

## STRAIN DIFFERENCES IN MERINOS FOR CARCASE AND MEAT QUALITY

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The increased emphasis on the Merino for meat production has heightened the need to quantify the variation across the breed for meat and carcase traits and to produce genetic correlations and heritabilities for these traits. Fogarty *et al.* (2003) showed differences between broad, medium and fine wool strains for traits such as meat colour, meat pH and carcase fat levels. In terms of meat pH more recently Hopkins *et al.* (2005) reported that superfine strains produced higher levels than broader wool strains. These authors argued that muscle glycogen was potentially limiting in the work of Fogarty *et al.* (2003) and to counter this supplemented their animals on pellets before slaughter. These relationships have been further studied using the QPLU\$ flock and this will yield enhanced genetic parameters for carcase and meat traits. This paper reports on some initial analysis of strain effects.

Briefly, the structure of the QPLU\$ flock is based on Merino strains derived from parent studs representing fine, medium and broad wool types. Across these strains, 6 lines selected on combinations of wool weight and fibre diameter and 3 control lines have been produced. Hogget rams (~19 months of age) were slaughtered over 3 years and data on 1509 animals from 192 sires has been collected. Every year, the hoggets were fed a formulated pellet at pasture for 5 weeks before slaughter. All animals were slaughtered in commercial abattoirs. Hot carcase weights were recorded and the GR measured using a GR knife. After overnight chilling (4–5°C), carcasses were cut between the 12th/13th ribs and the *longissimus thoracis et lumborum* (LL) was exposed to the air at chiller temperature for 30 minutes. Meat colour was measured on the cut surface using a Minolta Chromameter set on the  $L^*$ ,  $a^*$ ,  $b^*$  system. The pH of the LL and the *semitendinosus* (ST) muscles was also measured.

Data were analysed using a REML procedure, which contained the fixed strain effect (fine, medium, broad), with year of slaughter, sire identification and ewe identification included as random terms. For GR, hot carcase weight was included as a covariate and for the colour traits; muscle pH was used as a covariate. In agreement with Fogarty *et al.* (2003) and Hopkins *et al.* (2005), fine wool rams were the fattest when compared at the same carcase weight. As found by Hopkins *et al.* (2005), the broad wool strain had the lowest pH in both muscles and there were minimal differences between strains for meat colour. Higher average values for lightness were recorded than reported by Fogarty *et al.* (2003). The observed difference in muscle pH in our study may reflect a higher intake of the supplement in the broad wool strain and thus a higher glycogen concentration, or a difference between strains in the response of muscle glycogen under the same level of intake. Alternatively the response of the strains to the stress of slaughter may differ having an impact on muscle metabolism. Nevertheless, there are real strain differences, indicative of potentially useable genetic variation, which can impact on factors such as meat keeping quality and tenderness.

**Table 1. Animal numbers, hot carcase weight (HCW), GR (mm), pH (LL and ST) and colour parameters  $L^*$ ,  $a^*$ ,  $b^*$ , for the LL according to strains**

Strain	Number	HCW (kg)	GR (mm) <sup>A</sup>	pH <sub>LL</sub>	pH <sub>ST</sub>	$L^{*AB}$	$a^{*B}$	$b^{*B}$
Broad	324	29.6a	7.4c	5.88b	6.10c	34.6a	20.0a	9.4a
Medium	921	25.6b	8.6b	5.93ab	6.17b	34.1b	20.0a	9.3a
Fine	264	24.2c	9.2a	5.95a	6.23a	34.9a	20.1a	9.6a
<i>Av. s.e.d.</i>		0.32	0.24	0.025	0.027	0.22	0.19	0.11

<sup>A</sup>Adjusted to a HCW of 26.2 kg; <sup>B</sup>Adjusted to a pH of 5.92. Different letters represent significant differences ( $P < 0.05$ ).

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This work was funded by Meat & Livestock Australia