

# Diet and breed affected the ruminal microbiota of White Suffolk and Poll Merino ewes

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Diet is one of the main factors influencing ruminal microbial populations (de Menezes et al., 2011) and the microbiota in the ruminal is the link between diet and the host animal (Weimer et al., 1999). Research has assessed ruminal microbial differences related to breed, but focused mainly on cattle. In beef cattle, different sire breeds (Angus, Charolais and a hybrid) have been linked to particular ruminal microbiomes, more evident when the cattle are fed different diets, further differentiating the populations (Hernandez-Sanabria et al., 2013). In this study, we aimed to determine whether breed differences influence the ruminal microbiota composition of Poll merino and White suffolk ewes, and if their ruminal microbiota respond similarly to changes in diet.

The study utilised 24 White suffolk and 24 Poll merino ewes, randomly assigned to either a roughage type diet or a high-grain diet. The high-grain diet consisted of 80% pellet and 20% chaff, whereas the roughage diet consisted of 20% pellet and 80% chaff. Once the ewes had been on their allocated diet for 21 days they each had a ruminal sample taken and analysed for ruminal bacterial communities using 16S rRNA sequencing. The ewe's entry and exit weight, and feed intake were also measured.

There was a preference for the high-grain diet ( $P < 0.0001$ ), with greater amounts of this diet consumed, although no significant difference in ewe weights between the two dietary treatments were observed. However, the suffolk ewes lost weight on the roughage diet while all other groups gained weight (suffolk roughage  $5.91 \pm 2.62$  kg, suffolk high-grain  $7.83 \pm 1.66$  kg, merino roughage  $9.18 \pm 2.65$  kg, merino high-grain  $4.99 \pm 1.76$  kg). There were significant ruminal bacterial differences associated with both diet and breed, with breed differences most evident on the roughage diet. The average dissimilarity in ruminal bacterial phyla associated with diet was 14.13%, with the top 50% of phyla contributing to the dissimilarity being Verrucomicrobia, Lentisphaerae, Elusimicrobia, SR1 and Fibrobacteres, which were significantly more abundant in the roughage dietary group, and Proteobacteria, which were significantly more abundant in the high-grain dietary group. There was greater variation between individuals in ruminal bacterial populations on the high-grain diet but greater diversity within the populations of ewes on the roughage diet.

**Table 1: Two-way ANOSIM of ruminal bacterial communities associated with sheep breed and diet for each of the bacterial taxonomic groups investigated.**

Parameter	R and P values <sup>a</sup>					
	Phyla	Class	Order	Family	Genus	Species
Diet	<b>0.543</b> , <i>0.001</i>	<b>0.628</b> , <i>0.001</i>	<b>0.654</b> , <i>0.001</i>	<b>0.661</b> , <i>0.001</i>	<b>0.590</b> , <i>0.001</i>	<b>0.594</b> , <i>0.001</i>
Breed	<b>0.077</b> , <i>0.017</i>	<b>0.176</b> , <i>0.001</i>	<b>0.162</b> , <i>0.001</i>	<b>0.153</b> , <i>0.001</i>	<b>0.164</b> , <i>0.001</i>	<b>0.172</b> , <i>0.001</i>

<sup>a</sup> The Global R statistic (indicated in boldface) and significance (indicated in italics) are shown for each of the factor's bacterial taxonomic levels. The Global R value describes the extent of similarity between each pair in the ANOSIM, with values close to unity indicating that the two groups are entirely separate and a zero value indicating that there is no difference between the groups.  $P < 0.05$  is significant.

We hypothesised that a difference between breed would be seen and that breed would affect how microbial populations react and change with diet. We can show clearly that diet has affected both breed's rumen bacterial populations and that the microbiota of the two breeds react differently to changes in diet. We also hypothesised that the difference between the microbes would be greater with imposed diet than the differences created by genetic differences (breed). This hypothesis is supported by this study, as there are clear differences among microbial profile of ewes fed a high roughage and a high-grain diet following 21 days on a stable diet, regardless of breed. As expected, diet had a large effect on the microbial profiles of both breeds, but importantly we demonstrate that the microbiota was also strongly influenced by sheep genotype. The differences in microbial composition between breeds was related to some of the animal productivity differences of the two breeds, indicating that at least some of the genetic differences in animal productivity are generated by differences in the responsiveness of the ruminal microbiota to diet.

## References

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