Genotype and age effects on sheep meat production. 5. Lean meat and fat content in the carcasses of Australian sheep genotypes at 20-, 30- and 40-kg carcass weights

E. N. Ponnampalam\textsuperscript{A,B,E}, K. L. Butler\textsuperscript{B}, D. L. Hopkins\textsuperscript{C}, M. G. Kerr\textsuperscript{B}, F. R. Dunshea\textsuperscript{B,D} and R. D. Warner\textsuperscript{B}

\textsuperscript{A}Australian Sheep Industry Cooperative Research Centre, Armidale, NSW 2350, Australia. 
\textsuperscript{B}Department of Primary Industries, 600 Sneydes Road, Werribee, Vic. 3030, Australia. 
\textsuperscript{C}New South Wales Department of Primary Industries, Centre for Sheep Meat Development, Cowra, NSW 2794, Australia.  
\textsuperscript{D}Present address: The University of Melbourne, Melbourne, Vic. 3010, Australia. 
\textsuperscript{E}Corresponding author. Email: eric.ponnampalam@dpi.vic.gov.au

Abstract. Lean meat and fat content of Australian sheep genotypes were compared at 20-, 30- and 40-kg carcass weights. Sheep comprised Poll Dorset\textsubscript{growth} × Border Leicester Merino (PD\textsubscript{g} × BLM), Poll Dorset\textsubscript{muscling} × Merino (PD\textsubscript{m} × M), Border Leicester × Merino (BL × M) and Merino × Merino (M × M) genotypes. Lambs were raised as a mixed flock under grazing and slaughtered at 4, 8, 14 and 22 months of age with each slaughter time involving ~150 mixed sex animals. At 24 h after slaughter, chilled carcasses were halved along the backbone and the right sides were used for determination of lean, fat and ash percentages using dual energy X-ray absorptiometry. Within a particular age group and genotype, animals growing at faster rates and reaching heavier carcass weights had lower carcass lean meat content than slower growing animals. Merino carcasses weighing 20 and 30 kg had similar levels of lean meat to PD × M genotypes, which was greater than that from the BL × M genotype. Second-cross PD × BLM carcasses weighing 20 kg at 4 months and 30 kg at 8 months had similar carcass fat and lean percentages to 20-kg Merino carcasses at 8 months and first-cross PD × M carcasses weighing 30 kg at 14 months, respectively. At 40-kg carcass weight, 22-month-old Merinos had similar levels of leanness to carcasses from 22-month-old PD × M animals and carcasses from 14-month-old second-cross PD × BLM animals. Carcass lean meat content decreased with increasing carcass weight and first-cross BL × M animals had the lowest carcass lean across all weight categories. There was a major acceleration in carcass fatness between 14 and 22 months associated with a reduction in muscle deposition. Results indicate that age of the animal should be taken into account when carcass lean and fat contents are compared at a particular carcass weight. Merinos will achieve weight/composition specifications at least equally well to crossbreds but will take longer with a likely increase in production costs.

Introduction

Lambs for meat production in Australia are mainly from second-cross [Poll Dorset × (Border Leicester × Merino)], first-cross (Poll Dorset × Merino/Border Leicester × Merino) and straight Merino (M) genotypes and are grown under different production systems. In general, second-cross sheep would be expected to reach weight and carcass specifications at younger ages than first-cross sheep, which in turn would be expected to reach weight and fatness specifications at younger ages than pure M sheep (Ponnampalam et al. 2007\textsuperscript{b}). Different production systems will place different emphases on the importance of meat and wool production, and the balance between these two can change mainly with response to market and climatic conditions.

Recently, Ponnampalam et al. (2007\textsuperscript{b}) compared the carcass composition of young and old sheep among a range of genotypes slaughtered at different ages (4, 8, 14 and 22 months). They found that carcass lean percentage decreased from M to Poll Dorset (PD) to Border Leicester (BL) sires at each age when joined to M ewes, while fatness increased in the opposite direction. Comparisons at the same age are useful because those genotypes that reach a specification at younger ages will be more profitable for meat production. However, to compare different genotypes in their suitability to reach minimum specifications for size (carcass weight) and meat composition (percentage lean and/or fat), it is necessary to compare carcass composition between genotypes, when slaughtered at the same weight. Differences between genotypes made at the same age may or may not be similar to differences between genotypes made at the same weight. There have been studies that have directly compared carcass composition traits between genotypes at the same carcass weight (Cotterill and Roberts 1979; Hopkins et al. 1997; Johnson et al. 2005), but these studies have mostly been limited to a specific carcass weight.

