SUPERSYMMETRY PROBLEM IN BIOMORPHOLOGY

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The symmetry of proportions of human body as well as the algorithmic order of leaves on a plant (philotaxis) are known from ancient times. Arcy d'Thompson in the beginning of this century (1917) undertook an attempt to systematize the volume of empirical knowledge of bioforms of growth on the basis of similarity symmetry. After that D.V.Nalivkin put forward an idea of curve-linear symmetry.

It is common knowledge that isometric symmetry of bioforms on submolecular level is quite low: just bilateral (mirror) symmetry in the world of animals endowed with freedom of movement and pentagonal ones (in general) in flowers. Such scarcity is not correspond to the high level of organization of biological objects - philotaxis, cyclomery, proportionality of their structure and other types of algorithmic orderness. This contradiction brought V.I.Vernadsky to formulate the problem (1931): "It is necessary to develop the science of symmetry in close relation with morphology of life. Such is the new and enormous problem which is now on the agenda". V.I.Vernadsky suggested that to the drastic difference between living and non-living matter there correspond the non-Euclidean space or to be more precise the space-time of the living matter.

In 1940 A.V.Shubnikov in his book "Symmetry" (see also A.V.Shubnikov, V.A.Koptsik, 1972) summarized our knowledges in this field as follows: "As to living organisms we do not have any theory for them which could answer what kinds of symmetry are or are not compatible with the existence of living matter." Having introduced into the symmetry theory a notion of relative equality A.V.Shubnikov discovered in 1960 the point groups of similarity symmetry modelling cyclomeries for a number of geometric schemes. A.M.Zamerzaev extrapolated this model to the space similarity groups. Biologically important groups of Möbius, projective and tangent transformations, containing the subgroup of similarity, were discovered recently by S.V.Petukhov (1981, 1988) in cyclomeric biological objects and in kinematics of movements. Realization of these biosymmetries is connected with iteratively-algorithmic peculiarities of biological self-organization and information inheritance.

Does the discovery of non-Euclidean symmetry groups in biomorphology of submolecular level of organization verify Vernadsky's first hypothesis of non-Euclidean character of "the geometric space of living organisms"? The answer to this question should be polysystemic. According to the principle of relativity of symmetries revealed by A.V.Shubnikov, there are different groups of symmetry which act on different structural levels of the same material object. This statement also holds true for biological objects in which the hierarchy of structural levels and, hence, symmetries is most fully developed. "The principle of superposition of structures and the principle of symmetry for composite systems connected with the previous one acts in specific forms at every of the biological levels." (A.V.Shubnikov, V.A.Koptsik, 1972). It turns out that in biomorphology as well as in physics or crystallography the broken symmetries (isometry, similarity, affinity) do not disappear but are retained in the structure in the modified form on the level of generalized (so called coloured) positional groups (V.A.Koptsik, 1988). By choosing the proper local compensate transformations, each of the cyclomeries studied by S.V.Petukhov can be alternatively described not as global groups of Möbius or projective transformations, but as coloured affine groups. Such an alternative in description of biocyclomeries makes the problem of non-Euclidean character of biospace quite clear: such statements are only true for a given considered model and fixed level of its structure.

The study of laws and algorithms of organic biomorphology is one of the prominent directions of research in modern biology, which in accordance with general expectations should bring about fundamental discoveries and some practical outcome in the nearest future. In contrast with crystallography the modern mathematical biology does not have a generally accepted formalized theory of morphogenesis, although numerous attempts are known to develop this theory on the basis of different primary models - cybernetic, reaction-diffusion, etc. The difficulty of developing such a theory lies primarly in the lack of sufficient knowledge about general biological properties of morphogenesis which could be mathematically formalized and theoretically explained. The level of the mathematical biology of evolution requires yet a long way to go, accumulating knowledge of the key morphological qualities and adequate geometric classifications till it can arrive at the desired theory - a common way, already passed by crystallography and other natural sciences, which deals with far simpler objects than biology. Revealing non-Euclidean biosymmetries gives valuable material for development of formal theory of the morfogenesis, whereas the ability to account for the existence of those biosymmetries is an important criterion of adequacy of such a theory.

The authors of the present report are physicists, specialising in crystallography and biology who in their research are oriented by the tendency of "geometrization of biology", as well as on the experience of crystallography. They discuss fundamental problems of application of group-theoretical approach to mathematical biology, biomorphology and biomechanics.

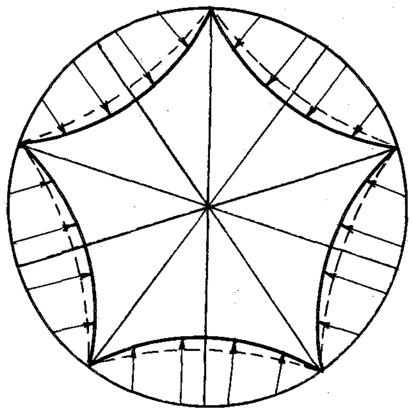

Fig.1. Scheme of polyblock structure of Ludvig perennis fruit and its orthogonal (G = 5 mm), conformal (spheric-reflectional) and coloured affine symmetry (field of arrows).

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