Vasily V. Zuev,
PhD, professor (Doctor) Philosophy,
ScD, associate professor, Biology
Novosibirsk State University,
Central Siberian Botanical Garden SB RAS

Methodological Programs of Modern Biological Taxonomy and Methodological Solutions

Annotation: The biological taxonomy developmentally handicaps were historically related with two main problems: 1) a problem of searching for essential features which was unachievable within the framework of empiric taxonomy and could be solved as a part of the mature theory; 2) a problem of developing of a model of the biological object the remedies of which were developed only in the XX century. Both problems are associated with the development of classificatory and system ontology and the relevant methodologies. The classificatory methodology from its inception was developed as the means of classification of biological diversity furthermore it was assumed that the features representing classes possess ontological nature that is they actually represent individual objects. Taking into account the empiric nature of taxonomy that assumption turned to be wrong. In the modern taxonomy along with the classical approach a classificatory-system approach was developed. Fundamentally, it is a transition from the classical approach to the modern one which is held to imply the development of a system model of the study subject.

The scope of our research is the literature on methodology and methodological problems of biological taxonomy. The method used in study is the analysis of methodological programs of biological taxonomy formed in the process of historical development of biological taxonomy: programs of classification of biological diversity (classificatory approach – XVIII-XXI cc.), programs aimed at revealing of links in classification systems (classificatory-system approach – XIX-XXI cc.), programs of construction of system models of biological taxonomy objects (system approach – XX-XXI cc.).

1. Program of classification of biological diversity (classificatory approach – XVIII-XXI cc.). In biological taxonomy, construction of taxonomic objects (classes, taxons) is still carried out within the framework of the classical Linnaean method developed on the basis of classificatory ontology formed way back by Aristotle. The classificatory approach assumes the possibility to construct objects (classes) based on the revealed essential features which serve as a type of a group of species, at the same time it is assumed that the essential feature not only integrates homotypic organisms into a class but also reflects the specific nature of the class as an individual subject. In modern classification theory, there are two different definitions of the concept "type": "It is noteworthy that there is an important difference between two scientific "type" concepts. The first is defined as a most characteristic singular

event which to the fullest extent possible captures the essence; the second is an antitype, basic waiving form. Conveniently, these notions may be discerned by using for the second one a term "archetype", dated back to Goethe", – wrote Y.A. Schreider (9). The first understanding of type was historically formed with the development of the classical approach in systematics, the second gained momentum in the concept of archetype proposed by S.V. Mejen.

Essential features have genus-species relations: the whole group of species possesses generic features whereas subgroups within the whole group possess species characters that can be expressed in a form of a hierarchic system where no relationship and interaction between features and the groups that represent these features are intended. The key role of essential features (those that reveal essences of classes of things) is the representation of classes of living organisms that meets the objective of classification of wild life objects. The founder of classificatory approach – Aristotle – thought that the formal essence of sensible things lies in specific differences of thing which are multiple[1], therefore, the majority of specific differences of thing are fundamental and reflect different sides of the essence. Hence stems the notion "essential feature" adopted by C. von Linné and dating back to the Aristotelian form which assumes direct observation of these features that capture essences of organisms as if "not hard to plumb" and reflecting the *true nature*.

In the works of C. von Linné and his disciples there was called into doubt the possibility of finding essential features empirically[2], little by little to methodologically thinking scientists it became evident that this approach is acceptable just in classification of biological diversity in form of living organism classes that are set by arbitrarily chosen "essential" features. This fact has not been realized yet by the whole academic community – the deep-seated tradition of searching essential features in the process of empirical study is still alive. Traditionally, a requirement to naturalness of the class (taxon) also remains assuming construction of a system model of a taxonomic object which is infeasible within the framework of the classical taxonomy. It was in a picture when in the XVII-XVIII centuries the problem of class naturalness was set as well as later in XIX-XX – the problem of reality of taxons of specific and supraspecific rank (5).

