SCIENCES &
BIOENGINEERING SCIENCES

The Research Group
Industrial Microbiology and Food Biotechnology

has the honor to invite you to the public defence of the PhD thesis of

Ana Sosa Fajardo

to obtain the degree of Doctor of Bioengineering Sciences

Title of the PhD thesis:
Competitiveness-enhancing factors in the fermented meat isolate *Staphylococcus shinii* IMDO-S216: a genomic and (meta)transcriptomic approach

Supervisor:
Prof. dr. ir. Frédéric Leroy (VUB)

The defence will take place on

Wednesday, April 1, 2026 at 5 p.m.

VUB Etterbeek campus, Pleinlaan 2,
Elsene, Learning Theatre (LIC.0.04)

The defence can be followed through a live stream:
https://teams.microsoft.com/meet/34582172765537?p=YTI0l7RJgfVSAjQNVA

Members of the jury

Prof. dr. Dominique Maes (VUB, chair)
Prof. dr. Bruno Pot (VUB)
Prof. dr. Catharina Olsen (VUB)
Prof. dr. ir. Chris Michiels (KU Leuven)
Prof. dr. Véronique Delcenserie (ULiège)

Curriculum vitae

Ana Sosa Fajardo (born June 7, 1992, in Seville, Spain) is a biochemist specializing in microbiology and biotechnology. She earned a Bachelor's degree in Biochemistry (2014) and a Master's in Advanced Biology (2015) from the University of Seville. In 2016, she worked as a research associate at the Health Research Institute of Santiago de Compostela studying cancer-related genomic variations. From 2017–2019 she was a proteomics engineer at the Structural Biology Institute in collaboration with the Center for Plant Biotechnology and Genomics. She began a PhD at Vrije Universiteit Brussel in 2019, researching genomic and transcriptomic traits of *Staphylococcus shinii* in fermented meat. She has co-authored five peer-reviewed papers, co-supervised an MSc student, coordinated practical courses, and presented at international conferences.

Abstract of the PhD research

Fermentation is among the oldest known techniques to preserve meat, which is otherwise a highly perishable food in the absence of a cold chain. Two main bacterial populations are key to obtain a safe and flavourful fermented end product, namely the lactic acid bacteria (LAB) and the Gram-positive catalase-positive cocci (GCC). The LAB constitute the major part of the microbial consortium, kickstarting the meat fermentation by the conversion of endogenous or added sugars into lactic acid, which in turn acidifies the product and renders it more stable and safer for human consumption. The GCC are mostly responsible for the establishment and stabilization of a desirable flavour and colour, so that their development plays a modulating role in quality generation.

Among the functionalities relevant for a successful fermentation event, both the LAB and GCC rely on competitiveness factors, which are dynamic mechanisms that improve bacterial fitness within the ecological niche. Competitiveness factors are thus primordial to the survival of a microbial community in a challenging and fluctuating environment, involving for instance the generation of antimicrobial activities against competitors, enhanced nutrient uptake, neutralization of acidic or oxidative stresses, or the establishment of biofilms. Despite the importance of such competitiveness factors for the successful outcome of a fermentation, more research is needed to fully understand their contribution to the quality and safety of the fermented end product. Moreover, most available information relates to the competitive behaviour of LAB in fermented meats, whereas the GCC are much less researched.

This PhD research focused on the presence and expression of competitiveness factors of a selected GCC strain, namely *Staphylococcus shinii* IMDO-S216, within a fermented meat environment. First, a review of the currently published transcriptomic and metatranscriptomic research in the area of fermented foods and beverages is provided (Chapter 1), followed by the specific aims and objectives of the research (Chapter 2). Next, key competitiveness factors within the genome of *Staphylococcus shinii* IMDO-S216 are mapped through a genomics approach (Chapter 3). To study the expression of these factors in solid and liquid growth conditions, a transcriptomic approach was followed (Chapter 4), after which a metatranscriptomic setup was used to monitor the expression of the staphylococcal community's genetic potential in an actual meat environment (Chapter 5). Finally, a general discussion is provided to put the obtained results in perspective (Chapter 6).