



Phenotypic and genetic analysis of carcass quality of different breeds' fatlings

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ABSTRACT

Dissection and quantitative-genetic analysis of carcass quality was performed on 318 fatlings of 5 different pig breeds: German, Dutch and Belgian Landrace, Yorkshire and Hampshire. Significant fixed effects (sex and genotype) and regression effects (age and body weight at slaughter) were fitted in the statistical model. Genetic parameters were estimated using the restricted maximum likelihood (REML) procedure based on an animal model with multivariate analyses. Heritability estimates for carcass traits were moderate to high except for back weight and neck weight. Among most of the carcass quality traits, the midrange strong and very strong positive genetic and phenotypic correlations were established. The traits that were analyzed showed sufficient genetic variation, indicating that their improvement is possible through genetic selection. Genetic variability was stable and expressed and justified further genetic changes in the desired direction.

Key words: Carcass quality, Fatlings, Genetic and phenotypic correlations, Heritability

Carcass and meat quality traits are of increasing relevance for the pig industry. This has led to the development of breeding objectives that includes pork quality traits with increasing muscle tissue and decreasing fat as two major objectives of breeding programs (Jiang *et al.* 2012, Newcom *et al.* 2004). As a result, dramatic improvements in body composition of pigs have been made through genetic selection (Latorre *et al.* 2008). Furthermore, because of consumer and industry demands for more uniform and higher quality meat, interest in improving meat quality traits is growing (Dransfield *et al.* 2005, Ngapo *et al.* 2007).

Pork quality and carcass characteristics are now being integrated into swine breeding objectives because of their economic value. Understanding the genetic basis for these traits is necessary for this to be accomplished (Dube *et al.* 2013, Miar *et al.* 2014). Genetic improvement of meat and carcass quality in swine breeding program requires estimating the genetic and phenotypic parameters of these traits. Estimates of heritabilities for carcass characteristics and genetic correlations between these economically important traits are limited but have received attention recently. Meat quality traits are low to moderately heritable while carcass composition traits are highly heritable (Ciobanu *et al.* 2011, Dube *et al.* 2013, Miar *et al.* 2014)

Given the importance of the carcasses quality of fatlings, the objectives of this research was: (a) dissection to determine the share of major carcass parts in specialized breed Landrace, Yorkshire and Hampshire, (b) to estimate heritability for various share of major carcass parts and (c) to estimate phenotypic and genetic correlations between share of major carcass parts.

MATERIALS AND METHODS

Dissection and quantitative-genetic analysis of carcass quality was performed on 318 fatlings produced on commercial farms within five different breeds: German Landrace – GL (57 fatlings), Dutch Landrace – DL (69 fatlings), Belgian Landrace – BL (59 fatlings), Yorkshire - Y (59 fatlings) and Hampshire – H (77 fatlings). After 24 h of cooling, weight of cold carcass (CCW) was measured and carcass quality was determined by partial dissection (Commission Regulation (EC) No 3127/94, 1994) which are explained in detail by Walstra and Merkus (1994). The carcass quality traits analyzed were: slaughter age (SA), slaughter weight (SW), hot carcass weight (HCW), cold carcass weight (CCW), carcass length (CL), chop length (CHL), head weight (HEW), lard weight (LW), *Musculus longissimus dorsi* area (MLDA), back weight (BW), neck weight (NW), ham weight (HW), ribs weight (RW), shoulder weight (SHW), share of meat in the carcass (SMC), share of fat in the carcass (SFC), share of bone in the carcass (SBC), less valuable parts in the carcass (LVC).

The significance of the fixed effects and inclusion in the models were determined for each trait using the general

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Table 1. Significance of the fixed, regression and random effect included in model for the analysis of carcass quality

Traits	Fixed effects		Regression effects		Random effects		
	Sex	Breed	Weight	Age	Dam	Sire	Animal
HCW, kg	NS	**	**	*	*	**	— ¹
CCW, kg	NS	**	**	**	*	**	— ¹
CL, cm	NS	NS	**	NS	**	**	— ¹
CHL, cm	NS	**	NS	NS	**	**	— ¹
HEW, kg	NS	**	*	**	**	**	— ¹
LW, kg	**	**	NS	**	*	**	— ¹
MLDA, cm ²	**	**	*	**	**	**	— ¹
BW, kg	NS	NS	**	NS	*	*	— ¹
NW, kg	**	**	**	NS	NS	*	— ¹
HW, kg	NS	NS	**	**	**	**	— ¹
RW, kg	**	NS	**	**	NS	**	— ¹
SHW, kg	NS	**	**	*	**	**	— ¹
SMC, kg	**	**	**	**	**	**	— ¹
SFC, kg	**	NS	**	**	*	**	— ¹
SBC, kg	**	**	**	NS	**	**	— ¹
LVC, kg	NS	NS	**	*	NS	**	— ¹

