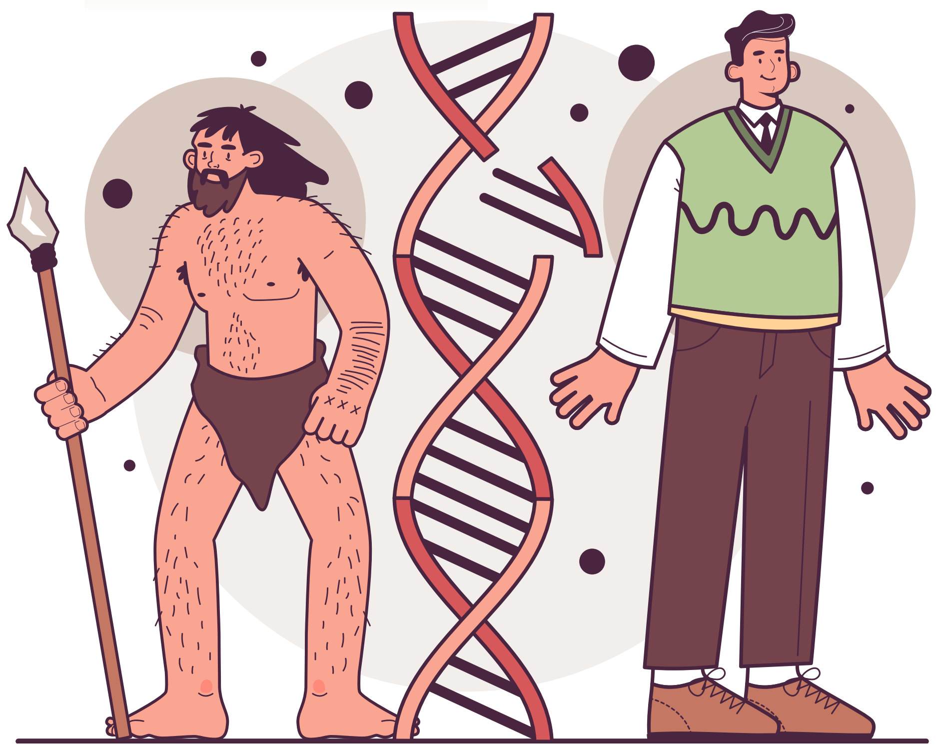
Evolutionary theory

Debating the origins of our DNA

For over a decade, Mr Shaojie Deng of Chongqing Municipal Bureau of Planning and Natural Resources, China, has been formulating and more recently presenting his new evolutionary theory to the academic world. Over time his thought processes too have evolved with his most recent manuscript centring around the stable complex model as an explanation for the evolution of enzymes and functional biomolecules. In his most recent manuscript, Deng details how the model provides an explanation for key evolutionary concepts and calls for current evolutionary theory to be expanded and alternative viewpoints taken on board.



How life on Earth evolved remains a much-debated topic. Cells form tissues, organs, and bodily systems, but at the heart of this all is the genetic information within each cell (our DNA, RNA, and associated enzymes). But how did this genetic information evolve? Like the chicken and egg analogy, what came first – RNA or DNA, genetic systems, or metabolic systems?

Mr Shaojie Deng initially proposed the stable complex evolution model in his 2015 book, *The origin and evolution of life*. He has now revised and refined these concepts, providing more detail for how his model can explain fundamental characteristics of life and the origins of the genetic and metabolic systems, whose evolution he proposes are intrinsically linked.

It is widely believed that DNA was formed from RNA through the mechanism of reverse transcription. But what evolutionary mechanism drove this? Deng believes the stable complex evolution model is key in understanding the origin of genetic systems, the origin of metabolic systems, and the origin of polymerases (enzymes that synthesise DNA or RNA). So what is this model, and can it give us the answers to these questions?

WHAT IS THE STABLE COMPLEX EVOLUTION MODEL?

Firstly, the stable complex evolution model is a structural model of evolution, meaning structural or physical forces are thought to be driving evolutionary change. The fundamental concept of this model is that biomolecules form stable, tight, and complementary complexes enabling them to carry out their function. Interactions between molecules are complementary, meaning their interaction improves or helps the other. Such interactions occur in all biological processes including those within genetic systems (transcription and translation) as well as metabolic reactions, for example, receptor-ligand interactions. Deng proposes the amount of complementary area between molecules dictates their binding affinity. This binding affinity provides the energy needed for conformational (or structural) change of the complex and it is through conformational change that certain molecules signal information. These tight complementary interactions are proposed to be at the heart of phenomena such as intrinsic selectivity of life and self-organisation, discussed later.

