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

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Denrées alimentaires

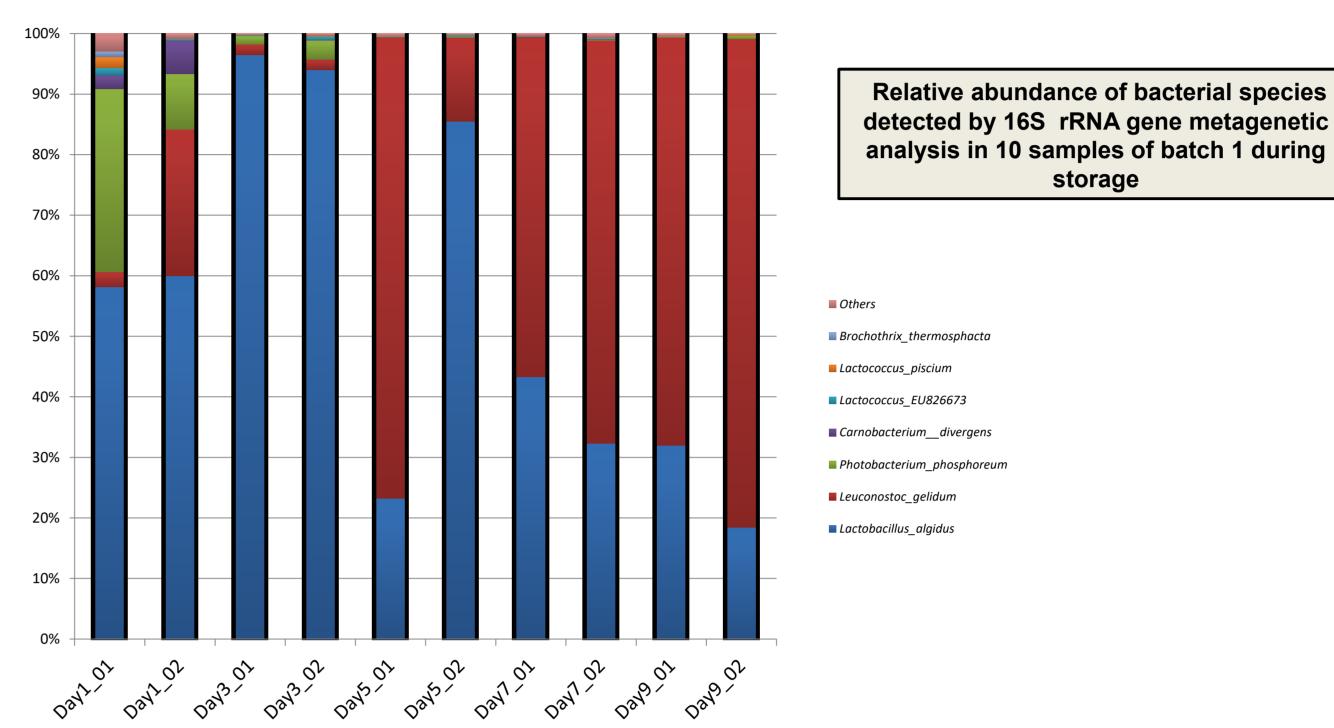
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INTRODUCTION