* P < 0.05; ** P < 0.01; NS, not significant.

linear model (GLM) procedures in software package Statistica 12. Table 1 shows the fixed, regression and random factors included in the final analyses for each trait. Genetic parameters, including variance components and ratios, were estimated using the restricted maximum likelihood (REML) procedure based on an animal model using the Wombat program (Meyer 2007) with multivariate analyses. To estimate genetic parameters, the model

constructed was:

$$Y_{ijklmn} = \mu + A_i + F_j + D_k + B_l + S_m + b_1(X - \bar{X}) + b_2(Y - \bar{Y}) + e_{ijklmn}$$

where Y_{ijklmn} , phenotypic values of traits; μ , average mean; A_i , random influence of animal; F_j , random influence of sire; D_k , random influence of dam; B_l , fixed influence of breed; S_m , fixed influence of sex; b_1 , regression influence of age at slaughter; b_2 , regression influence of body weight at slaughter; e_{ijklmn} , random error.

RESULTS AND DISCUSSION

The average weight (Table 2) at slaughter (SW) ranged from 101 kg in GL and DL to 104 kg in H fatlings. The lowest average weight of hot (HCW) and cold (CCW) carcass had GL (79.84 and 78.19 kg, respectively) and DL (79.14 and 77.90 kg, respectively), while the largest weight of hot and cold carcass had the BL (82.89 and 81.63 kg, respectively) and H (82.63 and 81.34 kg, respectively).

The shares of some parts of the carcass did not differ significantly between the 5 genotypes. The most important and largest part of the carcass was ham (HW) followed by shoulder (SHW), ribs (RW), back (BW), neck (NW) and head (HEW). Weight lard (LW) in all fattening pigs was less than 1 kg, and (MLDA) ranged from 34.44 (DL) to 41 cm² (BL and H).

Genetics parameters for carcass quality are shown in Table 3. Heritability estimates for carcass traits were moderate to high for HEW. Carcass traits generally have been reported as moderate to high heritable traits in previous studies. The estimated heritabilities of these traits were moderate or high indicating great opportunities to improve

Table 2. Least-squares means (LSM) and standard errors of the means (SE_{LSm}) share of major carcass parts

Traits	German landrace		Dutch landrace		Belgian landrace		Yorkshire		Hempshire	
	LSM	SE _{LSm}	LSM	SE _{LSm}	LSM	SE _{LSm}	LSM	SE _{LSm}	LSM	SE _{LSm}
SA, days	197	195	200	190	184					
SW, kg	101.75	0.79	101.21	0.72	103.30	0.80	102.47	0.78	104.68	0.68
HCW, kg	79.84	0.64	79.14	0.58	82.89	0.65	80.94	0.63	82.63	0.55
CCW, kg	78.19	0.67	77.90	0.61	81.63	0.68	79.85	0.66	81.34	0.58
CL, cm	97.64	0.35	96.86	0.32	96.22	0.36	96.16	0.35	97.18	0.30
CHL, cm	55.33	0.43	53.93	0.39	53.49	0.43	43.48	0.42	53.19	0.37
HEW, kg	2.86	0.03	2.91	0.03	2.79	0.03	3.03	0.03	3.01	0.03
LW, kg	0.92	0.03	0.97	0.02	0.90	0.03	0.76	0.03	0.79	0.02
MLDA, cm ²	39.48	0.70	34.44	0.63	41.06	0.70	38.78	0.69	41.01	0.60
BW, kg	6.50	0.07	6.40	0.06	6.73	0.07	6.48	0.07	6.68	0.06
NW, kg	3.13	0.04	3.10	0.04	3.21	0.04	3.24	0.04	3.34	0.04
HW, kg	11.54	0.09	11.38	0.09	12.27	0.10	11.60	0.09	11.78	0.08
RW, kg	6.74	0.08	6.68	0.07	6.64	0.08	6.81	0.08	6.87	0.07
SHW, kg	6.50	0.08	6.60	0.07	6.93	0.08	7.06	0.08	7.14	0.07
SMC, kg	22.15	0.21	20.72	0.19	23.12	0.21	22.27	0.21	23.07	0.18
SFC, kg	10.63	0.20	11.86	0.18	10.72	0.20	11.05	0.20	10.76	0.17
SBC, kg	3.57	0.04	3.61	0.03	3.80	0.04	3.77	0.04	3.87	0.03
LVC, kg	2.68	0.03	2.71	0.02	2.64	0.03	2.71	0.02	2.74	0.02