An alternative approach is to indirectly compare meat specifications between genotypes, at the same weight. This can be achieved using a study, such as that described by Hopkins et al. (2007) and Ponnampalam et al. (2007\textsuperscript{a}), where a range of genotypes were slaughtered at a range of specified ages. Using this approach, carcass composition traits are
modelled as a function of hot carcass weight (hcwt), genotype and slaughter age, taking into account extraneous source of variation. Model comparisons are then made between genotypes at specified carcass weights, using appropriate predicted values of the carcass composition trait. While this approach is powerful, it must be used carefully in order to avoid misleading conclusions. It is necessary to carefully verify that sources of variation are modelled in a way that is in accord with the data, and that predictions are not extrapolated outside the range of the data. This paper details the use of this approach using data generated from the study reported by Hopkins et al. (2007).

### Materials and methods

#### Sire and ewe selection

The detail of sires and dams joined to produce the progeny used in the study has been reported by Hopkins et al. (2007). Semen from four PD sires selected for growth (PDg), using LAMPLAN (Banks 1994), was used with both BL×M (BLM) and M ewes. Four PD sires selected for muscling (PDm), four M sires selected for growth, and four BL sires selected for growth were used only across M ewes.

#### Management of lambs from birth to slaughter

After marking, ewes and lambs with PDg×BL, PDg×M, PDm×M, BL×M, and M×M genetics were managed on pasture until weaning in November 2003. Lambs were vaccinated with a 6 in 1 vaccine, drenched for internal parasites at weaning and, except for those slaughtered at 3 months, shorn a week later. After weaning, the lambs were grazed as a mixed flock on a combination of lucerne and pasture grasses. Supplements and legume silage were offered, as appropriate, to maintain weight gain for the entire duration of the experiment and to allow the expression of genetic potential under grazing conditions.

#### Slaughter of lambs and measurement of carcass composition

Approximately 600 lambs were used in this study. At each age (i.e. 4, 8, 14 and 22 months), ~150 animals of mixed sex raised at the New South Wales Department of Primary Industries, Centre for Sheep Meat Development, Cowra were weighed, transported to a commercial abattoir within 2–3 h, kept overnight in lairage and slaughtered the next day. Water was freely available at all times in lairage. Animals were slaughtered on 2 days (Tuesday and Thursday) and within days they were allocated to two sessions, each 1–2 h apart. At 24 h after slaughter, chilled carcasses were halved along the midline and right sides and subsequently transported to the Meat Research and Training Centre, Werribee, Victoria for the assessment of carcass composition.

The composition of each carcass side was determined using a Hologic QDR4500 dual energy X-ray absorptiometry (DXA) machine, incorporating a calibration equation as described by Dunshea et al. (2007). The calibration related DXA determined readings to the measured percentage of lean, fat and ash calculated from chemical analysis of ground half carcasses (excluding head). Weight of lean tissue, fat tissue, bone mineral content and total tissue weight were calculated for each carcass and converted to percentages of total carcass weight.

#### Statistical analysis

The variates fat percentage and lean percentage were related to effects and interactions of carcass weight, slaughter age, genotype combination, selection group of PD sires, lamb gender, slaughter day, slaughter session, sire identity and dam identity using restricted maximum likelihood models (Payne 2008). The most parsimonious model for each variate was chosen using a combination of change in deviance tests for random effects and Wald tests for fixed effects. Predicted values for fixed effects were adjusted for all other terms in the chosen model. All s.e. were calculated using first order likelihood approximations.

#### Results

The parsimonious models chosen had the same form for both fat percentage and lean percentage. The fixed effects can be symbolically represented in Genstat 10 notation (Payne 2008) as:

\[
(\text{slaughter age} + \text{genotype}) \times \text{hcwt} + \text{hcwt}^2 + \text{lamb gender} \quad (1)
\]

where slaughter age, genotype and lamb gender are factors and hcwt is a variate representing observed hcwt. There was no

![Fig. 1. The relationships between (a) carcass lean percentage and carcass weight and (b) carcass fat percentage and carcass weight for Merinos (---), first-cross Border Leicester Merino (BL×M, --), first-cross Poll Dorset Merino (PD×M, ++) and first-cross Poll Dorset × Border Leicester Merino (PD×BLM, * * * *). For a genotype, there are four disconnected lines with the same drawing symbol representing, from left to right, at a slaughter age of 4, 8, 14 or 22 months.](image-url)
difference between PDg or PDm animals ($P = 0.72$ for fat percentage, $P = 0.94$ for lean percentage), and no effect of slaughter time ($P > 0.10$). The model includes random effects for sire identity, ewe identity and slaughter day within slaughter age, with the variance of sire and ewes being constrained to be equal. The model included a separate residual variation for each of the four slaughter ages. Some of the random terms not included in the model ($P > 0.10$) were: (i) the magnitude of the between sire variance being different to the magnitude of the between ewe variance; (ii) sire and ewe effects differing with slaughter; and (iii) the sire effect variance differing with slaughter.

