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Comparative fibrolytic activity of different microbial populations from rabbit caecum and bovine rumen

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As in the bovine rumen, plant cell walls are degraded in the rabbit caecum by enzymes produced by fibrolytic microbial flora. The caecal microflora contrasts from that of the rumen by absence of protozoa and predominance of Bacteroïdes species. In the rumen, solid-associated bacteria (SAB) represent the most important bacterial population (about 75 %) (Legay-Carmier and Bauchart, 1989, Br J Nutr, 61, 725-740), and differentiate from the liquid-associated bacteria (LAB) by both their chemical composition (Merry and Mc Allan, 1983, Br J Nutr, 50, 701-709) and their higher glycolytic activity (Martin *et al*, 1993, Curr Microbiol, 27, 223-228). In the rabbit caecum, distribution and enzyme activity of the microbial population are not well known.

The aim of this study was to evaluate whether the separation between liquid and solid-associated caecal bacteria is opportune or not, and to compare the fibrolytic activity of rabbit caecal bacteria and ruminal bacteria.

The experiment was conducted with rabbits fed *ad libitum* and cows restricted to 80 % *ad libitum*, on fibre rich diets : 40 % (NDF) for the two rabbit diets (diets 1 and 2) and 60 % for the cow diet (diet 3). Caecal contents were collected at the end of the caecotrophy period (11 am) and ruminal content 23 h after feeding. After sonication under anaerobic conditions, samples from SAB and LAB (diets 1 and 3) or whole bacteria (WB) (diet 2) were assessed for their cellulolytic (CMCase and avicelase) and hemicellulolytic (xylanase) specific activities (Williams and Strachan, 1984, Curr Microbiol, 10, 215-220).

Ruminal LAB were not involved in plant cell wall polysaccharides degradation. In the rabbit caecum, the fibrolytic activity was similar in SAB and LAB, but showed an important variability, suggesting a transitory or a random distribution between SAB and LAB population. In contrast, the fibrolytic activity of whole bacterial population (WB) had a variability similar to that registered for rumen SAB. In addition, the great homogeneity of caecal digesta and its high DM level (20 %), contrasted with those of the rumen. Thus, the fractionation of caecal flora into free and adherent bacteria seemed not justified. Activity of the caecal WB was lower than ruminal SAB, but contamination of the enzymatic extract by endogenous proteins may induce an underestimation of the specific enzyme activity in the caecum. Nevertheless, the measurement of enzyme activity seems to be an interesting approach to study the rabbit microbial caecum ecosystem and its eventual modifications by the dietary conditions.

Enzyme activity	caecum			rumen	
	diet 1		diet 2	diet 3	
nmole or reducing sugars released/mg proteins/min	SAB (n = 6)	LAB (n = 5)	WB (n = 8)	SAB (n = 4)	LAB (n = 4)
Xylanase	946 ± 955	1472 ± 1120	1446 ± 406	7706 ± 3514	0
CMCase	581 ± 436	362 ± 361	424 ± 92	838 ± 479	0
Avicelase	263 ± 193	206 ± 227	432 ± 130	760 ± 313	0