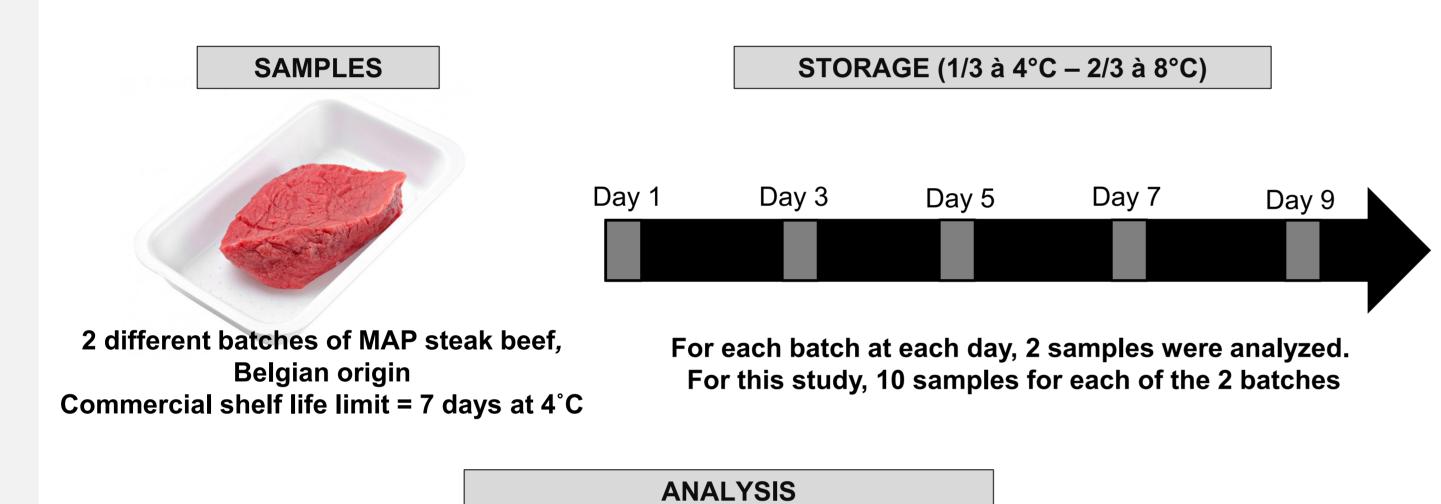
Meat is one of the most perishable food products on the market thus resulting in economic losses. Different parameters have an impact on the meat spoilage such as the initial microbial load, post-harvest processing, packaging method and the storage temperature. An approach combining classic microbiology 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.





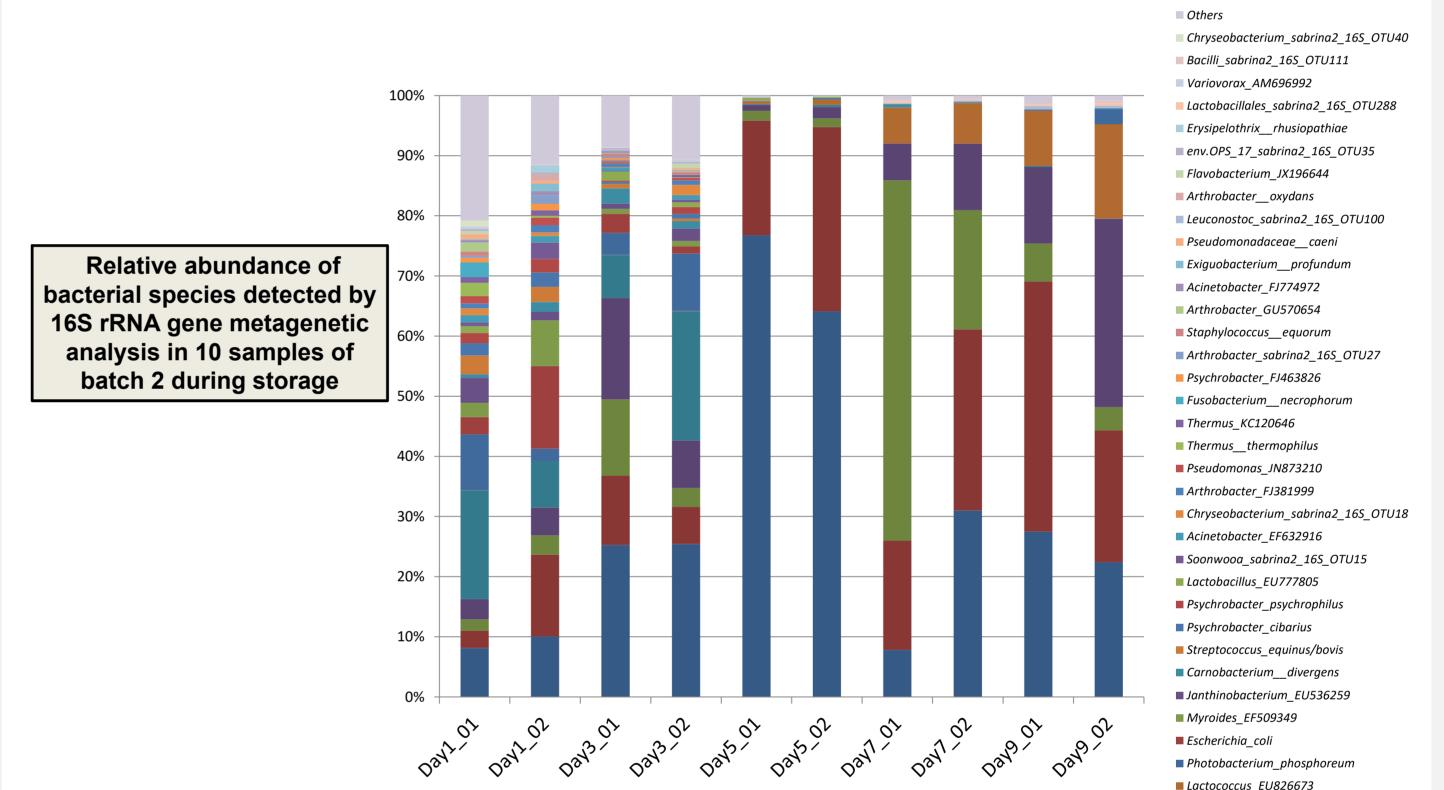
The purpose of this work is to characterize the dynamic of MAP beef spoilage microbiota and highlight among the identified species the most active populations during storage.

