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ON CERTAIN NON-HUMAN SIMILARITIES IN TYPOLOGY

(IN THE EXAMPLE OF BIOLOGY)

O. Y. Tukhtasinova
Associate Professor of the Kokan State Pedagogical Institute

Abstract

This article highlights the issues of biological evolution and biological taxonomy in biological science in understanding the problems of language development and genetic description of language.

Keywords: genetics, biological evolution and biological taxonomy, philosophy of language, taxonomic problem, genetic, genealogical, phenetic taxonomy

Linguists have turned to biological evolution and biological taxonomy in the biological sciences to understand the problems of language development and genetic description of language. But such an appeal did not mean that a structural harmony was found with the theory of biology and linguistics. (Not counting A. Schleicher's evolutionary concept of language). The romanticism of the philosophy of language led to the replacement of the "linguistic Darwinism" period with the pragmatic realism typical of the "Young Grammarians". By the beginning of the 20th century, the biological paradigm had lost its appeal to linguists as a model for the construction of science. [1.11]. A. Meye, in his article "The brotherhood of languages" (1914), noted that the genealogical classification of languages differs from the classification in biology, although he adopted the law of evolution in biology as a research technique. "If biologists have been able to observe evolution and determine the differentiation of species, their classification can be compared to the classifications of linguistics. This happens when the basis of biological classification is a hypothesis that helps to identify similarities between organisms. In this, taking into account the genetic relationships of different classes, forms belonging to the same class and originating from the same base are taken into account." [2.100]. At the time when A. Maye expressed the above thoughts, radical changes occurred in the science of biology. Biologists reread G. Mendel's works and moved to a new way of solving evolutionary and taxonomic problems based on genetic theory. After that, by the end of the 20th century, it was again possible to observe the convergence of biology and social sciences. Biologist M. Ryuza writes about this: "In the future, biological science will approach social sciences on the one hand, and physical sciences on the other." [3. 302]. Among the natural sciences, biology is close to linguistics. This is reflected in the following: the problem of the evolution of the studied phenomena, the problem of reconstruction of the oldest state of these phenomena, and the problems of rational classification are important for both sciences. Aspects shown by A. Maye in linguistics are the most relevant aspects of research for biological science today. The experience of biological science is useful for linguistics in two ways: first, the theoretical research of biological scientists is not alien to the linguist (in the fields of a deeper understanding of development and the development of more refined principles of classification); and secondly, the similarity of traditions in different paradigms of the two disciplines. This suggests that the difference in the ontological content of biology and linguistics suggests a certain degree of epistomological parallelism. This factor is useful in the selection of the main linguistic methods and the determination of research aspects.

Let's dwell on aspects related to taxonomic problems. Two different approaches to taxonomy are known in modern biology: 1) evolutionary taxonomy; 2) phenetic taxonomy (the 2nd spread in the 60s of the XX century).

Evolutionary taxonomy is derived from Linnaean classification. M. Ryuza divides this taxonomy into two more types: 1) genetic; 2) genealogical. The difference between them is determined by the degree of relation to phylogeny (the former is less, the latter is more) [3.179]. Although the concepts of "genetic" and "genealogical" are used synonymously in linguistics, they are different in biology: genetic taxonomy studies the structure of the organism in terms of genes (in the smallest units of function); genealogical taxonomy studies the pure phylogenetic history of a species. In linguistics, it is also useful to distinguish these concepts. Because in linguistics, genetic analysis is used to determine the aspect of comparative-historical study of languages and to find regular correspondences; and genealogical analysis is used to study the general history of languages.

Given the similarities between biology and linguistics, genealogical taxonomy in biology is paradigmatically similar to the genealogical classification of languages. The morphological similarities and differences between the organisms are related to the two different taxa. (This is evaluated in terms of the common origin of the taxa and their isolated existence over long periods of time).

We will give one example of parallelism between the sciences of biology and linguistics. This example relates to the general principles of phylogenetic analysis of morphological characters. J. Simpson describes these principles as follows: 1) generality of signs; 2) degree of divergence [4.192.3.181]. In biological taxonomy, a subtaxon corresponds to a species category, and the taxonomic hierarchy as a whole is expressed as: species - genus - family - order - class - phylum - kingdom. This taxonomy in biology is ontologically different from the classificatory hierarchy in linguistics.

Evolutionary taxonomy in biology is traditional and is the main type of classification.

