Host genetics a potent modulator of ruminal microbial activity in dairy ewes?

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Introduction: Weimer et al. (2010)[1] showed that their 4 dairy cows could totally or partly restore their bacterial activity after a total exchange of their ruminal contents, underlying that cow genetics could shape the ruminal microbial activity. Our preliminary study explores the possibility of a host genetics effect on ruminal microbial activity in dairy ewes, in particular towards *trans*11 fatty acids (FA) ruminal proportion, supposed beneficial for human health[2].

Material and methods: Four divergent lines of Lacaune ewes were used: one group selected on somatic cell count, called SCC- and SCC+ lines, and other on milk production persistency, called PERS- and PERS+ lines, for a total of 4 × 30 multiparous ewes. They were allotted by their lactation number and litter size, in order to have 4 homogenous groups. At the beginning, ewes weighed 77 kg, produced 1.5 kg of milk and were at 125 DIM, on average. Milk contained on average 9.6×10^5 cells / mL for SCC+ compared to 1.9×10^5 cells / mL for others. They were fed a 93% meadow hay and silage diet. Ruminal content were sampled twice on each ewe one week apart, using a stomach tube and a vacuum pump, and milk samples were done the same two days. Rumen volatile FA (VFA) and unsaturated FA (UFA) of rumen were assayed by GC. Statistic computations were done with a mixed model, taking into account the lines, days of measurements, parity and litter size as fixed effects, and the animal as random effect, with the Mixed procedure of SAS software. The intra-animal repeatabilities were estimated as the ratio between the animal variance and the total variance of the model. An ethic committee approved this experiment.

Results: Repeatability was moderate to high for rumen butyrate, monoUFA (MUFA), polyUFA (PUFA) and *trans*11 FA proportions but very low for total rumen VFA concentration. Among SCC lines, SCC- had slightly higher proportions of MUFA and *trans*11 in their rumen than SCC+. Among PERS lines, PERS- had a slightly higher proportion of acetate but a slightly lower proportion of butyrate than PERS+.

Table 1: Least squares means (± standard error) of the lines effect and repeatability estimates on ruminal VFA and UFA, and milk UFA in the divergent lines of Lacaune ewes.

	SCC+	SCC-	PERS+	PERS-	repeatability
Rumen					
Total VFA, mmol/L	52.74 ± 1.91	49.26 ± 1.89	66.57 ± 1.84	63.82 ± 1.88	5%
acetate, molar%	71.87 ± 0.24	71.78 ± 0.24	**69.71^{b} ± 0.23**	**70.41^{a} ± 0.24**	12%
propionate, molar%	14.37 ± 0.12	14.38 ± 0.12	15.59 ± 0.12	15.53 ± 0.12	14%
butyrate, molar%	10.50 ± 0.12	10.59 ± 0.12	**11.58^{a} ± 0.12**	**10.94^{b} ± 0.12**	36%
MUFA, % total FA	**8.83^{b} ± 0.09**	**9.17^{a} ± 0.09**	8.96 ± 0.08	8.94 ± 0.09	30%
PUFA, % total FA	6.69 ± 0.11	6.95 ± 0.11	7.72 ± 0.10	7.54 ± 0.10	44%
*trans*11, % total FA	**3.41^{b} ± 0.06**	**3.61^{a} ± 0.06**	3.30 ± 0.06	3.43 ± 0.06	30%

^{a,b} significant (P<0.05) difference intra line-group (SCC+ *vs.* SCC-; PERS+ *vs.* PERS-; n=30 per line)

Discussion and conclusion: The effects of genetic line were biologically slight, because of high individual variations in each group, suggesting that these selections have no strong effect on ruminal activity. Nevertheless the high repeatability of butyrate and UFA proportions is encouraging to pursue studies on the link between host genetics and the ruminal microbiota activities.

References: [1]Weimer et al. (2010): J Dairy Sci 93:5902-12; [2]Or-Rachid et al. (2009)-: Appl Microbiol Biotechnol 84 :1033-1043