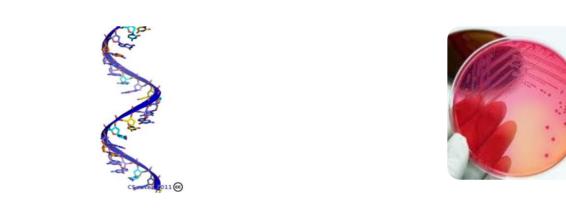
MATERIALS AND METHODS



For each of the 20 samples

In batch 1, only 7 OTUs are identified at a treshold > 1% of the global population detected. *Lactobacillus algidus* dominated the microbiota at the beginning of the storage. From day 5, the samples are dominated by *Lc gelidum and Lb. algidus*





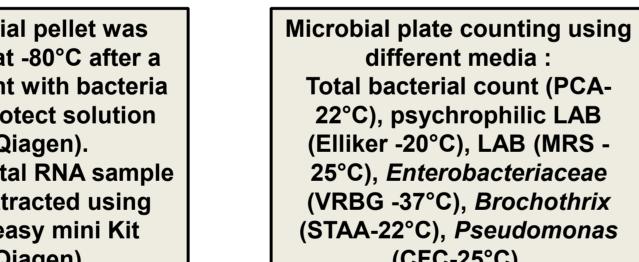
Total bacterial genomic **DNA** isolation and 16S rRNA gene (V1-V3) libraries construction were conducted by **Genalyse Patner** (Liège, Belgium). High throughput sequencing was performed with the Miseq Sequencing System (Illumina).

al., 2009).

Université

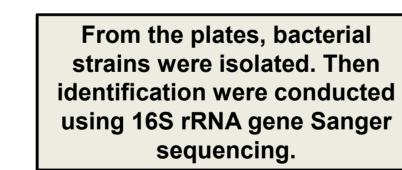
de Liège

Bacterial pellet was stored at -80°C after a treatment with bacteria **RNA** protect solution (Qiagen). Then, total RNA sample was extracted using RNA easy mini Kit



(Qiagen).

Sample preparation for library and RNAseq sequencing will be perfomed using a Hiseq Sequencing System (Illumina) by a technical sequencing platform.



different media :

