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Genotype Networks and Biological Evolution

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Abstract

Darwin proposed that the development and evolution of living beings is governed by natural selection of the fittest, which supposes that the different phenotypes existing in nature are a random product of such natural selection.

Although this is a consolidated scientific theory, there are still grey areas in the biological evolutionary process, among them, whether there has been enough time for point genetic mutations and natural selection to have been able to produce organs as complex as those in living beings.

This difficulty could be mitigated by the existence of so-called "genotype networks", and by their role in the production of all phenotypes that currently constitute the incomparable biodiversity of nature.

Genotype networks refers to a set of genotypes which, varying very little in their structure, are interconnected, producing the same phenotype.

Keywords: Theory of evolution; Biological evolution; Natural selection; Genotype networks

Introduction

In 1859, Charles Darwin published his book "The Origin of Species", in which he proposed that the development and evolution of living beings is governed by natural selection, which "let [s] the strongest live and the weakest die" [1]. This means that the different phenotypes that exist in nature are a random product of the aforementioned natural selection [1-3]. This hypothesis was not entirely shared by his contemporary and fellow proponent of biological evolution, Alfred Russel Wallace, who argued that natural selection was insufficient to explain the origin of different species; rather, he believed that the intervention of an external force-which could be divine-was necessary [4].

Following the proposed evolutionary theory of Darwin and Wallace, the Austrian monk Gregor Mendel discovered the role of inheritance in the biological evolutionary process, in light of observations made in the garden of his monastery [5].

Years later, in 1930, Darwin and Wallace's evolutionary theory was reformulated by Theodosius Dobzhansky who, combining natural selection with Mendelian inheritance, put forward the "synthetic theory of evolution" [6].

Natural Selection as the Foundation for Evolutionary Change

Without going into this in too much depth, we can say that, on the basis of the synthetic theory of evolution, the genes constitute the basic building blocks for constructing the phenotypes that are generated in this evolutionary building, and that its development is based on the fact that, in the evolutionary process, each gene gives rise to a protein; its natural selection and subsequent organization then produces the different phenotypes that exist in nature. This mechanism of biological evolution is what has come to be called "gradualism" [7], which argues that the profound biological changes that occur in nature are the result of small genetic modifications-specific modifications-that accumulate during a slow but sustained evolutionary process.

However, in the 1970s, better understanding of the fossil data that were being identified suggested that the evolutionary process could be produced by sudden large jumps (called "punctuated equilibrium"), which would be followed by periods of minimal evolutionary change (periods of stasis) [8].

The theory of evolution undoubtedly has great strengths, and today it can be said that it is a scientifically consolidated fact, albeit not fully defined, for it still has some grey areas. In the opinion of American biochemist, Michael Behe, these areas could be: the transition of asexual clones to sexed populations; replicating molecules to molecules structured in compartments; independent replicators to chromosomes; RNA as gene and enzyme, to DNA as the basis of the genetic code; solitary individuals to colonies of individuals; the transition of protists to animals, plants and fungi, i.e. cellularly well-differentiated beings; primate societies to human societies, in which

language appears; prokaryotes to eukaryotes; and invertebrates to vertebrates [9].

But certainly, one of those grey areas-for some the most significant-is that there has not been enough time since the beginning of the evolutionary process, so that, with the specific genetic changes needed for the production of individual proteins and subsequent random natural selection of the fittest phenotypes and their organization into biological structures. This difficulty was mathematically defined by Frank B. Salisbury, who estimated that the number of possible amino acid sequences needed to build a typical protein could amount to the incredible figure of 10540. Furthermore, the number of proteins that could have been produced by point genetic mutations on Earth since it was formed could only be slightly higher than 1065 [10], according to the theory accepted until that time that each DNA fraction, each gene, only produces one functional protein. Thus, the probability of producing each of the proteins capable of performing a certain function by random point genetic mutations was, in Salisbury's view, practically nil [10].

William Dembski also argues that it is highly unlikely that phenotypes as complex as those that exist in nature could have been produced by mutation and natural selection. To that end, he uses the bacterial flagellum as an example, stating that if each protein has about 300 amino acids, the probability of creating the aforementioned flagellum by chance is 10-1170. He therefore concludes that, "even if one takes into account that life has existed on Earth for 3.5 billion years, the assembly of a functional flagellum is impossibly improbable" [3]. According to Ayala though, this calculation is completely irrelevant because the assumptions on which it is based are erroneous, as natural selection and its gradual course can yield results with vastly lower pre-probabilities than Demski's calculations [3]. To this we would add that genotype networks could play a role in solving the problems raised by Salisbury and Demski.

