

2004 Yeast Genetics and Molecular Biology Meeting
University of Washington
Seattle, Washington USA
July 27 - August 1, 2004

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Abstract #536B

Presentation: Poster

Topic: Other yeasts

Yeast orthologues associated with glycerol transport and metabolism.

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In *Saccharomyces cerevisiae*, three genes had been described as involved in glycerol uptake as well as export, respectively, *GUP1/2* and *FPS1*. Altogether, these genes participate in the regulation of intracellular glycerol levels in a way not yet completely unveiled. Physiological adaptation mechanisms to osmotic stress, like the stimulation of glycerol production, intracellular accumulation and the presence of active transport for glycerol, are common to a series of other yeasts. However, not all yeasts present constitutively expressed glycerol active transport systems and it seems that the differences observed are related to salt tolerance. These physiological differences could presumably be explained by differences in the sequences of the genes that encode for proteins related to glycerol metabolism. Taking this into account, we searched for some of the genes related to it in different yeasts. Our search focused on the genes *GUP1/2*, encoding for proteins involved in glycerol uptake; *FPS1*, which product is involved in glycerol export under hypoosmotic shock; *GPD1/2*, which encode for glycerol 3-P dehydrogenases responsible for glycerol production; and *GUT1*, encoding for glycerol kinase, the first enzyme in glycerol catabolic pathway. Sequences obtained were used to create/enlarge protein families, to explore the evolutionary relationship of the yeast species used in this work and to establish the putative relation between sequence and function.



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