Total bacterial count (PCA-

22°C), psychrophilic LAB

(Elliker -20°C), LAB (MRS -

25°C), Enterobacteriaceae

(VRBG -37°C), Brochothrix

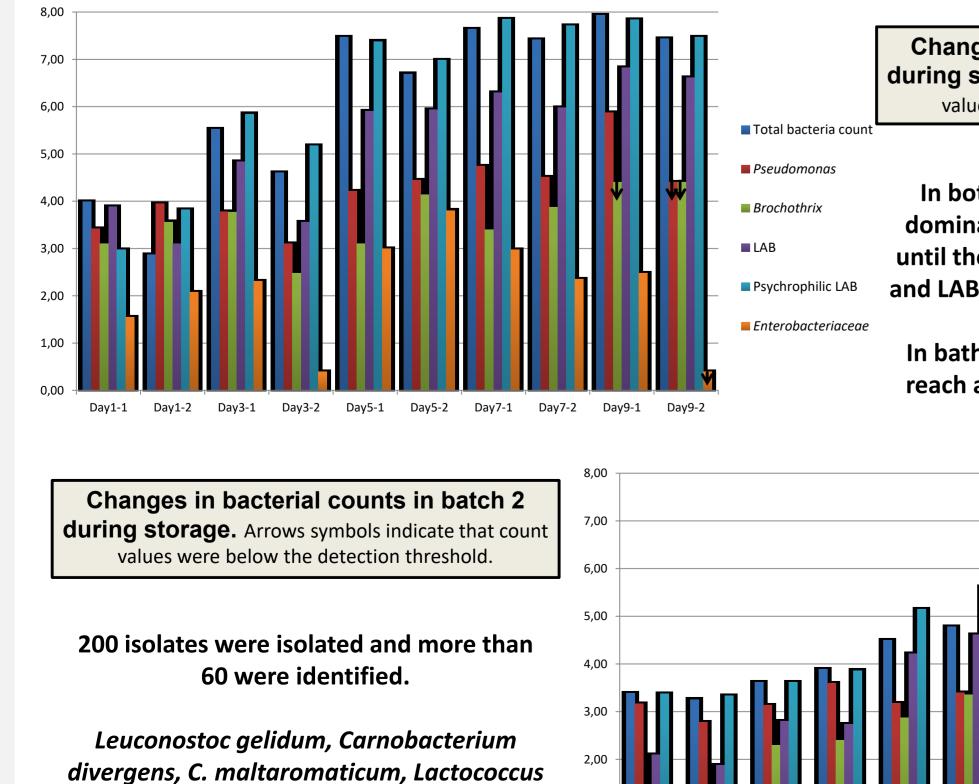
(STAA-22°C), *Pseudomonas*

(CFC-25°C).

Bioinformatic analysis were performed using the mothur software package (Schloss et

RESULTS AND DISCUSSION

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



Changes in bacterial counts in batch 1 during storage. Arrows symbols indicate that count values were below the detection threshold.

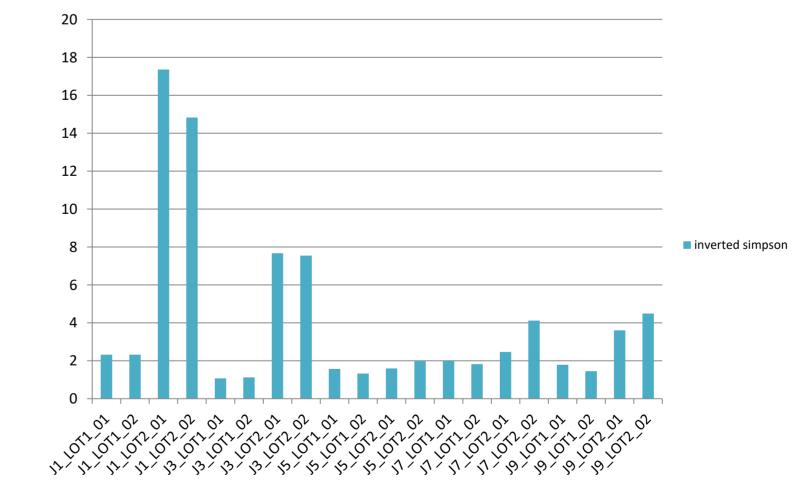
In batch 2, 39 OTUs are identified at a treshold > 1% of the global population detected. At the shelf life limit (7 days) days of storage B. thermosphacta and LAB: Lc. gelidium, Lactobacillus algidus and Lc. piscium at the dominant species.

Lactococcus_EU826673 Pseudomonas_fluorescens/poe/trivialis Lactococcus_piscium Brochothrix_thermosphacta Leuconostoc_gelidum Lactobacillus_algidus

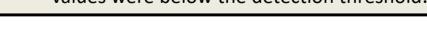
Biodiversity diversity index of the 20 samples

Batch 2 samples, clearly present an important diversity at the beginning of storage compare to batch .In batch, the samples present a low diversity during all the storage.

According the relative abundance and alpha-diversity results , it seems that's the meat in batch 2 was more fresh than in batch 1



piscium, Brochothrix thermosphacta and Pseudomonas spp



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)

Day5-1

Day5-2

Day7-1

Day7-2

In bath 2, *Pseudomonas* and *Brochothrix* reach almost 6 log (CFU/g) at the time of spoilage (7 days).

Total bacteria count

Pseudomonas

Brochothrix

Psychrophilic LAB

Enterobacteriaceae

LAB

Dav9-2

Day9-1

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

CONCLUSIONS

Among them, Lc. gelidum, Lb. algidus and Lc. piscium and C. divergens and C. maltaromaticum 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.



