

## GENETIC ANALYSIS OF PRODUCTION TRAITS IN PIGS MEASURED AT TEST STATIONS

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### ABSTRACT

In this study genetic and phenotypic analysis of the production traits measured at carcass stations in Slovakia from 1997-2007 was carried out. The data from 10636 purebred animals (Large White, Landrace, White Meaty, Yorkshire, Hampshire, Slovak Meaty, Pietrain and Duroc) were used for estimating of (co)variance matrices and genetic parameters. Following productive traits were analyzed: weight of neck, loin, ham, shoulder, percentage of valuable cuts, *longissimus dorsi* muscle area, backfat thickness and average daily gain. Different multivariate animal models were used to estimate genetic parameters (coefficients of heritability and genetic correlations) using VCE programme. The highest heritabilities were estimated for weight of ham ranging from 0.46 to 0.63 according to breed, while the lowest heritabilities were estimated for weight of shoulder ranging from 0.14 to 0.18 according to breed. Estimated heritability for weight of loin varied from 0.24 to 0.26 according to breed and estimated heritability for weight of neck varied from 0.14 to 0.25 according to breed. High genetic correlations were calculated among the traits of detailed carcass dissection (weight of neck, loin, ham and shoulder) and traits currently used in routine genetic evaluation (proportion of trimmed valuable cuts, backfat thickness). Phenotypic correlations among single valuable cuts ranged from 0.10 to 0.68.

**Key words:** pig; test station; genetic parameters; covariance matrices

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### INTRODUCTION

A multivariate animal model with seven traits is used in routine genetic evaluation of pigs in Slovak Republic (Peškovičová et al., 2002). The model includes three traits measured at test station – average daily gain, backfat thickness and proportion of valuable cuts (neck, loin, ham, shoulder). There are few works concerning the genetic analyses of single valuable cuts (neck, loin, ham, shoulder). The heritability values for single cuts vary across the studies. The highest estimates were presented for the weight of ham (0.36 – 0.76; Newcom et al., 2002; Wijk et al., 2005; Fernandez et al., 2003). The estimates for weight of loin ranged from 0.28 to 0.72. Low heritabilities (0.21 – 0.38) were estimated for the weight of shoulder (foreleg). Authors presented the

estimates for *longissimus dorsi* muscle ranging from 0.24 to 0.62. Generally, negative genetic correlations were found among single valuable cuts and backfat thickness (Newcom et al., 2002; Wijk et al., 2005; Chen et al., 2002). Low genetic correlations between single valuable cuts and average daily gain were also noted (Groeneveld et al., 1999; Peškovičová et al., 2002).

The aim of the work was to estimate the genetic and phenotypic parameters for single valuable cuts and *longissimus dorsi* muscle area measured on dissected carcass side and to analyze the relationships among these traits and the traits currently used in the routine genetic evaluation of pigs in Slovakia. The possibilities of including the single valuable cuts in the routine genetic evaluation were also discussed.

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## MATERIAL AND METHODS

### Data

The data from 10636 purebred animals (3 datasets) were used in this study. Dataset 1 included Large White breed (n = 6334), dataset 2 included Landrace and White Meaty breeds (n = 3200), while dataset 3 consisted of Yorkshire, Hampshire, Slovak Meaty, Pietrain and Duroc breeds (n = 1102). Test station data included following traits measured according to the methodology of the performance testing (Anonymous, 1992):

- Neck, loin, ham, shoulder – weights of single trimmed valuable cuts (in kg),
- VC – total proportion of trimmed valuable cuts (neck, loin, ham, shoulder) in the carcass side at a live weight of 100 kg on station (in %),
- MLD – *longissimus dorsi* muscle area (in cm<sup>2</sup>),
- BFT – ultrasonically measured backfat thickness on the carcass (in cm),
- ADG – average daily gain in the test station (from 30 to 100 kg live weight) with linear adjustment for weight at the beginning and at the end of test (in g/day),
- CSW – carcass side weight (in kg).

Data were collected during the period from 1997 to 2007 in the database of Breeding Services of the Slovak Republic. Considering data on dataset 1 progeny from 794 boars and 2858 sows were included. Average number of piglets per boar was 7.6 and average number of piglets per sow was 2.1. Considering data on dataset 2 progeny from 412 boars and 1425 sows were included. Average number of piglets per boar was 7.2 and average number of piglets per sow was 2.1. Dataset 3 comprised progeny from 177 boars and 533 sows. Average number of piglets per boar was 5.7 and average number of piglets per sow was 1.9.

