

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



S. MACÉ*, G. KERGOURLAY, B. TAMINIAU & G. DAUBE



Fundamental and Applied Research for Animal & Health (FARAH), Department of Food Science, Faculty of Veterinary Medicine, University of Liège

* sabrina.mace@ulg.ac.be

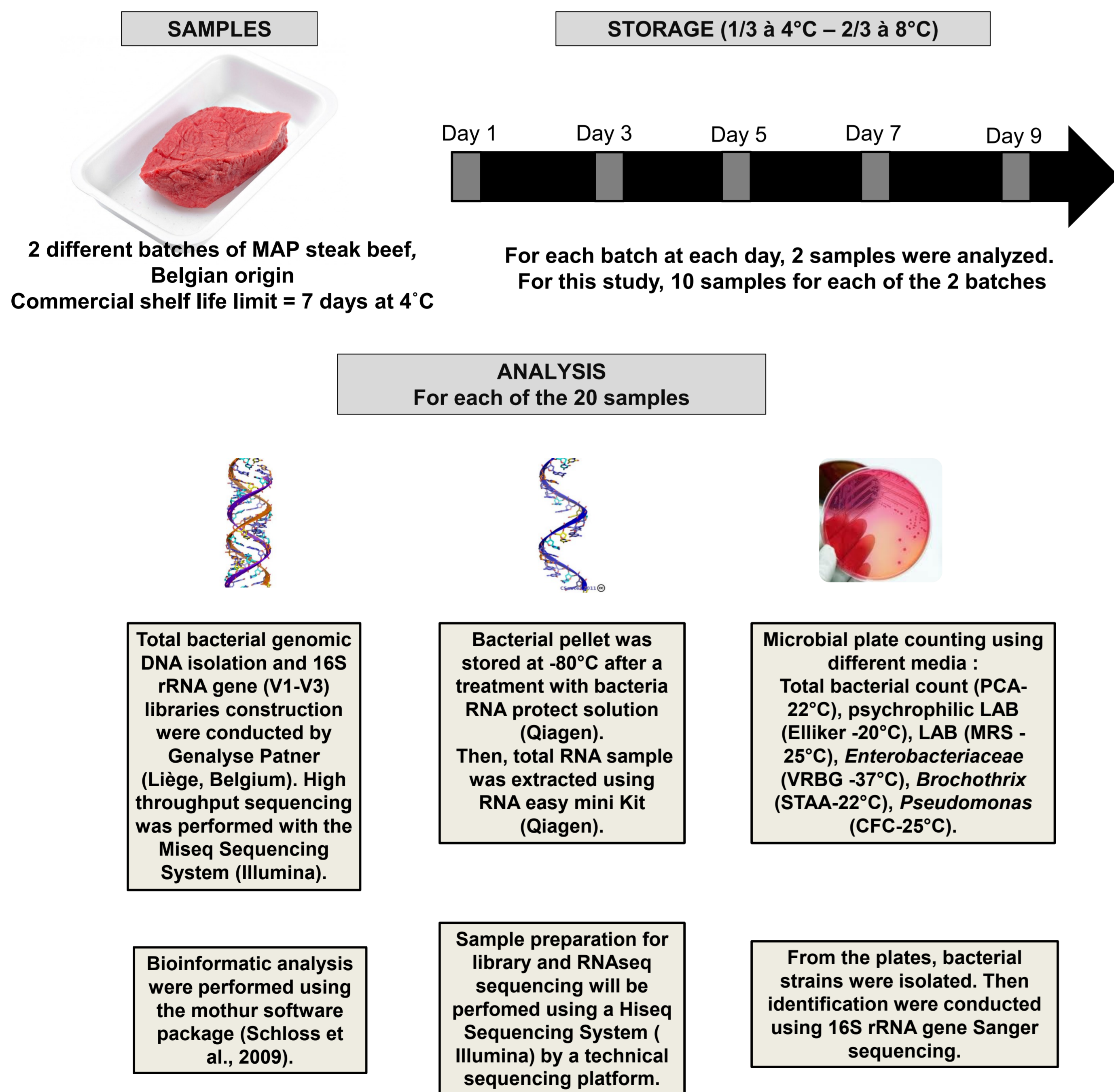


INTRODUCTION

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.

