

STABILITY OF VARIANCE AND COVARIANCE COMPONENTS FOR REPRODUCTION AND PRODUCTION TRAITS IN YORKSHIRE AND LANDRACE PIGS

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ABSTRACT

The investigation of changes in variance and covariance components is essential to save the time for re-estimating. The total 6477 growing pigs and 5932 litters of sows in Landrace (L00), and 5988 growing pigs and 5579 litters of sows in Yorkshire (Y00) between 2000 and 2007 were used to estimate the variance and covariance components for number born alive (SCS), litter weight at 21 days after birth (P21), days to 90kg (T90) and backfat thickness at 90kg (ML90) by using VCE5 software. When adding 24 months of new data, changes in genetic variances were 2.9 to 27.4% for studied traits in both breeds. Similarly, changes in residual variances were 0.4 to 18.2% accompanied by changes in genetic variances, and therefore the genetic parameters for studied traits had slightly negative trends. However, the spearman rank correlations of estimated breeding values obtained from variance components as new data accumulated over 24 months were still more than 0.99. This study suggests that variance and covariance components for SCS, P21, T90 and ML90 could be used for at least two years before re-estimating.

Key words: Variance components, correlation, production, reproduction traits, pigs

INTRODUCTION

For genetic valuation programs, the maximum accuracy of estimated breeding values is obtained when variance and covariance components reach to their true values (Henderson, 1973). At present, the method of REML (restricted maximum likelihood) allows to estimate variance and covariance with the highest accuracy (Wolf et al, 2001). However, this method consumes so much time and is very complicated. In order to save the computing time, the question raised is that is it necessary to estimate variance and covariance components at every time doing BLUP to get animal breeding values for selection? Or how long do we need to re-estimate variance components for performance traits in pigs? Therefore, the aim of this study is to investigate the change of variance and covariance components over time in Landrace and Yorkshire pigs as new data is accumulated.

MATERIALS AND METHODS

Data: Data sets of reproduction and production traits were obtained in Yorkshire and Landrace

at three pig breeding farms in South Vietnam between 2000 and 2007. The total animals of 6477 in Landrace (L00) and 5988 in Yorkshire (Y00) born were collected on growth and backfat traits, and the total litters of 5932 in Landrace (L00) and 5579 in Yorkshire (Y00) for litter traits. Data sets L12, L24, Y12 and Y24 were derived from L00 and Y00 by deleting data recorded from the most recent 12 and 24 months, respectively. All measurements were adjusted using the recommendations of NSIF (2002) for number born alive (SCS), litter weight (kg) at 21-days (P21), days to 90kg (T90) and backfat thickness (mm) at 90kg liveweight (ML90). The structure of data is indicated as table 1.

Statistical analysis: The genetic parameters were estimated by REML using VCE5 software and the breeding values (EBV) were estimated by BLUP using PEST software (Groeneveld, 2003) by the mixed animal models of (1) and (2), respectively for T90 and ML90, and for SCS and P21.

$$\mathbf{y} = \mathbf{Xb} + \mathbf{Zu} + \mathbf{e} \quad (1)$$

$$\mathbf{y} = \mathbf{Xb} + \mathbf{Zu} + \mathbf{Wpe} + \mathbf{e} \quad (2)$$

Where, y is vector $N \times 1$ of phenotypic observations; b is vector of fixed effects (herd-year-season); u is vector of random effects; pe is

vector of permanent environment; e is vector of random errors; and X, Z, W are matrixes related to vectors of $b, u,$ and pe .

Table 1. Data structure of Yorkshire, Landrace pigs recorded between 2000 and 2007

Measured traits	Number of records					
	Landrace breed			Yorkshire breed		
	L00	L12	L24	Y00	Y12	Y24
SCS, P21	5932	5076	3947	5579	4799	3870
T90, ML90	6477	5083	3792	5988	4825	3853
Measured traits	Population means and standard deviations					
	Landrace breed			Yorkshire breed		
	L00	L12	L24	Y00	Y12	Y24
SCS	9.2 ± 2.2	9.2 ± 2.2	9.2 ± 2.2	9.1 ± 2.4	9.1 ± 2.4	9.0 ± 2.4
P21	61.7 ± 6.9	61.8 ± 6.9	61.7 ± 7.0	60.9 ± 6.7	60.9 ± 6.7	60.5 ± 6.1
T90	178.5 ± 14.2	180.3 ± 15.9	181.2 ± 15.9	181.2 ± 17.3	182.1 ± 17.5	183.4 ± 17.1
ML90	9.8 ± 2.0	9.8 ± 2.1	9.9 ± 2.2	10.4 ± 2.3	10.5 ± 2.4	10.6 ± 2.5

Table 2. Additive genetic variance (σ^2_A), residual variance (σ^2_E) and heritability (h^2) for SCS, P21, T90 and ML90 in Landrace and Yorkshire pigs

