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TRANSCRIPTOME VARIABILITY OF YEAST STRAINS

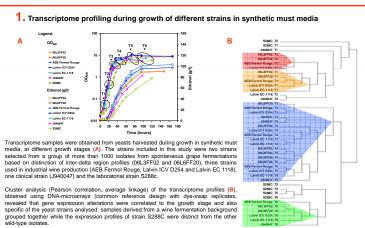
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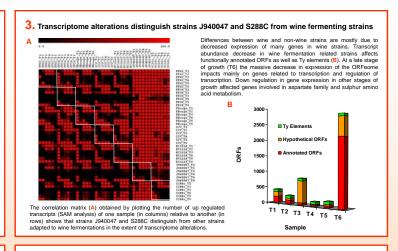
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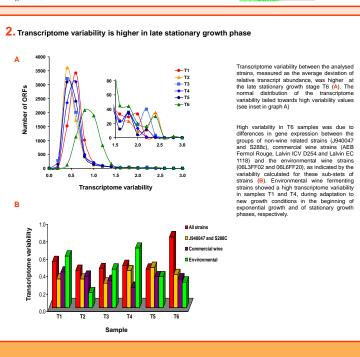
Introduction

Identifying genome and gene expression features associated with phenotypic variation is important to understand the mechanisms of adaptation to environmental change. We compared the genome and transcriptome of six wild-type Saccharomyces cerevisiae strains isolated from different biotopes and the laboratorial strain S288C, using oligo-DNA microarrays probing the yeast ORFeome. Comparative genome hybridization on array showed that only about 3 % of the ORFeome of the wild-type isolates had copy number alterations (mostly depletions) relatively to the laboratorial S288c strain (results not shown). Transcriptome profiling distinguished strains isolated from a wine fermentation background from the others (Figure 1) and showed high transcriptome variability in the late stationary growth phase (Figure 2), mostly due to the dramatic decrease of gene expression registered in wine fermenting strains (Figure 3). Transcriptome variability impacted different subsets of genes according to growth stage and affected key metabolic pathways associated to fermentation, among others (Figure 4).





4. Transcriptome variability affects different functional categories according to growth stage



Functional categories of the most variable transcripts at the different growth phases were obtained using the FatisCAN algorithm available in the BABELOMICS suit of annotation tools (http://babelomics.biointo.gi/tes/). The transcriptome list was ranked according to the average deviation value of the relative percentage of genes in the top of the list as compared between the top and the bottom of the list. The graphic shows the functional categories (Go level 7) identified as more variable (relative percentage of genes in the top of the list as compared to the relative percentage in the bottom of the list, which a corrected p-value above 0.05. Functional categories where average deviation was above 1.5 (see inset in Figure 3.4) were highlighted: (**e) Highly variable categories where deviation was above 1.5 (see inset in Figure 3.4) were highlighted: (**e) Highly variable categories where average deviation was above 1.5 (see inset in Figure 3.4) were highlighted: (**e) Highly variable categories where average deviation was above 1.5 (see inset in Figure 3.4) were highlighted: (**e) Highly variable categories where ORF copy number alterations were not detected.

Conclusions

Variability in gene expression in Sacchararomyces cerevisiae strains was found in genes belonging to functional categories related to metabolic pathways central to survival and adaptation to changing environments, such as sugar and metal intransport, nitrogen starvation and amino acid metabolism, throughout exponential and stationary growth stages. However, higher variability was found in late stationary growth, and this was mostly explained by repression of transcription of maggenes in wine fermenting strains relatively to the others monitored, namely the clinical isolate J490047 and the laboratorial strain S288c. Integration of comparative genome hybridization and the results from transcriptome profiling suggests that extensive changes in the global patterns of gene expression were associated to subtle, rather than to gross, genome alterations along with possible post-transcriptional gene expression regulation mechanisms.









GO Terms

