

On the role of natural selection in the genetic divergence of migration-coupled populations: results of mathematical modeling and experiments

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Motivation and Aim: The existence of stable differences in a uniform selection area seems somewhat paradoxical from the point of view of population genetics; however, it is precisely disruptive selection that can give such divergence [1]. Examples of population systems with stable divergence of genetic structures of subpopulations inhabiting a homogeneous area are found in nature and created experimentally [2–4]. Comparing these observations and modeling results allows us to explain the maintenance of the stability of natural genetic divergence by the interaction of disruptive selection (in the form of reduced fitness of hybrid forms) and weak migration process. The results of experiments performed by Yu.P. Altukhov and co-authors with populations of *Drosophila melanogaster*, in which primary divergence of the genetic structures of the subpopulation was obtained at the α -GDH locus, are in good agreement with this statement. One can assume that disruptive selection, in this case – reduced fitness of α -GDH heterozygotes, played a significant role in maintaining this divergence. An alternative hypothesis is the fixation of differences by genetic drift.

On the one hand, to identify and substantiate the possibility of the presence of this factor in the system, and on the other hand, to assess how significant a role disruptive selection plays in maintaining the stability of primary genetic divergence, in this work we analyzed mathematical models of the dynamics of allele frequencies in a large panmictic population and a system of 30 local migration-coupled populations, and also compared the model dynamics of allele frequencies under the action of selection and without it with the data obtained in the experiment.

Methods and Algorithms: In the experimental study [5, 6], Yu.P. Altukhov and colleagues studied the dynamics of allele frequencies of two autosomal diallelic loci α -glycerophosphate dehydrogenase (α -GDH: 2 alleles, chromosome II) and esterase-6 (Est-6: 2 alleles, chromosome III) in a system of 30 sequentially migration-related vial populations of *Drosophila melanogaster*. One hundred and fifty pairs of males and females heterozygous for both loci were placed in one of the compartments of the population vial and were allowed to reproduce freely and disperse throughout the area. After all compartments were populated and the number of flies stabilized (around 135 individuals), a panmictic population of the same size was founded, practically fully reproducing the gene pool of the evolutionary system. Both populations were kept in a thermostatically controlled carton and maintained under completely identical conditions, such as feeding, lighting, humidity, generation turnover, etc. The system evolved for about

70 generations. As a result of this experiment, the conditions that ensured a low migration rate and relatively random initial allele frequencies in most subpopulations, and local differentiation of allele frequencies at both loci appeared in the system despite completely identical conditions in the subpopulations. In addition, the displacement of one of the alleles of the α -GDH locus occurs, which was most noticeable in the large panmictic population.

To model the experimental dynamics of allele frequencies in the large panmictic population, we used the classic selection model in a population with non-overlapping generations, the coefficients of which were estimated from the experimental data by the least squares method. Furthermore, based on the fact that experimental results one can explain by at least two alternative hypotheses: the adaptive hypothesis, which assumes the presence of disruptive selection, and the fluctuation hypothesis, which assumes purely random drift differentiation. To assess the adequacy of these hypotheses, we used a mathematical model of the dynamics of gene frequencies in a chain of 30 migration-coupled ring populations and analyzed the results of its multiple implementations in a computer model [7].

Results and Conclusion: Based on the results of computer modeling, we can conclude that under disruptive selection, primary genetic divergence in a system of populations connected by stochastic migrations arises with a high probability and proves to be structurally stable. At the same time, comparing the experimental data with the modeling results shows that in the artificial population system constructed by Yu.P. Altukhov and colleagues, the disruptive selection contributed to the primary genetic divergence of populations.

Looking at the ongoing processes more broadly, we can obtain the following generalization. Since hybrid individuals created the original core of the experimental population system, we can assume that during the development of the system, two opposite processes took place in parallel. The first was the formation of gene blocks with increased fitness of heterozygous forms. The process of natural selection here maintained polymorphism of the alleles of these genes. The second process was associated with the segregation of heterozygous forms and the identification of genes characterized by increased fitness of homozygotes and disruptive dynamics of allele frequencies. Both of these processes involved alleles of genes that were adaptively neutral in this experimental system. For various reasons, the main of which is linkage, these neutral alleles turned out to be genetic markers of the corresponding adaptive processes. Thus, the esterase-6 locus turned out to be such a marker for processes aimed at maintaining allele polymorphism, and the α -GDH locus – a marker of disruptive selection occurring in the system and contributing to primary genetic divergence.

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