

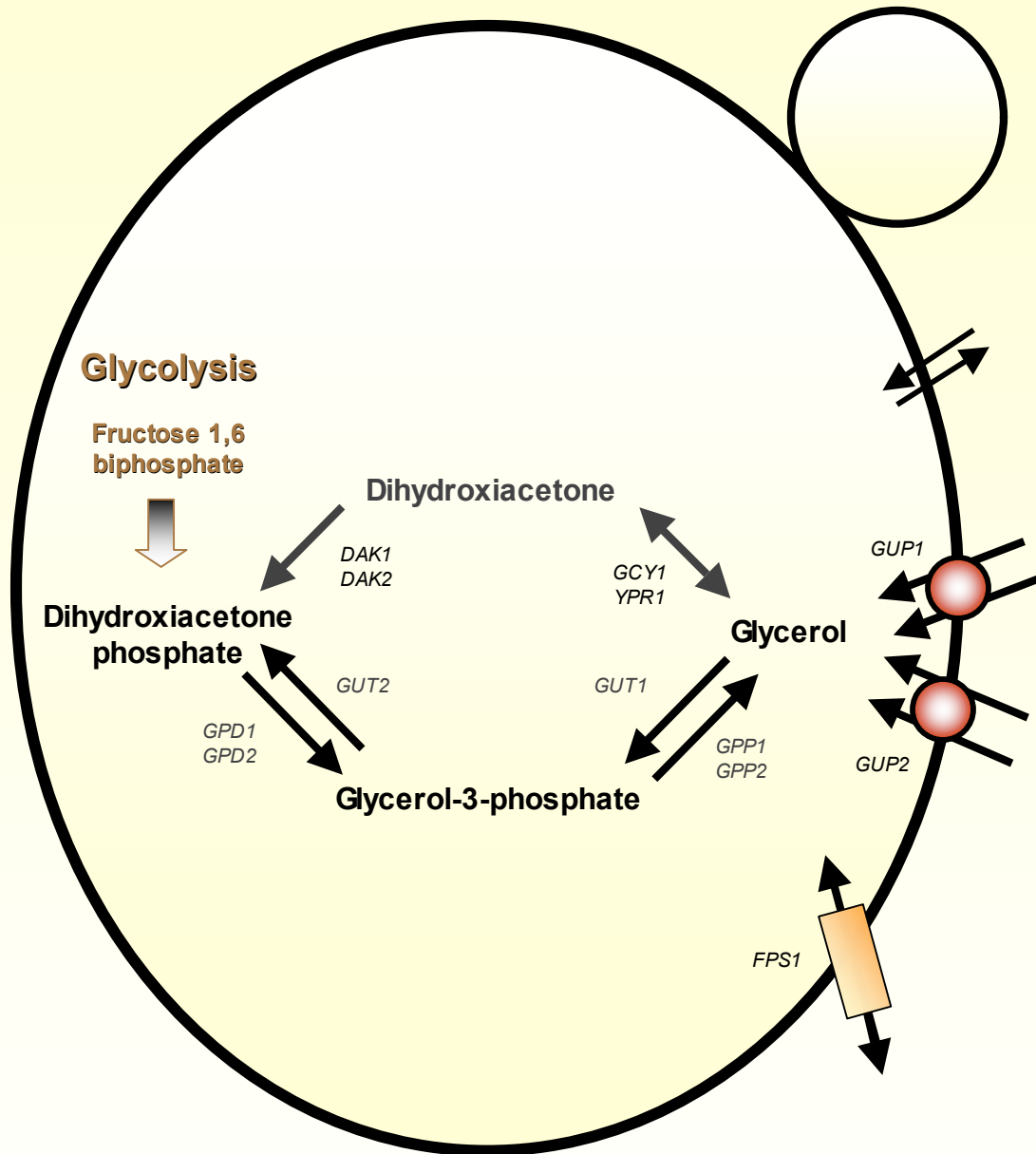
# Expressão dos genes *GUP1* e *GUP2* de *Saccharomyces cerevisiae*: influência da fonte de carbono e do stresse salino

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# Glycerol metabolic pathway in *Saccharomyces cerevisiae*



## GROWTH CONDITIONS

## Ethanol

(Exponential)

Strain	Active transport V <sub>max</sub> ( $\mu\text{mols h}^{-1} \text{g}^{-1}$ )
W303-1A	277 $\pm$ 26 (3)
<i>gpd1 gpd2</i>	237 $\pm$ 30 (3)
<i>gup1</i>	181 $\pm$ 12 (4)
<i>gut1</i>	205 $\pm$ 17 (4)
<i>gup1 gut1</i>	-
<i>gpd1 gut1</i>	248 $\pm$ 36 (4)
<i>gpd1 gup1</i>	nd
<i>gpd1 gup1 gut1</i>	-
<i>gup1 gup2</i>	169 $\pm$ 17 (3)
<i>gut1 gup1 gup2</i>	-
<i>gpd1 gut1 gup1</i>	-

