



Effect of live yeast on bacterial variability in the rumen of dairy cows

Objective: Evaluate the effect of Actisaf® Sc 47 on the ruminal microbiota in lactating dairy cows.

Trial design

Experimental study
Location: France

Species/life stage

Mid-lactation dairy cows
Breed: Holstein

Main criteria

Analysis of the bacterial population in the rumen of dairy cows.

Reference

Julien C. *et al.*, 8th INRA-RRI symposium, 2012.

Protocol

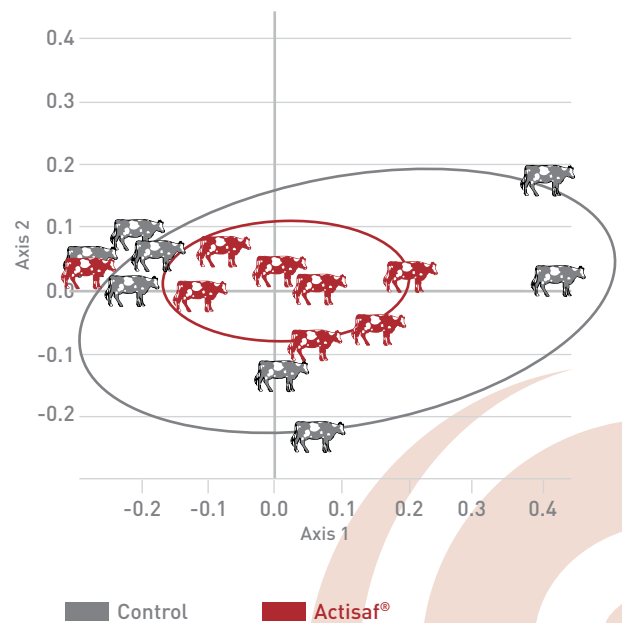
4 x 4 latin square design
4 cows
4 periods



Main results

Even minor changes to dairy cows' diet lead to significant changes in the ruminal microbiota. Actisaf® Sc 47 supplementation reduces these inter-individual variations, leading to more similar rumen bacterial profiles.

Effect of Actisaf® on bacterial variability in the rumen of lactating dairy cows



Conclusion

Actisaf® Sc 47 supplementation decreased the inter-individual variability of ruminal microbiota, suggesting that live yeast has a stabilising effect on the microbiota. Therefore, Actisaf® Sc 47 could help to decrease variability within the herd and stabilise the farm's milk production by enhancing microflora balance in cows under challenging conditions.

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Introduction

The aim of the study was to investigate the variability between cows of the rumen microbial population and their response to different diets.

Materials and methods

Four lactating Holstein cows in mid-lactation (DIM = 142±20; 32.3±4.2 kg milk/cow/day) were assigned to different diets according to a 4×4 Latin square design.

Specifically, they were fed two diets formulated to contain 65% maize silage, 18% soybean meal and 17% wheat (rapidly digestible starch - Diet A) or 16% maize (slowly digestible starch - Diet B).

The treatments were as follows:

- **Control group:** cows were fed Diet A or Diet B only, without any live yeast supplementation.
- **Actisaf® group:** cows were fed Diet A or Diet B and supplemented with 5g/cow/day of Actisaf® Sc 47.

Characterisation of the ruminal microbiota was achieved using the V3-V4 hypervariable regions of the 16S RNA gene by 454-pyrosequencing.

Results and discussion

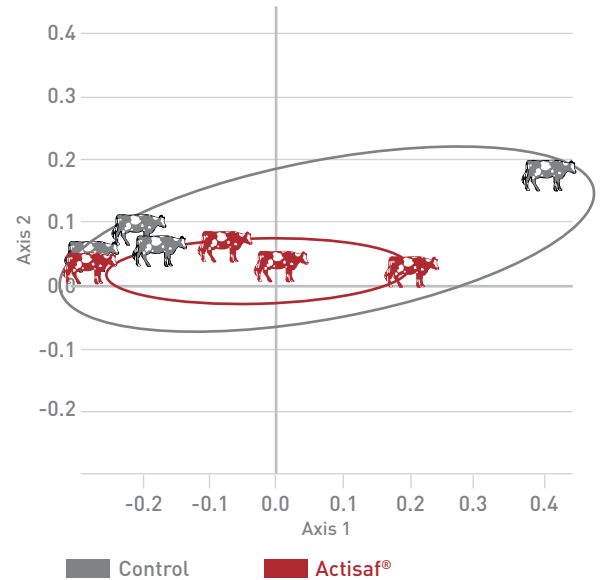
Among the 249 genera found, a total of 177 genera of rumen bacteria were identified (63.5% of total sequences):

- Dominance of *Prevotella* genus = 23.8% of sequences assigned at genus level.
- *Ruminococcaceae Incertae Sedis* relative abundance was significantly higher with Diet A than Diet B (7.74% and 0.68% of total sequences assigned to genus level, respectively).

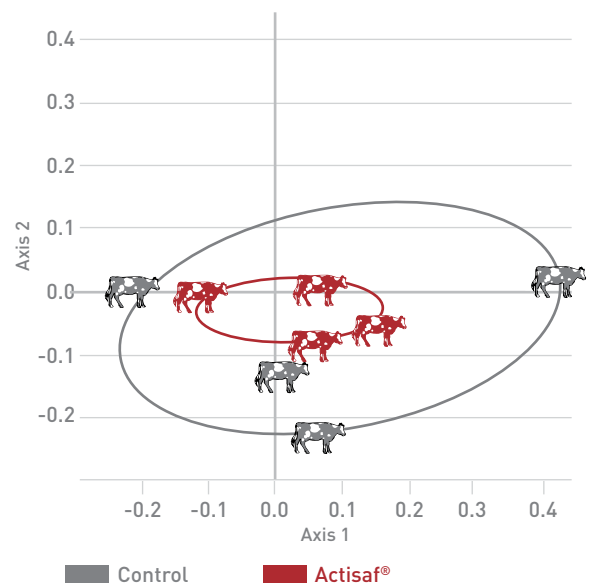
Bacteroidetes (44.8%) and *Firmicutes* (33.2%) were dominant and unaffected by diet and live yeast, as was the dominant *Prevotella* genus.

Adding 5g/cow/day of Actisaf® Sc 47 to the diet greatly reduced the inter-individual variability of the ruminal microbiota, suggesting a stabilisation of the ruminal ecosystem.

Effect of Actisaf® on bacterial variability in the rumen of lactating dairy cows fed with Diet A



Effect of Actisaf® on bacterial variability in the rumen of lactating dairy cows fed with Diet B



Conclusion

Actisaf® Sc 47 supplementation helps to decrease inter-individual variability of microbiota between cows whatever the diet, and therefore to reach a more consistent performance of the herd.

Keywords Actisaf® Sc 47, live yeast, rumen bacterial population.

Reference Julien C., Cauquil L., Combes S., Bouchez O., Marden J.P., Bayourthe C., Study of the effect of Live Yeast *Saccharomyces cerevisiae* (CNCM I-4407) on ruminal bacterial community in lactating dairy cows using 454 GS FLX pyrosequencing. 8th INRA-RRI symposium, 17-20 June 2012, Clermont-Ferrand, France.