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**The effect of high lipid sheep diets on fatty acids of liquid and solid associated rumen bacteria.** RJB Bessa, MA Almeida, JMR Ribeiro, AV Portugal (INIA, Estação Zootécnica Nacional, Department of Nutrition, Fonte Boa, Vale de Santarém, 2000 Santarém, Portugal)

Three rumen fistulated rams were used in a 3x3 Latin square experimental design in which the control diet (C) was dehydrated alfalfa pellets and wheat straw. The treatments consisted of soybean oil, mixed with milled alfalfa before pelleting which resulted in final lipid contents of 8% (SO6) and 14% DM (SO12). The rams were fed twice a day near maintenance (40g of lipid free DM gLW<sup>0.75</sup>). The rumen contents were collected before the morning meal, and 1.5, 3 and 6 hours after that meal. The liquid and solid phases of the four collection times were pooled. The solid phase

was washed with a 37°C isotonic solution and stored overnight at 4°C in a pH2 isotonic solution with 0.1% Tween 80 and treated as described by Whitehouse *et al* [1]. The samples were centrifuged for 20min at 500g and the resulting supernatants centrifuged for 30min at 20000g. Fatty acids (FA) analyses were made by a one-step extraction-methylation [2], using benzene as solvent and C19:0 as internal standard. Fatty acid methyl esters were analysed by GC.

The inclusion of soybean oil increased the FA contents of rumen bacteria although this effect was more evident in solid-associated (SAB) than liquid-associated bacteria (LAB). C18 acids contributed 80-90% of this increase. Among the C18 acids, C18:0 and C18:1 *trans*11 (C18:1t11) were the most important and contributed respectively 43 vs 31% in SO6 treatment and 28.5 vs 42% in SO12 treatment. This increase of C18:1t11 suggested a reduced ability for the complete hydrogenation of C18:2n-6. The quantity of odd-numbered FA (Odd-FA) did not vary between SAB and LAB

Fatty acid content of bacteria associated with the solid and liquid phases of rumen contents

Fatty acids	C		SO6		SO12		SEM	T	P
	SAB	LAB	SAB	LAB	SAB	LAB			
FA. Mg g <sup>-1</sup>	156.0 <sup>b</sup>	67.2 <sup>a</sup>	310.8 <sup>c</sup>	123.3 <sup>d</sup>	350.9 <sup>d</sup>	121.0 <sup>b</sup>	11.19	*	*
C18:0	32.08 <sup>bc</sup>	19.37 <sup>a</sup>	37.87 <sup>d</sup>	29.86 <sup>b</sup>	33.37 <sup>c</sup>	20.46 <sup>a</sup>	0.99	*	*
C18:1t11	5.25 <sup>a</sup>	2.81 <sup>a</sup>	20.03 <sup>bc</sup>	14.01 <sup>b</sup>	23.84 <sup>c</sup>	21.80 <sup>c</sup>	2.28	*	
C18:1cis9	10.48 <sup>d</sup>	2.95 <sup>a</sup>	8.37 <sup>c</sup>	4.59 <sup>b</sup>	7.47 <sup>c</sup>	3.90 <sup>ab</sup>	0.43		*
C18:2n-6	1.86	1.62	1.98	1.78	2.13	1.78	0.40		
C18:3n-3	1.09 <sup>b</sup>	1.98 <sup>c</sup>	0.33 <sup>a</sup>	0.51 <sup>a</sup>	0.30 <sup>a</sup>	0.64 <sup>ab</sup>	0.14	*	*
Odd-FA	3.16 <sup>b</sup>	5.91 <sup>c</sup>	1.14 <sup>a</sup>	2.81 <sup>b</sup>	0.88 <sup>a</sup>	2.58 <sup>b</sup>	0.23	*	*
BC-FA	3.03 <sup>b</sup>	8.11 <sup>d</sup>	1.30 <sup>a</sup>	4.49 <sup>c</sup>	0.91 <sup>a</sup>	4.65 <sup>c</sup>	0.40	*	*

\*Significance for error level P<0.01; T- treatment; P- SAB vs LAB. Averages with different index (a,b,c,d) are significantly different. SEM - standard error

and decreased with the treatment.

Branched chain FA (BC-FA) were higher in LAB than in SAB and were not affected by the treatment. The proportion of C18:2n6 remained constant, although its quantity increased in SAB when oil was included. The C18:3n3 decreased as oil inclusion increased. The table shows the total FA contents (mg g<sup>-1</sup>) and some FA expressed as a proportion of total FA.

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**Microbial forestomach populations of the sheep and kangaroo.** SK Baker (CSIRO Division of Animal Production, Floreat Park, 6019, Western Australia)

Classification according to size of the organisms in a community is a fundamental description of the structure of that community. When rumen microorganisms are classified according to cell size the population can be described by linear regression equations and comparisons of the regression coefficient (b) constitute comparisons of the size structures of the populations [1]. For a range of dietary conditions the size structure of the rumen population in sheep is unchanged and appears to be characteristic of a stable rumen population. The size structure of the microbial population in the forestomach of the quokka a macropod marsupial [2], resembles that of the rumen populations of the sheep. A comparison of the size structures of the microbial populations of the forestomach of the western grey kangaroo (*Macropus fuliginosus*) and of the rumen

of sheep when the animals grazed in the same pasture is reported here.

Digesta from the sacciform region of forestomachs of western grey kangaroos and from the reticulo-rumen of sheep with rumen cannulae were used as inocula in a study to determine if ciliate protozoa from the kangaroo would establish in the sheep rumen [3]. The sheep and kangaroos grazed in the same pasture. Digesta also was collected from sheep fed oaten hay, lupin grain and minerals (78:20:2). At each sampling digesta were combined from three animals and diluted in formol saline. Microorganisms comprising bacteria and archaea, were counted and classified according to cell size between ca. 0.5 and 9µm (expressed as the diameter of a sphere of equivalent volume) using a Coulter counter.

As found in sheep, concentrations of microorganisms in digesta from the sacciform region of the forestomach of western grey kangaroos were a decreasing function of cell size ( $p < 0.05$ ), and the size structures of the populations from sheep and kangaroos grazing together were similar. The ciliate protozoa in these kangaroos differed from recognised rumen species [4], yet the similarities in the size structures of the populations suggested that trophic relationships in the kangaroo forestomach may have evolved similarly to those in the rumen, despite the evolutionary differences of the host animals.

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