

## GENETIC PARAMETERS ASSESEMENT IN A ROMANIAN SWINE POPULATION

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### ABSTRACT

The genetic structure of a population is described by the number of the genotype categories and their frequencies. Regarding the productive characters, being involved a large number of genes with an additive effect, the describing of the genetic structure becomes difficult because it is possible to determine each gene category frequency and the genotype presents a very large reaction field that could not allow the sharing of the phenotypes in perfect distinct classes.

That is why for such features, the describing of the genetic structure of a population is made with the aid of the genetic parameters: heritability, repeatability and genotypic correlations.

Due to the fact that the genetic structure of a population modifies from a generation to other one, it is absolutely necessary to asses the genetic parameter of each generation.

Thus, the aim of our study is to asses the genetic parameter of a L.S.-345 Peris swine population, obtained by testing their own performances, being known their importance for the selection process of the reproductive individuals.

**Keywords:** boar, genetic parameters, heritability, biometric, variance, slight of lean

### INTRODUCTION

For animal breeding, the knowledge of the genetic parameters has a major importance, because they are necessary for giving the priority to the genetic breeding or global animal production increasing, choosing the breeding system, establishing the selection objective and setting up the breeding program.

The correlation between different characters shows indications on the selection range of a character and if it is correct or incorrect these two or more characters be in the same time the breeding objective.

The correlation could be:

- phenotypic, established by the values carried out by quantitative measures;
- genotypic, established by additive variance value;
- Environmental, the environmental factors could influence in the same direction or in different ones, two or more characters.

We know that genetic parameters and the economic values represent an important stage of an animal breeding program setting up and the fact that the consumers prefer a high quality meat, so the swine breeding efficiency depends on it, in this study we wish to give our contribution in the breeding work of a swine population.

## MATERIALS AND METHODS

The population of L.S.-345 Peris is a paternal line of swine, created in a Romanian Research Institute and it represents one of the using ways of pigs' genetic diversity along the whole world, having in view to emphasize the heterozis effect and complementarities between breeds.

In the present, it is used like a genitor population as a terminal sire for obtaining the pig hybrid for the Romanian pork market. The biologic material used in the present study was represented by 1620 tested individuals (young sows and boars) on their own performances, owing to 45 boar families.

For establishing the genetic parameters, there was applied a mix biometric model, a sire model:

$$y_{ijk} = S_i + V_j + e_{ijk}$$

Where:

$y_{ijk}$  = observed performance of k descendent, i sex, owed j boar;

$S_i$  = fixed effect of individual sex;

$V_j$  = compulsory effect of boar;

$e_{ijk}$  = each value error.

The studied characters were:

- the final body weight at the end of testing (carried out by their own growing performances);
- the slight of lean, corrected for 100 kg, carried out by ultrasound device Piglog 105;
- daily average gain (during the whole life);
- age at 100 kg.

Because all the characters were measured on each individual, it was used the canonic transformation of the phenotypic values. For obtaining the observational compounds of genotypic and environmental variances and covariance the results were transformed with the aid of the reverse matrix of the canonic transformation.

The matrix is iterative estimated till it is arrived to convergence. After these, the observational compounds are transferred in causal compounds.

$$V_f = S_F^2 = S_T^2 + S_E^2$$

## RESULTS AND DISCUSSIONS

In table 1 there are presented the average performances of the analyzed population.

**Table 1.** Average performances of the analyzed population

No.	Character	U.M.	N	$\bar{X}$	s	c.v.(%)
1	Body weight at the end of testing	Kg	1623	102,2286±0,1862	7,5024	7,2964
2	Slight of lean (corrected)	mm	1623	11,5946±0,0724	2,9204	25,1880
3	Daily average gain	g	1623	0,5651±0,0010	0,0414	7,3300
4	Age at 100 kg	Days	1623	178,7566±0,2649	10,6738	5,9711

**Table 2.** Presents the observational compounds of variances

Characters / pair of characters	$S_F^2$	%	$S_F^2$	%	$S_F^2$	%
Body weight at the end of testing (A)	63,1695	100	60,5252	95,81	2,6443	4,19
Slight of lean (corrected) (B)	8,5239	100	7,8228	91,68	0,7011	8,32
Daily average gain (C)	26,8055	100	25,6269	95,60	1,1786	4,40
Age at 100 kg (D)	115,5039	100	109,9895	95,23	5,5239	4,77

The observational compounds of the analyzed covariance are presented in table 3.

