VUB 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

# ir. Louise Vermote

to obtain the degree of Doctor of Bioengineering Sciences

Title of the PhD thesis:

## Metagenomics and meta-metabolomics of fruit, rice vinegar, and sour beer ecosystems

Promotors:
**Prof. Dr. Stefan Weckx**
**Prof. Dr. ir. Luc De Vuyst**

The defence will take place on

**Tuesday, August 19, 2025 at 5 p.m.**
**in the Promotiezaal (D.2.01)**

VUB Etterbeek campus, Pleinlaan 2,
Elsene

### Members of the jury

Prof. Dr. Dominique Maes (VUB, chair)
Prof. Dr. Bruno Pot (VUB)
Prof. Dr. Catharina Olsen (VUB)
Prof. Dr. ir. Katleen Raes (UGent)
Dr. Gert De Rouck (KU Leuven)

### Curriculum vitae

ir. Louise Vermote obtained her degree of Master of Science in Bioengineering Sciences with a specialization in Chemistry and Bioprocess Technology from the Vrije Universiteit Brussel in 2016. In 2017, she started her PhD research at the research group Industrial Microbiology and Food Biotechnology under the supervision of Prof. Dr. Stefan Weckx and Prof. Dr. ir. Luc De Vuyst. She is co-author of six publications in peer-reviewed journals, four of which as first author. She combined her research with supervising Master students during (practical) exercises.

### Abstract of the PhD research

Worldwide, more than 5000 different fermented foods and beverages exist, which are part of daily life. Recent advances in high-throughput DNA sequencing have resulted in an evolution in culture-independent techniques, such as shotgun metagenomic sequencing, which allows the detection of the complete microbial diversity, including unculturable microorganisms. Doing so, several novel insights into the microbial diversity and functional potential of microorganisms in different (fermented) food ecosystems were obtained.

First, large differences were encountered in the surface microbiota between different wild tropical fruits and flowers from Northern Argentina. The fruits' surface microbiota was dominated by bacteria, and mainly composed of flower, fruit, and/or plant surface inhabitants. A considerable fraction of the metagenomic sequence reads remained unidentified, suggesting that intrinsic species are still to be sequenced or discovered. Second, wooden barrels used during lambic beer production were shown to act as an additional inoculation source of key microorganisms during fermentation and maturation, which contributes to the characteristic stable microbial ecosystem. The reconstruction of metagenome-assembled genomes (MAGs) for *Acetobacter lambici* and *Pediococcus damnosus* revealed the mechanisms underlying their dominance. Third, three lambic-style acidic beer production processes carried out in Norway with addition of apples during wort cooling confirmed this additional inoculation source and showed that the apples' surface microbiota was not involved in the fermentation processes. The four microbial phases typical for Belgian lambic beer production processes were encountered, although the acidification and maturation phases overlapped. Finally, traditional Korean rice vinegar production processes at two different producers were highly dependent on the use of *nuruk*, a producer-specific starter composed of molds, yeasts, and lactic acid bacteria, which was responsible for the simultaneous rice starch saccharification and alcoholic fermentation phase. The acetic acid fermentation phases were characterized by the presence of several (novel) *Acetobacter* species, while several MAGs were reconstructed.