GENETIC PARAMETERS FOR PRIMAL CUT WEIGHTS IN PIGS

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SUMMARY

A study was conducted to estimate genetic parameters for phenotypes describing primal cuts recorded on 2,077 pigs with pedigrees comprising 5,011 animals over three generations. The four main primal cuts considered were: shoulder, leg, loin and belly. These were analysed as primal weights, or as a percentage of cold carcase weight. Heritabilities ranged from 0.10 (± 0.04) to 0.24 (± 0.06) for primal cut weights and from 0.12 (± 0.05) to 0.24 (± 0.06) for primal cut percentages. The loin primal was the least heritable. The genetic correlations between primal weights and primal percentages for the same primals ranged from 0.97 to 1.00. The genetic correlations among primal cut weights ranged from -0.45 to 0.07 which were similar to those found among the primal cut percentages (-0.63 to 0.06). The genetic correlations between the shoulder and leg primal with the belly primal were negative. The strongest negative genetic correlation was found between the leg and belly primals (-0.45 for weight trait and -0.63 for percentage trait). The leg weight was genetically uncorrelated with loin weight, suggesting that selection for high leg weights would not result in high loin weights. The phenotypic correlation between loin and belly was negative but the genetic correlation was not significant. Genetic correlations between the loin and other primal cut weights were weaker in comparison to the genetic correlations between the belly and other primal cuts. The genetic correlations amongst primal cut weight traits were similar to those found among the primal cut percentages. Incorporating these genetic parameters into a pig breeding program could help to increase the total economic return from pig carcases but would need to be done in association with other traits that impact pig production.

INTRODUCTION

Pork producers and retailers could make better marketing decisions if quantitative information on primal cut yield per carcase were available. A primal cut is a piece of meat initially separated from the carcase of an animal during butchering. Until now, the weight of each primal cut has not been considered in the price Australian farmers receive for pigs. Producers or wholesalers are currently paid on the basis of hot standard carcase weight (HSCW) and back fat. Total carcase weight and leanness do not provide complete information about carcase market value. The economic return per carcase could be determined by the market value of each of its primal cuts and in turn increase returns to farmers (Hermesch 2008). The Australian pig industry lacks classification systems to measure variation in primal cut weights in commercial abattoirs that is required to quantify the economic benefits of higher saleable meat yield for a given carcase weight. Therefore, determining the weight of primal cuts is an important area of interest worth exploring (Lisiak et al. 2015). This study aimed to estimate the genetic parameters of primal cut weights and primal cut percentages in pigs and to determine the relationships between these traits.

MATERIALS AND METHODS

Animals. Data on primal cut traits were combined with pedigree and performance records from 2,077 pig carcases recorded in 2012. The pedigree was extended back three generations for parameter estimation which comprised 5,011 animals including 523 sires and 2411 dams. The subset of pigs

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* A joint venture of NSW Department of Primary Industries and the University of New England

with primal cut records was represented by 98 sires and 1135 dams. Pigs were recorded on one farm and represented three different breeds. There were 25 contemporary groups defined by the week of slaughter, which were fully nested within five different grow-out facilities.

Traits. The four main primal cuts weighed (kg), and expressed also as percentages (relative to cold carcase weight, %) were shoulder (S_WT and S_P), leg (L_WT and L_P), loin (LN_WT and LN_P) and belly (B_WT and B_P). All primal cut weights were recorded on one side of the carcase only. Each primal cut weight was multiplied by two to express them on a per carcase basis.

Statistical analysis. Descriptive statistics for carcase measurement and Pearson correlations were calculated using the statistical package SAS. The (SAS) procedure GLM was used to test for the significance of fixed effects for each trait. All genetic parameter estimates were obtained under an animal model using ASReml (Gilmour *et al.* 2015). Two mixed linear animal models were used: for primal cut weight: $Y_{ijkmn} = \mu + b_i + c_j + cw_k + an_m + pe_n + e_{ijkmn}$ and for primal cut percentage: $Y_{ijmn} = \mu + b_i + c_j + an_m + pe_n + e_{ijmn}$ where, Y = observation for of a trait, μ= overall mean, b_i = fixed effect of the i_{th} breed, c_j = fixed effect of the j_{th} contemporary group, cw_k = linear covariate (cold carcase weight), an_m = random effect of the m_{th} animal, pe_n = common litter effect of n_{th} litter and e_{ijkmn} = error. The common litter effect was only retained in the models for the loin and belly primals, because it was not significant for the shoulder and leg primals.

