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## Introduction

With the development of the high throughput sequencing and bioinformatics, targeted metagenomic analysis has become a powerful tool to study the dynamic of bacterial flora in food products during their shelf life.

## Objectives

A new approach was investigated to follow bacterial population dynamics in perishable foods (white pudding) under different environmental conditions by combining the results of targeted metagenomics and classical microbiology for predictive microbiology models.

## Results and discussions

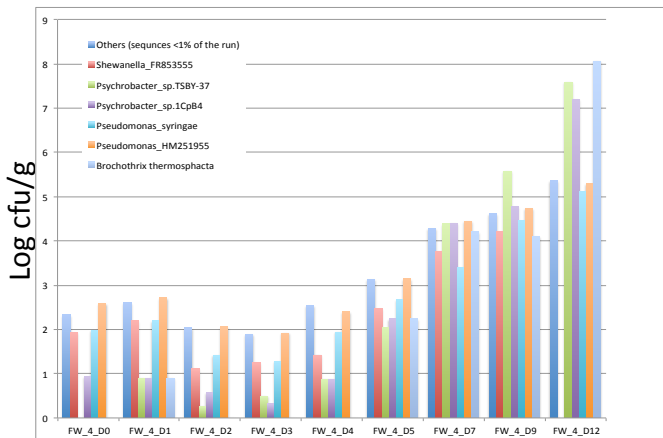


Fig. 2: Example of evolution of bacterial species concentrations in white pudding along the shelf life under food wrap stored at 4°C based on targeted metagenomic and classical microbiology analysis (total flora at 22°C)

## Materials et methods

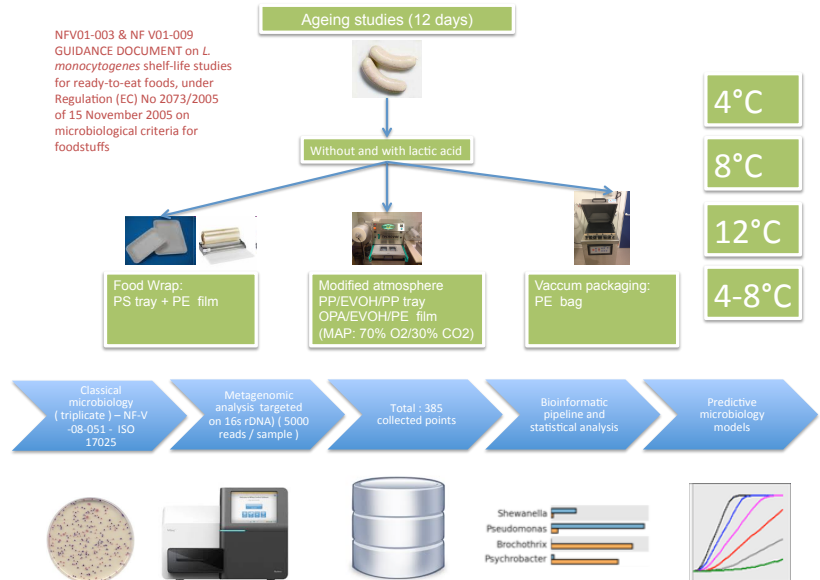


Fig. 1: Figure 1. Procedure to collect kinetic data of microorganisms from targeted metagenomic and classical microbiology analysis for predictive models

Figure 2 shows an example of bacterial evolution in white pudding along the shelf life stored at 4°C and packed under food wrap (FW). Bacterial species present at less than 1% of sequences are gathered in the group "Others", reducing at 6 the number of bacterial species with a proportion equal or higher than 1%. In that environmental condition, Gram-negative bacteria, as *Pseudomonas* and *Shewanella* were mainly present at day 0. Two Gram-positive bacteria, *Brochothrix thermosphacta* and *Psychrobacter*, were identified as the main bacterial species at the end of the shelf live at whatever the temperature. The simulations of the *Brochothrix thermosphacta* and *Psychrobacter* seem to be sufficient for this food product to predict 75 - 95 % of the bacterial population at the end of the shelf life in function of the temperature

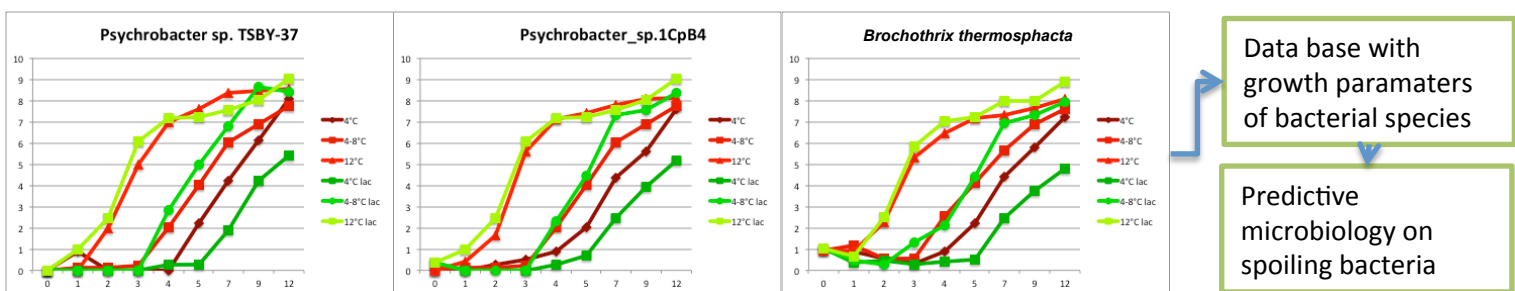


Fig. 3: Kinetics for *Psychrobacter sp* and *Brochothrix thermosphacta* along the shelf life of white pudding packed under food wrap in function of temperature

The main bacterial population identified by metagenomic was analyzed as a proportion of the aerobic colony count of the sample. The figure 3 gives the extracted kinetics for two *Psychrobacter sp* and *Brochothrix thermosphacta* along the shelf life packed under food wrap in function of temperature. Growth parameters for each microflora was estimated with a one step fitting of the primary model of Baranyi and Roberts (Baranyi and Roberts, 1994) and the square root type secondary model (Ratkowsky et al., 1982) using the nls function of the open source software R (© The R Core Team). The data collected will be included in a data base and used as growth parameters for predictive microbiology models in order to predict the potential growth of spoiled bacteria in function of temperature.

## Conclusions

Targeted metagenomics combined with classical microbiology is a useful tool to identify spoiled bacteria in perishable foods during the shelf life and to collect growth kinetics of bacterial species for predictive microbiology models. This new approach takes into account the initial bacterial contamination in terms of abundance and diversity. This methodology gives new perspectives to manage microbiological quality of foods during their shelf life.