

Deletion of novel genes of an industrial strain of  
*Saccharomyces cerevisiae*

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Fermentation of sugar cane for industrial ethanol production is mainly performed by the yeast *Saccharomyces cerevisiae*. In Brazil, it's the most economically viable process for producing fuel from renewable energy sources. The strains used in the industrial process, for example PE-2, must be highly adapted to various stress conditions.

The genome sequencing of a haploid (JAY291) of PE-2 strain revealed that the genetic structure of the strain has a high frequency of polymorphisms and rearrangements, also containing some genetic regions not identified in S288c (standard laboratory strain).

Recently, new data from JAY270 genome were generated and analyzed by the bioinformatics team of LGE/UNICAMP resulting in a more complete assembly than the previous one. The computationally-predicted genes from the current JAY270 assembly were aligned to all the genes from the S288c genome and 21 of the predicted genes in JAY270 were not found in S288c. These genes may be associated with the high fermentation performance of the PE-2 strain. Therefore, this work aimed to analyze the hypothetical functions and the distribution of putative genes in PE-2 genome and evaluate their influence on fermentation process through gene disruption. The study of the hypothetical functions of putative genes was performed by alignment with sequences from other microorganisms through the program BLASTX. The result revealed that some genes may be involved in crucial functions of the fermentation process, such as carbon and nitrogen metabolism, membrane transport and stress tolerance. This analysis also revealed that new genes in PE-2 are divided into five clusters. We deleted four clusters of genes and three genes individually (21 putative genes in total). The mutants will be evaluated phenotypically and physiologically. We hope to identify whether these genetic regions are associated with the fermentation performance characters and can be used in future studies for improvement of strains.

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