

The Research Group of

Industrial Microbiology and Food Biotechnology (IMDO)

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

MSc. Marko Verce

to obtain the degree of Doctor of Bioengineering Sciences

Title of the PhD thesis:

Omics approaches to unravel fermented food ecosystems

Promotor:

Prof. Dr. Stefan WECKX

The defence will take place on

Monday, July 13, 2020, at 17 h

Given the COVID-19 regulations, the capacity to attend the defence on the Campus Humanities, Sciences and Engineering of the Vrije Universiteit Brussel, Pleinlaan 2, 1050 Elsene, is limited. The defence can also be followed through a live stream. Contact stefan.weckx@vub.be for more information.

Members of the jury

Prof. Dr. ir. Geert ANGENON (VUB, chairman)

Prof. Dr. Joske RUYTINX (VUB, secretary)

Prof. Dr. Sonia VAN DOOREN (VUB)

Prof. Dr. Peter VANDAMME (Ghent University)

Prof. Dr. Danilo ERCOLINI (University of Naples Federico II, Italy)

Prof. Dr. Stefan WECKX (VUB, promotor)

Curriculum vitae

Marko Verce was born on May 9, 1989, in Mostar, Bosnia and Herzegovina. In 2010, he graduated at the University of Ljubljana, Slovenia, obtaining a Bachelor degree in Biotechnology. He obtained a Master degree in Biotechnology at the University of Ljubljana in 2013. In March 2014, he started his PhD at the Research Group of Industrial Microbiology and Food Biotechnology of the Vrije Universiteit Brussel under the supervision of Prof. Dr. Stefan Weckx and Prof. Dr. ir. Luc De Vuyst, at first with the financial support of the Vrije Universiteit Brussel and from October 2015 onward with a PhD fellowship fundamental research from the Research Foundation – Flanders (FWO-Vlaanderen). Marko Verce is co-author of nine peer-reviewed publications and one genome announcement, among which are six first-author publications. During his PhD, he has participated in one field experiment in Northern Argentina and three in Costa Rica. He gave in total five oral presentations at national and international conferences and symposia.

Abstract of the PhD research

Food fermentation processes are an interesting example of microbial ecosystems. Metagenomics and metatranscriptomics are culture-independent approaches for studying microbial ecosystems that rely on high-throughput DNA and RNA sequencing, respectively. In this PhD study, omics methodologies were used to explore the microbial diversity of food fermentation processes of different complexities and to gain insight into the possible roles of the microorganisms present, extending our knowledge of food fermentation ecosystems.

The complete genome of a candidate sourdough starter culture strain, *Lactobacillus fermentum* IMDO 130101, was sequenced and annotated. A species-wide comparative genomics analysis shed light on traits potentially relevant to sourdough fermentations in this bacterial species, opening up new avenues in sourdough starter culture strain research.

Metagenomics of two cheese brines from commercial manufacturers in Flanders revealed a major microbial group consisting of halophilic and halotolerant species, and a minor microbial group of cheese ingredient-associated microorganisms. The former group likely grows in these extreme environments and the knowledge gained can be used to assess its impact on cheese quality.

Metagenomics of a water kefir fermentation process showed a restricted microbial diversity and the reconstruction of a metagenome-assembled genome revealed a novel *Oenococcus* species. The assignment of metabolic functions to microbial species revealed indications of cross-feeding.

Finally, the application of omics and metabolite target analysis on Costa Rican cocoa bean fermentation processes revealed microbial species from 82 genera and a decreasing trend in microbial diversity along the fermentation. The yeasts, lactic acid bacteria, and acetic acid bacteria typical for cocoa bean fermentation processes were also found and assigned to dedicated metabolic activities, some of which have so far been unreported. For pectin degradation, a possible complementary role of distinct microbial species was discovered.

Overall, this PhD study demonstrated a variety of ways of omics data analysis in terms of microbial composition and functional potential, resulting in the discovery of microbial ecosystem members and functional traits not revealed before using more conventional methodologies.