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Phenotypic analysis and transcriptome profiling of Saccharomyces cerevisiae response to medium chain fatty acids


Introduction

Medium chain fatty acids (MCFA) produced by Saccharomyces during fermentation are well known fermentation inhibitors, which toxicity is enhanced by ethanol and low pH encountered in wine making process (1). On the one hand the accumulation of medium chain fatty acids during wine fermentation is considered as a contributor to sluggish fermentation but on the other hand, fatty acid ethyl esters do contribute positively to the sensory aspect of wine. When exposed to these acids, Saccharomyces acquires greater resistance. For example, octanoic acid induction results in the synthesis of a membrane transporter not characterized until now (2). To investigate the Saccharomyces genes involved in the response to octanoic and decanoic acids we combined both transcriptome profiling and phenotypic analysis.

Results

Transcriptome profiling

The transcriptome of the oenological resistant S. cerevisiae U13 strain was studied after exposure to octanoic or decanoic acid.

Phenotypic analysis

The ability of 80 knocked-out strains to grow on YPG media containing octanoic or decanoic acid was tested on solid or liquid YPG (pH 4.5).

Analysis of PDR12 mRNA levels

PDR12 mRNA levels were measured by Real Time PCR after exposure to 0.1 mM octanoic acid.

Conclusion

Octanoic and decanoic acids induce different sets of genes partially overlapping. Saccharomyces cerevisiae response to octanoic acid share common features with weak acid response (3), essentially with activation of Pdr12 transporter.

Moreover, Tpo1 transporter is also involved in octanoic acid expulsion. Adaptation to decanoic acid is more complex, including expulsion of C10 by the Tpo1 transporter, and activation of a metabolic pathway able to detoxify decanoic acid to generate flavour-producing ethyl-esters.

References

(3) Schuller C. et al., 2004, Mol Biol Cell 15, 766-720