**V<sub>max</sub>** Determined using one glycerol concentration in the range of active transport V<sub>max</sub> ( 2mM )

(-) < 50 $\mu\text{mols h}^{-1} \text{g}^{-1}$

(../..) Number of replicates / number of independent batches of cells



## GROWTH CONDITIONS

**Glucose + 1M NaCl + 15mM Gly**  
(Exponential)

Strain	Active transport	
	<sup>14</sup> [C]Gly uptake Vmax ( $\mu\text{moles h}^{-1} \text{g}^{-1}$ )	H <sup>+</sup> uptake
<b>W303-1A</b>	-	-
<b><i>gpd1 gpd2</i></b>	<b>630 <math>\pm</math> 18 (3)</b>	<b>+</b>
<b><i>gup1</i></b>	-	-
<b><i>gut1</i></b>	-	-
<b><i>gup1 gut1</i></b>	-	-
<b><i>gpd1 gut1</i></b>	<b>165 <math>\pm</math> 9 (2)</b>	<b>+</b>
<b><i>gpd1 gup1</i></b>	<b>182 <math>\pm</math> 0.5 (2)</b>	<b>+</b>
<b><i>gup1 gup2</i></b>	-	-
<b><i>gpd1 gup1 gup2</i></b>	-	-
<b><i>gpd1 gpd2 gup1</i></b>	<b>379 <math>\pm</math> 37 (2)</b>	<b>+</b>

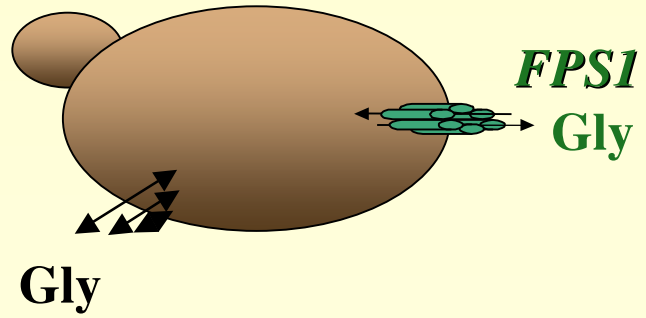
**Vmax** Determined using one glycerol concentration in the range of active transport Vmax ( 2mM )

