The Genetic Determinism of Biochemical Systems Polymorphous From the Blood Serum in Pigs

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Abstract
The study of genetic markers and identification of new markers make the subject of an increasing number of research projects in various fields such as genetics of immunology, biochemical genetics, molecular genetics, quantitative genetics and the genetic amelioration of animals. The information provided by electrophoresis graphs has been used to determine the frequency of various categories of alleles (for the loci of pre-albumin, transferines and serum amylases), the frequency of various phenotypes and the genetic structure for each and every locus and, simultaneously, for the loci being studied. The discussion over the varieties of serum proteins was carried on for the purpose of using them as genetic markers, in order to appreciate the levels of genetic unity or diversity within the stock of swine that has been studied. A pair of simple alleles has been determined for each of the three loci. When the three loci were studied simultaneously, out of the 27 possible combinations, only 15 have been found. The sample studied has found to be genetically balanced for every of the three loci. However, when the simultaneous study has been applied, the same sample has not been found genetically balanced.

Keywords: amylases, combined genotype, genetic polymorphism, pre-albumin, transferines.

1. Introduction

The study of genetic markers and identification of new markers make the subject of an increasing number of research projects in various fields such as genetics of immunology, biochemical genetics, molecular genetics, quantity genetics and the genetic amelioration of animals.
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2. Materials and methods

In order to determine the types of serum proteins, blood samples were collected from 72 individuals of the Syntetic line 345.
The technique of vertical electro-phoresys was employed in order to determine the *transferine* and *pre-albumine* types in the analysed samples, using polyacrylamidae as migration support, the same technique used by Meriaux J.C. [2].
Electrophoresis in starch gel, in a discontinuous system of buffers was employed, in order to emphasize the types of *serum amylases*, as in Smithies [4].

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3. Results and discussion

The locus of serum pre-albumins

Three categories of individuals have been described within the lot and they are as following: homozygous Pa^A/Pa^A, heterozygous Pa^A/Pa^B and homozygous Pa^B/Pa^B .

The heterozygous individuals Pa^A/Pa^B represent approximately one quarter of the sample.

The three genetic categories are genetically determined by the presence, at the serum pre-albumins locus, of two categories of genes, Pa^A and Pa^B (table 1).

Tablel 1. Distribution of gene and genotype categories at serum pre-albumin locus

Genotype categories	N	The ratio of genotype categories	The distribution of gene categories	
			Pa^A	Pa^B
Pa^A/Pa^A	9	12.5	27.1	72.9
Pa^A/Pa^B	21	29.2		
Pa^B/Pa^B	42	58.3		

The locus of serum transferines

The interpretation of electrophoresis graphs for the 72 individuals has detected three categories of individuals: homozygous for gene Tf^A, heterozygous Tf^A/Tf^B and homozygous for gene Tf^B [1].

The presence of the three genotype categories in the lot proves the presence of two categories of genes, Tf^A and Tf^B, identified with different frequency (Table 2).

Table 2. Distribution of gene and genotype categories at serum transferines locus

Genotype categories	N	The ratio of genotype categories	The distribution of gene categories	
			Tf^A	Tf^B
Tf^A/Tf^A	4	5.6	16.7	83.3
Tf^A/Tf^B	16	22.2		
Tf^B/Tf^B	52	72.2		

Locus of serum amylases

The interpretation of electrophoresis graphs led to the identification of three categories of individuals in the sample. They are as following: homozygous Am^A/Am^A, heterozygous Am^A/Am^B and homozygous Am^B/Am^B.

The highest percentage of individuals in the sample was homozygous Am^B/Am^B. The heterozygous Am^A/Am^B represents a quarter of it. After calculating the frequency of the genes categories, the gene Am^A seems to be expressed at a very low frequency (Table 3).

Table 3. Distribution of gene and genotype categories at serum amylases locus

Genotype categories	N	The ratio of genotype categories	The distribution of gene categories	
			Am^A	Am^B
Am^A/Am^A	3	4.2	16	84
Am^A/Am^B	17	23.7		
Am^B/Am^B	52	72.1		

Determining the ratios of the genotype categories and, as a result, the genetic structure of the sample in this study allowed building an estimate for the state of genetic equilibrium, for each of the three loci analyzed. The results are presented in Table 4.

The analysis of genetic equilibrium was made using χ^2 test [5], and it led to the conclusion that the studied sample express genetic equilibrium for each of the three loci.