TIGHT BONDS AND ENZYMES

Enzymes are needed for cellular function because they speed up essential chemical reactions by

DNA polymerases create DNA molecules by assembling nucleotides

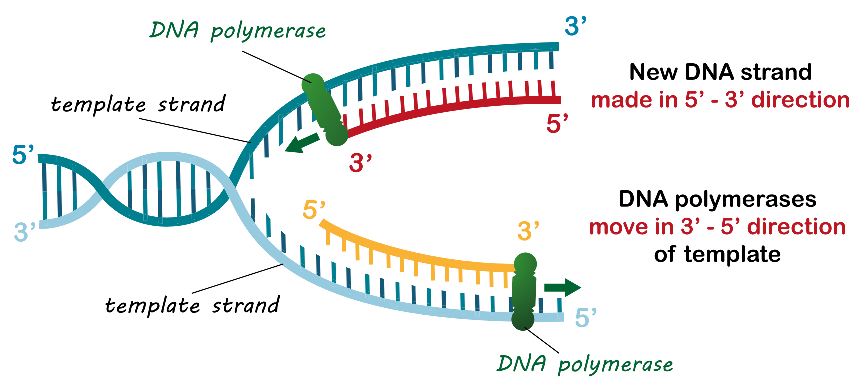


Figure 1. Polymerase enzymes are vital for making our genetic material, DNA and RNA.

binding and converting substrates into molecules or product. The tight binding of an enzyme to the active site of its substrate causes conformational changes in the enzyme itself. This conformational change is needed for catalytic reactions to occur, therefore such reactions are regulated by this binding. This close or tight bonding between molecules is essential for the functioning of many molecules and its evolution was crucial in the origin of life. Deng believes the stable complex evolution theory can explain the evolution of enzyme substrate complexes. He proposes that local mutations (possibly away from the active site) were, in part, responsible for such evolution by altering the enzyme substrate complex active site itself, ultimately affecting its catalytic ability. Mutations may also be responsible for altering the binding affinity of an enzyme for a substrate and, in some cases, act to improve such affinity.

POLYMERASES: LIFE'S ESSENTIAL BUILDING BLOCKS

In his recent manuscript, Deng states, 'Life originates from polymers.' Biopolymers are produced by cells and engineered by enzymes using building blocks of amino acids, fatty acids, and sugars to form larger molecules. These polymers therefore formed the foundation of the complex biological systems we know today, with polymerase enzymes helping to assemble DNA or RNA from these polymers. Considering their importance, Deng argues that any theory about the origin of life must be able to explain how polymers came about. He suggests his stable complex evolution model can explain the origin of these polymers and complementary interactions, providing an explanation by which functional molecules evolved.

The model does not detail the evolution of RNA but rather assumes its prior existence. What the model does provide is an explanation for the mechanism of reverse transcription in the evolution of DNA from RNA. For reverse transcription to occur, firstly there needed to be enough building blocks of DNA, namely deoxynucleotide triphosphate (dNTPs). These are assumed to have already evolved because protein-based ribonucleotide reductases exist. Secondly and of vital importance is the evolution of polymerase enzymes central to the process which Deng suggests evolved from RNA replicase through a series of mutations. The evolution of RNA transcriptase from RNA replicase illustrates the stable complex model evolution process. He suggests that an RNA replicase mutant formed a tight structural bond with an RNA template, eventually evolving into reverse transcriptase. Furthermore, he argues that DNA polymerase evolved from a mutant reverse transcriptase. This demonstrates that through tight structural bonds, evolution of these molecules and systems was able to occur.