The difficulty and the impossibility of finding essential features empirically was periodically manifested itself as a reference problem (fixed and described only in the end of the XX century) of instable connection between object names, "essential" features and objects. The problem of reference is conditioned by regulatory rules of any theoretical work of the empirically arranged discipline (4), therefore it is feasible to set theoretically an essential feature under constitutive rules adopted by the developed science (9), however establishment of constitutive rules of theoretical work in modern taxonomy suggests construction of a system model of taxonomic object according to modern science standards which consider to be *artificial any dissociation of the essential feature from the holistic phenotype*, that may be divided into parts only for the sake of convenience of organism description.

Practically, the modern taxonomy does not differ from the Linnaean taxonomy (at least in large part exclusive of methodologically thinking taxonomists): adopting as a type of taxon (= class) not a single essential feature but a set of essential features the modern taxonomists,

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1 Aristotle. Metaphysics. 1042 b 11 – 25.

2 C. von Linné wrote in "Philosophy of botany": "The *artificial* feature is a surrogate, the *essential feature* is the best but it is hardly possible everywhere".

the same as Linné, are faced with the problem of reference[3] – instable link between elements of knowledge and objects-referents by virtue of empirical character of modern taxonomy (4). As both the Linnaean class based on the single essential feature (type), and the modern taxon based on the feature complex (type) are constructed in the process of empiric search of type that captures the essence they can be thought as virtually counterparts. The modern taxonomy just elaborates the concept of taxon nature by the species system model (population model of biological species) that does not shade light on taxon, creating additional difficulties such as a problem of sibling species, a problem of sterile hybrid taxon status etc. (5).

Thus the problem of essential features actually hides two challenges:

1) The problem of constructing a developed theory because empiristic search of essential features is an unattainable task.

2) Revealing of natural objects of taxonomy. As such, only integral objects are taken since solution of essential feature problem is insufficient in the light of modern science – the modern theory is built within the framework of system approach. That is exactly why the theoretical objective of taxonomy is a problem of individuality (integrity) of taxonomic objects – classes and taxons - is manifested in a wide range of ontological problems appeared in the process of historical development of biological taxonomy as it was thought that the individual nature of taxonomic objects was at the back of essential features. By means of classificatory approach these problems cannot be solved because their objective is classification of diversity, and only the system approach describes natural objects.

In the process of historical development of taxonomy the following ontological problems of taxonomy stood up: 1) search of essential features as basis of class individuality (later - taxon), 2) search of boundaries between classes as basis of class individuality (taxon), 3) search of taxon rank stability as basis of its individuality, 4) search of correspondence of typology in objective reality as basis of type reality, 5) search of reality basis of taxons as individua in time (3). These problems that need the development of system methodology for their solution eventually resulted in the development of the concept of "limited transformism" (2) which combined specific features of both classificatory and system ontology which turned to be not sufficiently efficient for problem solution. It gave occasion to statement of reality problem in taxonomy throughout the twentieth century.

2. Program of recognition of relations in classification systems (classificatory-system approach – XIX-XXI cc.). In modern taxonomy along with the classical approach the classificatory-system approach is also developing that comprises different trends of phylogenetic systematics and theory of archetypes. In the phylogenetic systematics the classical understanding of type remains unchanged. The phylogenetic system is constructed as a form served for the expression of connections between the groups which are related as ancestor/descendant within a certain space of time. Connections between groups of organisms are structured as a system of relationships between empirically selected essential features – types. Thus these systems reflect the genetic sequence of different kinds of adjustment common to the groups of organisms which are still presented in form of classes arranged in the system through connections between complexes of features – types and not Gestalts of

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3 Linné called this a "problem of order of nature features" – he clearly realized the impossibility of finding essential features of orders of nature and stated his beliefs in conversation with his disciple Gizeke.

group of organisms – phenotypes. In other words, the phylogenetic system reflects coupling not between groups of organisms but between features which represent such groups.

