

Linking the genotype of the host with rumen bacterial communities in sheep

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Divergent genetic selection for wool growth as a single trait has led to major changes in sheep physiology, including variations on rumen microbial protein production and uptake of amino nitrogen in portal blood. **This study was conducted to determine if sheep with different genetic merit for wool growth under commercial conditions have distinct rumen bacterial populations.**



- Eighteen Merino wethers were separated into two groups of contrasting estimated breeding values for clean fleece weight (Low and High).
- They were fed oaten/lucerne chaff at two levels of intake (1.0-M or 1.5-M maintenance) for two seven-weeks periods in a crossover design.
- Bacterial diversity, in rumen fluid, was characterised using 454 amplicon pyrosequencing of the V3/V4 regions of the 16S rRNA gene.
- Data was analysed using Mothur, Acacia, Qiime and SAS software packages with operational taxonomic units (OTUs) determined at 97% sequence similarity.

Effect of wool genotype and level of intake

	Wool genotype		Level of intake	
	Low	High	1.0-M	1.5-M
Chao1	2292	2385	2362	2314
Phylogenetic distance	61.8	64.0	64.1	61.7
Observed species	914	954	945	923
Shannon-Wiener index	7.67 ^b	8.02 ^a	7.94	7.75
Phylum (% of sequences)				
Bacteroidetes	71.9 ^a	66.5 ^b	68.6	69.8
Firmicutes	26.6 ^a	31.6 ^b	29.8	28.5

^{ab}Means within rows and factors (wool genotype and level of intake) with differing letters are significantly different ($P < 0.05$). There were no interactions between the evaluated factors.

- Bacterial diversity estimated by Shannon-Wiener diversity index differed between wool genotypes.
- Differences (% of sequences) at Phylum, Class, Order, Family and Genus level were found between both wool genotypes.
- Principal Coordinate Analysis did not indicate any particular cluster according with wool genotype, level of intake or their interaction.
- Twenty-four specific OTUs, belonging to Firmicutes and Bacteroidetes phyla, were shared among all the samples.
- Thirty-seven specific OTUs varied significantly in presence/abundance ($P < 0.05$) between wool genotypes and fifty varied ($P < 0.05$) between levels of intake.



Conclusion:

Sheep with divergent estimated breeding values for fleece weight may harbour different rumen bacterial communities that persist across different feeding levels