EXPRESSION OF *GUP1* AND *GUP2* IN *SACCHAROMYCES CEREVISIAE*: INFLUENCE OF CARBON SOURCE AND SALT STRESS

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In *Saccharomyces cerevisiae*, *GUP1 and GUP2* genes were identified as responsible for glycerol transmembrane active transport. *GUP1* was identified by increased salt-stress tolerance phenotype in a mutant impaired in glycerol synthesis by deletion of glycerol-3P dehydrogenase genes, *GPD1* and *GPD2*. According to previous results[1], glycerol active transport could be detected in derepression conditions, by growing cells in either ethanol or glycerol. Transport was not detected in glucose-grown cells neither in the presence nor in the absence of NaCl. On the contrary, strain *gpd1gpd2* showed glycerol transport activity when cells were grown on glucose in the presence of NaCl. Further deletion of *GUP1* in this *gpd1gpd2* background, did not abolish transport activity, being this one attributed to its close homologue: *GUP2*[2].

The expression of *GUP1* and *GUP2* was determined by relative quantitative RT-PCR and could be detected on every growth condition, including glucose with or without salt-stress, ethanol and glycerol, suggesting post-transcriptional regulation of glycerol transport activity. Accordingly to data from microarrays[3] available at the *Saccharomyces* Genome Database, we observed constitutive transcription of both genes, with a decrease in mRNA levels during the shift from fermentative to respiratory metabolism. Results obtained in parental strain cells showed that *GUP1* mRNA levels were higher in exponential glucose-grown cells than in any other growth condition, including non-fermentable carbon sources and salt stress. On the contrary, *GUP2* mRNA levels were highest in salt stress glucose-grown cells or ethanol-grown cells. These results indicate that the expression of *GUP1* and *GUP2* are differently regulated at transcriptional level, nevertheless, both genes are constitutively expressed, thus, the major steps in regulation, determining glycerol active transport activity, must lie downstream mRNA synthesis.

1. Hölst, B., Lunde, C., Lages, F., Oliveira, R., Lucas, C. and Kielland-Brandt, M. (2000) *Mol. Microbiol,* 37: 108-124.

2. Lages, F., Lucas, C (1997) *Bioch.Biophys Acta,* 1322: 8-18

3. deRisi et al. (1997) *Science*, 278: 680-686