Within any genotype and slaughter time cohort, slower growing animals were leaner and had lower carcass fat than faster growing animals. However, between 14 and 22 months, there was a major acceleration of the increase in carcass fatness in the slower growing sheep, within any genotype (Fig. 1a, b). As expected, second-cross animals grew faster than first-cross animals that in turn grew faster than pure M animals (Fig. 2).

Table 1 shows the comparative fat and lean percentages between genotypes slaughtered at 20-, 30- or 40-kg carcass weight. In this case, the term ‘fast’ indicates that animals reaching slaughter weight at a nominated slaughter are among the fastest growing third of animals in the genotype group. ‘Slow’ indicates that animals reaching slaughter weight at a nominated slaughter are among the slowest growing third of animals within the genotype group and ‘typical’ indicates that animals reaching slaughter weight at a nominated slaughter are among the middle growing third of animals within a particular group. At any given genotype and carcass weight, animals slaughtered at 22 months have more fat and less lean. At younger ages (4–14 months), the BL×M genotype had a greater level of carcass fat and lower lean than other genotypes, with other genotypes being similar (Table 1). Around 10% of the total variation was contributed by variation between sires and 10% by variation between ewes (Table 2). The variation due to slaughter day is comparatively small. For any given carcass weight and genotype, the lean percentage was 3.4% (s.e. ± 0.50%) greater in wethers than ewes, and the fat percentage was 3.4% (s.e. ± 0.42%), less in wethers than ewes.

**Discussion**

Results show that within a given age and genotype category, sheep with smaller carcasses deliver less fat and more lean than sheep with larger carcass counterparts. For example, at 8 months of age, a BL×M carcass weighing 20 kg had 22% carcass fat while a BL×M carcass weighing 26 kg had 25% carcass fatness (Fig. 1b). This implies that within a genotype at a particular age, there is variation in fat and muscle deposition with faster growing animals diverting more energy into fat deposition than muscle growth compared with smaller growing animals. This may have been due to a variation in selection of diet under grazing conditions, which may result in the faster growing animals having increased feed intake and a lower protein : energy ratio of the diet being consumed. This could also be due to a difference

![Fig. 2. Boxplots of the carcass weight of pure Merino, first-cross Border Leicester Merino, first-cross Poll Dorset Merino and first-cross Poll Dorset × Border Leicester Merino at a slaughter age of 4, 8, 14 or 22 months.](image-url)
Table 1. Comparative fat percentage and lean percentage between genotypes (M, Merino; BL, Border Leicester; PD, Poll Dorset) slaughtered at a hot carcass weight of 20, 30 or 40 kg
Results are adjusted for all other terms in the model.

<table>
<thead>
<tr>
<th>Genotype</th>
<th>Slaughter age</th>
<th>Growth rate within breed</th>
<th>Lean %</th>
<th>Fat %</th>
</tr>
</thead>
<tbody>
<tr>
<td>Pure M</td>
<td>8 months</td>
<td>Fast*</td>
<td>76.4</td>
<td>20.4</td>
</tr>
<tr>
<td>BL × M</td>
<td>8 months</td>
<td>Slow*</td>
<td>74.9</td>
<td>22.2</td>
</tr>
<tr>
<td>PD × M</td>
<td>4 months</td>
<td>Fast*</td>
<td>77.5</td>
<td>19.5</td>
</tr>
<tr>
<td>PD × M</td>
<td>8 months</td>
<td>Slow*</td>
<td>77.1</td>
<td>20.1</td>
</tr>
<tr>
<td>PD × BLM</td>
<td>4 months</td>
<td>Typical</td>
<td>76.8</td>
<td>20.6</td>
</tr>
<tr>
<td>Pure M</td>
<td>14 months</td>
<td>Fast*</td>
<td>71.5</td>
<td>24.3</td>
</tr>
<tr>
<td>Pure M</td>
<td>22 months</td>
<td>Fast*</td>
<td>67.2</td>
<td>28.5</td>
</tr>
<tr>
<td>BL × M</td>
<td>14 months</td>
<td>Slow*</td>
<td>68.3</td>
<td>28.1</td>
</tr>
<tr>
<td>PD × M</td>
<td>14 months</td>
<td>Slow*</td>
<td>71.3</td>
<td>25.2</td>
</tr>
<tr>
<td>PD × BLM</td>
<td>8 months</td>
<td>Fast*</td>
<td>70.8</td>
<td>26.0</td>
</tr>
<tr>
<td>Pure M</td>
<td>22 months</td>
<td>Fast*</td>
<td>65.0</td>
<td>30.2</td>
</tr>
<tr>
<td>BL × M</td>
<td>14 months</td>
<td>Fast*</td>
<td>64.0</td>
<td>32.1</td>
</tr>
<tr>
<td>BL × M</td>
<td>22 months</td>
<td>Slow*</td>
<td>60.0</td>
<td>36.0</td>
</tr>
<tr>
<td>PD × M</td>
<td>14 months</td>
<td>Fast*</td>
<td>67.8</td>
<td>28.4</td>
</tr>
<tr>
<td>PD × M</td>
<td>22 months</td>
<td>Slow*</td>
<td>63.9</td>
<td>32.3</td>
</tr>
<tr>
<td>PD × BLM</td>
<td>14 months</td>
<td>Typical</td>
<td>65.9</td>
<td>30.7</td>
</tr>
<tr>
<td>PD × BLM</td>
<td>22 months</td>
<td>Slow*</td>
<td>61.9</td>
<td>34.6</td>
</tr>
</tbody>
</table>