**Table 3.** Observational compounds of covariances

Couple of characters	$cov_F$	$cov_I$	$cov_i$
<i>Body weight at the end of testing X</i>			
Slight of lean (corrected) 100 Kg	1,8278	0,1940	1,6338
Daily average gain	-0,9493	-0,0403	-0,9090
Age at 100 kg	36,1867	1,7417	34,4450
<i>Slight of lean (corrected) 100 Kg X</i>			
Daily average gain	-0,1472	-0,0114	-0,1357
Age at 100 kg	39,0380	1,8549	37,1831
<i>Daily average gain X</i>			
Age at 100 kg	38,9512	1,8614	37,0899

There were also calculated the values of heritability for the analyzed characters:

**Table 4.** Heritability values of the analyzed characters

Couple of characters	$h^2$	$S_{h^2}$
Body weight at the end of testing (A)	63,1695	100
Slight of lean (corrected) (B)	8,5239	100
Daily average gain (C)	26,8055	100
Age at 100 kg (D)	115,5039	100

Following the data in table three there were analyzed the correlation between the pairs of the studied characters and the results are presented in table5.

**Table 5.** Components

Couple of characters	$r_F$	$Sr_F$	$r_G$	$Sr_G$	$r_e$
<i>Body weight at the end of testing X</i>					
Slight of lean (corrected) 100 Kg	0,0788 <sup>NS</sup>	0,02384	0,1425 <sup>*</sup>	0,07111	0,0662 <sup>NS</sup>
Daily average gain	-0,5958 <sup>***</sup>	0,03138	-0,5781 <sup>***</sup>	0,02861	-0,5986 <sup>***</sup>
Age at 100 kg	0,2918 <sup>**</sup>	0,02090	0,3135 <sup>***</sup>	0,04423	0,2886 <sup>**</sup>
<i>Slight of lean (corrected) 100 Kg X</i>					
Daily average gain	-0,6705 <sup>***</sup>	0,03210	-0,6544 <sup>***</sup>	0,02198	-0,6756 <sup>***</sup>
Age at 100 kg	0,6771 <sup>**</sup>	0,01411	0,5974 <sup>***</sup>	0,02662	0,6936 <sup>***</sup>
<i>Daily average gain X</i>					
Age at 100 kg	0,7000 <sup>***</sup>	0,01360	0,7301 <sup>***</sup>	0,02124	0,6953 <sup>***</sup>

NS = no-nsignificant;

\* = significant differences;

\*\* = distinct significant differences;

\*\*\*= very significant differences;

It could notice that, regarding the genetic correlations, they are very significant for all the studied couples, that denoting the existence of some common genetic mechanisms involved in their determinism, with only one exception, the couple: body weight at the end of testing – slight of lean, where the recorded genetic interdependence is just significant from the statistical point of view.

The phenotypic correlation follows the same trend as the genetic ones, their interdependence being very significant, with the same exception as above. Generally, the genotypic correlation coefficients have values between -0.6705 and 0.7000. Only two of the six phenotypic correlations are negative, the others are significant and positive. From all the correlation, the genotypic correlation is the most important. A comparative study emphasizes the fact that they could not be known upon appearances. Generally, the way that animals are exploited influences very much the genetic value of the individuals. So, it could conclude that their simultaneous breeding is possible and we could introduce both characters in the objectives of the selection.

## CONCLUSIONS

1. The determined values for the analyzed population are typical for a paternal swine population.
2. The high variability coefficient of the character slight of lean shows the fact that in this population there is a high variability for this character, so it could apply a severe selection for its improving.
3. In the analyzed population, the values of the heritability coefficients frame the most characters in the category of the easy heritable ones.
4. The estimated heritability values for the body weight at the end of the testing and the age at 100kg, does not recommend the applying of the selection based on their own performances, being necessary other information sources. It could recommend the applying of the combined selection index.

5. The intense negative correlation between the slight of lean and the daily gain show the fact that in the analyzed population the average gain is realized mainly on the base of muscular tissue growth and less on fat depositing, a specific fact for the paternal population.
6. The genetic positive and significant genetic correlation between the slight of lean and the age at 100 kg, represents a benefit fact, because the improving of the speed of growth and the decreasing of the age realized two important goals: the economic efficiency and the main wish of the consumers and the processors to obtain leaner carcasses.

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