### FARAH Day 2017 Liège, October 13<sup>th</sup> 2017



A NMR-based metabolomics study of minced pork meat inoculated with Brochothrix thermosphacta, Leuconostoc gelidum and Pseudomonas fragi



# CAUCHIE E.<sup>\*1</sup>, LEENDERS J.<sup>2</sup>, BARÉ G.<sup>1</sup>, TAHIRI A.<sup>1</sup>, DELHALLE L.<sup>1</sup>, KORSAK N.<sup>1</sup>, DE TULLIO P.<sup>2</sup> AND DAUBE G.<sup>1</sup>

<sup>1</sup>Food Science Department, Food Microbiology, FARAH, ULiège. <sup>2</sup>Center for Interdisciplinary Research on Medicines (CIRM), Laboratory of Medicinal Chemistry, ULiège, 4000 Liège, Belgium.

\* ecauchie@ulg.ac.be

# INTRODUCTION

FÁRÁH

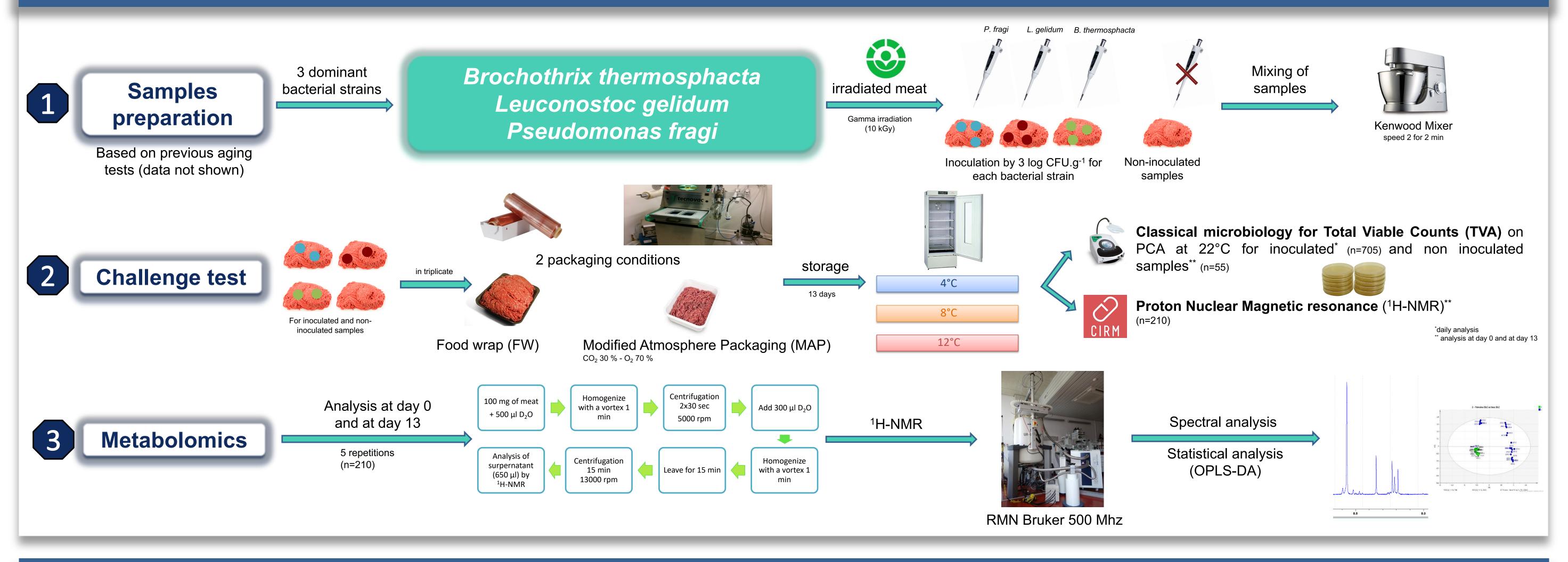
# **OBJECTIVES**



The aim of the current study was to assess meat spoilage through the evolution of bacterial counts and changes in the metabolic profile of minced pork meat using Proton Nuclear Magnetic Resonance (<sup>1</sup>H-NMR).

In order to control food waste, studies have highlighted the importance of monitoring the microbial diversity of food products.