RESULT AND DISCUSSION

Descriptive statistics. Animals were on average slaughtered at 168 days of age with an average hot carcass weight of 79.0 kg. Considerable variation was observed in all four primal cuts (Table 1). The coefficients of variation (CV) were higher for the loin (18%) and belly (17%) cuts which may be due inconsistencies during the butchering process.

Table 1. Descriptive statistics for the weights and percentages of four primal cuts

Trait		N	Mean	SD	CV	Min	Max
Shoulder weight (kg)	S_WT	2064	22.7	2.56	11.3	12.0	32.2
Leg weight (kg)	L_WT	2068	23.2	2.40	10.3	14.6	31.5
Loin weight (kg)	LN_WT	2073	12.9	2.30	17.8	6.8	30.0
Belly weight (kg)	B_WT	2038	10.2	1.75	17.1	5.2	16.2
Shoulder percentage (%)	S_P	2061	32.8	1.71	5.2	21.9	41.8
Leg percentage (%)	L_P	2065	33.6	1.53	4.6	22.1	41.6
Loin percentage (%)	LN_P	2070	18.7	2.45	13.2	9.4	35.7
Belly percentage (%)	B_P	2035	14.7	1.67	11.3	8.7	22.6

N: number of pigs, SD: standard deviation, CV: coefficient of variation, Min and Max: minimum and maximum

Model fit. The total variation accounted for by the GLM model (R^2; Table 2) was high for all primal cut weights due to the adjustment for cold carcase weight. The R^2 values were 0.86 and 0.87 for S_WT and L_WT and slightly lower at 0.62 and 0.77 for LN_WT and B_WT, respectively. As expected, when compared with the R^2 values for the primal weights those for the primal percentages were lower without carcass weight adjustment (0.10 to 0.28) and when adjusted for cold carcase weight (0.32 to 0.48) because part of the variance in primal cut percentages is masked by the variance in cold carcase weight which is part of the percentage trait.

Heritabilities. The heritabilities for primal cuts were low to moderate, ranging from 0.10 to 0.24 for cut weights and 0.12 to 0.24 for percentages with or without adjustment for cold carcase weight (Table 2). The loin and belly primal traits were less heritable than the other primals. Adjusting primal cut percentage traits for cold carcase weight did not affect heritability estimates significantly and the phenotypic variances were only slightly reduced. The reduction in additive genetic variation resulting from this adjustment supports the simpler model for primal cut percentages. Higher heritabilities for primal cut weight traits compared to the current study have been observed previously (Newcom *et al.* 2002; Van Wijk *et al.* 2005). However, primal cuts definition differed between studies and it is difficult to directly compare heritability estimates. Nonetheless, Newcom *et al.* (2002) estimated heritabilities of 0.60, 0.61, 0.24 and 0.23 for ham, loin, belly and shoulder weights of Yorkshire and Duroc breeds, whereas Van Wijk *et al.* (2005) reported heritabilities of 0.40 and 0.29 for leg and loin weights. Mérour *et al.* (2009) reported higher heritabilities for loin and leg (0.43 and 0.46) than belly and shoulder (0.35 and 0.23).

Table 2. Estimates of heritability (h^2) and common litter effect (c^2) with standard errors (se) along with variance components for primal cut traits[a]

