

Screening of non-Saccharomyces wild yeasts for biotechnological applications

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In nature, a wide diversity of yeast species can be found even in wastes from food industries. The exploration of this yeast biodiversity has captured great interest from food, pharmaceutical and even fuel companies due to the interesting properties of such microorganisms [1]. These microorganisms can transform sugars present in raw materials into different valuable compounds as several chemical building-blocks and biofuels, in a process more sustainable than those based on fossil fuels and refineries [2]. Within yeasts, *Saccharomyces cerevisiae* is considered the model organism, being the most widely used industrially for the production of added-value products [3]. Properties that range from its simple cultivation, short replication period, sporulation efficiency, easy genetic manipulation and rare pathogenicity have turned it in an ideal organism for various biotechnological processes [3]. Nevertheless, other non-Saccharomyces yeasts are being increasingly used for the heterologous production of valuable products [4]. In this work, a group of isolates from the TransBio collection (Project FP7 KBBE–Nº289603) was selected based on their ability to grow in organic acids. Microorganisms were identified by molecular typing (DNA sequencing of the ITS regions) and characterized regarding morpho- and physiological features. The morphological traits and sporulation patterns were evaluated for cell cycle determination. The selected yeasts revealed interesting physiological features regarding growth profiles using carboxylic acids as sole carbon and energy source. The full characterization of these wild yeast strains is underway.

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References

1. Barnett, J. A., and Barnett, L. (2011). *American Society for Microbiology Press*.
2. Nandy, S. K., and Srivastava, R. K. (2018). *Microbiological research*, 207: 83-90.
3. Gibbon, B., Geertman, J., Hittinger, C. T., Krogerus, K., Libkind, D., Louis, E. J., Magalhães, F. and Sampaio, J. P. (2017) *FEMS Yeast Research*, 17: 1-13.
4. Satyanarayana, T., and Kunze, G. (Eds.). (2009) *Dordrecht: Springer*, 78.