

The Research Group of

Industrial Microbiology and Food Biotechnology (IMDO)

has the honour to invite you to the public PhD defence of

ir. Emiel Van Reckem

to obtain the degree of Doctor of Bioengineering Sciences

Amplicon-based high-throughput sequencing exploration of the fermented meat microbiota as a function of geographical origin and process parameters

Promotor:

Prof. Dr. ir. Frédéric Leroy

The defence takes place on

Monday, July 5, 2021 at 16 h

Due to COVID-19 measures, the capacity to physically assist the event at the Campus of Humanities, Sciences and Engineering of the Vrije Universiteit Brussel, Pleinlaan 2, 1050 Elsene, will be limited. The defence can also be followed via livestream. Contact stefan.weckx@vub.be for more information.

Composition of the jury

Prof. Dr. Steven BALLEET (VUB, president)
Prof. Dr. ir. Wim DE MALSCHE (VUB, secretary)
Prof. Dr. Joske RUYTINX (VUB)
Prof. Dr. Bruno POT (VUB)
Prof. Dr. ir. Stefaan DE SMET (Ghent University)
Dr. Monique ZAGOREC (INRAE Centre Angers-Nantes Pays de la Loire, Nantes, France)

Curriculum vitae

Emiel Van Reckem was born on October 12, 1993, in Mechelen, Belgium. He obtained a Master of Science (MSc.) of Bioengineering Sciences: Chemistry and Bioprocess Technology from the Vrije Universiteit Brussel (VUB) in 2016. He started his PhD in January 2017 at the Research Group of Industrial Microbiology and Food Biotechnology of the VUB under the supervision of Prof. Dr. ir. Frédéric Leroy, after obtaining a PhD Fellowship for Strategic Basic Research of the Research Foundation Flanders (FWO-Vlaanderen). Concurrently, he obtained a MSc. in Management from the VUB in 2020. Emiel Van Reckem is co-author of eight scientific papers published in peer-reviewed international journals, among which four times as a first author. He attended two international scientific conferences and gave a total of five oral presentations at national and international scientific conferences and symposia.

Abstract of the PhD research

During meat fermentation, diverse microbial communities can be encountered, mostly consisting of lactic acid bacteria (LAB) and coagulase-negative staphylococci (CNS). This PhD study focussed on improving the understanding of the intrinsic relationships between the community dynamics of the dominant meat microbiota, the geographical origin of the products, and the processing conditions applied.

An overview of the bacterial species diversity in commercially available European fermented meat products was obtained using established culture-dependent methods, and potential links with key processing conditions and geographical origin were explored. It was found that the geographical origin impacted the composition of the LAB and CNS communities, which can most likely be ascribed to the combination of differences in process technology as well as starter culture use.

Whereas amplicon-based high-throughput sequencing (HTS) methods are becoming increasingly popular to study microbial communities, existing methods were lacking in taxonomic resolution power to unravel the phylogenetically diverse group of CNS. Therefore, a primer set for amplicon-based HTS was developed, amplifying a region of the *tuf* gene with enough discriminatory power to distinguish different CNS species. From the three primer sets designed, one set outperformed the two other primer sets for studying *Staphylococcus*-rich microbial communities using amplicon-based sequencing, as it resulted in no false positives and precise species-level identification.

Thereafter, a combined amplicon-based sequencing approach, targeting the 16S rRNA and *tuf* genes, was applied to characterize the bacterial communities of European fermented meat products in greater detail. This resulted in an improved taxonomic exploration by also encompassing several subdominant bacterial species that previously may have been underreported using culture-dependent methods.

Finally, a closer look was taken at the influence of different processing conditions on microbial communities during meat fermentation, using the aforementioned combined amplicon-based sequencing approach. It was elucidated that the fermentation temperature was the most influential processing condition in shaping the bacterial communities during spontaneous meat fermentation. Furthermore, CNS communities showed a great level of variability, depending on the initial bacterial communities present and their competitiveness. Therefore, both the processing conditions applied and the respective adaptations of the background microbiota to these sets of conditions, were crucial in determining the composition of CNS communities during spontaneous meat fermentation.

Overall, the present study used both an established culture-dependent method and a novel amplicon-based HTS method to improve the understanding of the ecological behaviour of the meat microbiota, highlighting the importance of the background microbiota, and the meat processing conditions applied