Semiosis and Evolution

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For several years I have been working on a project whose goal it is to demonstrate that living nature is structured and organized in a language-like and communicative manner. I investigate processes involving characters (semiosis) within cells, i.e., those involved in reading the DNA code, its translation into the protein language, specific communication malfunctions, and special repair mechanisms. An additional study dealt with communication processes between cells and cell associations.

Communication processes between honey bees formed a further topic of research. The work has proved to be successful in that I was able to achieve consensus with some molecular biologists, biochemists, sociobiologists and ethologists that living nature is in fact structured and organized in a language-like, communicative manner. In addition, agreement was reached that enzyme proteins are the actual character-users in the DNA language. Through their incredible variety they can be said to have a text-editing capability.

Here, I would like to briefly present the consequences of my "theory of communicative nature" for evolutionary theory. It allows certain inconsistencies in conventional approaches in the theory of evolution to be avoided.

If one examines the evolution of life from the earliest bacteria (with a DNA length of approximately 1 millimeter and containing several thousand genes) to man (whose DNA is approximately 1 meter long and contains 2 million genes), then evolution can also be understood as the history of DNA chain growth. This history is an elusive subject of scientific research, as growth of DNA chains does not involve processes that can be arbitrarily reproduced in experiments.

In the mid-1980s, a representative from the field of industrial macro-molecular chemistry, Bruno Vollmert (1985: 31-141), pointed out that, under the assumption of chance mutations, this chain growth could be understood merely as a statistical polycondensation. While such polycondensation processes must have occurred in the higher development of species, the question remains how these new genes arose and were incorporated into the established genome. Another consideration is the fact that one new gene in a cell has virtually no effect. As a rule, at least 10 enzymes are necessary for the synthesis of a single, new, physiologically active substance. The production of such substances involves a number of intermediate stages, each of which - in the correct sequence - requires its own enzyme for the appropriate chemical reaction. In the genetic text, however, each enzyme corresponds to a separate gene. The various synthesis stages form interconnected series and cycles, resulting in a spatial and temporal dependence of the reactions. A single reaction, or one cycle without the succession of the others, is inconsequential for the total cycle and useless for the cell.

Consequently, in the development of a new cycle leading to a possible new enzyme (which itself is part of an entire series of enzymes which could constitute a new gene), the new cycle remains irrelevant and without effect until it is entirely functional, i.e., until it is constitutive for the structure of the genetic text of the genome. In addition, the numerous intermediate products in the biosynthesis of physiologically active substances are mere intermediate products and themselves have no significance in changing the feature: only the end product is part of a character- changing cycle. Such changes in features typically manifest themselves only after cycles of 30 to 50 enzymes are appended.

Mutations represent interventions on already established genetic texts. They often lead to conspicuous alterations of features which, in the sense of Darwin´s survival of the fittest, inevitably lead to selection. Selection in the case of polycondensation, i.e., in the growth of DNA chains, however, is not possible because the addition of new genes remains without consequence for the organism until these new genes express new features. After all, the addition of new genes does not change the function of established genes or the life of the cell. Since those new genes, arising from or being attached by a polycondensation, find no expression, there is no test situation to determine whether that new gene happens to be adequate and whether it can enter a cooperative relationship with other, established genes. No selection can take place in polycondensation processes. The development of new organisms with new features is therefore not the product of a new gene: a single new gene cannot create a new substance, much less a new feature. New species require a great number of new genes. This great number of new genes, however, cannot arise from mutations (changes) of already available genes.

New genes first manifest themselves when their effect leads to the formation of many new substances which actually alter the genotype. Only at this time, and no earlier, is the organism bearing the new features subject to selection. It requires the development of a harmonious sequence of genes to provide the cell with that protein sequence which, as enzymes, enable a cooperative, stepwise reaction sequence (including intermediate stages) leading to new characters.

The entire sequence of substance modification in the evolutionary process from one species to the next (along with the corresponding DNA chain growth) had to take place without selection. The development of new species had to be preceded by the development of new genes, in an orderly fashion and in a specific sequence of becoming operative. This required a large number of new substances, each of which necessitated a synthesis of five to twenty steps. This, in turn, required the repeated occurrence of a thoroughly improbable event. Mutants, i.e., organisms having undergone changes on the established gene complement, are in fact subject to selection; this clearly leads to a stronger adaptation to the environment. This, in turn, inevitably leads to the stabilization of a species, not, however, to the complex process of DNA chain growth (with all its repercussions) that is responsible for the origin of new species. Under the perspective of macromolecular chemistry, the process called upon by evolutionary theorists to explain the higher development of species is actually not responsible for this advanced development, but rather for the stabilization of a species that has newly arisen.

