

### 364A Genetic fingerprinting of *Brettanomyces* yeast strains

Sam Crauwels<sup>1</sup>  
Annelies Justé<sup>1</sup>  
Fatemeh Bajoukakahi<sup>2</sup>  
Pieter Busschaert<sup>1</sup>  
Jan Steensels<sup>3</sup>  
Guy Derdelinckx<sup>2</sup>  
Gorik De Samblanx<sup>4</sup>  
Kathleen Marchal<sup>5</sup>  
Kevin Verstrepen<sup>3</sup>  
Kris Willems<sup>1</sup>  
Bart Lievens\*<sup>1</sup>

<sup>1</sup> Laboratory for Process Microbial Ecology and Bioinspirational Management (PME&BIM), Consortium for Industrial Microbiology and Biotechnology (CIMB), Department of Microbial and Molecular Systems (M2S), LForCe, KU Leuven Association, Lessius Mechelen, Campus De Nayer, B-2860 Sint-Katelijne-Waver, Belgium,

<sup>2</sup> KULeuven -FBIW-M2S-LForCe - LIBR:

site MBS, Kasteelpark Arenberg, 33 PO box 2463 B -3001 - HEVERLEE - Belgium,

<sup>3</sup> VIB Lab for Systems Biology and CMPG Lab for Genetics and Genomics, M2S, KU Leuven, B-3001 Leuven, Belgium,

<sup>4</sup> Laboratory for Process Microbial Ecology and Bioinspirational Management (PME&BIM), Consortium for Industrial Microbiology and Biotechnology (CIMB), Department of Microbial and Molecular Systems (M2S), LForCe, KU Leuven Association, Lessius Mechelen, Campus De Nayer, B-2860 Sint-Katelijne-Waver, Belgium and Department of Computer Science, KU Leuven, B-3001 Leuven, Belgium,

<sup>5</sup> Centre of Microbial and Plant Genetics (CMPG), M2S, KU Leuven, B-3001 Leuven, Belgium

*Brettanomyces* (teleomorph: *Dekkera*) is a yeast with high importance in the beer and wine industry, mainly due to the production of aromatic compounds. The production of "off-flavours" makes that the yeast is mostly considered as a spoilage microorganism. However, it is also appreciated and encouraged in a few beers, particularly in certain traditional Belgian ales. By influencing the acidity level and production of secondary metabolites, such as volatile phenol derivatives and isovaleric acid, the yeast is responsible for the typical flavor characteristics of these beers. Despite its economic importance, *Brettanomyces* has remained largely unstudied at the genetic level, and little is known about the genetic diversity between different *Brettanomyces* species or strains belonging to the same species. The objective of this study was to investigate the phylogenetic relationships between *Brettanomyces* strains belonging to all species presently classified within the genus. To this end, a collection of over 60 *Brettanomyces* strains, originating from both reference culture collections and isolations from a beer brewery, was used in this study. Strains were examined for their partial 26S rRNA large subunit sequences. In addition, all strains were characterized by genetic fingerprinting using four Random Amplified Polymorphic DNA primers, one Repetitive Extragenic Palindromic primer, three M13 primers and one primer set amplifying repetitive elements in the *Brettanomyces* genome. Fingerprints were clustered using GelCompar software, version 6.6. Data analysis was performed using both separate and combined data sets. In general, similar results were obtained for the different methods, although some techniques yielded more resolving power. Obtained results will be discussed in relation to the used techniques. Combined

with phenotypic assays and whole genome surveys, this study will contribute to a better understanding of the genetic basis of the physiological capabilities of *Brettanomyces* strains.