HERITABILITY ESTIMATES FOR CONFORMATION TRAITS IN PIGS

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SUMMARY

Data from 1006 pigs selected for breeding and subsequently scored at 22-24 weeks of age were used to estimate heritabilities for conformation traits. Front wrists, front pasterns, back hocks, back pasterns, front view, rear view and back shape were each subjectively scored by a single operator on a 1 to 7 scale. Heritability estimates ranged from high (0.42 ± 0.09 for front pasterns) to negligible (0.01 ± 0.04 for back hocks and body shape). Results suggest that at least some conformation traits would respond to selection. Week off test, sex, performance test system and breed affected conformation scores in diminishing order, but overall explained relatively little variation (generally R^2<3-5%). Variation in finishing weight, average daily gain, eye muscle depth or backfat further explained relatively little of the variation in conformation scores (additional R^2<1-2%).

Keywords: Conformation, pigs, heritability, selection, culling

INTRODUCTION

Independent culling for poor conformation in nucleus breeding herds results in reduced response to selection for traits explicitly included in the breeding objective. In addition, subjective phenotypic evaluations that lead to animals being culled for poor conformation generally do not account for systematic effects influencing the animals' appearance. Assessing the relative influence of genetic and non-genetic effects on conformation traits can determine whether culling on conformation traits could improve future herd conformation, providing a positive outcome that partially offsets losses in the otherwise defined breeding objective. The aim of this study was to assess whether aspects of conformation, for which animals with less desirable characteristics are often culled, are heritable.

MATERIALS AND METHODS

Conformation traits were scored for 1006 animals selected for breeding between May and September 2002 at QAF Meat Industries (QAF). Traits were scored on both male and female pigs from five lines immediately following performance testing: conformation was not considered prior to this point. Front wrists (FW), front pasterns (FP), back hocks (BH), back pasterns (BP), front view (FV), rear view (RV) and back shape (BS) were each subjectively scored by a single scorer on a 1 to 7 scale (Table 1). Injuries were recorded for those animals having correct conformation but displaying signs of injury. These records were re-assigned to the "Correct" conformation class for analyses. The original scores of 6 and 7 for front and rear views were not consistent with a continuous scoring system, and new categorical variables were created from these scores. The new front (FVNEW) and rear (RVNEW) view traits were created to reflect whether an animal was standing outwards slightly (1), heavily (2) or not at all (0).

Several binary traits were also created by combining information across traits. These included: INJ (injured (1) or not (0)); COR_L (legs all correct (1) or not (0)); and COR_B (body shape (back shape + FVNEW + RVNEW) all correct (1) or not (0)).

Table 1. Scoring systems used for conformation traits (Stdg Out: standing out)

	Score						
Trait	1	2	3	4	5	6	7
Score intensity	Heavily	Slightly	Correct	Slightly	Heavily		
Front Wrists	Buckled	Buckled	Correct	Sickled	Sickled	Injured	
Front Pasterns	Straight	Straight	Correct	Weak	Weak	Injured	
Back Hocks	Steep	Steep	Correct	Sickled	Sickled	Injured	
Back Pasterns	Straight	Straight	Correct	Weak	Weak	Injured	
Score intensity	Heavily	Slightly	Correct	Slightly	Heavily	Slightly	Heavily
Front view	X-shaped	X-shaped	Correct	O-shaped	O-shaped	Stdg Out	Stdg Out
Rear view	X-shaped	X-shaped	Correct	O-shaped	O-shaped	Stdg Out	Stdg Out
Back shape	Weak	Correct	Dipped	Arched			

Systematic effects were investigated and estimates of genetic parameters were obtained using ASREML (Gilmour *et al.* 1999). The initial model contained week off test and testing system (electronic feeder versus finisher pens, both with concrete slatted flooring) along with line and sex (fitted as class effects nested within testing system) as fixed effects. Linear regressions for age at selection, end of test weight or lifetime daily gain (ADG), and the performance traits (EMD: eye muscle depth; AVFAT: average backfat) were evaluated within testing system. Models for each trait were subsequently reduced in a stepwise fashion to retain only significant ($P<0.05$) effects. However, week off test and performance testing system were always retained in the final models for parameter estimation, since groups of animals from each test procedure were evaluated separately. Parameter estimates for the categorical traits were obtained under an animal model, implying approximate normality of scores. Estimates of genetic parameters for binary traits were obtained using generalised linear model procedures, using a probit link function under a sire model (Gilmour *et al*. 1999). Due to the low number of animals scored per litter, data were not adequately structured to separate additive genetic from common environmental (litter) effects.