Therefore, in the phylogenetic system the features of holistic phenotypes are categorized according to historical phases of their formation by individuals, respectively, in graphic terms the phylogenetic system is presented as a tree with branches – different rank features – coinciding with historical phases of their generation. The features of holistic phenotypes distributed in hierarchal and phylogenetic systems as taxons of various ranks do not generate natural objects that possess the basic property of the systematic object – integrity. In nature such object is in congruence with groups of individuals which in common with classes are characterized by one or several features that are observed in specific individuals and present just some parts of the holistic object – phenotype. Indeed, the features are of interest in study of history of development of adjustments by living organisms but the concept of the "taxon" as a natural, holistic object can be related only to the phenotype which includes all organism features and forms the holistic taxon image.

When taxonomists rank characters (features) and qualify them with groups of individuals with different degrees of similarity, they hold in place the historical stages of generation and development of features. By doing so, they consider these groups as taxons which appeared in different historical eras and build bridges between them in form of the phylogenetic system. Trying to solve the problem of taxon integrity, taxonomists assign a status of reality only to taxons of trivial rank because in their opinion owing to their "youth" these taxons have not "lost integrity!", consequently the supraspecific taxons are thought to be the "systems with a small degree of entirety". However the presently existing individuals of any kind possess features of every rank that generate the phenotype as a certain holistic formation – image (habitus) of taxonomic object, and when taxonomists distribute features of holistic phenotypes by taxons of various ranks they at once deprive these phenotypes of their entirety and receive a host of problems which cannot be solved. It was clearly demonstrated by the taxonomy through the whole history of development – in all historical periods these attempts created different kinds of difficulties associated with taxonomic reality (3).

Therefore, phylogenetic systematics could not have solved the objective of natural classification but could reveal the historical aspect of development of features as organisms' adaptive flexibility that without doubt is a major accomplishment.

Within the framework of the classificatory-system approach the problem of naturalness was partly solved by S.V. Mejen in his concept of archetype. Giving the definition of archetype, Mejen notes: "Homologized i.e. arranged and becoming merons, parts of organisms of this taxon combine altogether the taxon archetype. Usually, in biology the archetype is understood to be a plan of construction (morphological) of all organisms of this taxon (Kanaev, 1963, 1966). Archetype in a more comprehensive sense adopted in this paper embraces not only morphological but also all other properties of taxon representatives. Clarification of archetype concept with regard to any objects as well as a more detailed characterization of other meronomic concepts and approaches to their formalization can be found in literature" (6).
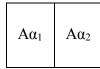
Mejen's archetype – is still a hierarchal structure – and in this sense it is an intermediate formation, an element of classificatory-system formations. However the archetype has one significant property: "Of theoretical and practical interest is a case with the available system diversity of archetypes. If the K_{A1} class is a subclass of the K_A class then any object having

archetype A_1, at the same time has also archetype A. All common things inherent in objects of K_{A1} are also common to all objects of K_A. Therefore the description of such commonness must belong within not only archetype A, but also within archetype A_1" (9: 3), i.e. in practice the archetype of species incorporates features of holistic phenotype that represents the organism. Arguably, the foundering fathers of archetype theory S.V. Mejen and Y.A. Schreider run short of the new vision of hierarchy of features in the taxonomic system to understand the nature of system presentation of taxon.

3. Program of formulation of system models of objects of biological taxonomy (system approach – XX-XXI cc.). Modern scientificity standards necessitate construction of system models of objects based on the holistic principle. From the current point of view, holistic concerns "biological, psychological, social and complex technical systems, i.e. systems which possess not only functionalities but also their own behavior, own history, development and as a rule being hierarchal according to their structure etc." (1: 18). The classes constructed within the classificatory approach conceptually cannot be holistic objects. We cite the simplest example. Let us assume that the diagnostic feature A was revealed in a group of individuals, and inside this group we single out two subgroups of individuals with diagnostic features α_1 and α_2. From the standpoint of classificatory approach, there are two levels of feature hierarchy: upper – with feature A evidenced among all individuals of the group, and lower – with features α_1 and α_2 observed in two subgroups inside the entire group of individuals, correspondingly *one can single out three classes*: **genus** with the diagnostic feature **A** and two **species** with diagnostic features α_1 and α_2:

