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Data Article

Functional analysis of stress protein data in a flor yeast subjected to a biofilm forming condition

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ABSTRACT

In this data article, an OFFGEL fractionator coupled to LTQ Orbitrap XL MS equipment and a SGD filtering were used to detect in a biofilm-forming flor yeast strain, the maximum possible number of stress proteins under the first stage of a biofilm formation conditions (BFC) and under an initial stage of fermentation used as reference, so-called non-biofilm formation condition (NBFC). Protein functional analysis – based on cellular components and biological process GO terms – was performed for these proteins through the SGD Gene Ontology Slim Mapper tool. A detailed analysis and interpretation of the data can be found in "Stress responsive proteins of a flor yeast strain during the early stages of biofilm formation" [1].

1. Specifications Table

Subject area	*Biology, Microbiology and Biochemistry* *Proteomics, Bioinformatics*

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More specific subject area	
Type of data	*Tables*
How data was acquired	*Protein identification: 3100 OFFGEL Fractionator (Agilent Technologies, Palo Alto, CA) and LTQ Orbitrap XL mass spectrometer (Thermo Fisher Scientific, San Jose, CA, USA) equipped with a nano LC Ultimate 3000 system (Dionex, Germany); Protein quantification: emPAI; Bioinformatic analyses: SGD*
Data format	*Filtered and analyzed*
Experimental factors	*Saccharomyces cerevisiae G1 flor yeast strain; biofilm formation condition and non-biofilm formation condition as control; bioinformatic analyses of the stress response-related identified proteins*
Experimental features	*Saccharomyces cerevisiae G1 flor yeast was exposed to a biofilm formation condition with ethanol and glycerol as main carbon sources and non-biofilm formation condition with glucose. After protein fragmentation using OFFGEL and the identification of the stress response-related proteins, bioinformatic analyses were performed to investigate the protein sub-cellular localization and biological functions*
Data source location	*Agrifood Campus of International Excellence ceiA3, University of Cordoba, Spain*
Data accessibility	*Data are within this article*

2. Value of the data

- Through the SGD Gene Ontology Slim Mapper tool, flor yeast stress proteins were sorted in cellular components and biological GO Terms. Comparison among stress and non-stress conditions of protein frequency sorted in each term, allows to highlight relevant GO Terms.
- The bioinformatics tools applied in this study allows to interpret biological information to be used for comparative proteomics studies.
- The association of proteomic data with protein activity assays and genetics may lead to the genetic improvement of flor yeast strains.

3. Data

Here, we show sub-cellular localizations (Table 1 in supplementary data) and biological processes (Table 2 in supplementary data) GO Terms in which the flor yeast stress related-proteins detected in stressed biofilm formation condition (BFC) and non-biofilm formation condition (NBFC) were sorted. Each type of biofilm formation stresses (lack of fermentable carbon source, ethanol, acetaldehyde and oxidative) were considered separately. Comparison with the *Saccharomyces cerevisiae* proteome frequency, *p*-value and the "GO Term frequency BFC/GO Term frequency NBFC" ratio highlighted most relevant cellular components and biological processes in each condition.

4. Experimental design, materials and methods

The effects of two different biofilm formation conditions (BFC and NBFC) on *S. cerevisiae* G1 flor yeast stress response related-protein expression patterns have been analyzed by using an offgel-based approach. Culture conditions were performed as described in the Process Biochemistry journal paper [1]. Briefly, after growing until the yeast viability reached 90% at the exponential phase, under the two different conditions: BFC with ethanol and glycerol and NBFC with glucose as the main

carbon sources; yeasts were collected and proteins extracted. In both conditions, for triplicates, three aliquots for proteomic analysis were carried out. OFFGEL fractionation, LTQ Orbitrap XL mass spectrometer identification, emPAI quantification [2] and SGD filtration were used to obtaining the stress response proteins in each condition. Bioinformatic tool Gene Ontology Slim Mapper from SGD (http://www.yeastgenome.org/), were applied in order to clarify the sub-cellular localization and biological processes of the identified proteins.

Acknowledgments

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Appendix A. Supplementary material

Supplementary data associated with this article can be found in the online version at http://dx.doi.org/10.1016/j.dib.2016.03.072.

References

[1] J. Moreno-García, J.C. Mauricio, J. Moreno, T. García-Martínez, Stress responsive proteins of a flor yeast strain during the early stages of biofilm formation, Process Biochem. (2016) (in press), http://dx.doi.org/10.1016/j.procbio.2016.02.011.

[2] Y. Ishihama, Y. Oda, T. Tabata, T. Sato, T. Nagasu, J. Rappsilber, M. Mann, Exponentially modified protein abundance index (emPAI) for estimation of absolute protein amount in proteomics by the number of sequenced peptides per protein, Mol. Cell. Proteom. 4 (2005) 1265–1272.