RESULTS AND DISCUSSION

Of the original 1006 records, 950 were retained for analyses after removing progeny data for sires with less than five progeny scored. The latter editing was performed to reduce the level of uninformative sire progeny means for the binary traits. The edited data contained progeny of 59 sires and 461 dams (Table 2). Mean values and ranges for both conformation and performance traits were almost identical for the original and edited data sets.

Table 2. Number of animals present in each scoring category, raw data means and coefficients of variation for conformation traits (-: score not relevant)

	Score							Raw Data	
	0	1	2	3	4	5	Total	Mean (SD)	CV (%)
FW	-	19	324	563	44	0	950	2.67 (0.59)	22
FP	-	1	6	523	332	88	950	3.52 (0.67)	19
BH	-	5	135	637	170	3	950	3.03 (0.59)	19
BP	-	3	119	718	107	3	950	2.99 (0.52)	17
FV	-	1	28	648	0	0	677	2.95 (0.21)	7
FVNEW	677	264	9	-	-	-	950	0.31 (0.48)	157
RV	-	3	92	762	2	0	859	2.89 (0.34)	12
RVNEW	859	87	4	-	-	-	950	0.10 (0.31)	316
BS	-	0	937	11	1	-	949	2.01 (0.12)	6
Injured*	852	98	-	-	-	-	950	0.10 (0.30)	291
COR_L*	844	106	-	-	-	-	950	0.11 (0.32)	286
COR_B*	434	516	-	-	-	-	950	0.54 (0.50)	93

Fixed Effects. Week off test, sex, performance test system and breed affected conformation scores in diminishing order, but overall explained relatively little variation (generally $R^2<3$-5%). The exceptions were FP and COR_L, where 8-10% of the variation in scores was associated with scoring week, and sex+breed explained a further 10% of the variation in FP. While there were significant regression coefficients for some conformation on performance traits, variation in weight, ADG, EMD or AVFAT explained relatively little of the variation in conformation scores (additional $R^2<1$-2%). Generally, regression coefficients suggested that faster growing, leaner animals with larger EMD were slightly more likely to appear as O-shaped or standing outwards and to have superficial injuries.

Parameter Estimates. Estimates of heritabilities and corresponding variances are presented in Table 3. Heritability estimates for leg conformation traits ranged from negligible (hocks) to high (pasterns). Estimates for body conformation traits were negligible (shape) to low (front and rear view traits). The binary traits (INJ, COR_L, COR_B) were highly to lowly heritable. Corresponding estimates of heritability from linear methods, converted to the underlying scale, were 0.32, 0.19 and 0.14 respectively, supporting the magnitude of estimates for these traits.

Phenotypic variances for all conformation traits were low, which is characteristic of categorical traits with few scoring categories. Phenotypic variances for the binary traits (INJ, COR_L and COR_B) are inflated, because residual variances for binary traits are fixed to 1.0 (Gilmour *et al.*, 1999).

Table 3. Estimates of heritabilities (h^2 ± standard error), additive genetic (σ^2_a), between sire variances (σ^2_{sire}) and phenotypic (σ^2_P) variances for conformation traits

Trait	h^2 ± se	σ^2_a	σ^2_{sire}	σ^2_P
FW	0.16 ± 0.07	0.05	-	0.34
FP	0.42 ± 0.09	0.16	-	0.37
BH	0.00 ± -	0.00	-	0.35
BP	0.27 ± 0.08	0.07	-	0.26
FV	0.12 ± 0.08	0.01	-	0.04
FVNEW	0.12 ± 0.05	0.03	-	0.23
RV	0.12 ± 0.07	0.01	-	0.11
RVNEW	0.06 ± 0.05	0.01	-	0.10
BS	0.01 ± 0.04	0.01	-	0.02
INJ*	0.42 ± 0.20	-	0.12	1.12
COR_L*	0.30 ± 0.19	-	0.08	1.08
COR_B*	0.14 ± 0.10	-	0.04	1.04

- not fit; *estimates are on the underlying scale, residual variance fixed to 1.0

Larochelle (1999), in a review of conformation related literature, reported average heritabilities of 0.40 for front pasterns, 0.19 for back pasterns, 0.18 for front legs and 0.12 for back hocks. Average heritabilities for leg weakness traits reported by Clutter *et al.* (1998), who reviewed different conformation studies, ranged from 0.16 to 0.30. While direct comparisons between these studies are hindered because of different scoring systems, similar estimates of heritabilities are generally indicative of the low to moderate heritability of leg conformation traits and moderate to high heritability of feet conformation traits in pigs. The binary traits, INJ and COR_L were moderately to highly heritable. Further investigation is necessary to determine whether there are economic benefits to directly improving heritable conformation traits through selection, and whether there are genetic associations between these conformation traits and economically important performance traits.

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