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Law of Taxon Formation and Mechanism of Living Organisms Evolution

Annotation: *A unit of evolution of living organisms is a phenotype – a stable manifestation of genetic program which has been historically formed in the course of adaptation of animal units to varied environment. Phenotype includes invariable phenes which determine a basis of organism habitus (background phenes), and variable (mendelevian) phenes which determine a changing nature of some parts of organism. Mendelevian, variable phenes present opportunities for an organism to adapt to the varied environment as exemplified by reduction of frequency of phene of white coloration among butterflies Biston betularia in the areas of high pollution load – white butterflies are more frequently eaten by birds than dark ones as they become easy-to-see on dirty birch trunks. Therefore, it can be believed that phenotype evolution occurs at the level of mendelevian phenes – as a result of adaptive processes a frequency of non-adaptive mendelevian characters is greatly reduced whereas a frequency of adaptive characters is increased. After passing of different versions of mendelevian characters through the "filter" of adaptation the least successful combinations are eliminated and adaptive ones are included in stable characters forming the basic organism habitus. Against stable phene populations the newly emerged mendelevian characters are evolving and the cycle is repeated. Among organisms a "nucleus" is eventually formed – a population of stable highly adaptive characters forming the basis of organism facies, and variable characters as a material for evolution. Within classification systems of allied organism groups phenes of various level of adaptation and hence different frequency are fixed in a form of a many-staged hierarchical structure of phenes of different degree of community as a consequence of genetic program implementation within species groups.*

Introduction

Specific features of character inheritance from the earliest times were of interest mostly of plant and stock breeders whose major concern was breeding of high-yielding varieties: plants with larger fruitage, more resistant to unfavorable environment, having larger sugar content; animals with a higher milking ability etc. All experiments aimed at fancying were conducted mostly on breeding organisms as in the process of species mating the characters quite frequently produced a speciose range of different combinations from which the breeders chose interesting properties and consolidated in subsequent generations by

selection of the most promising species. The researchers noted that in the process of organism mating the characters had a different behavior. It was found out that in the mating of one breed specie a part of characters typical for main lines of habitus remained unchanged whereas a certain part of other characters could change both qualitatively and quantitatively in next generations. Most breeders were interested in qualitative changes of characters because they allowed for improving valuable performance indicators of breed and cultivars. At the same time people were not aware that quantitative character ratios kept inheritance mechanisms and mechanisms of living organism evolution in the dark. The first researcher who took note of the quantitative side of character ratios in breeding was G. Mendel who registered different variants of quantitative character ratios in hybrids of different generations and reflected them as the rules of character inheritance which were named the G. Mendel laws.

The same as the precedent breeders, Mendel was mainly interested in characters forming different combinations which changed the habitus of individual parts of species, and specific features of their inheritance while the range of unchangeable characters was not included in analysis by Mendel. He took as a point of departure the assumed in that time biological concept within the framework of classification approach that stated that the properties of organisms were determined by essential characters which fixed organism classes and determined their individuality. Nevertheless, in G. Mendel's studies the elements of systematic approach were well-marked: he envisaged the systems of interrelated characters.

It is of interest the examination of inheritance rules from the standpoint of systematic approach adopted by contemporary science. So we will proceed from the assumption of "integral phenotype" which includes all characters, phenes combining an organism habitus. Needless to say, one may distinguish an infinite set of characters, but we will mainly focus on the characters which define the organism as an integral system and allow for fixing the organism integrity by letter symbols designating the parts of organism habitus, phenotype – phenes. An integral phenotype is of paramount importance for understanding the interconnection between different parts of organism, fixation of organism habitus as a certain stable image which allows for separating it from other organisms, or vice versa, relating it to a group of similar organisms etc. The entire range of characters – phenes combining phenotypes of organisms was resulted from a centuries-old meticulous work with organisms, their descriptions, classification through which it was found out that it was convenient to define similarities and differences between organisms by distinguishing alternative states of characters. Later it turned out that alternative states of characters – phenes – made possible not only to fix similarities and differences between organisms but also describe regularities of character inheritance by living organisms. For the first time it was clearly and plainly made by G. Mendel for mating organisms. It is been a long time since the discovery of G. Mendel. In our opinion, the time is ripe for re-thinking of this discovery with consideration for new data accumulated by biology, as well as systematic methodology developed by contemporary non-classic science.

As data for study, there were taken literature and author's reports on research in quantitative ratios between characters in laboratory and in vivo. The method used to study is philosophical and scientific analysis and generalization of the whole bulk of literature data.

