

Delhalle L.¹, Taminiau B.², Nezer C.¹, Ferauche C.¹, Picollo D.¹, Daube G.²

¹Quality Partner sa, 62 Rue Hayeneux, 4040 Herstal, Belgium ; T+32 (0)4 240 75 00 / F+32 (0)4 240 75 10

² University of Liège, Food Science Department ; B43 Bis, 4000 Liège, Belgium ; T+32 (0)4 366 40 29 / F+32 (0)4 366 40 44

Introduction

Steak tartare is a popular meat dish in Belgium and other European countries. This meat preparation, due to its raw nature, is highly sensitive to bacterial spoilage. A better understanding of the bacterial content of this product will thus be insightful to control the risk of spoilage. Metagenomics targeted on the 16S ribosomal DNA has appeared as a powerful tool to study bacterial composition of food samples. The aim of this study is to identify the bacterial populations of steak tartare from different origins along their shelf life and determine the main spoilage bacterial species.

Results and discussions

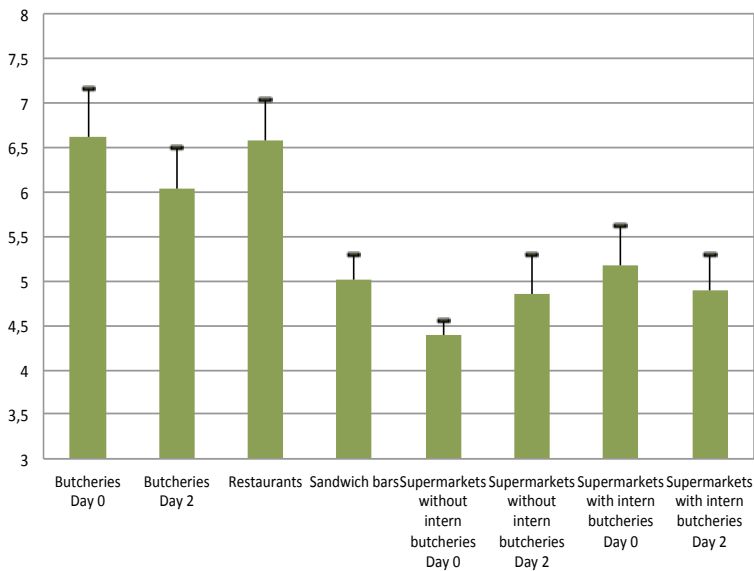


Fig. 2: Results of the classical microbiological analysis on psychrotrophic aerobic flora determined on PCA at 22°C during 72h (log cfu/g)

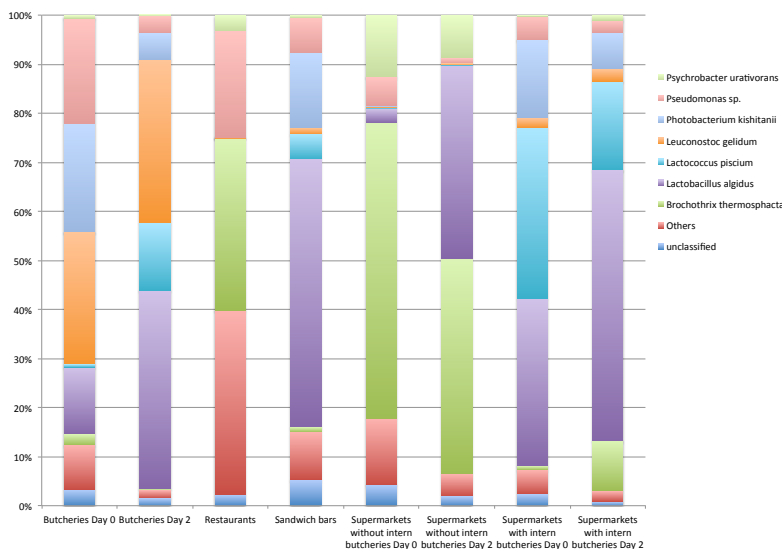


Fig 3: Results of the metagenomic analysis on steak tartare

Conclusions

The metagenomic analysis is a powerful tool to identify and to measure the relative proportions of dominant bacterial species in the steak tartare from different origins. Some bacterial species could be indicators of the meat quality. The identification of bacterial species over time give information on the evolution of the spoilage process. Therefore, metagenomic analysis could be an additional tool to control and to manage the quality of meat and the risk of spoilage.

Materials et methods

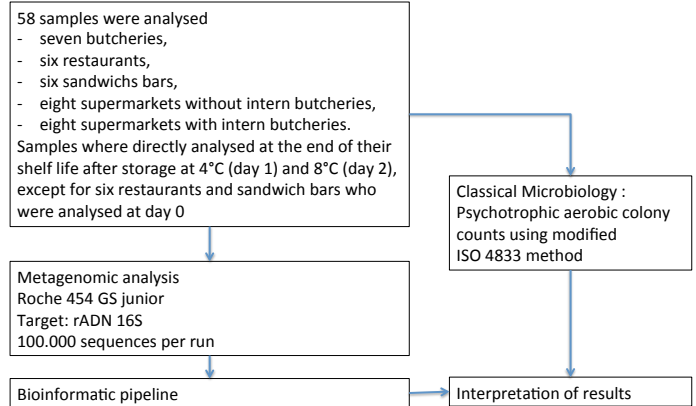


Fig. 1: Description of a metagenomic analysis

- The psychrotrophic aerobic flora counts were between 3,9 and 7,4 log cfu/g depending of the origin of the samples and day of analysis. The flora grows few over time between day 0 and day 2.
- A total of 32 bacterial species were identified in the steak tartare samples by the metagenomic analysis.
- *Brochothrix thermosphacta*, *Lactobacillus algidus*, *Lactococcus piscium*, *Leuconostoc gelidum*, *Photobacterium kishitani*, *Pseudomonas sp.* and *Psychrobacter urativorans* are the most predominant bacterial species in the samples and represent 89% of the detected bacterial species.
- *Brochothrix thermosphacta* and *Lactobacillus algidus*, represent 50% of all the detected species. *Brochothrix thermosphacta* is detected mostly in samples from restaurants (2,8-93,9 %; n=4/6) and supermarkets without intern butcheries (0,3-83,2 %; n=8/8).
- *Lactobacillus algidus* is present in each category but in low proportion for restaurants (2,3-5,5 %, n=3/6)
- *Pseudomonas sp.*, *Brochothrix thermosphacta* or *Leuconostoc gelidum* are present in high proportion in some samples at Day 0. These bacteria are well known to spoil meat product and samples which contain these bacteria in high proportion are more susceptible to spoil rapidly.
- Some samples (data not shown) contain a high level of *Steptococcus* or *Enterobacter* resulting probably of cross contamination during the meat process.
- A food with a concentration of 6 log CFU/g is generally considered as spoiled. However, the results indicate that some samples have a concentration around this theoretical limit and contains a high proportion of bacteria which are not considered as spoilage bacteria like *Lactobacillus algidus*.