¹SA, Slaughter to age; SW, slaughter to weight; HCW, hot carcass weight; CCW, cold carcass weight; CL, carcass length; CHL, chop length; HEW, head weight; LW, lard weight; MLDA, *Musculus longissimus dorsi* area; BW, back weight; NW, neck weight; HW, ham weight; RW, ribs weight; SHW, shoulder weight; SMC, share of meat in the carcass; SFC, share of fat in the carcass; SBC, share of bone in the carcass; LVC, less valuable parts in the carcass.

Table 3. Variance and heritability for carcass quality

Traits	V_e	V_a	V_p	h_e^2	SEh_e^2	h^2	SEh^2
HCW, kg	16.097	8.231	24.328	0.662	0.05	0.338	0.05
CCW, kg	16.599	8.560	25.159	0.660	0.05	0.340	0.05
CL, cm	3.795	3.670	7.465	0.508	0.05	0.492	0.05
CHL, cm	6.231	4.925	11.156	0.558	0.05	0.441	0.05
HEW, kg	1.532	0.515	0.789	0.347	0.05	0.653	0.05
LW, kg	0.372	0.184	0.556	0.668	0.05	0.332	0.05
MLDA, cm ²	18.788	7.516	26.304	0.714	0.04	0.286	0.04
BW, kg	0.293	0.043	0.336	0.871	0.05	0.129	0.05
NW, kg	0.120	0.006	0.126	0.951	0.04	0.049	0.04
HW, kg	0.419	0.154	0.573	0.730	0.04	0.270	0.04
RW, kg	0.256	0.134	0.390	0.656	0.05	0.344	0.05
SHW, kg	0.287	0.116	0.403	0.710	0.05	0.290	0.05
SMC, kg	1.600	0.988	2.588	0.618	0.04	0.382	0.04
SFC, kg	1.725	0.513	2.238	0.771	0.04	0.229	0.04
SBC, kg	0.071	0.029	0.100	0.701	0.05	0.299	0.05
LVC, kg	0.332	0.197	0.529	0.627	0.05	0.372	0.05

V_e , residual variance; V_a , additive genetic variance; V_p , phenotypic variance; h_e^2 , heritability of residual variance; h^2 , heritability; SEh^2 , standard error of heritability.

these traits in swine breeding programs. Zumbach *et al.* (2008) and Miar *et al.* (2014) reported low to moderate heritability for HCW and CCW. Heritability estimate for CL was more heritable (0.49) than CHL (0.44), which is in agreement with the average (0.51, 0.57 and 0.56) of all studies reviewed by Miar *et al.* (2014). Dube *et al.* (2013) recorded lower value of heritability (0.33) for the CL. These moderate to high heritabilities would be expected because pig breeders have known that these carcass traits are easy to change by selection.

For MLDA, the heritability estimate in the present study (0.28) was higher than estimates reported by Miar *et al.* (2014) (0.22), but was lower than that of Suzuki *et al.* (2005) (0.41) and Dube *et al.* (2013) (0.55). Most of the phenotypic variation for MLDA is under genetic control, hence its improvement by direct selection is possible.

The genetic (r_g) and phenotypic (r_p) correlations and their standard errors are reported in Table 4. Overall, among the majority of carcass quality traits were determined medium to strong and very strong positive genetic and phenotypic correlations. A strong positive genetic and phenotypic

Table 4. Estimates of genetics (above diagonal) and phenotypic (below diagonal) correlations, and their standard error of estimates among carcass quality