In the 60s of the 20th century, in addition to evolutionary taxonomy, phenetic taxonomy was also formed. This type of taxonomy is based on quantitative analysis of physical similarities between organisms based on distinguishing characters. By its very nature, this type of taxonomy is anti-evolutionary. Proponents of this type study phenetic similarities rather than genetic similarities. (Reuse M. Source cited, p. 219). R. Sokel and P. Snit, theorists of the phenetic approach, comment: "We cannot use phylogenies for classification, because in most cases phylogenies are not known" [5.21]. It follows that any comments about the past or about the genetic basis must be made after classification (not before, and not during the classification process) [3.237].

Phenetic taxonomy differs from evolutionary taxonomy not only in its orientation in the object of study, but also in the fact that the number of taxon classification levels is not clearly defined. Because determining the degree of similarities can be different according to the purpose of the researcher. In this case, the similarity coefficient is used as a taxonomic parameter. This range includes morphological, physiological, behavioral traits. Ecological markers and markers of geographic distribution are also taken into account [3.223].

Thus, the phenetic direction in biological systematics is manifested in typological classification. Genetic problems can be solved by means of typological classification.

Along with the phenetic direction in biology, the typological direction also developed in linguistics. Proponents of this line conducted comparative-historical episystem analyzes from the point of view of typology [6.]. J. Greenberg's quantitative typology in linguistics is close to the quantitative coefficient of phenetic taxonomy in biology. J. Greenberg E. After Sepir, he is a scientist who made a significant contribution to the theory of typology [7.]. J. Greenberg made observations both in the field of typology and in the field of comparative studies. Even at the level of taxonomy, he did not consider one of these two directions (typology and comparativistics) subordinate to the other.

A. Kreber, a linguist who is closest to the biologist-pheneticists, was a supporter of a single linguistic taxonomy [8.] .

As a result of research in the field of cybernetics, such universal structural mechanisms were sought, which were necessary to coordinate the work of self-developing systems. This is also how language emerged (synchronically and diachronically). And in biology, bionics has developed. This necessitated the need to understand the "feedback" between the paradigms of different disciplines.

In modern biological science, it is considered appropriate to re-evaluate the previous evolutionary paradigm both as a mechanism of evolution and as a relationship between systematics and morphology. A similar process can be observed in linguistics. In "Evolutionary Linguistics", a certain comparative-historical method was surrounded by theoretically new, improved and enriched research methods. This situation gave E.A. Makaev the basis to draw the following conclusion: "The current stage of comparative linguistics is characterized by having an incomplete paradigm. This paradigm replaced the complete paradigm recommended by the supporters of the stream of "Young grammarians" [9.14] .

There are two ways to fill the incomplete paradigm in science: 1) by means of intensification of one or another method (or direction); 2) as a means of extensification of an incomplete paradigm. Both ways are used in modern genetics. On the one hand, this is observed in molecular biology, and on the other hand, it is observed in population genetics. The transition from the individual level to the molecular level transforms the gene from an abstract formal unit into a material structure with specific physical and chemical properties. The transition at the population level makes it possible to imagine en masse evolution, taking into account the complex relationship of genotypes with each other and with the external environment [10.10].

Both ways are used in linguistics. The second way is especially effective in solving taxonomy problems.

Фойдаланилган адабиётлар

1. Кун Т. Структура научных революций. М., 1975, с.11.
2. Meillet A. Linguistique historique et linguistique generale. Paris, 1926, p.100.
3. Рьюза М.Философия биологии. М., 1977, с.30
4. Sımpson G.G. The major features of evolutıons. New York, 1953, p.192. Бу ҳақда қаранг: Рьюз М.Кўрсатилган манба, 181-бет.
5. Sokal R.R., Sneath P.H. A Principles of numerical taxonomy. San Fransisco, 1963, p.21
6. Якобсон Р. Типологические исследования и их вклад в сравнительно-историческое языкознание. – Новое в лингвистике, вып. III. М., 1963 [1957 йилги маъруза матнининг таржимаси]; Иванов В.В. Типология и сравнительно-историческое языкознание. – ВЯ, 1958, № 5; Макаев Э.А. Сравнительная, сопоставительная и типологическая грамматика. – ВЯ, 1964, №1; Макаев Э.А.Общая теория сравнительного языкознания. М., 1977.
7. Гринберг Дж. Квантитативный подход к морфологической типологии языков. – Новое в лингвистике, вып.III. М., 1963 [1960 йилда эълон қилган мақоласининг таржимаси]
8. Kroeber A.L. Statistics, Indo-Evropean, and taxonomy. – Language, 1960. V.36, № 1 (pt.I). p.21.
9. Макаев Э.А. Общая теория сравнительного языкознания. М., 1977, с.14.
10. Рейвин А. Эволюция генетики. М., 1967, с.10.