A	
α_1	α_2

The system approach suggests that holistic objects in this case will be the phenotype, while singled out generic and specific features cannot be treated as independent essences because they present interrelated parts of the holistic phenotype. In fact, it is observable among individuals: features of all ranks are observed in case of every individual and form the holistic phenotype, accordingly in the context of system approach in the example above *two phenotypes may be singled out* (**taxons**): **Aα_1** and **Aα_2**, where features are interrelated and represent the **holistic phenotype**:

Aα_1	Aα_2

Obviously, in the case of classificatory approach the integrity (consequently naturalness) of object – phenotype is violated right from the start: holistic phenotypes **Aα_1** and **Aα_2** are split into parts which are determined by diagnostic features – classes. In point of fact, if we speak about holistic objects, how can we single out, for example, geni by specific characteristics of fruit, and species – by specific characteristics of petals? In doing so we would split the holistic phenotype into parts.

The integral phenotype is only a part of the system taxon model that includes genetic material which determines phenotype development, aside from this the taxon as a living system is in a close coordination with different environmental factors that specify the form of its existence.

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I.I. Schmalhausen clearly demonstrated that the taxon as a holistic system could not be built outside of adaptation factors which constitute the character and form of the taxon existence (8). It is believed that the holistic taxonomic system incorporates the following components: 1) **group of individuals**, 2) **genetic program** realized among the group of individuals as a form of preservation and translation of features appeared in the course of evolution, 3) **inherited material** (genetic system which includes the genetic program) as a potential basis for formation of 4) **phenotype** that includes two types of features: 5) **constant features** that form the basis of phenotype as compliance with the existing habitat conditions, 6) **changeable features** that form the material for evolution of individuals [4]. Apart from this the system should be added with 7) **taxon formation factors** (divergence, hybridization and adaptation) which eventually form the vectors of development of taxonomic systems, and bring about well-defined phenotypes (10).

The genetic system in the process of organism development is manifested in the phenotype form while the basis of its existence is the genetic program "stored" in genetic material of the organism. Consequently in terms of mode of being the taxon may be defined as a genetic system-cumatoid – genetic program that each time reproduces in a new material and lives in this material. Alternately stated, living organisms present living "waves" running from the depth of the centuries and lapping in our time, more or less quickly regenerating in their material.

The cumatoid ontology was developed by M.A. Rozov (7) to explain the mode of being of social systems. Social cumatoids according to Rozov are not systems as the social program exists in a great measure independently of material. Biological systems can be viewed as genetic cumatoids[5] – genetic programs which have been historically formed in the process of transformational growth of living systems and realized in specific periods in the living material. A genetic program, contrary to the social one, exists as a part of living organism directly in the cell genetic material that is why the biological cumatoid is a special type of cumatoid – system-cumatoid. Use of cumatoid ontology allows for more clear describing of the taxonomic reality as a reality of a special biological program which similar to wave skims along the living material. The taxon can be presented as a genetic program capturing more and more new material and existing in time due to the capacity of genetic substance self-replication. That particular property of taxonomic systems allows for reproducing the mechanism of their evolution since the genetically fixed specific features of the system, as it was established by paleontology, are preserved in many generations.

Implementation of genetic program in material is carried out via genetic system so the principal way for research of genetic programs is through the investigation of genetic systems and their phenotypical manifestations. Material carriers – individuals – contain many features of different rank among which one can distinguish the invariable part of the phenotype of individuals which is specifically arranged – in form of genetically bound features. It is reproduced as a single structure. Phenotype invariability is due to a number of reasons. First, the peculiarities of genetic substance variability – genes: their discrete behavior and self-

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4 Without division of features into constant and changeable it is impossible to explain the capacity of recognition and classification of taxons as well as the propensity of organisms themselves for evolution (V.Z.).
5 Cumatoid – "wavelike", derived from the Greek "cuma" – "wave". *(V.Z.)*

replication property, second, compliance of phenotype with environmental conditions that is its adaptivity.

