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# Northern and Southern European fermented meat products in the Belgian retail display differences in their microbial communities (#159)

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# Introduction

The geographical origin is often linked to the cultural meaning and technological properties of traditional fermented foods (Leroy *et al.*, 2013). This is also the case for fermented meat products, of which a wide variety is manufactured across Europe (Ojha *et al.*, 2015). The main microbial groups occurring during meat fermentation are lactic acid bacteria (LAB) and coagulase-negative staphylococci (CNS). CNS communities are generally more diverse in traditional fermentations. However, only two species (*Staphylococcus xylosus* and *S. carnosus*) are commonly used as starter cultures in industrial fermentations (Stavropoulou *et al.*, 2018). Due to the wide variety of processing conditions across Europe, it is unclear which microbial communities are dominant in commercially available fermented meat products from different origins. Therefore, the present study aimed to assess the biodiversity of fermented meat products in the Belgian retail and to investigate potential links with the country of origin and the product characteristics.

# Methods

In total, 80 randomly selected fermented meat products were purchased from small and large retail vendors in and around Brussels, Belgium. For each product, the pH was measured and the country of origin was catalogued according to the producer. Samples were plated on de Man-Rogosa-Sharpe (MRS) agar and on mannitol-salt-phenol-red agar (MSA) to enumerate LAB and CNS, respectively. Isolates picked up from these agar media were subjected to (GTG)<sub>5</sub>-PCR fingerprinting and clustered using BioNumerics 5.1 software. The identity of each (GTG)<sub>5</sub>-PCR fingerprint cluster was further confirmed via sequencing of the 16S rRNA, *rpoB*, and *tuf* genes of representative isolates. A detrended correspondence analysis (DCA) was performed, followed by a series of pairwise permutational multivariate analysis of variance (PERMANOVA) comparisons and similarity percentage analysis (SIMPER) to assess microbial differences between products from different countries (R Core Team, 2018).

# Results

The collected fermented meat products originated from Italy (17), France (32), Spain (14), Belgium (13), and Germany (4). Generally, Southern European products had a higher pH than the Northern European ones, with the average pH being  $5.71 \pm 0.47$ ,  $5.56 \pm 0.40$ ,  $5.43 \pm 0.25$ ,  $4.92 \pm 0.16$ , and  $4.77 \pm 0.09$  for Italian, Spanish, French, Belgian, and German fermented meat products, respectively. DCA indicated differences in microbial communities

between products originating from different countries (Figure 1). Pairwise PERMANOVA and SIMPER revealed that microbial communities of mainly lactobacilli and CNS from Belgian and German products were significantly different from their Southern European counterparts, showing a high prevalence of *Pediococcus pentosaceus* and *S. carnosus*. Furthermore, microbial communities of Spanish fermented meat products were significantly different from Italian and French ones, with *S. equorum* and *S. xylosus* as the prevailing CNS species, respectively (Figure 2).

## Conclusion

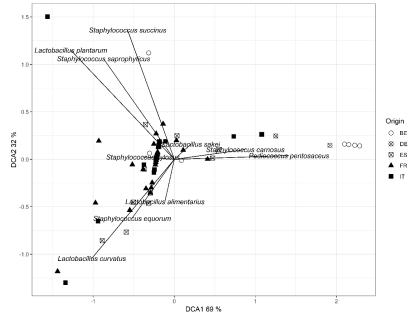
The present study highlighted differences in microbial communities of LAB and CNS between Northern and Southern European fermented meat products. This was likely due to differences in ingredients, processing conditions, and starter culture formulations.

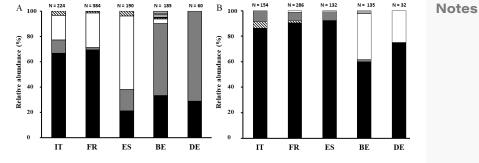
#### Literature

Leroy, F., Geyzen, A., Janssens, M., De Vuyst, L., Scholliers, P., (2013). Meat fermentation at the crossroads of innovation and tradition: a historical outlook. *Trends Food Sci. Tech.*, 31, 130-137. Ojha, K. S., Kerry, J. P., Duffy, G., Beresford, T., Tiwari, B. K. (2015). Technological advances for enhancing quality and safety of fermented meat products. *Trends Food Sci. Tech.*, 44, 105-116. R Core Team (2018). *R: A Language and Environment for Statistical Computing*. R Foundation for Statistical Computing,Vienna, Austria. Stavropoulou, D. A., De Vuyst, L., Leroy, F. (2018). Non-conventional starter cultures of coagulase-negative staphylococci to produce animal-derived fermented foods, a SWOT analysis. J. Appl. Microbiol., 125, 1570-1586.



Notes





#### Figure 2 ∎ п

Total relative abundances of (A) Staphylococcus xylosus (black), S. carnosus (darkgrey), S. equorum (white), S. saprophyticus (diagonal parallel lines), and S. succinus (parallel lines), and (B) Lactobacillus sakei (black), L. curvatus (darkgrey), Pediococcus pentosaceus (white), L. plantarum (diagonal parallel lines), and L. alimentarius (parallel lines) in fermented meat samples from Italy (IT),

Spain (ES), France (FR), Belgium (BE) and Germany (DE)

### Figure 1

Detrended correspondence analysis biplot based on Bray-Curtis dissimilarity scores of the microbial communities of fermented meat samples from Italy (IT), Spain (ES), France (FR), Belgium (BE) and Germany (DE).