Traits[a]	R^2	h^2	c^2	σ_{pe}^2	σ_a^2	σ_p^2
S_WT	0.86	0.24 (0.06)	-	-	0.44	1.82
L_WT	0.87	0.23 (0.06)	-	-	0.35	1.53
LN_WT	0.62	0.10 (0.04)	0.09 (0.03)	0.28	0.30	3.07
B_WT	0.77	0.09 (0.04)	0.16 (0.04)	0.18	0.10	1.16
S_P	0.12	0.24 (0.06)		-	0.64	2.67
S_P (adjusted for CW)	0.34	0.23 (0.06)		-	0.60	2.60
L_P	0.10	0.23 (0.06)		-	0.49	2.16
L_P (adjusted for CW)	0.32	0.24 (0.05)		-	0.48	2.01
LN_P	0.15	0.12 (0.05)	0.07 (0.03)	0.38	0.61	5.23
LN_P (adjusted for CW)	0.36	0.12 (0.05)	0.07 (0.03)	0.36	0.62	5.19
B_P	0.28	0.16 (0.06)	0.15 (0.04)	0.31	0.32	2.05
B_P (adjusted for CW)	0.48	0.14 (0.05)	0.13 (0.04)	0.25	0.27	1.91

[a] For trait abbreviations see Table 1; CW: cold carcase weight; R^2: coefficient of determination; σ_{pe}^2: variance due to common litter effect; σ_a^2: additive genetic variance and σ_p^2: phenotypic variance

Correlations. The genetic correlations between primal weights and primal percentages for the same primal ranged from 0.97 to 1.00 (Table 3). These very high correlations indicate that the weight and percentage traits for the same primal are essentially the same trait. The genetic correlations among primal cut weights ranged from -0.45 to 0.07 which were similar to those found among the primal cut percentages (-0.63 to 0.06). The genetic correlations the shoulder and leg primals have with the belly primal were negative. The strongest negative genetic correlation was found between the leg and belly primals (-0.45 for weight trait and -0.63 for percentage trait), suggesting that selection for longer pigs would be associated with lower leg weights. The leg weight was genetically uncorrelated with loin weight, which means selection for high leg weights would not result in high loin weights. This result was also found by Mérour *et al.* (2009). In comparison, Van Wijk *et al.* (2005) reported positive genetic correlations (0.22 to 0.58) between leg and loin weights. The phenotypic correlation between loin and belly primals was negative but the genetic correlation was not significant. In comparison, a number of studies (Newcom *et al.* 2002; Mérour *et al.* 2009) reported moderate to high negative genetic correlations (-0.54 to -0.57) between loin and belly primals. Genetic correlations between the loin and other primal cut weights were weaker in comparison to the genetic correlations the belly primal has with the other primal cuts. The genetic correlations amongst the primal cut weight traits were similar to those found among the primal cut percentage traits.

Table 3. Estimates of phenotypic (above diagonal) and genetic correlations (below diagonal) with standard error (se) among primal cut weight and percentage traits

Traits	S_WT	L_WT	LN_WT	B_WT	S_P	L_P	LN_P	B_P
S_WT		38(2)	8(2)	21(2)	90(0)	4(3)	-18(3)	-9(3)
L_WT	22(17)		16(2)	18(2)	5(3)	88(1)	-5(3)	-16(3)
LN_WT	1(27)	-4(28)		-14(3)	-14(2)	-3(2)	99(0)	-47(2)
B_WT	-10(29)	-45(31)	7(34)		-7(2)	-14(2)	-54(2)	99(0)
S_P	97(2)	-8(19)	5(25)	-11(27)		7(2)	-16(2)	-11(2)
L-P	-18(18)	97(2)	-7(26)	-54(23)	-19(18)		-5(2)	-20(2)
LN_P	-17(24)	-21(25)	100(0)	-4(34)	-3(24)	-10(25)		-42(2)
B_P	-27(22)	-63(19)	-0(31)	100(0)	-33(20)	-63(18)	6(29)	

All correlations and se were multiplied by 100

CONCLUSION

Overall, these results suggest that the size of the most valuable primals (loin and belly) could be improved through breeding, which may also reduce the size of the least valuable primals (shoulder and leg). This could in-turn increase the total economic value of pig carcases. The primal weight traits were genetically highly correlated with the percentage traits, so the primal cut weight and percentage traits are basically same trait. The actual primal weight is needed to calculate primal percentages so breeders need only use primal weights adjusted for cold carcass weight. In breeding programs, these primal traits need to be used with respect to other production and welfare traits in order to change overall profit per carcase without causing detrimental changes in the pig.

ACKNOWLEDGEMENTS

Data recording was funded by Australian Pork Limited (Project 1025). The first author was supported by an Australian Government RTP International Scholarship.

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