FLOCCULIN-ENCODING GENES IN WILD AND INDUSTRIAL STRAINS OF *Saccharomyces cerevisiae*

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Introduction. Flocculation is one of the most important characteristics for industrial yeast; the cell-cell aggregation of the yeast *Saccharomyces cerevisiae* enables it to sediment at the end of fermentation. The brewing industry has used the natural flocculating ability of *S. cerevisiae* to cost-effectively, environmental-friendly separate biomass from the fermented product. The flocculation is mediated for lectins-like proteins that bind mannose residues in the cells walls of adjacent yeast cells; these proteins are encoded by specific genes, the so-called *FLO* genes, which include *FLO1, 5, 9, 10* and *FLO11*. Besides *FLO* gene activity being regulated at the transcriptional level, it has also been shown to be modulated by other regulatory systems. In particular, environmental factors that influence *FLO* gene expression, and factors that act upon the physical interactions between yeast cells (1).
In this study, we evaluated the presence of *FLO1, FLO5, FLO9* and *FLO11* genes in native and industrial strains of *S. cerevisiae*, providing information about the distribution of these genes, highlighting the importance of this process in yeast applicability for industrial

Methods. The yeast strains used in this study are *S. cerevisiae* S288C(2) as a reference strain, nine industrial and six native *S. cerevisiae* strains. Yeast isolates were characterized biochemically by use of the API 20C Aux. Genomic DNA extraction of the yeast isolates was performed using a Linda Hoskins's lab protocol. All primers used in the PCR amplification of the *FLO* genes were designed based on the genomic sequences of S288c strain, and annealing temperature was determinate for each gene. The flocculating ability of yeast strains was assayed according to the method described by Zhao et al. (3).

Results. The *FLO* genes were distributed as follows: *FLO1* gene was presented in 10 strains, *FLO5* in 13 strains, *FLO11* in 10 strains and *FLO9* gene was not amplified in these yeast strains. Table 1 shows the occurrence of the *FLO* genes in native and industrial yeast isolated from various sources.

***FLO* genes**	**Native yeasts**	**Industrial yeasts**
FLO1	83%	56%
FLO5	83%	89%
FLO11	100%	45%

Table 1. Distribution of *FLO* genes in native and industrial *S. cerevisiae* strains isolated from various sources.

Although we demonstrated the presence of *FLO1, 5* y *11* genes in fourteen *S. cerevisiae* strains, no strain showed positive results in flocculation assay. Figure 1 shows percentage of flocculent cells of each yeast strain evaluated.

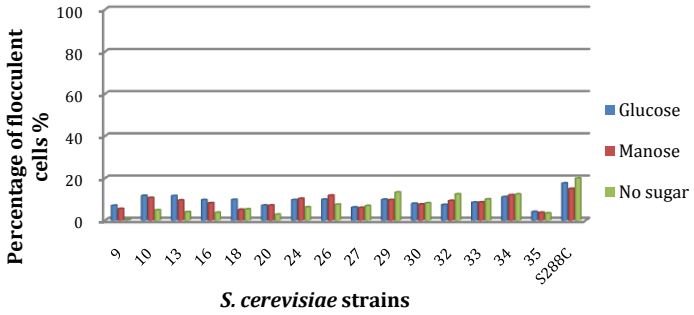

Fig. 1.Flocculation of different *S. cerevisiae* strains isolated of various sources. Inhibition of flocculation by different sugars.

The presence of *FLO* genes ensures no flocculation of yeast even in the presence of calcium, was observed only natural sedimentation process. Sugars did not influence the percentage of flocculent cells, indicating no inhibition of flocculation process.

Conclusions. *FLO* genes are widely distributed in native yeasts are subjected to stressful environmental conditions; these strains become a resource for obtaining strains of wide applicability flocculants in the industry. However, it was demonstrated that flocculation is a complex process involving multiple factors besides the presence of *FLO* genes and is important to identify the variables that influence epigenetic control of flocculation.

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