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Bacterial diversity and its evolution during storage of fresh beef from different origins under different atmosphere and temperature conditions

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INTRODUCTION

Food contamination and food spoilage by bacterial organisms have always been a source of concern in food microbiology.

Despite a diverse initial microbial population, vacuum-packaging (VP) or modified atmosphere packaging (MAP), associated with chilling temperatures, will select specific flora in meat.

Furthermore, the study of the microflora of chilled beef remains a challenge since some members of the microflora may be missed or not identified by cultivation-based methods.

OBJECTIVE

The purpose of this study was to evaluate the bacterial diversity and its evolution during storage of fresh beef, depending on its origin, packaging and storage temperature, by metagenomic approach.

MATERIALS AND METHODS

Samples

- Vacuum-packaged striploins from:

United Kingdom (UK) (n = 3)

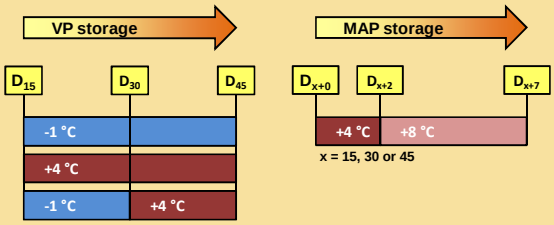
and

Belgium (BE) (n = 3)

- 15 days after slaughter: cut in slices individually vacuum-packaged. Analysis on days 15, 30 and 45.

- Each 15 days: part of VP slices were repacked under modified atmosphere (70 % O_2/30 % CO_2). Analysis on days 15+7, 30+7 and 45+7.

Storage design

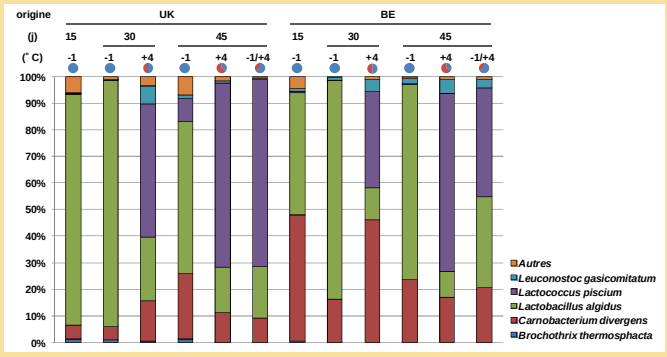


Metagenomic analysis

total DNA extraction
↓
DNA pooling (within the same batch)
↓
16S rRNA gene amplification
↓
pyrosequencing
↓
data processing

RESULTS

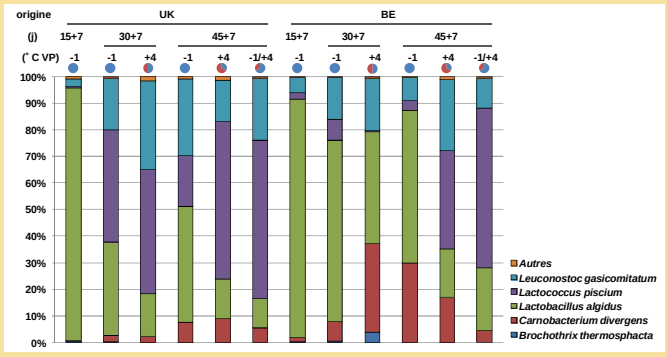
Vacuum-packaged samples



VP and −1 °C : favored *Lactobacillus algidus* growth

VP and +4 °C : favored *Lactococcus piscium* growth

Modified atmosphere-packaged samples



MAP and T > +4 °C : favored *Leuconostoc gasicomitatum* growth

Already isolated from beef, but no study has evaluated their role in meat preservation.

Spoilage of cold-stored, modified-atmosphere-packaged (MAP), nutrient-rich foods.

CONCLUSIONS

Metagenomics showed to be a useful tool to study the microbial population of a complex matrix since some of the identified genera could not have grown or have grown slowly in media commonly used. Furthermore, it helped to clarify the evolution of the bacterial ecosystem associated to meat during its storage.

The next step of this study will be to isolate and characterize strains of *Lactobacillus algidus* from meat and to assess their bioprotective potential.

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