From the vantage point of a language-pragmatic oriented philosophy of biology, the process of DNA chain growth in the development of a new species is, in all its complexity, the result of enzyme proteins or enzyme groups exhibiting a text-editing type of competence; this complexity involves not only growth, but also the coordinated incorporation into the established genome. To date, such enzyme proteins have only been demonstrated in the areas of productive, regulative, and constative communication processes of the intra- and intercellular type. These communication processes correspond with the three known and differentiated code types: protein code, regulatory code, structure code.

In gene manipulation, certain enzymes are used for the text separation and insertion processes. They are known to be able to identify insertion sequences as such and are therefore competent in text splicing or, more broadly, text editing. Enzymes operating in this text-generating manner, i.e., which effect DNA chain growth along with the coordinated intermediate stages so as to give rise to a truly new form of life, have yet to be demonstrated. This may perhaps be due to their being detectable only in a revolutionary-evolutive phase, during the development of a new species; thereafter they may disappear or remain behind as gene wrecks after mutations, something we would refer to as useless "junk DNA".

This would come as no surprise, since the development of a true new species is not a daily event but rather a historical process occurring during certain times in earth history and leading to the differentiation of five different organismic kingdoms (or six communication forms in living nature). Let us assume the presence of such text-generating enzyme proteins capable not only of extending available texts, but also of constituting new genes (I) and inserting them with numerous other enzymes (II) via numerous intermediate stages (III) at the right place (IV) and right time (V) in the proper sequence (VI). Then, we necessarily require genes that are capable of coding these enzyme proteins.

My hypothesis (Witzany 1993) is based on the assumption that specific text-generating genes must be or must have been present. Within the context of specific, pragmatic interactions which organisms experience, these genes are made available for reading and initiate the production process of such gene-constituting enzyme proteins competent in text editing. Under this aspect it is irrelevant how many generations are required to realize this text generating process. The text-generating process is largely independent of selective processes since no effect on the phenotype and the function of the established genome occurs up until the corresponding gene sequence is created and inserted into the genome. The genetic text creation appears rather suddenly; the resulting organisms of a new species are (and must be) fully functional, since they are subject to immediate selective processes after their actual conception.

When a new species (or in extreme cases a new species representing a new organismic kingdom) enters evolutionary history, this text-generating, text-creative process ceases to function, and the reading of the text-generating genes is interrupted. This is probably due to a further special enzyme or enzyme group which stops the expression of the text-generating genes. Perhaps the production of special gene-constituting or text-generating enzyme proteins is interrupted when the new genes constituting the new organism are incorporated or successfully integrated into the genome. At this point a truly new organism has entered history. Only at this juncture do mutation and selection again become important and lead to phenotype changes which themselves immediately underlie selective pressure. The stabilization phase of a new species can begin. At this point the revolutionary-evolutive phase is completed and the normal-evolutive phase, which merely serves to improve the prototype, is initiated. In this sense, successful evolutionary processes constitute themselves through the comple-mentarity of revolutionary- and normal-evolutive phases.

This hypothesis renders several developments understandable: the process of DNA chain growth in the higher evolutionary development of species and the differentiation of various organismic kingdoms (I), the sudden appearance of new species (II), and the lack of numerous intermediate stages (III). It also affords an explanation for the absence of numerous "not-quite-yet" life forms. In explanatory attempts based on continuity theory, such forms should be present in large numbers, but are de facto lacking.

Notwithstanding the development of the first living cell with functional DNA, the first historically reconstructable revolutionary-evolutive phase is the jump from unicellular organisms without to those with a true nucleus. According to my hypothesis, one or more text-generating genes must have already been at work in this evolutionary hyper-event. The origin of such text-generating genes might be sought in the realm of associative processes of the anucleate unicells giving rise to the basic form of unicells with true nucleus.

Since the genetic text is complementary yet consists of quite different substructures (protein code, regulatory code, structure code), one can assume that a comparable innovation code (which could also be termed as text-generating code, evolution code or creation code) exists or once existed. No information is available on its substantive structure because to date no such code has even been postulated. Perhaps it deviates significantly from conventional, known codes or is subject to completely different rules of expression. Since its expression

involves historically singular events and is not arbitrarily reproducable, it could have long since disappeared again (with the exeption of remnants) from the established genome.

References

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