GENETIC VARIATION IN PORK TRAITS OF AUSTRALIAN COMMERCIAL PIG LINES

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Abstract – The aim of this experiment was to evaluate several meat quality and production traits recorded in 7 commercial pig lines bred in Australia and to determine the heritability of these traits. Carcase weight, P2 fat depth and pH_{24} (recorded 24 hours post slaughter) differed between the lines ($P < 0.05$) and sexes ($P < 0.05$). P2 fat depth was highly heritable (0.56), unlike carcase weight and pH_{24} which were both very lowly heritable (0.05 and 0.02 respectively). This study confirmed little potential for genetic improvement of pH_{24} of commercial Australian pig lines through within-line selection.

Key words – pH, meat quality, commercial lines, heritability.

I. INTRODUCTION

One of the attributes that influences pork meat quality is pH, because it can affect several other attributes, such as shelf life, color, texture and flavour. Like other traits, the expression of pH is influenced by genetic and environmental factors and their interactions [1]. Expression of these characters can be regulated by genetics through exploitation of genetic variation between and within breeding lines. There is interest from commercial operations in examining differences between breeding lines and so a study was undertaken to evaluate these differences for pigs raised in Australia under a controlled breeding program. As well, the design of this study allowed the heritability of a number of important production traits to be estimated.

II. MATERIALS AND METHODS

Seven different pig lines were sampled from maternal breeds (Australian Landrace, Line 2; Australian Large White, Line 3; Colored Duroc, Line 4) and terminal sire breeds (Colored Duroc, Line 7; Duroc, Line 9; Belgium Landrace, Line 61; and cross-breed 50% Line 9 x 50% Line 61, Line 400) bred at a PIC piggery in Grong Grong NSW, Australia. Each pig was individually branded and recorded against their (pedigreed) ID on farm before being transported to the abattoir. The brand was then recorded against their slaughter records, which allowed assigning of the correct pedigree to each record. Over 9 weeks, pigs from the seven different genetic lines were weighed (final weight) and transported to the Cowra abattoir (Olympic Way, Cowra, NSW). After slaughter and overnight chilling pH_{24} was measured in the *m. longissimus thoracis* using a meter with temperature compensation (WP-80, TPS Pty Ltd, Brisbane, Australia) and a polypropylene spear-type gel electrode (Ionode IJ 44) after calibrating the meter at chiller temperatures. This measurement was taken at the 10^{th} rib after an incision was made through the skin and fat. Carcase weight and fat at the P2 site were recorded and the slaughter data matched with the PIC database that includes pedigree information. A total of 597 pigs were measured, the progeny of 45 sires.

The data available for each animal included: animal identity, line, pH_{24}, carcass $T°C_{24}$, carcase weight, P2 fat depth, sex, slaughter day, and identity of the sire and dam. The data were firstly analysed using

a linear mixed model (LMM) analysis in GENSTAT (17th Ed.). The model for pH_{24} included slaughter day as a random term and line and sex as fixed effects. The interaction between line and sex was tested. The impact of carcase weight and P2 fat depth was also tested. Another model was used to test the effect of line and sex on carcase weight and P2 fat depth with carcase weight included as a covariate for P2 data. Differences between means were detected using a least significant difference (LSD) test at the P = 0.05 level. Heritability estimates were derived from an animal model fitted to the data for each trait using ASReml (Version 4). Fixed effects fitted to the data included line, slaughter group and sex, with age at recording fitted as a covariate and a direct additive genetic effect fitted as a random term.

III. RESULTS AND DISCUSSION

There were differences in pH_{24} between lines ($P < 0.05$; data not shown) and there was a difference between males and females ($P < 0.05$), with mean ± s.e. values of 5.47 ± 0.046 and 5.51 ± 0.045 respectively. There was also a significant effect ($P < 0.001$) of line (data not shown) and sex on carcase weight (77.0 ±1.10 and 79.3 ±1.06) and P2 fat depth (9.3 ± 0.385 and 10.2 ± 0.374) respectively. Of the lines, Line 7, a Duroc terminal sire line, tended to have the lowest values of pH_{24} and P2 fat depth and the highest carcase weight. Line 61, which is known to carry the halothane gene, and to a lesser extent the crossbred line 400 tended to have lower P2 fat depths and carcase weights, though higher values of pH_{24}, than the other lines. There was phenotypic variation in all traits (Table 1), except pH_{24}. P2 fat depth was estimated to be of high heritability, and pH_{24} very lowly heritable. If final weight was included in the model for P2 fat depth, the heritability increased to 0.67 (0.13), while for pH_{24} it decreased to 0.01 (0.06). The high heritability for P2 fat depth indicates that this trait will respond to genetic selection. High heritability estimates (0.34, 0.46) for carcase fat depth of Australian pig carcases have been reported previously [2]. Conversely, the very low heritability for pH_{24} suggests that this trait would not respond to genetic selection in this population.

Table 1 Heritability estimates (± s.e.) for pork traits.

Trait	Number of records	Phenotypic variance (s.e.)	Heritability (s.e.)
Final weight (kg)	489	58.27 (3.95)	0.19 (0.10)
Carcase weight (kg)	591	43.14 (2.57)	0.05 (0.06)
P2 far depth (mm)	591	3.90 (0.27)	0.56 (0.12)
pH24	591	0.0188 (0.0011)	0.02 (0.07)

IV. CONCLUSIONS

This study has identified differences between Australian commercial pig lines in meat quality traits of pH_{24}, carcase P2 fat depth and carcase weight. P2 fat depth was found to be of high heritability, indicating sufficient genetic variation exists for this trait, which could be exploited through within-line selection.

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