The goal of research is rethinking of the character inheritance by living organisms, which up to date has been developed by classical science within classification approach, in the light of modern systematic approach developed by non-classic science.

Mechanism of character inheritance and mechanism of evolution of living organisms

The nature of variability of characters of living organisms and main types of their inheritance we defined in the Law of taxon formation (1, 2):

1. Formation of taxons takes place due to elementary evolution processes – ***divergence*** and ***hybridization*** influencing the genetic level, as a result, ***taxon-forming hereditary units*** are formed – genes and supergenes as a material display of ***genetic program***, which is fixed by observation in the form of phenotypical gene displays: taxon phenes-markers.

2. ***Divergence*** – is a basic elementary evolution process of character "discrepancy" – formation of a new character on the basis of an old one in the process of adaptation occurring at the genetic level having phenotypical displays.

3. ***Hybridization*** – is a secondary elementary evolution process – interrelation of newly emerged taxon-forming units specifying taxons, as a result, ***intermediate taxon-forming hereditary units*** are formed and their phenotypical displays.

4. As a consequence of elementary evolution processes, formation of taxon-forming hereditary units follows well-defined tracks (types) with two most important:

$A + \alpha$ (divergence),

$A + A\alpha + \alpha$ (hybridization with formation of an intermediate type which can be thought as a special case of hybridization with formation of several intermediate types: $nA + (n–1) A 1\alpha + (n–2) A 2\alpha + ... + 1A (n–1) \alpha + n\alpha$ (1, 2, 3).

5. ***Taxon*** is a genetic program implemented in species in a form of a phenotype; a phenotype presents an adaptive part of phenome –stable phenotypical display of genome – population of phenes and superphenes representing salient features of constitution, physiological peculiarities and habitus of species of common kindred which has been implemented in all species (which ever were, vanished or are living at this moment), which have relationship with a specific species taken as a taxonomic type.

In order to study in the integral phenotype within systematic approach one may propose a more correct rendering of Mendel's laws: the whole system of characters should be distinguished within which the unchangeable characters are distinguished – background ones which form a stable habitus of organism inherited as a complete unit – 1 part (O), and variants of mendelevian – recombinant characters which define instability of habitus of certain parts of organism which inheritance takes a form of either incomplete dominancy – $1A + 2A\alpha + 1\alpha$ (3 parts: A, Aα, α), or complete dominancy – $3A + 1\alpha$ (two parts: A, α). Hence, two basic types of ratios of characters are distinguished in the system of phenes making up the phenotype of an organism:

1. relation between background (stable) characters / recombinant characters with incomplete dominancy – O: $A + A\alpha + \alpha$ (1:3);

2. relation between background (stable) characters / recombinant characters with complete dominancy – O: $A + \alpha$ (1:2).

In these relations are of interest both qualitative characteristics of organisms (O, A, Aα, α), and quantitative ratios (1:3, 1:2), which are registered by researchers in the process of taxonomic observations and experiments and described in scientific papers.

Within the entire system, it is also possible to describe the inheritance of recombinant characters according to incomplete $1A + 2A\alpha + 1\alpha$ (1:2:1) or complete dominancy $3A + 1\alpha$ (3:1), that was carried out by G. Mendel.

Asexual organisms will mostly have the elementary evolution process – divergence resulting in one variant of character inheritance:

3. relation between background (stable) characters / diverging characters – O: A + α (1:2).

Correction of the rules of character inheritance by G. Mendel is very important as a specific feature of character inheritance is dependent on their adaptive characteristics emerging as a result of adaptive processes passing in the organism-environment system, that is directly reflected in increase or decrease of a number of organisms in the course of evolution (1, 4). The adaptive nature of character variability governs similar changes of organisms as a response to certain changes of environmental conditions directly reflected in habitus of organisms: one may distinguish similar characters of different level of affinity which is shown by classic taxonomy in form of hierarchical classification system. A different level of affinity of characters depends on two factors stemming from the above calculations: first, frequency of stable phenes in populations which form the core of phenotype and determine basic adaptive properties of organism, second, different frequency of recombinant phenes in populations which determine adaptability of variants deviated from the basic phenotype. Hence, hierarchical classification system reflects different evolution stages of living organisms as a consequence of alteration of their adaptive characteristics and therefore quantitative ratios.

