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Induction of stress genes of *Saccharomyces cerevisiae* during starvation

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Introduction

Saccharomyces cerevisiae shows a typical pattern of gene expression if exposed to stress like heat, aridity, high salt concentrations or starvation. The induction of heat shock proteins for example is a well-known response not only to heat but to other stress conditions as well. However, genes of diverse other groups and metabolic pathways are

also activated. More than 200 genes are classified as “stress genes” in literature. These genes were divided into eight groups, four of which will be discussed in detail.

In this contribution, the reaction of *Saccharomyces cerevisiae* to starvation is examined.

Methods

The gene expression of yeast cells starved for 4 h was compared to those from cells grown at glucose concentrations above 50 mg/L, employing whole-genome microarrays (MWG Yeast 2 Array).

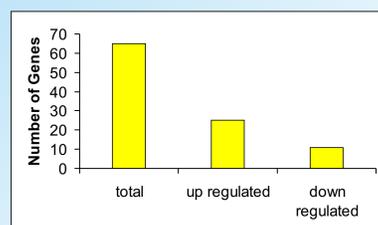
The data processing consisted of the following steps:

- image processing (commercial software ImaGene)
- subtraction of local background from signal (median)
- removal of badly shaped spots and all signals below a chosen threshold are given a value of 1 (Matlab)
- array-to-array standardisation (Matlab)
- addition of Cy3 and Cy5 signals (Matlab)

Stress Response

Among the categories, into which the involved genes have been splitted, the Stress Response Group is the largest. It contains 65 genes. Only a part are regulated at all and not all of these are up regulated. The induced genes mainly encode chaperones. About half of the genes of the Hsp family show an increased expression. Genes responding to high heavy metal ion concentrations or oxidative stress are not activated.

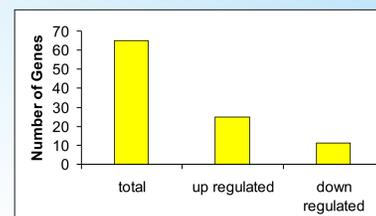
Figure 1



Cell wall

Under stress conditions like heat or aridity, the yeast cells depend on an intact and perhaps fortified cell wall. However, this is not essential during starvation and therefore, *Saccharomyces cerevisiae* does not show a significant increase in the expression of the relevant genes.

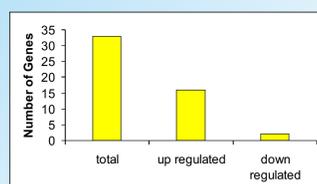
Figure 2



Metabolism

The majority of the genes assigned to the category “Metabolism”, is up regulated during starvation. Especially genes connected with the trehalose synthesis are induced, as well as genes involved in the energy generation.

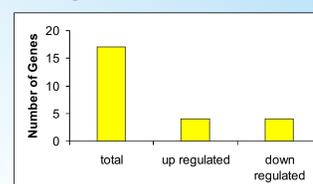
Figure 3



Cell Cycle & Sporulation

Starvation does not have an influence genes of the group “Cell Cycle & Sporulation”, which are activated at other stress conditions. The same amount of genes that is up regulated is down regulated. The expression of most genes does not change.

Figure 4



Further stress induced genes

As the data set included the complete genes belonging to the stress genome of *Saccharomyces cerevisiae*, it was possible to look out for genes induced by the stress condition starvation, which were not yet considered as

Group	Number of regulated genes
Cell wall	5
Proteins	35
Transcription	6
Glycolysis, Citrate Cycle & Glucogenese	7
Metabolism	26
Cell Cycle & Sporulation	9
Others	2

response. A search was run for significantly up regulated genes. Table 1 presents the number of genes found in each category.

Table 1

Conclusions

- *Saccharomyces cerevisiae* is capable to respond to stress situations in a sophisticated way. It adjusts its reaction to the respective condition.
- 90 genes, which are significantly up regulated during starvation and were not classified as part of the stress response, have been identified.