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Association of wool growth with gut metabolism and anatomy in sheep

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ABSTRACT

The hypothesis tested by this study was that sheep with divergent estimated breeding values (EBV) for fleece weight differ in gut metabolism and anatomy; regardless of the level of intake. Adult Merino wethers with contrasting EBVs for fleece weight were fed at two levels of intake in two 7-week periods in a crossover design, where wool growth, gut metabolism and anatomy of the sheep were evaluated. Regardless of the level of intake, wool genotype affected wool growth ($P < 0.05$); however, rumen metabolism and gut anatomy did not differ between wool genotypes ($P > 0.05$). Increases in the level of intake increased the supply of nutrients to the animal and the measured end-products of the process (wool production, live weight, methane) independent of wool genotype. The results obtained in this study indicate that differences in gut fermentation and anatomy are not a major cause of differences in wool production among sheep of different estimated genetic merit for fleece weight when fed restricted intakes.

1. Introduction

Improving nutrient utilization and the efficiency of feed conversion into animal products is a constant major challenge in animal nutrition (Poppi and McLennan, 2010; Herrero and Thornton, 2013). Changing the yield of animal product (i.e. wool and meat) arising from feed consumed can be achieved by dietary change (Leng, 1990) or by selecting animals for either smaller residual feed intake (Waghorn and Hegarty, 2011) or greater animal growth efficiency (Oddy, 1999). As wool growth is a trait expressed on the periphery of the animal, Oddy (1999) suggested that selection for wool growth may affect the environment in the rumen, and consequently the amount of nutrients produced by the bacterial population, and available to the animal.

Sustained divergent genetic selection for wool growth has demonstrated that differences in wool growth are associated, at the micro-structure of the skin, with: follicle density, ratio of secondary to primary follicles, depth of the follicles into the skin, area of mitotically active follicle tissue and rate of incorporation of cortical cells into fibre (Williams and Winston, 1987; Nancarrow et al., 1998). At the whole-animal level, selection for wool growth changes fractional protein synthesis rate and total protein synthesis in the skin, proportion of follicular tissue in the skin, proportion of active follicles and the efficiency of follicles and turnover rate of body protein (Masters et al., 2000; Adams et al., 2004). Li et al. (2006–2008) working with two groups of Merinos that differed in their average estimated breeding value (EBV) for clean fleece weight found that the differences in wool growth were also

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associated with differences in skin and protein masses, methionine usage in the skin, efficiency of utilizing amino acids available to the body for wool production and retention of ingested protein in wool and body tissue.

In addition, evidence of differences in portal amino acid uptake and ruminal microbial protein supply between genetic lines of sheep selected for or against wool growth has been documented. Sheep selected for more wool growth have, at the same feed intake, a greater uptake of α amino nitrogen in portal blood than animals selected for less wool growth (Lush et al., 1991) and a greater microbial protein outflow from the rumen (Kahn, 1996). Kahn (1996) found the differences in the yield of microbial protein from the rumen are explained by the variation in the yield of microbial protein per unit of dry matter intake (35% of the variation) and the variation in dry matter intake (65% of the variation), while digestibility of feed did not differ between these lines of sheep. Herd and Arthur (2009), based on these results, indicated that genetic differences in the processes of digestion and in nutrient availability can occur, hence, may explain the observed variation in efficiency of feed utilization.

It is hypothesized that differences in fleece production between sheep divergently selected for wool growth based on EBVs may be partially explained by differences in gut metabolism and morphology. This experiment also sought to detect the robustness of these relationships across different levels of intake.

2. Materials and methods

All research work was conducted in accordance with the University of New England Animal Ethics Committee (AEC approval no. 12/045).

