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

Time course of PDR12 overexpression

![Diagram](image)

Genes involved in the detoxification of fatty acids and production of esters

References