Traits	HCW	CCW	HEW	LW	MLDA	BW	NW	HW
HCW	-	0.99 ± 0.01	0.65 ± 0.16	0.69 ± 0.21	0.22 ± 0.31	0.75 ± 0.23	0.98 ± 0.53	0.77 ± 0.13
CCW	0.93 ± 0.00	-	0.52 ± 0.19	0.67 ± 0.22	0.17 ± 0.32	0.74 ± 0.24	0.97 ± 0.47	0.76 ± 0.15
HEW	0.47 ± 0.04	0.44 ± 0.05	-	0.08 ± 0.25	0.96 ± 0.11	0.17 ± 0.36	0.88 ± 0.59	0.16 ± 0.27
LW	0.39 ± 0.05	0.35 ± 0.05	0.08 ± 0.06	-	0.96 ± 0.01	0.46 ± 0.41	0.82 ± 0.35	0.58 ± 0.33
MLDA	0.27 ± 0.05	0.26 ± 0.05	0.96 ± 0.00	0.97 ± 0.03	-	0.94 ± 0.24	0.99 ± 0.00	0.83 ± 0.25
BW	0.66 ± 0.03	0.60 ± 0.03	0.23 ± 0.05	0.16 ± 0.05	0.31 ± 0.05	-	0.93 ± 0.60	0.67 ± 0.30
NW	0.40 ± 0.04	0.39 ± 0.04	0.35 ± 0.05	-0.02 ± 0.05	0.16 ± 0.05	0.37 ± 0.04	-	0.54 ± 0.57
HW	0.75 ± 0.02	0.70 ± 0.03	0.32 ± 0.05	0.13 ± 0.05	0.33 ± 0.05	0.52 ± 0.04	0.30 ± 0.05	-
RW	0.67 ± 0.03	0.66 ± 0.03	0.34 ± 0.05	0.31 ± 0.05	-0.01 ± 0.00	0.41 ± 0.05	0.28 ± 0.05	0.40 ± 0.05
SHW	0.65 ± 0.03	0.62 ± 0.03	0.41 ± 0.05	0.04 ± 0.05	0.17 ± 0.05	0.81 ± 0.00	0.18 ± 0.05	0.28 ± 0.05
SMC	0.68 ± 0.03	0.65 ± 0.03	0.29 ± 0.05	-0.05 ± 0.06	0.53 ± 0.04	0.45 ± 0.04	0.32 ± 0.05	0.63 ± 0.03
SFC	0.57 ± 0.04	0.65 ± 0.03	0.36 ± 0.05	0.49 ± 0.13	-0.21 ± 0.05	0.28 ± 0.05	0.20 ± 0.05	0.33 ± 0.05
SBC	0.44 ± 0.04	0.41 ± 0.05	0.30 ± 0.05	0.13 ± 0.05	-0.01 ± 0.06	0.26 ± 0.24	0.20 ± 0.03	0.27 ± 0.05
LVC	0.37 ± 0.05	0.36 ± 0.05	0.80 ± 0.02	0.12 ± 0.06	0.04 ± 0.06	0.24 ± 0.05	0.19 ± 0.05	0.18 ± 0.05
CL	0.41 ± 0.05	0.39 ± 0.05	0.87 ± 0.03	0.94 ± 0.00	0.82 ± 0.00	0.96 ± 0.00	0.94 ± 0.00	0.96 ± 0.02
CHL	0.16 ± 0.06	0.17 ± 0.06	0.90 ± 0.00	0.96 ± 0.00	0.81 ± 0.00	0.96 ± 0.00	0.96 ± 0.00	0.97 ± 0.00
Traits	RW	SHW	SMC	SFC	SBC	LVC	CL	CHL
HCW	0.76 ± 0.15	0.86 ± 0.13	0.84 ± 0.11	0.53 ± 0.25	0.55 ± 0.24	0.48 ± 0.23	0.18 ± 0.27	0.39 ± 0.27
CCW	0.93 ± 0.10	0.95 ± 0.11	0.89 ± 0.11	0.53 ± 0.26	0.66 ± 0.22	0.33 ± 0.27	0.16 ± 0.27	0.45 ± 0.26
HEW	0.31 ± 0.23	0.76 ± 0.17	0.35 ± 0.21	0.35 ± 0.21	0.46 ± 0.23	0.86 ± 0.07	0.91 ± 0.02	0.96 ± 0.01
LW	0.47 ± 0.31	0.23 ± 0.42	0.14 ± 0.36	0.76 ± 0.26	0.87 ± 0.43	0.54 ± 0.32	0.92 ± 0.03	0.94 ± 0.02
MLDA	-0.27 ± 0.34	-0.02 ± 0.38	0.71 ± 0.17	-0.50 ± 0.35	-0.18 ± 0.38	-0.01 ± 0.32	0.79 ± 0.02	0.80 ± 0.02
BW	0.05 ± 0.42	0.80 ± 0.02	0.99 ± 0.18	-0.46 ± 0.37	0.68 ± 0.0	0.99 ± 0.22	0.94 ± 0.01	0.96 ± 0.12
NW	0.29 ± 0.54	0.40 ± 0.00	0.19 ± 0.78	0.99 ± 0.01	0.99 ± 0.79	0.99 ± 0.43	0.85 ± 0.10	0.93 ± 0.03
HW	0.29 ± 0.30	0.33 ± 0.37	0.85 ± 0.15	0.22 ± 0.39	-0.11 ± 0.44	0.58 ± 0.29	0.95 ± 0.01	0.96 ± 0.00
RW	-	0.37 ± 0.35	0.26 ± 0.29	0.60 ± 0.26	0.80 ± 0.25	0.48 ± 0.27	0.95 ± 0.01	0.96 ± 0.01
SHW	0.30 ± 0.05	-	0.53 ± 0.25	0.58 ± 0.43	0.84 ± 0.29	0.99 ± 0.18	0.94 ± 0.01	0.96 ± 0.01
SMC	0.34 ± 0.05	0.56 ± 0.04	-	-0.15 ± 0.35	0.44 ± 0.25	0.69 ± 0.20	0.97 ± 0.00	0.97 ± 0.02
SFC	0.59 ± 0.05	0.25 ± 0.05	-0.04 ± 0.04	-	0.05 ± 0.38	0.32 ± 0.31	0.97 ± 0.03	0.97 ± 0.00
SBC	0.26 ± 0.05	0.29 ± 0.05	0.49 ± 0.04	0.05 ± 0.05	-	0.72 ± 0.22	0.89 ± 0.04	0.94 ± 0.02
LVC	0.18 ± 0.06	0.36 ± 0.05	0.24 ± 0.05	0.15 ± 0.05	0.33 ± 0.05	-	0.90 ± 0.03	0.94 ± 0.02
CL	0.96 ± 0.00	0.96 ± 0.00	0.97 ± 0.00	0.97 ± 0.00	0.93 ± 0.00	0.91 ± 0.00	-	0.97 ± 0.00
CHL	0.96 ± 0.00	0.96 ± 0.00	0.97 ± 0.00	0.97 ± 0.00	0.95 ± 0.00	0.94 ± 0.00	0.97 ± 0.00	-

