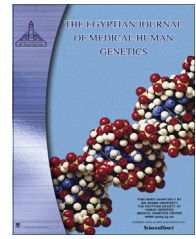




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REVIEW

Biological evolution: Some genetic considerations

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Phylogenetic divergence

Abstract *Background:* The concept of biological evolution has long been accepted as a palatable theory aiming at explaining how life began and how creatures diverged so widely along the life span of the earth. Meticulous analysis and criticism of the different postulations of this concept, however, reveals that evolution is an illogic concept based on theoretical hypotheses that can never be tested. Creation, on the other hand, represents the other side of the coin, and up till now debates confronting creation versus evolution are still occupying much interest of atheist as well as of believer biologists.

Aim of this article: The motive for accepting the concept of evolution by most biologists, stems solely from their atheism and their saying that creation can neither be experimented nor validated, the same criticism directed against their assumptions regarding the basic aspects of evolution. This article, through analysis, criticism and reevaluation of some relevant genetic considerations that have long been traditionally considered as observations in support of the concept of evolution, viz. genetic memory and evolutionary variations, genomic adaptations to stress and evolution, comparative genomics and natural versus targeted selection, tries to elucidate and reveal some insensible assumptions embodied within the core ideas of evolution that stand in direct controversy with many well-known facts regarding the structure, function and behavior of living matter.

Conclusion: Natural selection might be observed in nature but not in life. The concept of biological evolution is an illogic and insensible hypothesis since it stands in direct contradiction with our current knowledge regarding the behavior as well as the structural and functional characteristics of the human genome and human proteome. Additionally, almost all basic postulations of this concept can neither be tested nor imitated for experimentation, which is a prerequisite for acceptance and validation of any scientific hypotheses.

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Introduction

The concept of biological evolution needs reevaluation as regards most of its basic assumptions. There is no logic in postulating that performing a particular physiological function in human cells necessitates more complicated genetic systems or more complex metabolic pathways than corresponding requirements for performing the same function in lower or any other species. Also, the presence of endogenous retroviral elements in the human genome and their roles, not only as a subset of transposable elements but also as regulators of gene expression, could be interpreted in an equally plausible different contrasting way. Acquired elements, following viral infection and insertional mutagenesis, might have been used by the host genome for its own benefit to perform the functions attributable to these elements. Obviously, this explanation seems to be more plausible than nonsense postulations attributing super capability and dominance of inserted viral genomes over infected human genome that enable it to induce evolutionary changes or directed adaptations in the human genome. Presence of similar, even identical, genetic sequences in different organisms irrespective of their phylogenetic positions, humans and drosophila for instance, need not be an indication of anything other than that similar biological functions in living organisms are expected to be regulated by similar genetic sequences and mediated by similar proteomic networks. Phylogenetic taxonomy of living organisms clearly discriminates between human beings, *Homo sapiens*, on one side and all other living organisms, viz. animals–plants–micro-organisms including archaea, and reveals the uniqueness of humans as distinct single species compared to thousands of species comprising each of the three other kingdoms of living organisms. The persistence of this characteristic phylogenetic distinction between humans and all other creatures withstands as coherent theoretical and logical obstacle against the core concept of evolution, and points to the existence and persistence of the human genome as a unique bio-system all through human life on earth.

In fact, logical analysis of the concept of evolution reveals, in a very obvious manner, that evolution is an insensible idea. Postulations regarding final chance occurrence of self-assembly of biomolecules that started life activities, i.e. nucleic acids and proteins, after innumerable random reactions ignore the simple and firm fact that chance, by definition, has no memory. The Regular recurrence of biological phenomena in the same persistent, strict and repetitive pattern as seen in growth and development of living organisms, as well as in all their life activities, can never be attributed to chance and demolish these postulations. Regular recurrence of specific behavior patterns

of biomolecules is a solid indication of their being pre-programmed to behave in the same way under similar environmental effectors. Similarly, the construction of pre-programmed structured systems, like the genome, the transcriptome and the proteome, that obey definite physical laws and behave in accord to strict regulatory principles applicable to solid and living matter, as well, nullifies allegations as regards the ability of biomolecules to evolve, depending on innate self-assembly, in a selective pathway away from these laws. If we accept the idea that deeply seated roots of evolution began by chance event, then stochastic behavior of components undergoing evolution would be the rule in view of the continuous and persistent external effectors and stimuli they are exposed to. The exquisite control of structures and functions of biomolecules, living matter and living organisms throughout their life span invalidates any significance to these postulations regarding origin of life and evolution.

Genetic memory and evolutionary variation

In spite of the exquisite ability of the protein translation system to recognize and decode the mRNA transcript and to harmonize the actions of tens to hundreds of factors involved in protein synthesis, it cannot recognize changes of the original genetic code embodied within the codon sequence of the mRNA transcript. It decodes and recognizes triplets of bases, or codons, along the transcript without giving attention to whether they are complementary to the original sequences of the gene or not. It seems that the protein translation system has no prior memory to predict the validity of the codon sequence of the mRNA transcript with respect to both the gene sequence and the amino acid sequence of the protein. Though this apparent defect might be considered a prerequisite for evolutionary variation of protein phenotypes necessary for acquisition of new functional abilities, e.g. formulation and construction of new metabolic pathways or acquisition of favorable selective advantages, since it allows for synthesis of different new proteins, it is a major cause of pathogenesis of genetic defects due to the absence of a translation proofreading and repair system comparable to those of DNA and mRNA repair systems.

Absence of genetic memory necessary for proofreading of translated proteins is enigmatic and bewildering in view of the prime and critical significance of the translation process, since the majority of genetic diseases result from synthesis of defective proteins or deficient synthesis of required proteins. Though it might be considered as a genomic regulatory mechanism allowing for selective pressure to proceed in favor of evolutionary variation, it results in marked pathological effects on

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