s.e.d. within columns: a v. a, 0.40; b v. b, 0.72–0.75; a v. b, 0.80–0.87

Table 2. Sources of random variation in lean and fat percentages of animals with the same breed, time of slaughter and carcass weight at slaughter

<table>
<thead>
<tr>
<th>Source of variation</th>
<th>Variance</th>
<th>Lean % of variance</th>
<th>Standard error</th>
<th>% of total variation</th>
<th>Variance</th>
<th>Fat % of variance</th>
<th>Standard error</th>
<th>% of total variation</th>
</tr>
</thead>
<tbody>
<tr>
<td>Sire</td>
<td>0.7</td>
<td>0.25</td>
<td>9–13</td>
<td></td>
<td>0.8</td>
<td>0.27</td>
<td>8–14</td>
<td></td>
</tr>
<tr>
<td>Ewe</td>
<td>0.7</td>
<td>0.25</td>
<td>9–13</td>
<td></td>
<td>0.8</td>
<td>0.27</td>
<td>8–14</td>
<td></td>
</tr>
<tr>
<td>Slaughter day</td>
<td>0.2</td>
<td>0.16</td>
<td>2–3</td>
<td></td>
<td>0.2</td>
<td>0.19</td>
<td>2–4</td>
<td></td>
</tr>
<tr>
<td>Residual variation at 3-month slaughter age</td>
<td>4.4</td>
<td>0.64</td>
<td>74</td>
<td>4.0</td>
<td>0.61</td>
<td>70</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Residual variation at 8-month slaughter age</td>
<td>3.7</td>
<td>0.56</td>
<td>71</td>
<td>3.7</td>
<td>0.57</td>
<td>68</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Residual variation at 14-month slaughter age</td>
<td>4.7</td>
<td>0.69</td>
<td>75</td>
<td>4.9</td>
<td>0.72</td>
<td>74</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Residual variation at 22-month slaughter age</td>
<td>6.2</td>
<td>0.85</td>
<td>80</td>
<td>7.5</td>
<td>1.01</td>
<td>81</td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

*Value depends on slaughter age.*
The present study shows that the metabolic rate of adipose tissue differs with age and genotype of sheep. When an animal is growing from a young age (from birth), bone and muscle growth continues in preference to fat deposition (Searle et al. 1972; Bergen 1974). During the growth phase of a lamb, nutrients are partitioned towards muscle and bone development and the rate of fat deposition in the body is relatively low. As the muscle growth begins to slow with age, the rate of fat deposition increases in the body and the animal enters into the fattening stage, where accumulation of fat occurs. Vernon (1980) reported that sheep enter into a fattening stage from 200 to 250 days (7–8 months) and this may be earlier in rapidly maturing breeds.

Around 10% of the total random variation of fat and lean content at the same carcass weight is contributed by variation between sires and 10% by variation between ewes. This equates to a heritability of \( \frac{4s^2}{s^2 + \sigma^2_{	ext{residual}}} \). This implies that there is plenty of scope for genetic selection to change carcass composition within genotypes grown to the same carcass weight (i.e. to reduce fatness at the same weight). However, there was no difference between the PDm sires compared with the PDg sires in this study in either fatness or lean meat content. This implies that the process used for selection of PDm sires was not beneficial for improving the lean meat content of animals slaughtered at the same carcass weight, given the sires sampled for this study. Our results indicate that there is plenty of scope to research and implement new strategies for improving lean meat content and fatness at given weights, within genotypes or breeds. The greater leanness and lower fat percentage in wethers compared with ewes slaughtered at the same weight was expected (e.g. Lee et al. 1990).

**Conclusions**

There is plenty of scope for genetic selection to change carcass composition within sheep genotypes grown to the same carcass weight (i.e. to increase lean meat content at the same weight), although effective measurement strategies to identify the best animals might need further research and development. Purebred M animals are able to achieve similar weight/composition specifications to crossbreds, albeit at a later age and with increased costs of production.

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**References**


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