

# MICROBIOTEC 19

December 5<sup>th</sup>-7<sup>th</sup>, 2019  
University of Coimbra (Pólo II)

CONGRESS OF MICROBIOLOGY  
AND BIOTECHNOLOGY 2019

## BOOK OF ABSTRACTS

 **SPM**  
Sociedade Portuguesa de Microbiologia

 **spbt**  
sociedade  
portuguesa de  
biotecnologia

1 2  9 0  
UNIVERSIDADE D  
COIMBRA

### P323. Unveiling the role of the elusive HgAATs in ester production by *Hanseniaspora guilliermondii*

Isabel Seixas<sup>1,2</sup>, Isabel Vasconcelos<sup>3</sup>, Nuno Mira<sup>4</sup>, Ana Mendes-Ferreira<sup>1,2</sup>

<sup>1</sup> WM&B—Laboratory of Wine Microbiology & Biotechnology, Universidade de Trás-os-Montes e Alto Douro, Vila Real, Portugal

<sup>2</sup> BioISI-Biosystems and Integrative Sciences Institute, Campo Grande, Lisbon, Portugal

<sup>3</sup> CBQF/Centro de Biotecnologia e Química Fina, Escola Superior de Biotecnologia, Universidade Católica Portuguesa, Porto, Portugal

<sup>4</sup> IBB, Institute for Bioengineering and Biosciences, Department of Bioengineering, Instituto Superior Técnico, Universidade de Lisboa, Lisbon, Portugal

E-mail: [iseixas@utad.pt](mailto:iseixas@utad.pt)

The wine yeast *Hanseniaspora guilliermondii* (Hg) has the ability to produce aromatic compounds which greatly contribute to the fruity and floral aroma of alcoholic beverages. Recently, through the reconstruction of the metabolic network of Hg UTAD222 we identified a set of genes predicted to be involved in aroma formation, representing the Hg “flavorome”. Notably, within this cohort of proteins we could not identify homologues for known acetyl transferases (AATs), involved in formation of acetate esters, contrasting with the reported high production of these compounds. A deeper analysis of the Hg UTAD222 ORFeome led us to identify four proteins (HGUI\_006997, HGUI\_00952, HGUI\_01907 and HGUI\_01910) that harbor motifs conserved within the AATs enzyme family, these proteins only having orthologues in other *Hanseniaspora* species.

The present work intends to establish a relationship between ester formation with expression levels of these putative alcohol acetyl transferase coding genes.

This data will pave the way for a better elucidation of the putative role of these proteins in acetate ester formation, which in turn will accelerate research focused on its more rational utilization by the wine industry, and also by other bio-industries where they could be explored as cell factories for the production of biobased acetate esters.

#### Acknowledgements

This work was financed by FEDER through POCI-COMPETE 2020 and by Fundação Ciência e tecnologia (BI/PTDC/AGR-TEC/3315/2014, Project SMARTWINE “Smarter wine fermentations: integrating omic-tools for development of novel mixed starter cultures for tailoring wine production”), and supported by FCT to Biosystems and Integrative Sciences Institute (BioISI; UID/MULTI/04046/2019) and to iBB- Institute for Bioengineering and Biosciences (through contract UID/BIO/04565/2013). Programa Operacional Regional de Lisboa 2020 is also acknowledged for its financial support to iBB (project no. 007317). I.S. is a recipient of a Ph.D. grant from FCT (SFRH/BD/122200/2016).