

Genetic parameters in a Swine Population

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Abstract

The estimation of the variance-covariance components is a very important step in animal breeding because these components are necessary for: estimation of the genetic parameters, prediction of the breeding value and design of animal breeding programs.

The estimation of genetic parameters is the first step in the development of a swine breeding program, using artificial insemination.

Various procedures exist for estimation of heritability. There are three major procedures used for estimating heritability: analysis of variance (ANOVA), parents-offspring regression and restricted maximum likelihood (REML). By using ANOVA methodology or regression method it is possible to obtain aberrant values of genetic parameters (negative or over unit value of heritability coefficient, for example) which can not be interpreting because is out of biological limits.

Keywords: animal breeding, genetic correlations, heritability

1. Introduction

The accuracy of variance-covariance components estimation is related with choose of method and model used in data analysis.

There are three major procedures used for estimating heritability: analysis of variance (ANOVA), parents-offspring regression and restricted maximum likelihood (REML). By using ANOVA methodology or regression method it is possible to obtain aberrant values of genetic parameters. In case of regression method it is a must to underline that the value which is in numerator, like any covariance, may be negative and heritability will be negative also. In case of ANOVA methodology, the variance between families is obtain like difference between inter families and residual average square, divided by

average number of descendants per family.

Sometimes, the residual average square is bigger than inter families average square and, in consequences, the heritability will be negative.

These aberrant values of heritability can not be interpreting because is out of biological limits.

They are obtained either in case of existence a reduce biological material numerical point of view, or in situation of using an inadequate model of variance analysis which not describe correct the observation data. Even in case of big samples existence, the genetic parameters can be out of (0; +1) limits for heritability and (-1; +1) limits for correlations.

The scope of this paperwork is to estimate the genetic parameters in a swine population using REML methodology, which give maximum accuracy of estimation.

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2. Materials and methods

The research was made on 125 “LSP 2000” (a swine synthetic line) individuals performances, divided in 15 sire families. The analyzed traits are: live weight at 181 days, average daily gain, back fat depth and age at 100 kilo.

The used method for genetic parameters estimation was REML, developed by Patterson and Thompson in 1971 [1]. Using REML it is possible to taking in account complex models, which permit an accurate describe of observation data. So, with REML we can to take in account some elements ignored by “classical methods” (ANOVA and regression method): the correction of phenotypic values for factors with systematical effects; the overlapping generations; the inbreeding level and selection practiced during generations; the genetic relationships between individuals (other than those considerate by ANOVA) [2, 3].

3. Results and discussion

In table no 1 is presented the value of variance-covariance components for the considerate traits. The results present in table no. 1 show that the residual variance/covariance has the highest weight of total variance/covariance, for all traits. The values of heritability coefficients are presented in table no 2. According to these values, in analyzed sample, “live weight at 181 days” and “average daily gain” are classified in medium

heritable traits group, “back fat depth” is classified in high heritable traits group and “age at 100 kilo” has a low genetic determinism.

For underline the possibility of existence of a common gene pool from polygenic complexes which determinate the analyzed traits, it was determinate the values of phenotypic, genotypic and environmental correlations (traits interrelation). These values are presented in table no 3.

According to data shown in table no 3 it can be observed that “weight at 181 days” is high and positive related with “average daily gain” for all correlation categories. This fact underline that these traits have a high weight of common genes in their polygenic complexes.

Between “weight at 181 days” and “back fat depth” are low and negative correlations and, in consequence, these traits have a small common gene pool.

Between “weight at 181 days” and “age at 100 kilo” it can be observed an algebraic sign difference between phenotypic and genotypic correlations, and genotypic and environmental correlations also. Such algebraic sign difference between genotypic and environmental correlation underline that the genetic and environmental sources of variance affected traits by different physiological mechanisms.

It can be observed a low and negative correlation between “average daily gain” and “back fat depth”. This fact finding to conclude that daily gain is realized basically by virtue of meat, not fat.

Table 1. The observational components of the variance and covariance for considered traits

Traits / traits couple	S_F^2 / cov_F	S_I^2 / cov_I	S_i^2 / cov_i
Live weight at 181 days (A)	26.512	2.253	24.259
Average daily gain (B)	782.750	82.190	700.560
Back fat depth (C)	0.164	0.022	0.142
Age at 100 kilo (D)	189.870	5.221	184.650
AxB	135.912	11.970	123.942
AxC	-0.397	-0.031	-0.428
AxD	3.340	-0.980	4.320
BxC	-3.850	-0.190	-4.040
BxD	-280.780	-7.490	-288.270
CxD	1.143	0.032	0.091

Table 2. The heritability values for considered traits

Trait	$h^2 \pm S_{h^2}$
Live weight at 181 days	0.340 ± 0.29
Average daily gain	0.420 ± 0.33
Back fat depth	0.540 ± 0.37
Age at 100 kilo	0.109 ± 0.21

Table 3. Traits interrelation

Traits couple	$r_F \pm S_{r_F}$	$r_G \pm S_{r_G}$	r_e
AxB	0.940 ± 0.03	0.880 ± 0.13	0.970
AxC	-0.190 ± 0.09	-0.139 ± 0.53	-0.263
AxD	0.047 ± 0.09	-0.280 ± 0.83	0.040
BxC	-0.340 ± 0.08	-0.140 ± 0.46	-0.504
BxD	-0.728 ± 0.09	-0.380 ± 0.74	-0.894
CxD	0.204 ± 0.09	0.094 ± 0.80	0.0065

4. Conclusions

The heritability values classified the analyzed traits in high heritable traits group for “back fat depth”, in medium heritable traits group for “live weight at 181 days” and “average daily gain”, and low heritable traits group for “age at 100 kilo”; “live weight at 181 days” is high and positive related with “average daily gain” and low and negative with “back fat depth”; Between “weight at 181 days” and “age at 100 kilo” it can be observed an algebraic sign difference between phenotypic and genotypic correlations, and genotypic and environmental correlations also;

Between “average daily gain” and “back fat depth” is a low and negative correlation. The heritability and genetic correlation values permit a correct chooses of genetic improvement system and establish the selection criteria.

References

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