process that eventually led into something that resembles a cell. According to Ref. 25, 5 steps are involved; 1) Synthesis of polynucleotides, 2) Development of RNA replication, 3) RNA dependent peptide synthesis, 4) Development of translation, 5) Emergence of protein synthesis. Stage 3 and on is proposed to have developed in some sort of proto-cell. Ref. 25 gives brief comments on some of the chemistry that could have been involved in these steps; however, the further one investigates the chemistry of hypothetical scenarios the more one discovers problems for the RNA-World Hypothesis. In order to determine if an abiogenesis proposal presented on a superficial conceptual level is actually viable, the details of proposed molecular structures need to be investigated.

RNA has been discovered to act as a catalysis, so it can promote reactions. Once a RNA chain gets to be more than 15 units it will typically fold over; thus, have the self-replicating difficulties mentioned in section 8.2.3. Ref. 25 nor any other reference that I am aware of that present a solution to this apparently fundamental problem. With no apparent solution to step 2, step 3 appears impossible to obtain because step 3 involves an interdependent system. A solution to step 3 requires the RNA being replicated by peptide (proteins) and the peptides and these peptide have to be replicated to. Without a solution to how the different parts of an interdependent system develop individually, one is left with a paradox that appears impossible to solve naturally. This creates the chicken and the egg paradox, which came first?. This issue is a serious problem for all abiogenesis scenarios including the RNA world hypothesis as Orgel (14) points out,

"Hence, the central problem of origin of life research can be refined to ask, by what series of chemical reactions did this interdependent system of nucleic acids and proteins come into being? Anyone trying to solve this puzzle immediately encounters a paradox. Nowadays nucleic acids are synthesized only with the help of proteins, and proteins are synthesized only if their corresponding nucleotide sequence is present. It is extremely improbable that protein and nucleic acids, both of which are structurally complex, arose spontaneously in the same place at the same time. Yet it also seems impossible to have one without the other."

The interdependency of proteins and nucleic acids gives the impression that no matter how you arrive on the fitness terrain, the pathway to anything that resembles a cell, appears insurmountable considering the limitations of

the size and age of the observable universe. Ref. 27 shows a wide variety of success that can be achieved when using already synthesized polymerase proteins and designed experiments to select out preferred results. But these successful results are the result of already having in place important parts of the process such as enzymes which are used for replication. Also, filtering and sifting is done through an intelligently designed process which selects out the preferred molecules.; Thus, these results do not represent appropriate analogies for the question of the origin of self-replicating RNA and cells. The blind evolutionary process does not have the foresight of these intelligent experimenters in Ref. 27.

The cell wall is crucial for keeping together the proper constituent so that they will be available for the cell to perform the proper reactions. Modern cells have special proteins lodged in the wall that selectively control the flow of molecules in and out of the cell. This is an important feature in origin of life scenarios because certain concentration of the molecules have to be maintained so that side reaction are minimized so that a certain minimum level of efficiency is maintained. Microspheres have been proposed as the first proto-cells (26). Microspheres grow by accretion which is the attraction of like molecules to the micelle by simple physical forces. The process of microsphere growth has little if any similarity to the process which contemporary cells grow. There is nothing about the accretion that is analogous to the replication process of information (RNA sequences) within the cell that has to occur in order to pass down the cells heritage as is done in the Mitosis process.

The constant stereochemistry issue is also a problem for the RNA world hypothesis as Orgel acknowledges in Ref. 14, "Equally disappointing we can induce copying of the original template only when we run our experiments with nucleotides having a right-handed configuration. All nucleotides synthesized biologically today are right-handed. Yet on primitive earth, equal numbers of right and left handed nucleotides would have been present. When we put equal numbers of both kinds of nucleotides in our reaction mixture, copying was inhibited."

Clay can serve as a catalyst and concentrator for biochemical compounds. However, the clays do not produce constant stereo chemistry and they do not have any preference for forming sequences that are suited for self-replication. In addition, if clay absorption did occur there should be an abiological kerogen (kerogen with certain carbon-13 abundance) in the rocks dated to 4×10^9 years old but according to Ref. 21 no such feature has been discovered.