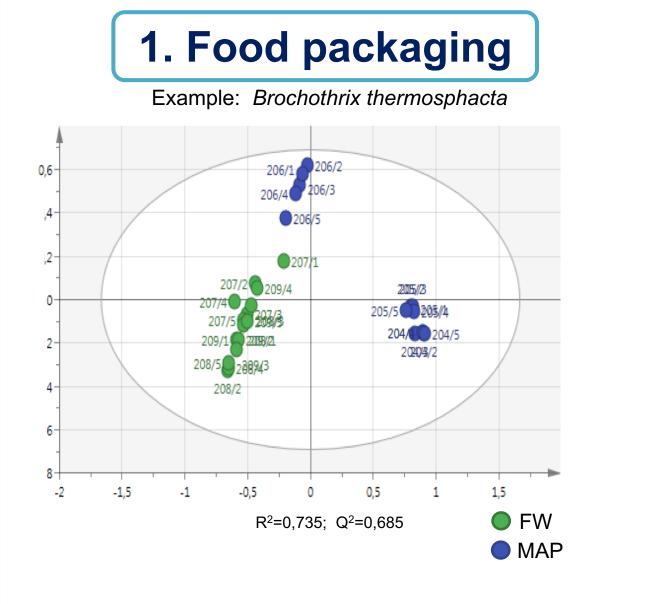
# **MATERIALS AND METHODS**

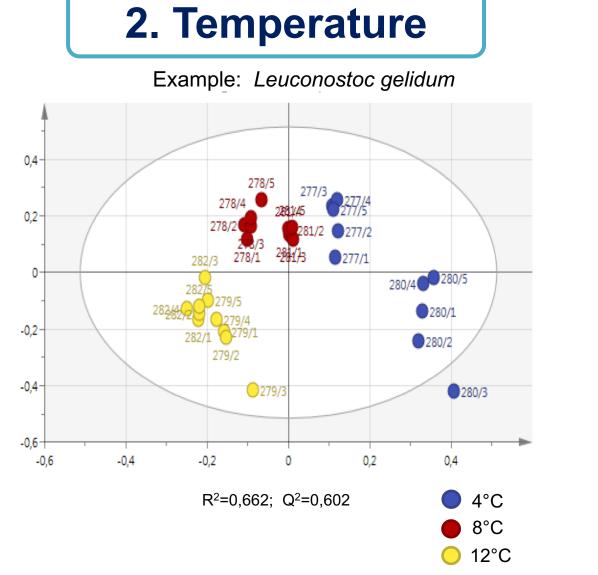


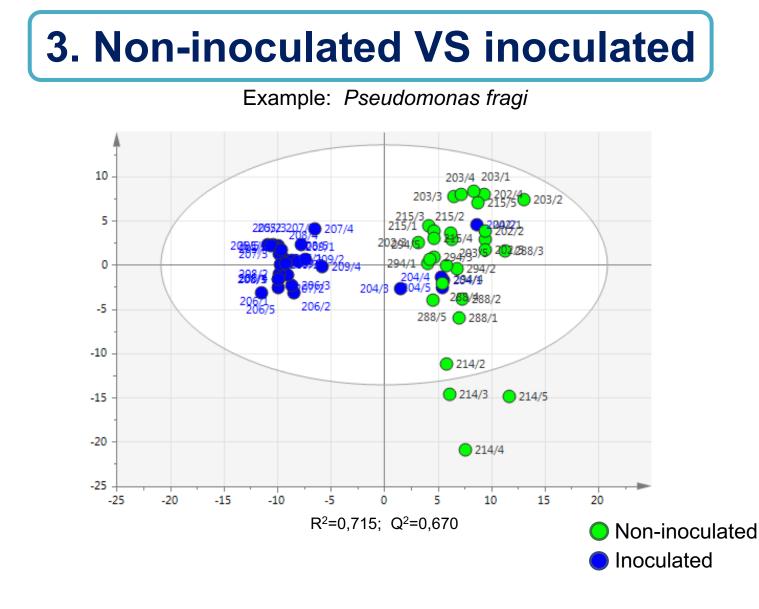
**RESULTS AND DISCUSSION** 

#### **Metabolomics pattern**

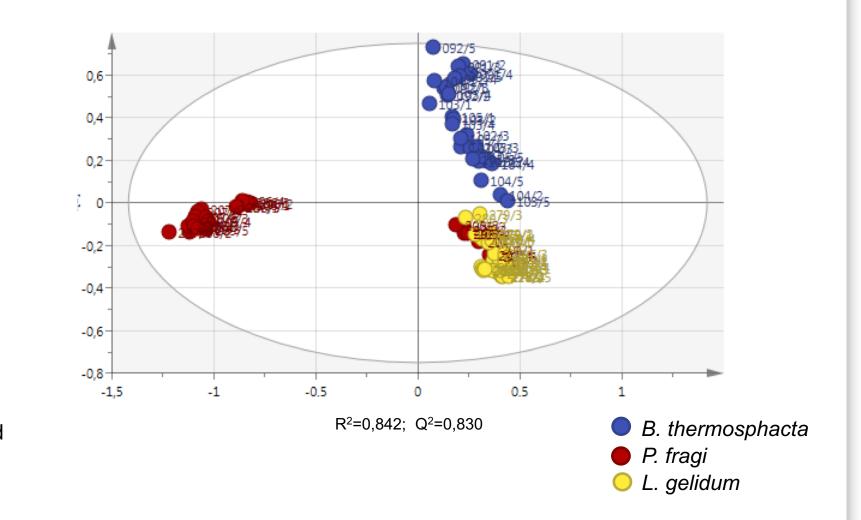
Samples discrimination into 3 groups based on their spectral pattern is observed for each bacterial strain (1, 2, 3) and between the type of strain inoculated (4).







## 4. Type of strain inoculated



# 2

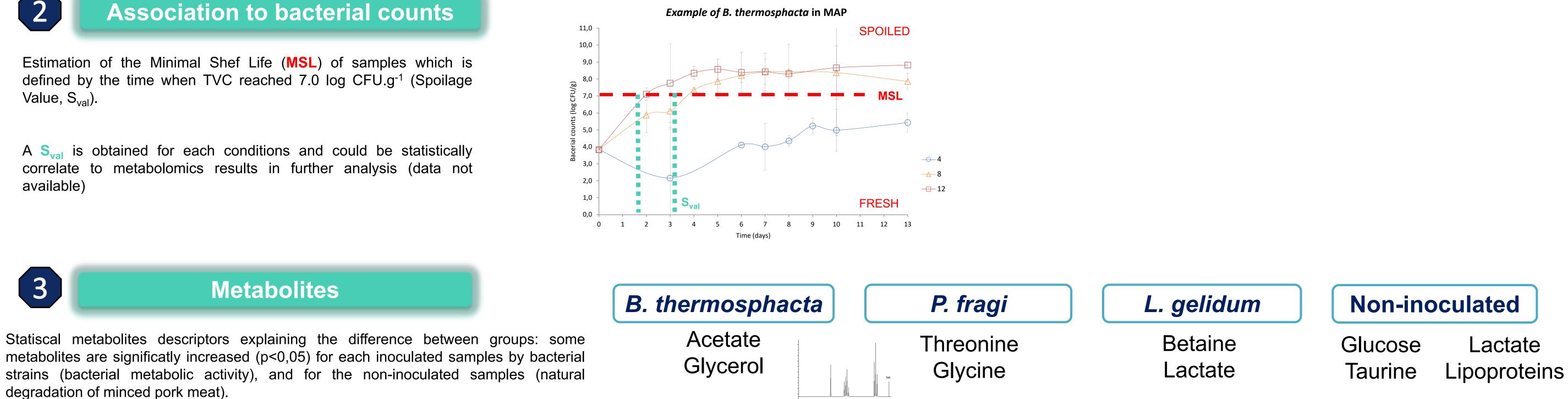
available)

3

#### **Association to bacterial counts**

Estimation of the Minimal Shef Life (MSL) of samples which is defined by the time when TVC reached 7.0 log CFU.g<sup>-1</sup> (Spoilage Value, S<sub>val</sub>).

A S<sub>val</sub> is obtained for each conditions and could be statistically correlate to metabolomics results in further analysis (data not



# CONCLUSIONS

Exploration of the correlation of these metabolites with microbial counts (Spoilage Value (S<sub>val</sub>) at 7.0 log CFU.g<sup>-1</sup>) suggested their use as possible spoilage indicators. These results support the use of NMR-based metabolomics as a valuable tool to provide information on pork meat spoilage and to follow intrinsically the evolution of the metabolomics pattern linked to a specific strain in a complex bacterial ecosystem.