### Statistical Model

Due to relatively small datasets (dataset 2 and 3) it was not possible to run only 1 multiple animal model for all traits studied. High number of traits and effects included in the model resulted in over-parametrized model and problems with convergence of the system of mixed model equations.

The four trait animal model was used for estimation of covariance matrices for single valuable cuts and MLD area (Peškovičová et al., 2002). This included valuable cut, percentage of valuable cuts, backfat thickness and average daily gain. The three trait animal model was used for estimation of covariance matrices for percentage of valuable cuts, average daily gain and backfat thickness. Five-trait (dataset 1 and 3) and two-trait (dataset 2) animal models were used for estimation of covariances and correlations between single valuable cuts (including MLD area). All animal models included random effects of breed (dataset 2 and 3), herd, litter and stys (station-year-season). The VCE-5 package was employed for the estimation of genetic analyses (Kovač et al., 2002).

## RESULTS AND DISCUSSION

Basic statistics of studied traits are given in Table 1. The average weight of neck and loin varied from 3.14 to 3.25 and from 4.76 to 4.98, respectively. The higher average weight of ham in the dataset 3 reflected high selection pressure for meat traits in sire breeds. The same trend was observed when comparing the average MLD area and proportion of valuable cuts. On the other hand, breeding focused on lean meat percentage led to reduction of backfat thickness, therefore the lowest average BFT was observed in the dataset 3.

**Table 1: Basic Statistics**

Variable	Dataset 1 (n = 6334)		Dataset 2 (n = 3200)		Dataset 3 (n = 1102)	
	Mean	SD.	Mean	SD.	Mean	SD.
NECK, kg	3.15	0.231	3.14	0.222	3.25	0.275
LOIN, kg	4.76	0.372	4.85	0.384	4.98	0.458
HAM, kg	8.72	0.602	8.76	0.616	9.44	0.850
SHOULDER, kg	4.78	0.396	4.79	0.386	4.96	0.494
MLD, cm <sup>2</sup>	47.46	5.989	48.24	5.887	53.84	8.073
VC, %	53.48	2.602	53.77	2.696	56.65	3.474
BFT, cm	1.72	0.33	1.63	0.328	1.47	0.354
ADG, g/day	792	104.51	807	109.22	806	100.86
CSW, kg	40.04	1.432	40.06	1.441	39.94	1.428
Number of tested boars	794		412		177	
Number of tested sows	2858		1425		533	
Average number of progeny per boar	7.6		7.2		5.7	

### Heritability

Heritability values for test station traits are given in Table 2. Variance ratios for random effects included in the model are shown in Tables 3, 4 and 5. The heritabilities estimated in our study were in agreement with estimates of ham (0.57), loin (0.51) and shoulder (0.21) reported by Newcom et al. (2002) in station test with Yorkshire and Duroc pigs. Wijk et al. (2005) reported similar heritabilities for proportion of lean meat (0.43), ham (0.40) and loin (0.29) in commercial crossbred line. Fernandez et al. (2003) reported lower heritability estimates for weight of ham (0.36) and loin (0.28) but higher heritability estimates for foreleg (0.41). Higher heritability estimates for MLD area from 0.45 to 0.62 were presented by Suzuki et al. (2005) in Duroc pigs, Hoque et al. (2009) and Newcom et al. (2002). Johnson et al. (1999) in dataset of Large White boars, Chen et al. (2002) in dataset of Yorkshire, Duroc, Hampshire

and Landrace pigs and Johnson and Nugent (2003) in Landrace, Yorkshire, Duroc and Hampshire breeds estimated similar heritability coefficients for MLD area.

Heritability estimate for backfat thickness is varying across the studies. Newcom et al. (2002) reported heritability for BFT 0.40. Similar heritabilities were reported by Johnson and Nugent (2003; 0.32 – 0.47), Chen et al. (2002; 0.48 – 0.49), Johnson et al. (1999; 0.36), Groeneveld et al. (1999; 0.28 – 0.38) and Peškovičová et al. (2001; 0.39 – 0.50). Higher estimates were presented by Imboonta et al. (2007; 0.61), Suzuki et al. (2005; 0.72) and Peškovičová et al. (2002; 0.58). In our study heritability estimates for backfat thickness ranged from 0.46 to 0.53.

Heritability estimates for average daily gain vary from 0.19 to 0.47 across the breeds. In our study heritability for ADG were low (0.13 to 0.23) and did not exceed the values of estimates reported by Peškovičová et al. (2001) ranging from 0.28 to 0.42.

