

PROTEIN POLYMORPHISM ON THE ARTIFICIAL AND NATURAL SELECTIONS:
use of electrophoretical variants of proteins as means to
investigate the process of domestication
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SUMMARY

Comparison of data on the laws of genetical variability in natural populations and populations of agricultural animals shows the absence of essential differencies between them. Variability on the certain set of biochemical markers is supposed to be bound with the specific conditions of selection.

INTRODUCTION

One beleives traditionally that nature populations and populations of agricultural animals differ in the level of latent genetical variability: natural, in spite of their external homogeneity, have the high level, whereas for agricultural, in spite of the external heterogeneity (the huge amount of morphotypes) this level is proposed to be low. The reason for it is found usually in specific tricks of breeding - artificial insemination, assortment, small numbers etc. - but the real investigatios of such problems as: what are the level and range of genetical variability in agricultural animals, what defines the degree of interspecies genetical differentiation, speed and range of new form-developing processes, is in the very beginning now. It can be explained by purely technical reasons - work with such objects as agricultural animals is hard bulky, needs much time and facilities expenses. Just the last time the successes in rapidly developing biochemical genetics make such investigations much easier, giving, for example, the possibility to compare the variability of homological loci in different species without crossing, as the proteins revealed by the electrophoretical methods can be considered as the markers of the corresponding structural genes. In our investigations of breedforming process in sheep (Glazko, 1985) we revealed the positive correlation between the values of genetical distances (the measure of genetical remotness), based on the analysis of phenotype traits (productivity traits) and those based on the analysis of biochemical markers.

In present work we set next problems: 1- to evaluate the level of genetical variability in agricultural species - (sheep, cattle, horses, goats and pig) and 2 - to compare it with the literature data on other animal species under the pressure of natural selections.

MATERIALS AND METHODS.

Purebred and mixed animals of following breeds: sheep - Clun forest, Finn-Landras sheep, Altai fine-wool, Romni-marsh, Lincoln, Romanian; cattle - Black-Patch, Simmentale, Ukrainiar Beef, Brown Carpathian breeds; horses - Orlov's and Russian Trotters; pig - Large White breed were investigated. All the animals were kept in the experimental farms of the Kiev, Lvov and Novosibirsk regions.

Methods of collection of whole blood, separation into plasma, red blood cells and white blood cells, and assay methods using starch electrophoresis for genetic loci have been described by H. Harris and D.A.Hopkinson (1976). Allele frequencies at all loci were estimated by the direct count method.

Genetic variation in each breed was measured as the percentage of loci that were polymorphic and mean heterozygosity.

Each group of animals was investigated on 14-30 systems: Lactate dehydrogenase (EC 1.1.1.27. - LDH), Diaphorase (EC 1.6.4.3. - DIA), Malic enzyme (EC 1.1.1.40 - MOD or ME), Malate dehydrogenase (EC 1.1.1.37. - MOR or MDH), Superoxide dismutase (EC - 1.15.1.1. - SOD), Carbonate dehydratase (4.2.1.1. - CAR), Nucleoside phosphorilase (EC 2.4.2.1. -NP), 6-Phosphogluconic dehydrogenase (EC 1.1.1.43. - 6-PGD), Glucose-6-phosphate dehydrogenase (EC 1.1.1.49 - 6GDP), Aryl- and Carboxylic esterases (EC 3.1.1.1. and 3.1.1.2. - EST), albumin (AL), haemoglobin (HB), transferrin (TF) and some others.

RESULTS

On the analyzing the summary distribution of gene frequencies in purebred animals it's necessary to notice, that each breed has its own, peculiar for its only, distribution pattern of genetical markers. We compare the data obtained for different agricultural species (to determine the percentage of loci that were polymorphic - P, and mean species heterozygosity - H, we used both own and literature data) (Tabl.1).

Table 1. Degree of genetic variability of loci coding biochemical markers in various species of agricultural animals

Species	Number of breeds	P	H
Goats	20	0,03-0,29	0,000-0,050
Swine	203	0,16-0,21	0,028-0,066
Horses	400	0,14-0,40	0,030-0,160
Sheep	603	0,16-0,42	0,073-0,181
Cattle	1100	0,29-0,52	0,069-0,260

As one can see, the level and range of genetical variability do not differ for nature populations of mammals (see Nevo et al., 1984). There are species both with high level and with low one in both groups. The values of M.Nei's genetic distances, calculated on the basis of allelic frequencies of various biochemical markers, between breeds of agricultural animals is within the bounds of amongsts characteristic if geographically isolated populations which diverged long ago. An overall analysis of the genetic variability of biochemical markers for various species of agricultural animals makes it possible to suggest the existence of a definite connection between the degree of a species' genetic variability and the rate of intra-specific processes of development of forms (Table 1). Thus, the least degree of genetic variability (P and H) was found in goats and swine. The greatest degree of genetic variability is characteristic of cattle, which also corresponds to the greatest number of breeds. For horses and sheep the degree of genetic variability also proved to be lower than for cattle.

We compare the portion of proteins with different biochemical functions in mean heterozygosity of natural and agricultural species (Tabl.2).

Table 2. The contribution to mean heterozygosity (mean values by all studied species) of species, supporting in conditions of natural (A) and artificial (B) selections, of the variability of the protein groups with the different biochemical functions: I - the enzymes of the intracellular energy metabolism, taking part in glucose destroying; II - enzymes of exogenous substrate metabolism; III - transport proteins.

Protein groups Species groups	I	II	III
A	0,38	0,23	0,39
B	0,23	0,43	0,34

Comparison was done by the same biochemical markers.

It appeared, that the contribution of variability to the mean heterozygosity of agricultural animals (B) of enzymes: of the intracellular energy metabolism (I) is essentially less; of the exogenous substrate metabolism enzymes (II) is essentially bigger, than their contributions in wild species (B) (Tabl.2).

DISCUSSION

It is known, that phenotype variabilities under conditions of natural and artificial selections have principal distinctions. The range of phenotype changes of domestic species is wider than that of wild species. The phenotype variabilities of domestic species do not lead to new species formation. The domestic species have some common morphological characters, that may be determined as the domestication traits (Bogolubskii, 1959). It allows one to suppose of the presence of common characteristics of general metabolism and genetic-biochemical specificities, distinguishing between domestic and wild species, that are involved to processes of domestications and phenotype variabilities. The need to switch from quantitative evaluation of genetic variability to qualitative identification of the genetic systems subject to variability can be seen especially clearly in comparing genetically determined protein polymorphism in natural populations and among domestic animals. Thus, in comparing genetic variability with respect to biochemical markers for groups of animals kept in conditions of artificial and natural selection, a contradiction is found between well-known differences in phenotypic diversity and similarity in the range of genetic variability in these conditions. The polymorphism of enzymes, metabolized the exogenous substrate, have more part in the general variabilities of domestic, than wild species, but wild species have more variabilities at the enzymes of intracellular energy metabolism. Such analysis will make it possible to discriminate precisely those metabolic links the variability and plasticity of which are most significant for the involvement of animals in the process of domestication, and it can probably be expected that it is precisely these links which are associated with the broad phenotypic variability of domestic animals.

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