

Metagenetic analysis of the bacterial flora dynamics of biopreserved pork meat

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Introduction

The objective of this study was to evaluate the dynamics of the bacterial flora of biopreserved and vacuum-packed pork meat stored at a temperature of -1.5° C for 12 weeks. The use of metagenetic analysis allowed a new insight into the bacterial competition taking place during storage.

Materials and methods

Pork loin was cut into three pieces and biopreserved with either *Pediococcus acidilactici* (culture 1) or *Lactobacillus sakei* (culture 2). A control sample without any added culture was also included. The study of the microbial ecosystem of pork meat was analyzed using the targeted approach of metagenetics.

The microbiological evolutions of the total flora (ISO 4833-1), the lactic acid bacteria (ISO 15214) and *Enterobacteriaceae* (NF V08-154) were monitored. At each stage of the analysis (carried out over 12 weeks), bacterial counts were obtained from five pooled samples for each treatment. Statistical analysis were performed using SAS software (V 9.2).

Results

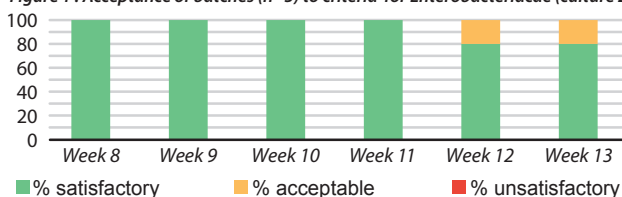
Microbiological monitoring

- Both biopreserved pork meats showed levels of total flora ranging from 7 to 8 LOG CFU/cm² over the 12 weeks.
- Total flora was mainly composed of lactic acid bacteria.
- Both cultures prevented the growth of *Enterobacteria* until W4. Culture 2 prevented the growth of *Enterobacteria* from W8 to W13 ($p < 0,005$).



Photo 1: Application of culture on pork loin

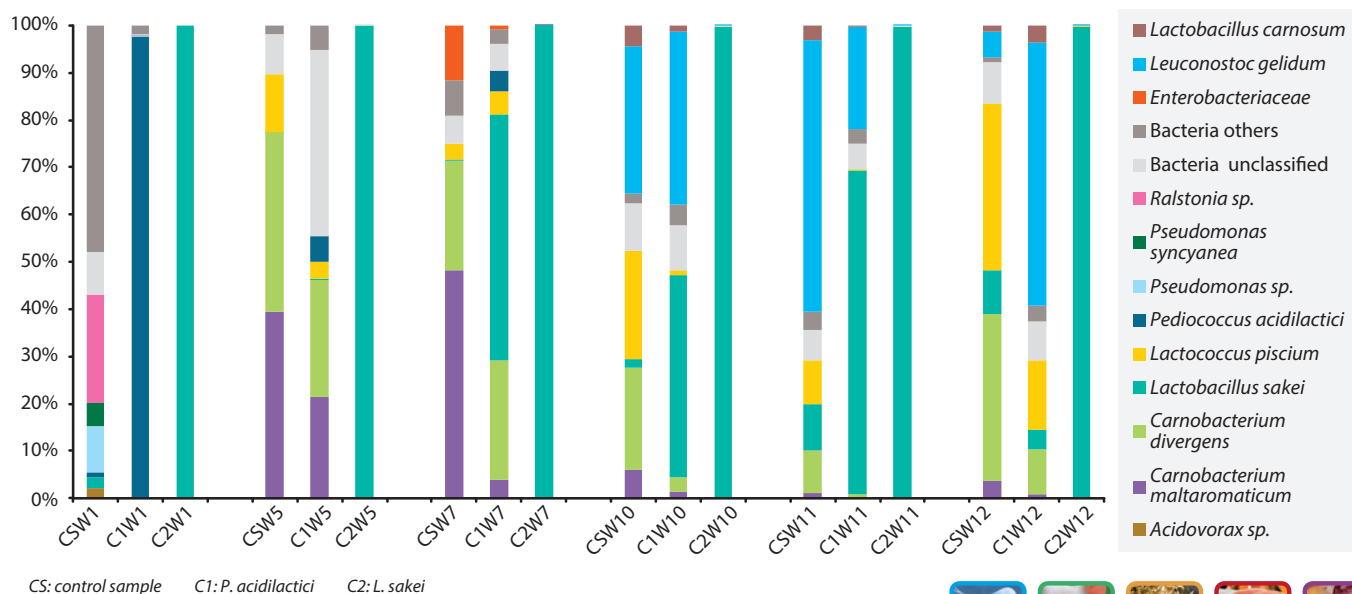
Figure 1 : Acceptance of batches (n=5) to criteria for *Enterobacteriaceae* (culture 2)



Metagenetic monitoring

- A very diverse bacterial composition of the control sample at W1 with 54 bacterial taxa and one major one : *Ralstonia* sp. Lactic acid bacteria were predominant at the end of the storage with *C. divergens* and *L. piscium* considered as spoiling bacteria.
- Culture 1 was dominant until W4 only. Then the control sample and the sample with C1 showed a similar bacterial composition. Thus C1 was not competitive and quickly supplanted by the naturally occurring bacteria in pork meat.
- L. sakei* (C2) was largely dominant regardless of the stage of the analysis. It was particularly adapted to this pork meat matrix.

Figure 2 : Proportion (%) of bacterial species in samples from weeks 1-12



Conclusions

The results of this study are very encouraging. The metagenetic analysis of the dynamic of the bacterial flora of the meat samples followed for 12 weeks has given us a new insight in bacterial competitions taking place during storage. Biopreservation represents a new breakthrough in the long-term conservation of pork cuts. However, the choice of a protective culture which is adapted to the food matrix is paramount so that the strain used is not overridden by naturally occurring microbial flora.