It is now wonder why Orgel, a leading evolutionist in the abiogenesis field, states in Ref. 14 where he discusses the RNA-world hypothesis, "those of us who favor the RNA-world hypothesis still have to explain self-replicating RNA was created from these constituents" ... "The precise (chemical) events giving rise to the RNA world remain unclear".

As shown in Figure 1 and Figure 2, the ribozyme rRNA plays a key role in the translation of RNA into a protein; thus, are needed for proteins and nucleic acids to replicate. But the production of the ribozyme is dependent upon the nucleic acid replication process. Thus, the development of a functioning ribozyme is key to resolving this paradox. It appears impossible for a molecule to perform the function of a ribozyme without any folding. The 3-D structure is a key feature that allows a molecule to act as a catalyst or enzyme. Thus, a functioning ribozyme could never develop independently because it could not self-replicate because it would be folded over, making the development of a solution to this paradox appear impossible. Leading evolutionist in the field of abiogenesis, Joyce and Orgel conclude in Ref. 28, "This discussion .. has, in a sense, focused on a straw man: the myth of a self-replicating RNA molecule that arose de novo from a soup of random polynucleotides. Not only is such a notion unrealistic in light of our current understanding of prebiotic chemistry, but it should strain the credulity of even the optimist's view of RNA's catalytic potential .. Without evolution it appears unlikely that a self-replicating ribozyme could arise, but without some form of self-replication there is no way to conduct an evolutionary search for the first, primitive self-replicating ribozyme."

Without providing solutions to the serious and fundamental problems listed in this article, Ref. 12 (Talk.Origins FAQ on abiogenesis) makes the following conclusion.

"The synthesis of larger nucleic acids from small is, as we say, academic. While I am sure that most critics will stumble here ("By God even E. coli has 3 million base pairs and you expect us to think it is descended from six???"), the hard parts were really all that I have described above. It is relatively easy to grow the 6 to teens and the teens to hundreds by obvious mechanisms. Once you have teens to hundreds the molecules can in fact fold and catalyze reactions. Random sequence polymers should thus have been present in the primordial soup. Many authors (including myself) have shown how, in defiance of the nonsensical 747 analogy, functional nucleic acids can be selected from random sequence mixes. Given natural selection on a molecular population, one can do literally almost anything: create binding species, anti-virals, new catalysts, new recognition sites for nucleic acid binding proteins"

This conceptual proposal is not plausible because as explained in Section 8.2, folded over molecules are not suited for self-replication. Ref. 12 neither discusses or presented solutions to getting these 3-D folded molecules to replicate.

9. CONCLUSION

There appears no special symmetry about life forming DNA or protein that causes the proper nucleic acid or protein sequences to form. In addition, there is apparently no special feature in nature that causes the proper

nucleic acids or protein structures to form, even in an environment which has energy flowing through it. Thus, the only natural mechanism left for naturally producing the proper nucleic acid or protein sequences for the 1st replicator is essentially just the pure chance of them forming through random intermingling in a prebiotic soup.

The requirement of constant stereochemistry produces a fundamental barrier that applies to all pathways. The proper sequence that will perform the important functions are apparently a very small fraction of the total possible sequences. The coiled up biological molecules appear impossible to self-replicate; thus, obtaining a realistic single protein or RNA strand that can self-replicate appears to be implausible. The interdependency of the nucleic acids and proteins which are crucial for replication in all cells appears impossible to achieve by replicators progressing in a step by step sequence guided by natural selection but limited by mutations, copying errors and the finite size of the observable universe.

The problems mentioned in this article and others gives evidence that all routes on the fitness terrain leading to the important development of the nucleic acid based cell are insurmountable by natural processes. It is no wonder why the discover of DNA, Francis Crick concedes in Ref. 8, "A honest man, armed with all the knowledge available to us now, could only state that in some sense, the origin of life appears at the moment to be almost a miracle".

The fundamental and serious difficulties for a natural explanation for abiogenesis appear to indicate that something else than natural processes were involved with forming the nucleic acid based cell. Certainly research should continue in looking for a natural explanation for abiogenesis; however, the longer the research continues without providing a plausible natural explanation, the stronger the case that something else than just natural processes was at work.

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