**Table2: Heritabilities (on the diagonal), genetic correlations (above the diagonal) and phenotypic correlations (below the diagonal)**

Variable	NECK	LOIN	HAM	SHOULDER	MLD	VC	BFT	ADG
NECK	<b>0.16<sup>a</sup></b>	0.72	0.66	0.71	0.61	0.77	-0.65	-0.03
	<b>0.14<sup>b</sup></b>	0.82	0.58	0.74	0.56	0.78	-0.82	-0.16
	<b>0.25<sup>c</sup></b>	0.90	0.64	0.72	0.69	0.74	-0.61	0.35
LOIN	0.41	<b>0.36</b>	0.76	0.80	0.93	0.88	-0.77	0.05
	0.33	<b>0.42</b>	0.81	0.79	0.84	0.93	-0.71	-0.20
	0.48	<b>0.24</b>	0.89	0.70	0.99	0.99	-0.91	-0.07
HAM	0.46	0.65	<b>0.46</b>	0.95	0.83	0.96	-0.86	0.09
	0.46	0.61	<b>0.57</b>	0.84	0.85	0.96	-0.81	-0.15
	0.53	0.68	<b>0.63</b>	0.71	0.89	0.97	-0.90	-0.33
SHOULDER	0.10	0.62	0.57	<b>0.14</b>	0.85	0.96	-0.86	-0.01
	0.21	0.66	0.62	<b>0.15</b>	0.90	0.91	-0.75	-0.41
	0.11	0.59	0.58	<b>0.18</b>	0.61	0.80	-0.99	-0.30
MLD	0.33	0.30	0.39	0.11	<b>0.21</b>	0.89	-0.73	0.05
	0.34	0.31	0.45	0.25	<b>0.23</b>	0.88	-0.84	-0.17
	0.30	0.39	0.58	0.36	<b>0.24</b>	0.98	-0.92	-0.24
VC	0.37	0.66	0.77	0.62	0.37	<b>0.49</b>	-0.89	0.05
	0.36	0.65	0.77	0.67	0.41	<b>0.60</b>	-0.84	-0.23
	0.47	0.72	0.85	0.67	0.60	<b>0.54</b>	-0.91	-0.13
BFT	-0.30	-0.36	-0.54	-0.33	-0.42	-0.66	<b>0.46</b>	-0.10
	-0.32	-0.39	-0.54	-0.38	-0.42	-0.66	<b>0.53</b>	-0.02
	-0.33	-0.53	-0.64	-0.49	-0.55	-0.77	<b>0.53</b>	0.35
ADG	-0.12	-0.15	-0.13	-0.07	0.01	-0.16	0.14	<b>0.22</b>
	-0.02	-0.09	-0.02	-0.03	0.03	-0.10	0.09	<b>0.23</b>
	-0.14	-0.13	-0.08	-0.02	0.02	-0.11	0.18	<b>0.13</b>

<sup>a</sup> – dataset 1, <sup>b</sup> – dataset 2, <sup>c</sup> – dataset 3

The lowest standard errors of heritabilities were estimated in dataset 1 (0.007 – 0.029) and the highest in dataset 3 (0.047 – 0.088), with intermediate error values in dataset 2 (0.011 – 0.045).

The low variance ratios were estimated for litter and herd effects (Tables 3, 4 and 5). Johnson and Nugent (2003) reported estimates for common environmental litter effects for MLD area (0.09 – 0.15) and BFT (0.08 – 0.10). Peškovičová et al. (2001) reported variance ratios for litter: 0.19 – 0.25 (ADG), 0.02 – 0.03 (VC), 0.00 – 0.05 (BFT) and for effect of herd-year-season: 0.14 – 0.16 (ADG), 0.14 – 0.20 (VC) and 0.10 – 0.25 (BFT). The variance ratios were estimated in all datasets for calculating the effect of station-year-season. High STYS effect was observed for weight of shoulder and neck. This can be due to differential dissection of these parts and the effect of technician should be involved in the model. Some distinctions in the methodology application of neck and loin dissection were found during the testing period. Therefore the STYS also affected the weight of these valuable cuts.

