INTRODUCTION

Meat is one of the most perishable food products on the market thus resulting in economic losses. Different parameters have an impact on the meat spoilage such as the initial microbial load, post-harvest processing, packaging method and the storage temperature. An approach combining classic microbiology methods and metagenomic approach was used to monitor changes in bacterial populations during the refrigerated storage of 2 different batches of naturally contaminated raw beef meat under modified atmosphere packaging.

The purpose of this work is to characterize the dynamic of MAF beef spoilage microbiota and highlight among the identified species the most active populations during storage.

MATERIALS AND METHODS

**SAMPLES**

- 2 different batches of MAF steak beef, Belgian origin
- Commercial shelf life limit = 7 days at 4°C
- For each batch at each day, 2 samples were analyzed
- For this study, 10 samples for each of the 2 batches

**STORAGE (10 ± 4°C – 20 ± 8°C)**

- Day 1
- Day 3
- Day 5
- Day 7
- Day 9

**ANALYSIS**

- Total bacterial genomic DNA isolation and 16S rRNA gene (V1-V2)
- Libraries construction were conducted by Genalyse Patcon (Liège, Belgium). High throughput sequencing was performed with the Minio Sequencing System (Illumina).
- Bacterial pellet was washed at 80°C after a treatment with bacterial RNA protect solution (Qiagen).
- Then, total RNA sample was extracted using RNA easy mini Kit (Qiagen).
- Microbial plate counting using several different media:
  - Total bacterial count (PCA – 25°C), psychrophilic LAB (Elliker – 0°C), LAB (MRSS – 37°C), Enterobacteriaceae (VREB – 37°C), Brochothrix (STARR), Pseudomonas (IPC – 20°C).
- Bioinformatic analysis were performed using the mothur software package (Schloss et al., 2009).
- Sample preparation for library and Illumina sequencing will be performed using a Mega Sequencing System (Illumina) by a technical sequencing platform.
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  - Total bacterial count (PCA – 25°C), psychrophilic LAB (Elliker – 0°C), LAB (MRSS – 37°C), Enterobacteriaceae (VREB – 37°C), Brochothrix (STARR), Pseudomonas (IPC – 20°C).
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**RESULTS AND DISCUSSION**

**METAGENOMIC AND METATRANSCRIPTOMIC ANALYSIS OF NATURALLY CONTAMINATED BEEF MEAT PRODUCTS UNDER MODIFIED ATMOSPHERE PACKAGING DURING STORAGE**

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**RESULTS AND DISCUSSION**

**After 7 days of storage (shelf life limit), both batches present sensory properties linked to spoilage: racinal odor, brown coloration and slime**

- Changes in bacterial counts in batch 1 during storage. In each graph, the mean of the detection threshold.
- Changes in bacterial counts in batch 2 during storage. In each graph, the mean of the detection threshold.
- In both batches, psychrophilic LAB are dominant after the 5 days of storage and until the end with more than 7 log (CFU/g) and LAB more between 6 and 7 log (CFU/g).
- In both 2, Pseudomonas and Brochothrix reach almost 6 log (CFU/g) in the time of storage (7 days).

**CONCLUSIONS**

Using conventional methods and 16S rRNA gene metagenetic analysis, LAB are the dominant bacteria at the time of spoilage.

Among them, Lc. gelidum, Lb. algidus and Lc. piscium and C. divergens and C. marshallum were identified. B. thermosphacta and Pseudomonas spp were also isolated from the samples.

Focusing on the dominating species, metatranscriptomics analysis will be conducted on those 20 samples to highlight the most active bacterial populations and the bacterial genes involved in beef meat spoilage.

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