Breeds/data sets	SCS			P21		
	σ^2_A	σ^2_E	h^2	σ^2_A	σ^2_E	h^2
1. Landrace						
- L00	0.7469	3.9965	0.140 ± 0.018	5.8779	36.0894	0.135 ± 0.014
- L12	0.7501	4.0066	0.148 ± 0.018	6.3854	36.5463	0.144 ± 0.017
- L24	0.6985	4.0429	0.141 ± 0.022	7.3249	37.4589	0.159 ± 0.020
2. Yorkshire						
- Y00	0.8129	4.7543	0.136 ± 0.008	5.4380	34.3255	0.132 ± 0.017
- Y12	0.8373	4.8536	0.141 ± 0.018	5.8762	34.7525	0.139 ± 0.019
- Y24	0.6916	4.2605	0.136 ± 0.019	5.2799	29.9791	0.147 ± 0.020
Breeds/data sets	T90			ML90		
	σ^2_A	σ^2_E	h^2	σ^2_A	σ^2_E	h^2
1. Landrace						
- L00	59.2054	128.796	0.315 ± 0.022	1.5808	1.2220	0.564 ± 0.019
- L12	73.1782	153.542	0.323 ± 0.023	1.7125	1.3500	0.559 ± 0.028
- L24	75.4629	150.740	0.334 ± 0.025	1.9706	1.4450	0.577 ± 0.023
2. Yorkshire						
- Y00	91.8368	178.325	0.340 ± 0.022	1.4751	1.5533	0.487 ± 0.024
- Y12	99.0950	180.420	0.354 ± 0.024	1.6833	1.6620	0.503 ± 0.026
- Y24	89.9280	179.009	0.334 ± 0.023	1.8481	1.7700	0.511 ± 0.030

Table 3. Additive genetic covariance ($\sigma_A(xy)$) residual covariance ($\sigma_E(xy)$) and genetic correlation (r_G) between SCS-P21, and between T90-ML90

Breeds/data sets	SCS-P21			T90-ML90		
	$\sigma_A(xy)$	$\sigma_E(xy)$	r_G	$\sigma_A(xy)$	$\sigma_E(xy)$	r_G
1. Landrace						
- L00	0.7596	0.6161	0.363 ± 0.096	1.9968	1.3050	0.206 ± 0.060
- L12	0.9028	0.7016	0.413 ± 0.098	2.5167	1.5140	0.225 ± 0.062

- L24	1.3284	1.0223	0.487 ± 0.110	3.6924	1.4500	0.303 ± 0.069
2. Yorkshire						
- Y00	0.3522	0.3458	0.167 ± 0.011	0.8319	2.2920	0.100 ± 0.061
- Y12	0.4779	0.3772	0.216 ± 0.018	1.5181	2.2070	0.118 ± 0.064
- Y24	0.5969	0.3628	0.312 ± 0.020	2.1185	1.7750	0.164 ± 0.066

RESULTS

Variance component changes

As indicated in Table 2, the genetic variances estimated for traits SCS and P21 changed respectively by 0.4 to 6.5% and 8.6 to 24.6% in Landrace, and by 3.0 to 14.3% and 2.9 to 8.1% in Yorkshire. For T90 and ML90, the change of genetic variance was respectively by 23.6 to 27.4% and 8.3 to 25.0% in Landrace, and by 3.7 to 7.9% and 14.1 to 25.2% in Yorkshire. The changes in genetic variance were always accompanied by similar changes in residual variance. Therefore, heritability of measured traits decreased very little along with the time. Maximum changes in estimated heritability over 24 months were 0.003 for SCS, 0.014 for P21, 0.019 for T90 and 0.024 for ML90.

Covariance component changes

Changes in estimated genetic covariance over 24 months were larger than that in genetic variances and very different from trait to trait (table 3). The greatest change was found for genetic covariance of T90 and ML90 by 155% in Yorkshire and the smallest change in this covariance component was 69.5% for the pair of SCS and P21 in Yorkshire. These changes in genetic covariance could be caused by the immigration of new genetics and by the genetic evaluation programs, which may result in increasing the inbreeding rate during the selection (Wolf et al, 2001). In addition, due to finite population size, the randomly genetic drift may occur and influence the genetic variation (Hill, 2000). However, residual covariance also changed similarly to genetic covariance, so genetic correlations for studied trait pairs did not change much in both Yorkshire and Landrace. The change in genetic correlation estimates varied from 0.064 to 0.145 in absolute value.

Rank changes of animals

Spearman rank correlations between breeding values obtained using variance components from L00 and from L12, L24 were 0.978 to 1.000 for measured traits (table 4). Similarly, Spearman rank correlations between breeding values obtained using variance components from Y00 and from Y12, Y24 varied between 0.985 and 0.999. Spearman rank correlations between multi-trait selection indexes based on the sets of L00, L12, L24, Y00, Y12 and Y24 were greater than 0.99. This means that there was nearly no change in the rank of animals based on selection indexes obtained using different variance components from data sets L00, L12 or L24 in Landrace pigs, and from data sets Y00, Y12 or Y24 in Yorkshire breed.

Table 4. Spearman rank correlations between sets of breeding values for SCS, P21, T90 and ML90, and SPI index SPI and TSI index

Traits/ index	L00 - L12	L00 - L24	Y00 - Y12	Y00 - Y24
SCS	0.999	0.986	0.999	0.992
P21	0.999	0.979	0.998	0.989
T90	0.999	0.986	0.995	0.985
ML90	1.000	0.993	0.996	0.991
SPI	0.999	0.991	0.999	0.994
MLI	0.999	0.990	0.999	0.990

CONCLUSIONS

From 2005 to 2007, as new data added, the genetic parameters for studied traits had slightly negative trends. The spearman rank correlations of estimated breeding values obtained from variance components as new data accumulated over 24 months were still more than 0.99. Therefore, this study suggests that variance and covariance components for SCS, P21, T90 and ML90 could be used for at least two years before re-estimating.

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