Genotype Networks

It is known that a protein, or more generally a phenotype or a biological function, is not associated with a single DNA sequence. Rather, a large number of different sequences can give rise to the same protein. All sequences of a given length that encode a protein can be considered nodes in a network. From this, one of the key concepts in the study of the relationship between sequences and phenotypes can be defined, that of the network of genotypes.

Each node of that network corresponds to a sequence and two nodes can be interlaced if their respective sequences differ by a single letter. Given a sequence, or node, the number of nodes that can be intertwined is generally variable, so the size of these networks can span many orders of magnitude. Most of the networks are small, or very small, however, there are huge networks in which there are an immensity of genotypes; so many that, in fact, those few large networks can generate all possible genotypes [10]. That is, genotype networks are the set of genotypes that, varying very little in their structure, are interconnected, producing the same phenotype [3].

In relation to the evolutionary process, genotype networks allow an adequate solution for each evolutionary situation that may arise [11-16].

With respect to the theory of evolution, it is thought that these genotype networks may facilitate evolutionary innovation, favouring the evolutionary process as a whole [17-18].

Indeed, the vast experimental evidence accumulated over the last few decades clearly indicates that some of the hypotheses of classic evolutionary models require a thorough overhaul, as the viability of organisms does not seem to depend on a single genotype, but also on large sets of genotypes (or neutral networks) that give rise to the same phenotype, and ultimately, to an organism [19].

According to all this, "contrary to what had long been believed, different phenotypes may have small variations in their primary genetic sequence without causing changes in their molecular structure or function". That is, many genotypes can produce the same phenotype [20-21], or in other words, organisms and macromolecules that express the same phenotype may have different genotypes [16].

In fact, sequences of DNA fragments that only vary by one letter can give rise to the same protein or the same phenotype, so it is impossible to unequivocally determine the sequence or genotype that produced a protein, if we attempt to do so through the phenotypic function that it eventually expresses. This supports the concept of a genotype network, as it considers that "all genetic sequences that give rise to the same protein or the same phenotype are considered members of the same genotype network. Each node in that network corresponds to a sequence and two nodes can be linked if their respective sequences differ by a single letter" [10]. This is how genotype networks are formed.

The vast majority of them are small, but there may be huge networks, containing countless genotypes, to the point that the largest networks include almost all the possible genotypes, making it easy for the biological evolutionary process to find solutions for the production of all kinds of functional proteins. Consequently, if a genotype is chosen at random, it most likely forms part of one of the existing genotype networks, as such networks may contain up to 1054 genotypes; however, in addition to this, "each network may be connected to a huge number of other networks so, in practice, it seems that it would be possible to access a phenotype from a genotype included in that 'network of genotype networks.'

This opens up enormous possibilities for biological evolution to explore innovations without having to sacrifice its functionality" [10]. It also suggests that, "neither genetic sequences are randomly distributed, nor does Darwinist evolution proceed completely erratically; rather, it does so through an elegant underlying structure that, in a natural manner, explains how organisms innovate without losing their biological functionality" [10].

Conclusion

The foregoing seems of interest to help better understand how natural selection might be a suitable mechanism for generating all the phenotypic functions existing in nature, for if the genotype network theory is correct, it could solve some of the problems that are currently being raised in the context of the theory of evolution, discussed above.

Nevertheless, there are still grey areas regarding the structure and functionality of genotype networks, especially insofar as refers to the fact that "major network changes may have no effect on phenotypic output at all. Unfortunately, we do not yet understand the complex and nonlinear chain of events that links evolutionary changes in regulatory network structure to changes in developmental mechanisms in any experimentally accessible system" [15]. Thus, in the opinion of some experts, little is known even about how genotype networks might influence biological evolutionary processes [22-25]. So far, we have a biological reflection on genotype networks and the role they may play in the theory of evolution. Nevertheless, we must ask whether genotype networks have the potential to have randomly produced all the phenotypes that currently constitute the incomparable biodiversity of nature.

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