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^{-1}) 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 fuligninosus*) 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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Size structure of rumen bacterial populations.

Digesta from:	*Date of sampling*	*b*[1]	*se*	*rsd*	r^2
Grazing sheep	October	-2.75 ab	0.105	0.036	0.966
Grazing kangaroos	October	-2.77 a	0.058	0.011	0.990
Grazing kangaroos	November	-2.41	0.034	0.004	0.995
Pen-fed sheep	December	-3.00 b	0.073	0.018	0.986

[1] Values followed by the same letter are similar ($p > 0.05$), indicating similar size structures.

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ANAEROBIC FUNGI

Molecular approaches to the characterisation and differentiation of the anaerobic gut fungi.

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Anaerobic fungi within the digestive tract of ruminants play an important role in the degradation of structural plant polysaccharides ingested by the host animal. Since their discovery, several different approaches have been adopted to isolate and characterise a variety of different fungal isolates. The fungi have been placed within the class *Chytridiomycetes* and assigned their own order *Neocallimastigales* which contains a single family the *Neocallimastigaceae*. To date, five genera have been described within the Neocallimastigaceae, as follows: *Anaeromyces, Caecomyces, Neocallimastix, Orpinomyces* and *Piromyces*. The designation of a genus is largely dependent upon morphological characteristics, such as the number of zoosporangia per thallus (i.e. one zoosporangium for a monocentric thallus or many zoosporangia for a polycentric thallus) and the number of flagella present on the uni-, bi- or multi-flagellated zoospore, whereas assignment at the species level is by zoospore ultrastructure. In addition to these classical taxonomic approaches, gut fungi have also been investigated using a variety of physiological, biochemical and (more recently) molecular techniques.

We have used the ribosomal ITS1 DNA sequence as a phylogenetic tool for comparing a variety of fungal isolates obtained from different host animals in widely-different geographical locations to assess the relatedness within and between different gut fungal genera. The ribosomal ITS1 sequence has been amplified from 22 different isolates spanning the *Neocallimastigaceae* family. The DNA sequence of this region has been determined and, together with other published sequences, used to construct a phylogenetic analysis of the order. Analysis of these ITS1 DNA sequences has enabled the production of a series of genera- and species-specific probes. These probes have then been used to develop membrane-based assays for the