The author's paper demonstrates that phenotypes present stable structures – taxons which can be constructed on the basis of system parameters. Contrary to the taxons constructed within the framework of classificatory approach, these taxons present a more realistic formation as they comprise all features regardless of rank which are observed in every individual belonging to a specific taxon. The advantages of the system model are obvious also in solution of taxonomic problems arising in the process of taxonomy development (10):

– **Problems of essential features and taxonomic boundaries** are eliminated as the phenotype comprises the phenome that consistently specifies the taxon.

– **The problem of taxonomic rank fades away** as the phenotype characterizes a rank-less group of individuals (ranks of genus and species may be separated conditionally), only phenes-markers are ranked as a primary material for taxon construction.

– **The problem of taxon existence in time (contingency)** is withdrawn by means of presenting it as a genetic program.

– **Phenotype presents a natural object**, as it is conditioned upon genetically and presents a totality of characteristics reflecting morphological and physiological peculiar properties of individuals as parts of the taxon, whereas the classical taxon includes only a part of all features and can be presented just in the logical possibility space (as abstraction).

Conclusions

Thus, the biological taxonomy developmentally handicaps were historically related with two main problems: 1) a problem of searching for essential features which was unachievable within the framework of empiric taxonomy and could be solved only as a part of a mature theory; 2) a problem of developing of a model of a biological object the remedies of which were developed only in the XX century. Both problems in implicit form were already present in works of C. von Linné.

The problems are also associated with the development of classificatory and system ontology and the relevant methodologies. The classificatory methodology from its inception was developed as the means of classification of biological diversity furthermore it was assumed that the features representing classes possess ontological nature that is they actually represent individual objects. Taking into account the empiric nature of taxonomy that assumption turned to be wrong. In the modern taxonomy along with the classical approach a classificatory-system approach was developed. Fundamentally, it is a transition from the classical approach to the modern one which is held to imply the development of a system model of the study subject.

Within the present-day ideas the holistic taxonomic system incorporates the following components: (1) group of individuals, (2) genetic program realized among the group of individuals as a form of preservation and translation of features appeared in the course of evolution, (3) inherited material (genetic system which includes the genetic program) as a potential basis for formation of (4) phenotype that includes two types of features: (5) constant features that form the basis of phenotype as compliance with the existing habitat conditions, (6) changeable features that form the material for evolution of individuals. Apart from this the system should be added with (7) taxon formation factors (divergence, hybridization and

adaptation) which eventually form the vectors of development of taxonomic systems, and bring about well-defined phenotypes.

References
1. *Blauberg IV, Sadovsky VN, Yudin EG. System studies and general system theory. System studies. M.: Nauka; 1969;7-28.*
2. *Zuev VV. Problem of reality in biological taxonomy. Novosibirsk, 2002.*
3. *Zuev VV. Peculiarities of development of biological taxonomy ontology: Philosophy of Science. Novosibirsk. 2011; № 4(51); 80-87.*
4. *Zuev VV. Reference problem as a problem of empiric classification in classical science: Epistemology and Philosophy of Science. 2014; № 2(40); 96-109.*
5. *Zuev VV. Development of a system model of biological taxon as the development basis of modern biological taxonomy: International Journal of Applied and Fundamental Research. 2014; 10(2); 101-108.*
6. *Mejen SV. Main aspects of typology of organisms: Zhurn. Obssh. Biol. 1978; № 39(4); 495-508.*
7. *Rozov MA. Theory of social relay races and problem of knowledge analysis. In: Theory of social relay races: History – Ideas – Prospects. Novosibirsk; 1997; 9-67.*
8. *Schmalhausen II. Factors of evolution. M.: Nauka; 1968.*
9. *Schreider YA. Typology as classification basis. Scientific and technical information. Series 2. Information Processes and Systems. 1981; 11; 1-5.*
10. *Zuev VV. Project of a theoretical biological systematics: on a way to rapprochement biological systematics and genetics: Eastern European Scientific Journal. 2014; 2; 23-48. DOI 10.12851/EESJ201404ART04.*