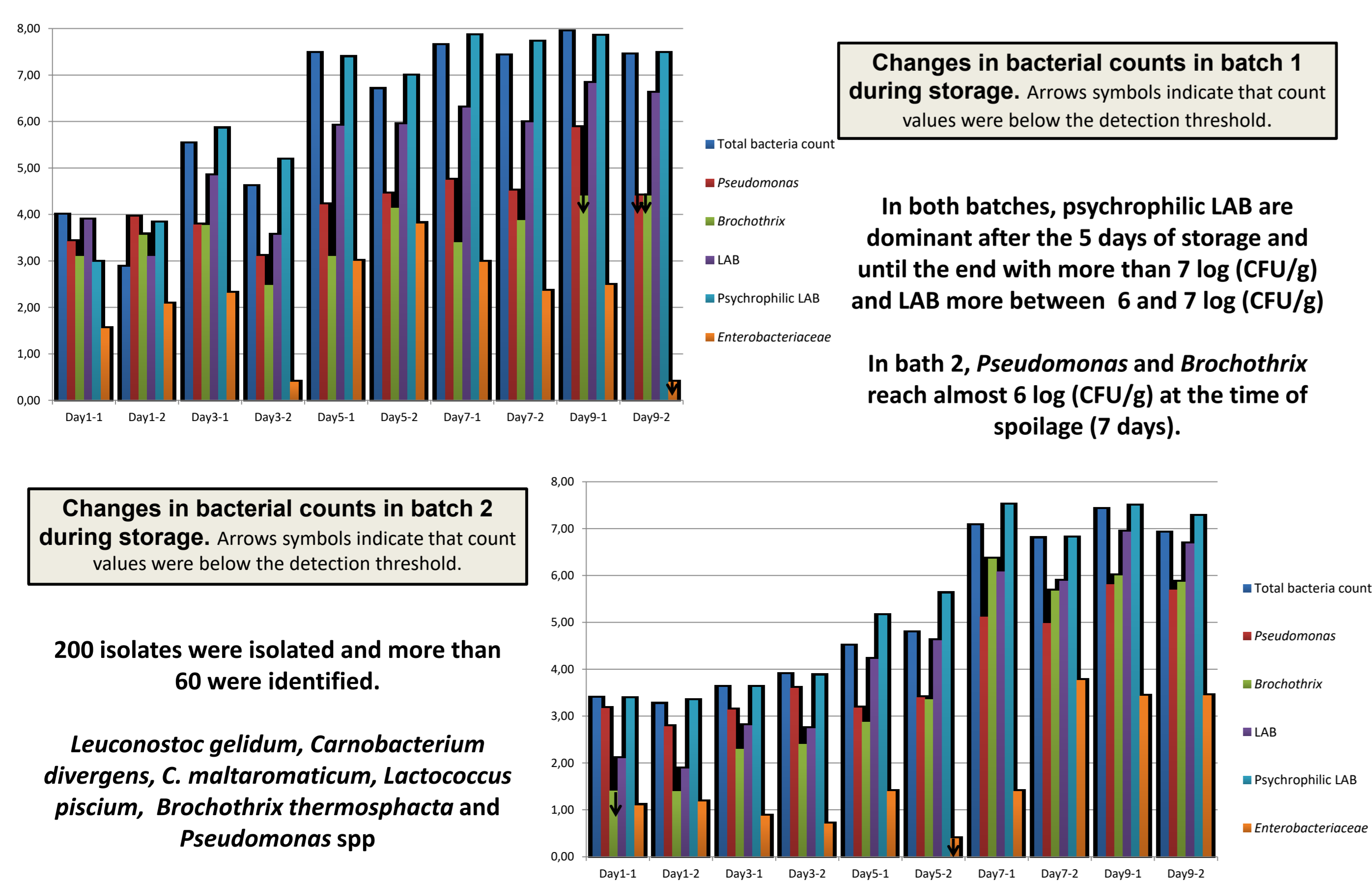
The purpose of this work is to characterize the dynamic of MAP beef spoilage microbiota and highlight among the identified species the most active populations during storage.