2.1. Animals, treatments and experimental design

Twenty 33-month-old Australian Merino wethers were selected from a group of 83 wethers at Trangie Agricultural Research Center (Trangie NSW, Australia). Selection was based on the following information: (a) estimated breeding values for yearling clean fleece weight, yearling fibre diameter and yearling live weight (EBV, MerinoSelect ASBV, www.sheepgenetics.org.au), (b) phenotypic information of greasy fleece weight, live weight and fibre diameter from the three previous shearing, and (c) pedigree information (sires and dams). From these sheep, two sub-groups ($n=10$) with divergent average EBVs for clean fleece weight (wool genotype, WG, plus and minus), but similar EBVs for live weight and fibre diameter were established (Table 1). The average clean fleece weight EBV for minus (WG−) and plus (WG+) wool genotype groups was 6.2% and 28.1%, respectively. Across all sheep average fibre diameter and live weight EBVs were −2.0 μm and 2.9 kg, respectively, and did not differ between groups. An incomplete cross-over design assessing the two factors (wool genotype and level of intake) was implemented. Two intake levels were evaluated, being 1.0× and 1.5× maintenance energy requirements (1 × M and 1.5 × M, respectively). The levels of intake were fixed for the experimental period and they were calculated (SheepExplorer, 2003) for wool-sheep housed indoors based on the average live weight of the 20 animals at the beginning of the experiment. The trial was divided in two periods of seven weeks each. In the first period half of the animals of each wool genotype were chosen at random to be fed at 1 × M and the other half were assigned to 1.5 × M. In the second period, the level of intake of each animal was swapped. Each period was comprised of an initial four weeks for acclimatization with three subsequent weeks when measurements were performed. Sheep were fed once a day in the morning (at 10:30 h) with a blend of oaten and lucerne chaff (Manuka Feeds Pty Ltd; CP, 14.5%; ME, 9.1 MJ/kgDM; DM, 89.5%; DMD, 61%). They weighed 57.2 ± 8.3 kg and their mean condition score was 3.1 ± 0.6 units (Russel et al., 1969). Animals had ad libitum access to fresh water and they were housed in individual metabolic cages.

Table 1
Genetic and phenotypic values for clean or greasy fleece weight, live weight and fibre diameter in accordance with the wool genotype group at the beginning of the experiment (mean ± s.e.).

	Wool genotype	
	WG+	WG−
Yearling clean fleece weight EBV (%)	28.1 ± 2.0[a]	6.2 ± 2.4[b]
Yearling live weight EBV (kg)	3.2 ± 0.8	2.5 ± 0.9
Yearling fibre diameter EBV (μ)	−1.7 ± 0.3	−2.3 ± 0.4
Yearling greasy fleece weight (kg)	5.09 ± 0.19[a]	3.83 ± 0.21[b]
Yearling live weight (kg)	49.0 ± 1.6	50.4 ± 1.8
Yearling fibre diameter (μ)	18.0 ± 0.5	17.0 ± 0.6

[a,b] Means within rows and factors with differing letter are significantly different ($P<0.05$). (WG+) greater EBV for wool fleece weight. (WG−) smaller EBV for fleece weight.

2.2. Live weight, condition score and wool measurements

Animals were weighed every 7 days in the morning prior to feeding, and condition score (Russel et al., 1969) was assessed fortnightly at the time of weighing. Greasy and clean wool growth rate, yield, fibre diameter and coefficient of variation of the fiber diameter were measured on the midside of the sheep between day 0 (after 28 days acclimatization period) and day 21 by clipping a patch approximately 10 × 10 cm (Oster Golden A5 clippers, blade size 30 model Cryogen X, USA) as described by Langlands and Wheeler (1968) in each period. Staple length (6 measures per patch) was measured on each animal using a metal ruler before the clipping of the wool. After the wool from the patch was clipped, four sides and one diagonal of the patch were measured and the area of the patch was calculated using Heron's formula for calculating both triangles included in each patch rectangle. Wool yield was estimated by the methodology of Thompson and Hynd (1998) with minor variations. Clipped wool was conditioned at 20 ± 2 °C and 65 ± 2% relative humidity and weighed 24 h later to determine greasy wool weight. Wool samples were cleaned in hexane (3 × 10 min) and water (65 °C; 2 × 10 min), dried to a constant weight at 70 °C, and re-weighed after 24 h at 20 ± 2 °C and 65 ± 2% relative humidity. The washing yield (%) was calculated using the following formula: clean wool weight (g/cm^2 per day)/greasy wool weight (g/cm^2 per day) × 100. After scouring, all wool samples were conditioned at 20 ± 2 °C and 65 ± 2% relative humidity for 24 h prior to