SCIENCES & BIOENGINEERING SCIENCES

The Research Group

Structural Biology Brussels

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

Beatrice Bernardi

to obtain the degree of Doctor of Bioengineering Sciences

Joint PhD with Hochschule Geisenheim University

Title of the PhD thesis:
Characterization of hybrid genes and copy number variations in lager yeast strains

Promotors:
Prof. dr. rer. nat. Jürgen Wendland
Prof. dr. ir. Ronnie Willaert

The defense will take place on
Friday, November 5, 2021 at 13h00

The defense can be followed through a live stream. Contact Beatrice.Bernardi@vub.be for more information

Members of the jury

Prof. dr. Annette Reineke (HGU, chair)
Prof. dr. Annette Reineke (HGU, secretary)
Prof. dr. Henri De Greve (VUB)
Prof. dr. Ralf Schweiggert (Hochschule Geisenheim University, Germany)
Prof. dr. Gerardo Puopolo (Universita di Trento, Italy)
Prof. dr. Stefanie Plöggeler (Georg-August-Universität Göttingen, Germany)

Curriculum vitae

In 2017, Beatrice graduated with greatest distinction as Master in Biology at University of Florence.
Having obtained a EU-Marie Skłodowska Curie fellowship, she started her doctoral studies in yeast microbiology and bioengineering at the Structural Biology research group of VUB in a joint PhD with the Biochemistry and Microbiology department of Hochschule Geisenheim University (HGU), Germany.
She studied a genome editing solution for allopolyploid genomes focusing on lager yeast.
She co-authored four publications in peer-reviewed scientific journals and partecipated in two international conferences.

Abstract of the PhD research

Lager yeasts are hybrid organisms that originated by cell-fusion of two species of the genus *Saccharomyces*, *S. cerevisiae* and *S. eubayanus*. Post-hybridization events such as copy number variations (CNV), chromosome loss, reciprocal translocations or inter-chromosomal rearrangements can affect genome size, ploidy or sporulation efficiency. In polyploidy hybrids, the presence of multiple alleles of one gene complicates functional studies that rely on genome manipulation, e.g. gene deletions. Most yeast genetic engineering methods are based on the yeast homologous recombination (HR) machinery, which works excellently in *S. cerevisiae* but has a low efficiency in lager yeasts.
In this thesis, I developed a strategy to improve the HR efficiency of lager yeast allowing short-flank (sf) PCR-based gene targeting. HR efficiency was successfully improved by overexpressing *RAD51*, which encodes a key regulator of the HR pathway that performs the search for complementary DNA strands during recombination.
Other mechanisms of genome evolution are by uptake of DNA through horizontal gene transfer or introgression. These were studied in more detail in a *S. uvarum* cider yeast isolate. Interestingly, in this strain we identified the acquisition of *S. eubayanus* and *Torulaspora microellipsoides* DNA. An analysis based on DNA polymorphisms suggests that a lager yeast strain is the likely parental donor of this DNA rather than a *S. eubayanus* strain.
Beer and wine yeasts are characterized by their flocculation properties at the end of fermentation. Flocculation is the ability to produced cell-flocs, a critical trait for industrial yeast, which enables facile separation of cells from the green beer. To implement non-conventional yeast (NCY) in an existing brewing process, these yeasts need to be adaptable to the current brewing technology. Therefore, in this thesis, the flocculation properties of a NCY, *Saccharomycopsis fermentans*, were characterized phenotypically and genotypically and compared to *S. cerevisiae*.