Table 4. The estimate of genetic equilibrium

Genotypes	Nr. of genotypes observed	Nr. of genotypes expected	d^2/A
Serum pre-albumins locus			
Pa^A/ Pa^A	9	5.288	2.606
Pa^A/ Pa^B	21	28.448	1.95
Pa^B/Pa^B	42	38.264	0.365
Total	72	72	$\chi 2 = 4.921$
Serum transferine locus			
Tf^A/ Tf^A	4	2.008	1.976
Tf^A/ Tf^B	16	20.032	0.811
Tf^B/ Tf^B	52	49.960	0.083
Total	72	72	$\chi^2 = 2.870$
Serum amylases locus			
Am^A /Am^A	3	1.843	0.726
Am^A /Am^B	17	19.354	0.286
Am^B /Am^B	52	50.803	0.028
Total	72	72	$\chi^2 = 1.040$

The analysis of combined genotypes at the loci of pre-albumins, transferines and serum amylases.

The simultaneous study of the three loci corresponding to the three types of serum proteins shows differences in the ratio of participation of the genetic categories in the genetic structure (figure 1).

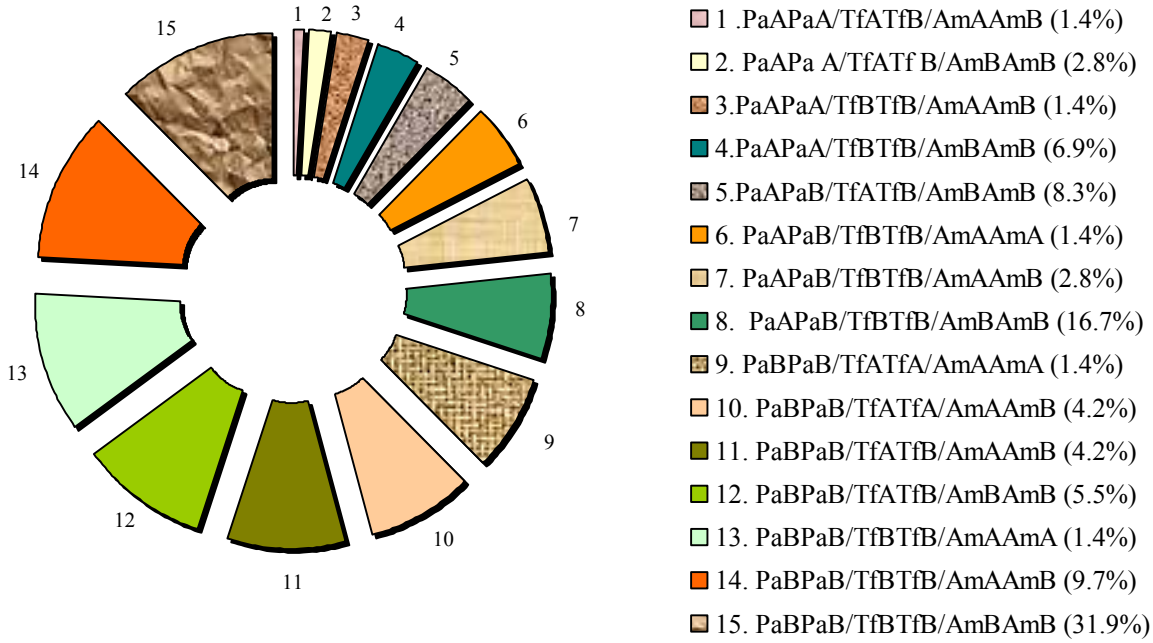

Figure 1. The distribution of the categories of combined genotypes (%)

The highest ratio was expressed by the individuals with the genotype combination $Pa^BPa^B/Tf^BTf^B/Am^BAm^B$, that represent about a third of the population studied. On the second place regarding the ratio of participation in the genetic structure, are the individuals expressing the pre-albumins AB, transferine B and amylases B (16.70%). This comes as a consequence of the high frequency of the homozygote individuals Tf^BTf^B at the locus of serum transferine and homozygote for gene Am^B at the amylases locus. The high frequency of gene Pa^B – described for this sample – also contributed to the ratio of this

category in the genetic structure of the population.