The adaptive nature of character changes is not always presented in an obvious form, and often requires long-term observations to reveal the nature of adaptations and their compliance with varied environment. The most important and obvious manifestation of adaptability or non-adaptability of a character is its rate in population of species (1, 4, 5). As a simplest model of character adaptability we may take the type of coloration inheritance by butterflies *Biston betularia* – peppered moth: in technogenic areas the birch bark is polluted and becomes brown so white peppered moth is more often eaten by birds than dark-colored as they are detectible on birch dark bark (3). Hence, the phene of white coloration is significantly reduced in populations of butterflies *Biston betularia*. We used this model added by mathematical calculations in study in phene frequency and indicators of their adaptability in populations of gentian family (*Gentianaceae*). The model turned out to be very efficient: it allowed for calculating the rate and indicators of adaptation of phenes and phenotypes, that was fully confirmed by factual material – data on ecological amplitude and scope of area of phenes and phenotypes (1, 4, 5, 6).

In light of the foregoing it is possible to offer the following living organism evolution (1, 2). As is shown above, phenes by their adaptive and evolution parameters may be divided into background (stable) and mendelevian (recombinant). Phene evolution starts from their "mendelevian" state – when they were formed as a result of divergence with ability for recombination in subsequent hybridization processes. From now forward, when different

combinations have passed through the adaptation "filter", the least successful combinations are eliminated and the adaptive combinations form a stable structure – background phene populations, later inherited with no recombinations, as a complete unit; they can recombine only as a result of chance mutations which usually turn to be nonviable. Against stable phene populations the newly emerged mendelevian characters evolve and the cycle is repeated.

The structure which emerges as a result of historical evolution of living organism system was defined by researchers as a multi-stage hierarchical classification interpreted as a consequence of evolution of different rank taxons. We have shown above that taxons of different rank defined by classical taxonomy actually present phenes (essential characters – in terms of classical taxonomy) representing the groups of organisms that do not have individual characters, and not integral phenotypes representing organisms and their groups as individual formations (1). Phenes or their populations are not natural subjects since they present manifestation of a part of genetic program, whereas the complete manifestation of genetic program is an integral phenotype.

Therefore, we offer a new interpretation of hierarchical classification within the framework of systematic approach. The processes occurring in groups of organisms similar to those in an individual organism as they are a consequence of implementation of the entire genetic program formed under the action of the environment. Each individual species has characters of all ranks which classical taxonomy qualifies as different rank taxons. Thus, as a result of implementation of genetic program in groups of affined species, the quantitative relations are observed between background and mendelevian phenes, similar to above-described for the individual organism. Background phenes form a stable "core" – phenotype, inherited as a complete unit in conjunction with which there are always also mendelevian phenes making up the "boiling" evolving layer of the whole phene hierarchical structure. Stemming from the calculations above, it may be thought that in hybridization and recombination of phenes disintegration takes place either in terms of different versions of incomplete phene dominance – $A + 2A\alpha + \alpha$, correspondingly, three phenes are formed (superphenes) – A, $A\alpha$, α, or complete one – $A + 3\alpha$, correspondingly, two phenes are formed – A and α, referring to which the whole remaining multi-staged structure is inherited as a complete unit. Two types of structure are obtained: the first – (background phenes as a complete unit) : (number of mendelevian phenes) = 1 : 3, and the second – (background phenes as a complete unit) : (number of mendelevian phenes) = 1 : 2.

The noted quantitative relations of phenes are confirmed on factual material in various systematic groups. Considering that each stage of hierarchical system on average contains two alternative and one intermediate phene-marker, the hierarchy can be described mathematically by raw estimation of a number of markers on each stage of hierarchy. Such calculations were performed by different authors in the XX century. There are used as quantitative parameters a number of phenes (taxonomic categories – in classical presentation) and different constants in description of hierarchical structure. For description of hierarchical structure different authors proposed the following formula:

$$N_n = k^n,$$

where N_n – number of phenes of rank n, k – constant which has different values in different taxonomic groups. For example, Guy Roberti (7) determined the formula for mathematical description of hierarchical structure as exemplified by sorghum family:

$$N_n = 3^n$$

L.L. Chislenko (8) for Harpacticoida (crustaceans) conceived the following formula for definition of complete taxonomic diversity:

$$H_T = \sum_{n=1}^{6} 3.3^n \ \sum lg\ N_n$$

where H_T – full taxonomic diversity, N – number of taxonomic categories (phenes), n – order number of taxonomic rank. He also found out that an average number of taxonomic categories of rank n–1 related to the n rank category were 3.3. Thus, with consideration for our calculations, a number of phenes of rank n can be derived from the formula $N_n = 3.3^n$. The author of this paper on the basis of structural analysis of family Gentianaceae derived the empiric dependence of the number of phenes on rank (9, 10):

$$N_n = 2.7^n$$

Among papers related to hierarchical structure, but without mathematical description, it is to be noted the paper by A.N. Golikov (11) about mollusks where was noted a consistent change of the number of taxonomic categories depending on taxonomic rank.