correlation was observed between CL, CHL and other carcass quality traits (r_g , 0.80 to 0.97; r_p , 0.81 to 0.97). Positive, but slightly lower genetic correlation was found by Dube *et al.* (2013) and Miar *et al.* (2014).

HAM as the largest and most important share in carcass was in moderate to high genetic and phenotypic correlations with BW, NW, RW and SHW. These results were in agreement with van Wijk *et al.* (2005) who reported the genetic correlations of 0.61 between HW and BW. Similar correlation relationship between HW and other parts of the carcass were found by Newcom *et al.* (2002) and Miar *et al.* (2014).

Genetic improvement of carcass quality is possible through indirect selection on performance traits, which requires knowledge of phenotypic and genetic parameters, and genetic parameters obtained herein are valuable for the design of a breeding program. The most important and largest part of the carcass for all genotypes was ham (11.38–12.27 kg) followed by shoulders (6.50–7.14 kg), ribs (6.64–6.87 kg), back (6.48–6.68 kg), neck (3.10–3.34 kg) and head (2.79–3.03 kg). The share of muscle tissues in carcass ranged from 53.26 to 57.39 %, the share of bone ranged from 26.61 to 30.48 %, the share of fat ranged from 9.14 to 9.65 % and share of less valuable parts 6.55 to 6.77 %. The traits that were analysed showed sufficient genetic variation, indicating that their improvement is possible through genetic selection. Heritability estimates for carcass traits were moderate to high, and ranged from 0.22 to 0.65 for HEW. Genetic and phenotypic correlations between carcasses parts are limited in the literature, most likely because these traits are difficult and expensive to measure. However, the obtained genetic and phenotypic correlations between body parts is moderate to high, enough to say that heavier pigs at slaughter yields heavier (or larger) body parts and that there is genetic relationship between whole body size and the size of body parts.

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