MATERIALS AND METHODS

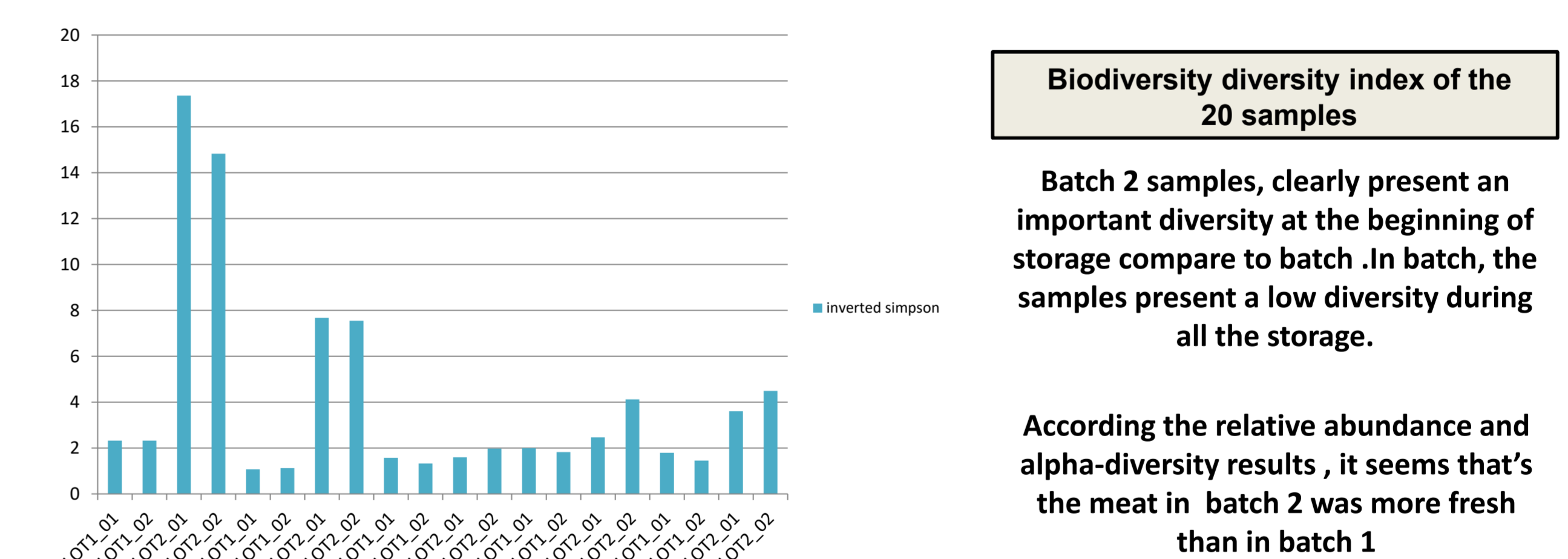
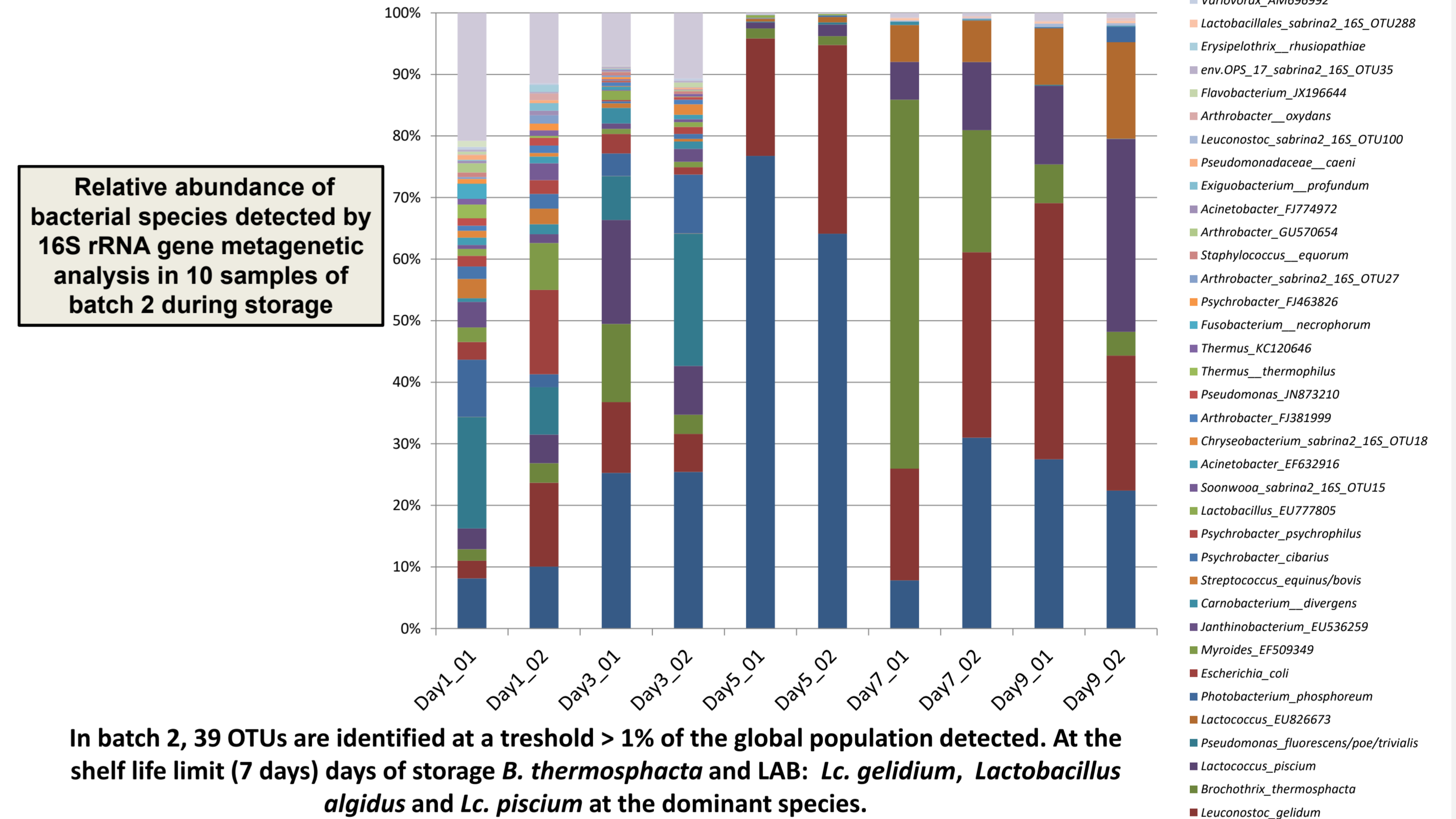
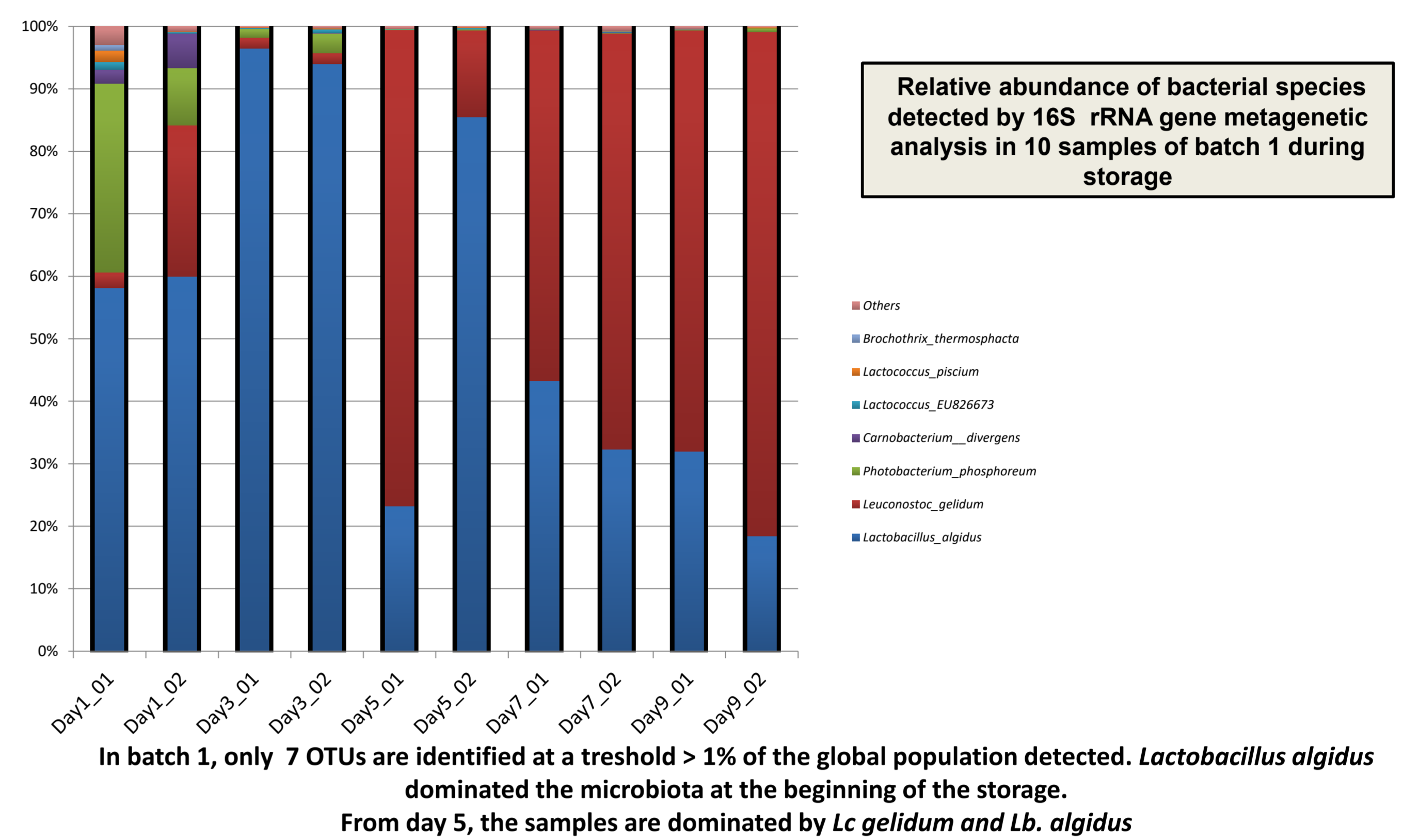


RESULTS AND DISCUSSION

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



RESULTS AND DISCUSSION



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. 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.