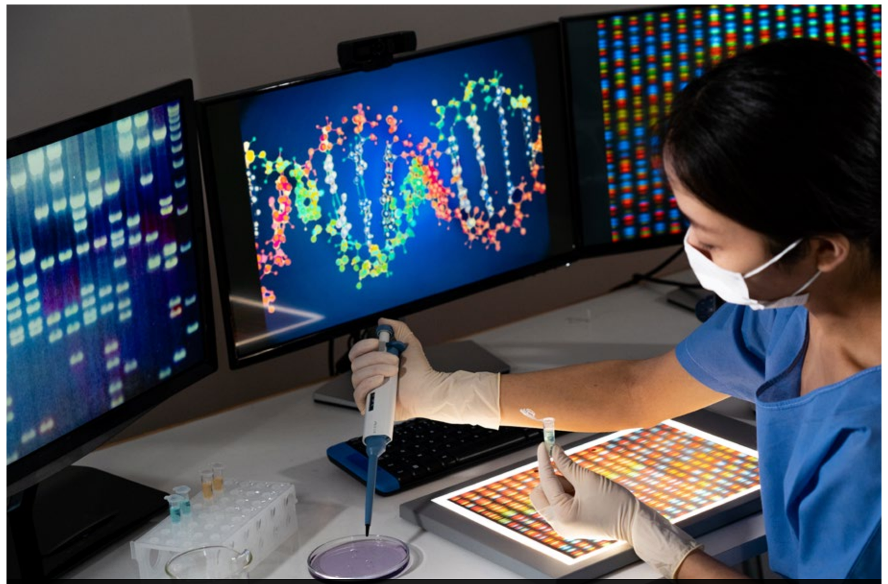
LOOK AT THESE NEW GENES!

Many studies indicate that the process of reverse transcription has enabled the evolution of genes and other parts of the genome, such as gene regulatory sequences including promoter regions and coding sequences. In primitive cells, Deng proposes that proliferation of gene regulatory sequences could have then led to the development of genes. Another school of thought is that new genes can form when stress induces mutations that enable them to relief that stress. On a separate note, a significant portion of the human genome consists of non-coding sequences that don't code for amino acids but maintain other roles in the genome. Various studies suggest these non-coding sequences can themselves evolve into coding sequences and subsequently new genes. Deng argues that for a gene to perform its function, it needs to form complementary interactions with other molecules, and these tight complementary interactions at the heart of the stable complex model theory have driven the evolution of new genes.

THE CO-EVOLUTION OF GENETIC AND METABOLIC SYSTEMS

Deng believes the evolution of the genetic and metabolic systems is closely linked and that they evolved together in a synchronised manner over time, and in doing so helped refine their functions. He proposes the stable complex evolution model is a unified model that could help explain both these evolutions. With a high number of enzymes required for the functioning of the metabolic system, Deng suggests the evolution of this system would have increased the quantity of enzymes and proteins in cells which in turn prompted the development of the DNA genetic system. Conversely, it is possible that

> ***The fundamental concept of this model is that biomolecules form stable, tight, and complementary complexes enabling them to carry out their function.***



The stable complex evolution model provides a fresh perspective in understanding the evolution of our genetic system. Deng advocates for the expansion or modification of his theory.

the metabolic system evolved only after DNA had already formed and because of changes in the environment. Lastly on this topic, Deng discusses the potential role of stress-induced adaptive evolution in the development and further refinement of the metabolic system. Importantly, he notes that such adaptive evolution could have added to the complexity of the metabolic system over time, making it the complicated system it is today.

ADAPTING TO SURVIVE

Adaptive evolution refers to adaptations of an organism to ensure they survive and thrive in their habitat. There are two principles of adaptive evolution, namely the function-based principle and the principle of cell selection. The former refers to the inclination for cells to maintain a stable function and a balance with the environment. The principle of cell selection proposes that cells maintain this stable function by acquiring mutations. Because cells want to maintain balance with the environment, any change in the environment can cause instability in cell function tipping it into a stress state. To counteract this instability and reinstate stability, the cell may select a mutation that enables this. Changes in the environment may therefore be one of the main driving forces of evolution and therefore cells need to adapt to survive. A real-life example of adaptive evolution can be found in a population living at high altitude with low-oxygen conditions. Research at the Tibet Institute of Medical Sciences discovered such populations develop a new protein called haemoglobin X. This protein is not present at birth but evolves to enable them to adapt to their low-oxygen environment because it improves oxygen use in an oxygen-depleted environment. Over a prolonged period under low-oxygen conditions, haemoglobin X could become integrated into the genetic structure to ensure survival of the species.

SELF-ORGANISATION, FUNCTIONAL STABILITY, AND INTRINSIC SELECTIVITY OF LIFE

Another evolutionary question that the stable complex model can help explain is self-organisation origin. Self-organisation refers to order in a complex system that occurs by itself and within itself as opposed to be induced by external factors. Deng reasons that the stable complex evolution model explains the self-organisation properties biomolecules display such as their natural tendencies to react with each other. The model emphasises two main aspects of the complementary interactions between molecules that are vital to induce evolution: one is high binding affinity and the second is the specificity of the interaction. He believes that stable binding provides the required high binding affinity that drives this self-organisation. This is key to understanding the origin of life, with Deng arguing that self-organisation has played as pivotal role as natural selection in determining it.