From the above materials on various taxonomic groups of plants and animals (sorghum family, gentian family and crustaceans – Harpacticoida) it may be seen that a number of phenes of rank n–1, linked with the phene of rank n varies from 2.7 to 3.3, and, on average, it probably approximates 3. From there it may be deduced that in hybridization of mendelevian characters an incomplete dominance prevails so the ratio between numbers of phenes on each stage of the whole hierarchical structure will be something like 3:

$$f^n: f^{n+1} \approx 3.$$

This specific feature of phenotypical systems constructed by researchers allows for describing mathematically the hierarchical structure as well as forecasting a number of phenes on different hierarchical levels, and guesstimating a number of specific phenes in various taxonomic groups. For a number of families the author calculated theoretically the numbers of different rank phenes which turned to be very close to the real quantities of phenes, for example, for the gentian family a calculated value of 4 rank phenes was 81, real – 83, a calculated value of phenes of 7 rank (species) – 972, real – 1050 (9). It confirms our thought that the development of taxonomic theory keeps the path of revealing alternative and intermediate phenes-markers.

Thus, a rank is determined by ranking of phenes-markers in terms of the level of affinity. A rank is a judgment-based category bringing to light a degree of phene-marker affinity in terms of representativeness among organisms: the more organisms are embraced by this phene-marker, the higher is its rank. For example, the highest rank (domain) is registered for phene which marks the availability or absence of nucleus cell characterizing large groups of organisms: procaryota (bacteria) and eucaryota (fungi, plants and animals). Ranking results in names, phenes-markers and corresponding symbols or terms which fix a rank. For example, *Gentiana – corolla with intermediate plicae – 1st rank* (*general*, within the framework of classical taxonomy – *genus*); *Gentiana lutea – yellow corolla, divided up to the base – 0th rank* (*partial*, within the framework of classical taxonomy – *species*).

So then, in groups of species we observe populations of different rank phenes, a part of them is background phenes – stable structure ("core" or phenotype) inherited as a complete unit, and a great diversity of evolving mendelevian phenes (specific and intraspecific), which in the course of recombinations generate a big range of variability of phenes-markers and their transient forms. On this basis, it is advisable to distinguish taxons of rank "genus" and "specie" according to adaptive and evolution characteristics of phenes. According to views of C. Waddington (12), it may be thought that the genus (stable part of phenotype) is a main development pathway (chreod) determining development of a normal (wild) phenotype of population, specie characters may be defined as subchreods (species – recombinant phenes), different deviations from the normal phenotype, still not having high adaptive properties which in the future may result in progressive adaptive changes.

Therefore, a unit of living organism evolution is a phenotype – a stable display of genetic program which has formed historically in the course of adaptation of species to varied environment. Specific features of character inheritance in groups of living organisms are determined by quantitative ratios of phenes which make up phenotypes, at the same time the quantification of phenes is conditioned by adaptive indicators. The mechanism of evolution of living organisms depends on processes of divergence and hybridization of characters having quantification values, in the course hereof a stable structure is formed – phenotype. The lability of phenotypic system is determined by evolving characters complimentary to the stable system core – phenotype.

Conclusion

A unit of living organism evolution is a phenotype – a stable display of genetic program which has formed historically in the course of adaptation of species to varied environment. Phenotype includes invariable phenes which determine the basis of organism habitus (background phenes), and variable (mendelevian) phenes which determine the variable nature of certain parts of organism. Mendelevian, variable phenes present opportunities for organism for adaptation in changing environmental conditions: reduction of frequency of white coloration phene of butterflies *Biston betularia* in areas with an elevated pollution level may serve as an example – white butterflies are more often eaten by birds than dark ones as they become visible on polluted birch bark. Therefore, it is believed that the evolution of phenotype occurs at the level of mendelevian phenes – as a result of processes of adaptation the frequency of non-adaptive mendelevian characters is drastically reduced whereas the frequency of adaptive characters is increased. When different combinations of mendelevian characters have passed through the adaptation "filter", the least successful combinations are eliminated and the adaptive combinations are included in stable characters which form the basic habitus of organism. Against stable phene populations the newly emerged mendelevian characters are evolving and the cycle is repeated. Finally, among organisms a "core" is formed – a population of stable highly adaptive characters, forming the basis of organism facies, and variable characters as a material for evolution. Within classification systems of allied organism groups, phenes of various levels of adaptation and hence different frequency are fixed in a form of a many-staged hierarchical structure of phenes of different degree of community as a consequence of genetic program implementation within specie groups.

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