**Table 3: Variance ratios (dataset 1 – Large White)**

Variable	litter	herd	stys	residual
NECK	0.07	0.01	0.40	0.36
LOIN	0.10	0.02	0.20	0.33
HAM	0.07	0.03	0.14	0.30
SHOULDER	0.06	0.01	0.58	0.22
MLD	0.15	0.02	0.34	0.27
VC	0.06	0.03	0.16	0.27
BFT	0.09	0.04	0.13	0.29
ADG	0.20	0.04	0.16	0.36

**Table 4: Variance ratios (dataset 2 – Landrace, White Meaty)**

Variable	litter	herd	stys	residual
NECK	0.07	0.02	0.36	0.41
LOIN	0.07	0.08	0.10	0.33
HAM	0.06	0.08	0.06	0.23
SHOULDER	0.04	0.02	0.56	0.24
MLD	0.16	0.14	0.14	0.33
VC	0.03	0.10	0.06	0.22
BFT	0.04	0.11	0.06	0.26
ADG	0.21	0.08	0.10	0.38

**Table 5: Variance ratios (dataset 3 – sire breeds)**

Variable	litter	herd	stys	residual
NECK	0.05	0.17	0.21	0.31
LOIN	0.12	0.13	0.10	0.41
HAM	0.02	0.06	0.10	0.18
SHOULDER	0.11	0.23	0.32	0.16
MLD	0.23	0.09	0.18	0.25
VC	0.001	0.12	0.14	0.20
BFT	0.04	0.07	0.11	0.25
ADG	0.33	0.09	0.16	0.29

### Genetic correlations

The genetic correlations are summarized in Table 2. The high positive correlations were calculated between valuable cuts percentage and single valuable cuts (0.74 – 0.99). These results are in agreement with statements of Wijk et al. (2005). High negative genetic correlations were calculated between backfat thickness and single valuable cuts including MLD area ranging from -0.61 to -0.99. These correlations were slightly higher than correlations presented by Newcom et al. (2002; -0.51 to -0.60). Wijk et al. (2005) reported genetic correlations between backfat and boneless primal cuts ranging from -0.60 to -0.86. Chen et al. (2002) reported genetic correlation between BFT and MLD area ranging from -0.35 to -0.45. Similar genetic correlation between BFT and MLD (-0.44) was noted by Hoque et al. (2009). The low correlations were found between ADG and single valuable cuts in dataset 1 (-0.03 – 0.09). Higher negative correlations were calculated in dataset 2 (-0.16 to -0.41). Also, negative correlations were noted in dataset 3 (-0.07 to -0.33) except for that between neck and ADG (0.35). These findings were similar to presented results of Wijk et al. (2005). Low genetic correlations between percentage of valuable cuts and ADG were in agreement with those presented in various studies (Groeneveld et al. (1999; Peškovičová et al., 2002).

High correlations were estimated between neck and other valuable cuts (0.56 – 0.90). Higher correlations were calculated between loin and other valuable cuts ranging from 0.72 to 0.99. Correlations between ham and other valuable cuts varied from 0.58 to 0.95. Correlations between shoulder and other valuable cuts ranged from 0.61 to 0.95. Fernandez et al. (2003) reported lower genetic correlations between loin and ham (0.68), loin and foreleg (0.50) and ham and foreleg (0.77) in group of castrated Iberian pig males.

### Phenotypic correlations

Phenotypic correlations are shown in Table 2. The correlations between valuable cuts ranged from 0.10 to 0.68 and were at high level of statistical significance ( $P < 0.001$ ). Fernandez et al. (2003) reported phenotypic correlations between ham and foreleg (0.36), ham and loin (0.24) and foreleg and loin (0.15). Weight of loin, ham and shoulder were highly correlated to portion of valuable cuts. These correlations varied from 0.62 to 0.85 and were statistically highly significant. The highest was the correlation between ham and VC. Phenotypic correlation between neck and VC was lower, ranging from 0.36 to 0.47. Correlations between MLD area and VC ranged from 0.37 to 0.60. The lowest value was observed in dataset 1, while the highest value was observed in dataset 3. Valuable cuts were negatively correlated ( $P < 0.001$ ) to backfat thickness (-0.30 to -0.64). Correlation between MLD area and BFT ranged from -0.42 to -0.55 ( $P < 0.001$ ) and are in agreement with findings of Chen et al. (2002; -0.38 to -0.47). Low negative correlations were calculated between ADG and valuable cuts including MLD area.

High genetic and phenotypic correlations between weight of single valuable cuts and proportion of valuable cuts showed that routinely used model involving proportion of valuable cuts is sufficient for routine genetic evaluation. If the situation is changed, e.g. breeding focused at ham production is prioritized then the weight of this part will be preferred in animal model.

### CONCLUSION

The heritabilities for weight of neck and shoulder were lower than heritabilities for loin and ham. The heritability estimates varied according to breed as well. The higher estimates in the dataset of sire breeds reflected high selection pressure for production characteristics in these populations. Genetic correlations between single valuable cuts and backfat thickness and average daily gain were negative. No need for replacing the proportion of valuable cuts with weights of single cuts in animal models for routine genetic evaluation was indicated.

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