Two other concepts that Deng touches on is the maintenance of functional stability trend and the intrinsic selectivity of life. The former centres around organisms wanting to maintain stability and homeostasis. Perhaps counterintuitively, it is proposed that cells have been able to maintain their basic function by evolving, a concept that is central to the stable complex model. Moreover, while keeping their functional stability, biological systems can also gain complexity. In fact, stability is needed to gain complexity. Regarding the intrinsic selectivity of life, Deng postulates that there is a natural selective force acting at the molecular level during evolution. He believes it is possible that the stable complex evolution model is central in this selective force.

The stable complex evolution model provides a fresh perspective in understanding the evolution of our genetic systems.

With the stable complex evolution model providing a fresh perspective in understanding the evolution of our genetic system, Deng advocates for the expansion or modification of the evolutionary theory. His work provides substantial insight into evolutionary theory, asking probing questions and shedding light on questions humankind has pondered for so many years. Deng's contribution to this field continues to grow with his most recent publication amongst other planned manuscripts.

Behind the Research

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Research Objectives

Mr Shaojie Deng proposes the stable complex evolution model, which offers an explanation for the fundamental characteristics of life: the origins of the genetic and metabolic systems, whose evolution he proposes are intrinsically linked.

Detail

Bio

Mr Shaojie Deng is a senior geological engineer at the Chongqing (Fengjie) Municipal Bureau of Planning and Natural Resources. Many years ago, he began conducting research on the origins and evolution of life, a subject for which he is very passionate. In 2020, he published a book in Chinese entitled, *The origin and evolution of life*, which discusses a wide range of biological phenomena.

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Personal Response

In an ideal world, how would you see your work taken forward and applied?

" The stable complex evolution model and the principles of adaptive evolution are a set of new concepts and methodologies. In a Chinese book published in 2020, I attempted to utilise these concepts to explain many biological phenomena. Currently, I am further demonstrating and expanding this theory. With the growing understanding of these new concepts, I hope that people will embrace, refine, and delve into this new field of biology. Our understanding of life faces certain impasses, such as the origin of the genetic code and the theory of evolutionary mechanisms. Breaking through these impasses may require trying new approaches. "

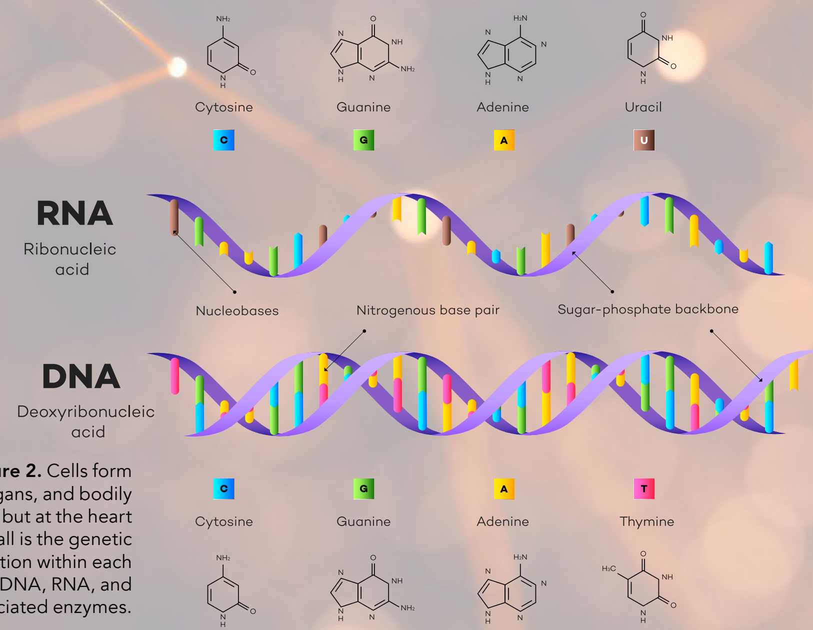

Figure 2. Cells form tissues, organs, and bodily systems but at the heart of this all is the genetic information within each cell – DNA, RNA, and associated enzymes.