The least ratio of participation (1.40%) was recorded by the individuals that expressed at least an A type for one of the three serum proteins, $\mathbf{Pa^APa^A}/Tf^ATf^B/Am^AAm^B$,$\mathbf{Pa^APa^A}/Tf^BTf^B/Am^AAm^B$,$Pa^APa^B/Tf^BTf^B/\mathbf{Am^AAm^A}$,$Pa^BPa^B/\mathbf{Tf^ATf^A/Am^AAm^A}$ şi $Pa^BPa^B/Tf^BTf^B/\mathbf{Am^AAm^A}$, respectively.

The determination of the genetic structure allowed the estimate for the genetic equilibrium for the Synthetic Line 345 lot. The twenty-seven categories of possible genetic combinations have been lined up to form a matrix with three rows and nine columns, having the following structure [6]:

$$G=\begin{bmatrix} G_{11} & G_{12} & G_{13} & G_{14} & G_{15} & G_{16} & G_{17} & G_{18} & G_{19} \\ G_{21} & G_{22} & G_{23} & G_{24} & G_{25} & G_{26} & G_{27} & G_{28} & G_{29} \\ G_{31} & G_{32} & G_{33} & G_{34} & G_{35} & G_{36} & G_{37} & G_{38} & G_{39} \end{bmatrix}$$

And when replaced with actual values:

$$G=\begin{bmatrix} 0 & 0 & 0 & 0 & 0.014 & 0.028 & 0 & 0.014 & 0.069 \\ 0 & 0 & 0 & 0 & 0 & 0.083 & 0.014 & 0.028 & 0.167 \\ 0.014 & 0.042 & 0 & 0 & 0.042 & 0.055 & 0.014 & 0.097 & 0.319 \end{bmatrix}$$

For each locus, at the population level, there are three possible categories of genotypes, enforced by the existence of a pair of simple alleles for each locus.

$Pa^ATf^AAm^A$ $Pa^ATf^AAm^B$
$Pa^BTf^AAm^A$ $Pa^BTf^AAm^B$

This means that, at population level, considering the categories of genotype combinations previously presented, the following categories of gametes are possible [3]:

$Pa^ATf^BAm^A$ $Pa^ATf^BAm^B$
$Pa^BTf^BAm^A$ $Pa^BTf^BAm^B$

Knowing the frequencies of the categories of genotypes we could calculate the gametes pool of the population.

As in the case of genotype categories, the gametes categories were lined up to form a matrix with two rows and four columns, as following:

$$g=\begin{bmatrix} g_{11} & g_{13} & g_{17} & g_{19} \\ g_{31} & g_{33} & g_{37} & g_{39} \end{bmatrix} \text{ and with values } g=\begin{bmatrix} 0.004 & 0.038 & 0.024 & 0.205 \\ 0.045 & 0.080 & 0.087 & 0.517 \end{bmatrix}$$

The condition for equilibrium is met when :

$$g_{11} \text{ x } g_{33} \text{ x } g_{17} \text{ x } g_{39} = g_{31} \text{ x } g_{13} \text{ x } g_{37} \text{ x } g_{19}$$

For the studied case, the condition of equilibrium is not met because:

$$0.004 \text{ x } 0.080 \text{ x } 0.024 \text{ x } 0.517 = 0.045 \text{ x } 0.038 \text{ x } 0.087 \text{ x } 0.205$$

$$0.000004 \neq 0.000030$$

It is to be remarked that, for the studied sample, even though for the three loci taken separately, the condition of equilibrium has been met, when working with combined genotypes (pre-albumins, transferines, and amylases) this condition is not achieved.

4. Conclusions

1.At the locus of serum pre-albumins three genotype categories have been identified, Pa^APa^A, Pa^APa^B and Pa^BPa^B. They are controlled by two categories of genes Pa^A and Pa^B.

2.At the locus of serum transferines we have identified a pair of simple alleles: Tf^A and Tf^B. The two gene categories can translate into three types of genotypes Tf^ATf^A, Tf^ATf^B and Tf^BTf^B.

3.At the locus of serum amylases, the two gene categories (Am^A and Am^B) lead to three categories of genotypes Am^A/Am^A, Am^A/Am^B and Am^B/Am^B.

4.Out of the 27 possible genotype combinations that can occur at the three loci, only 15 have been identified in the studied sample. Amongst the missing genotypes we counted the homozygous genotypes Pa^APa^A, Tf^ATf^A sau Am^AAm^A.
5.The sample studied has found to be genetically balanced for every of the three loci. However, when the simultaneous study has been applied, the same sample has not been found genetically balanced.

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