

Subject: Biopharmaceuticals & nutraceuticals

Title: Study of the microbial diversity in vacuum-packed chilled beef from different origins through a metagenomics approach

Summary

Max. 400 words

Imazaki, P. H., Taminiau, B., Nezer, C., Daube, G. and Clinquart, A.

Department of Food Science, University of Liège, Sart Tilman B43b, Liège, Belgium, 4000

Despite a diverse initial microbial population, bacterial spoilage of vacuum-packed chilled beef is mainly due to the growth of psychrotrophic bacteria. The study of the microflora of vacuum-packed chilled beef remains a challenge since some members of the microflora may be missed or not identified by cultivation-based methods. The aim of this study was to evaluate the microbial diversity in eight batches of vacuum-packed chilled beef from different origins (Australia, Belgium, Brazil, Ireland and United Kingdom) by metagenomics. *Longissimus dorsi* muscle samples were homogenized and analysed in early and late stages of their shelf life by metagenomics. The metagenomic assays consisted in DNA extraction, 16S ribosomal RNA gene amplification, pyrosequencing and data analysis. All samples, except for two batches from Australia, presented a high microbial diversity in the beginning of their shelf life. *Enterobacteriaceae*, *Pseudomonas*, *Burkholderia*, *Lactobacillus* and *Sterotrophomonas* were some of the major bacteria identified at this stage of storage. The dominant flora (> 80 % of relative abundance) in two Australian batches was composed by *Carnobacterium*. At the end of the shelf life of the samples, a decrease in microbial diversity was observed in almost all batches. At this stage of storage, *Carnobacterium*, *Lactobacillus*, *Lactococcus* and *Enterococcus* were some of the major genera identified. *Carnobacterium* remained the dominant flora in the two Australian batches cited above, which could explain the long shelf life applicable to this meat (140 days) as some *Carnobacterium* strains induce a biopreservative effect especially by producing bacteriocins with a wide inhibition spectrum. Metagenomics showed to be a very useful tool to study the microbial population of a complex matrix such as meat since some of the identified genera such as *Lactobacillus* and *Carnobacterium* are known not to grow or to grow slowly in media commonly used for the isolation and cultivation of total viable counts.

(Future) possibilities of valorisation

Max. 100 words

The study of the microbial diversity in vacuum-packed chilled beef is one of the keys to understand the conservability of this product. As metagenomics bypasses the need for laboratory cultivation and isolation, it is henceforth possible to identify bacteria involved in meat spoilage or biopreservation that would be missed by cultivation based methods.