(-) < 50 $\mu\text{moles h}^{-1} \text{g}^{-1}$

(../..) Number of replicates / number of independent batches of cells



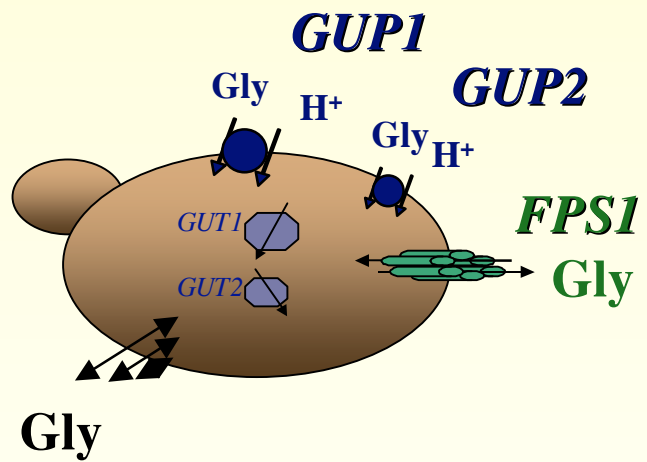
# Cells under glucose repression



# Induced cells

Growth on

ethanol  
glycerol

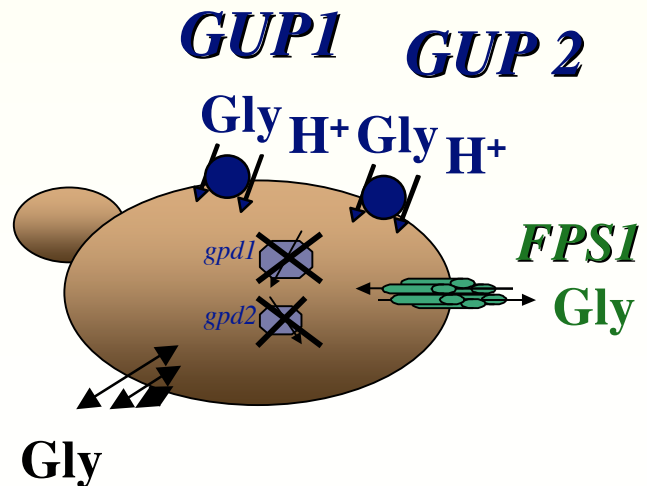


# Induced cells

Growth on

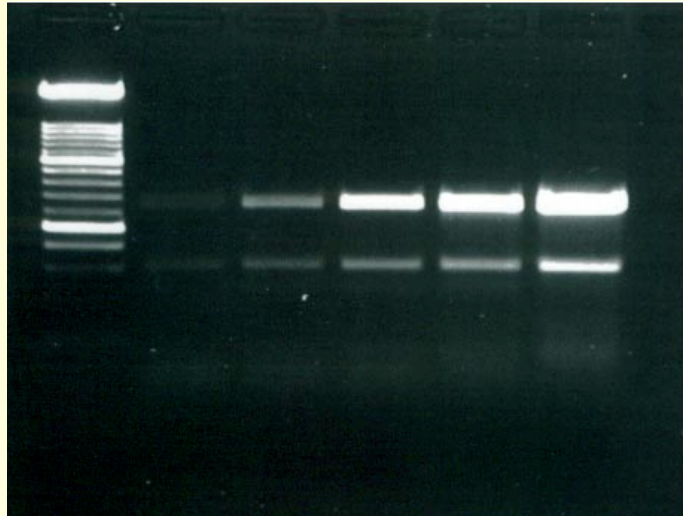
heavy salt stress  
with  
externally added

glycerol

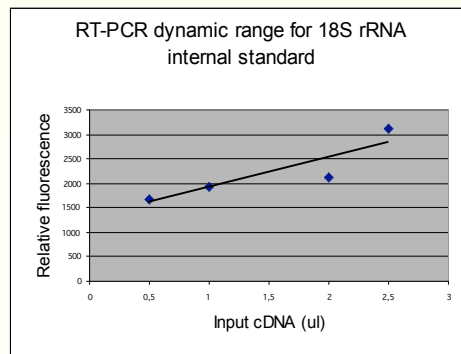
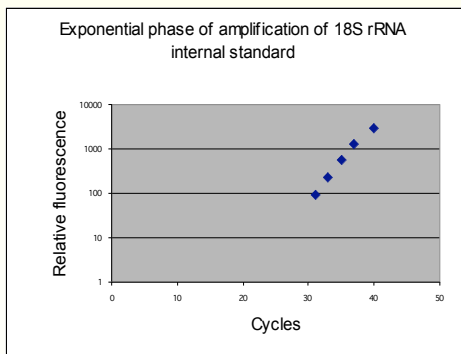
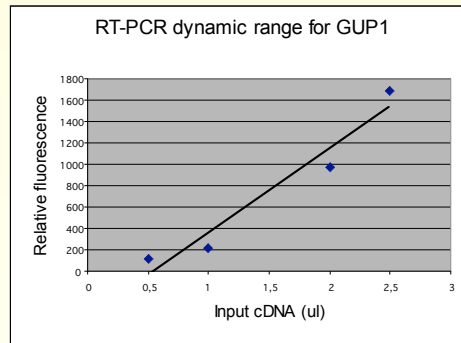
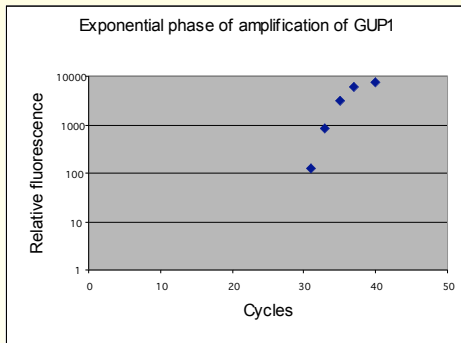


Cycle#

31 33 35 37 40



▶ GUP1  
▶ 18S rRNA



## **GUP1 mRNA relative amounts**

Strains	Growth conditions/carbon sources					
	Glucose (fermentative metabolism)	Glucose (respiratory metabolism)	Glucose + NaCl 1M	Glucose + NaCl 1M + glycerol 15mM	Ethanol	Glycerol
W303-1A parental strain	1.76±0.25 (3)	1.29±0.43 (3)	1.49±0.38 (4)	1.20±0.26 (3)	1.21±0.14 (4)	0.97±0.26 (3)
YSH642 <i>gpd1gpd2</i>	1.31±0.13 (3)	nd	1.35±0.39 (3)	1.61±0.15 (3)	nd	nd

( ) number of independent assays  
nd not determined



## **GUP2 mRNA relative amounts**

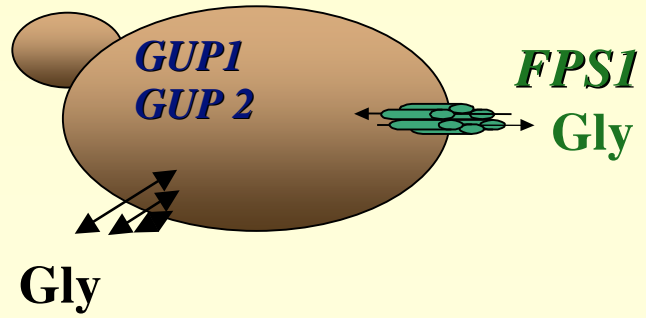
<b>Strains</b>	<b>Growth conditions</b>					
	Glucose (fermentative metabolism)	Glucose (respiratory metabolism)	Glucose + NaCl 1M	Glucose + NaCl 1M + glycerol 15mM	Ethanol	Glycerol
W303-1A	0.91±0.12 (3)	0.66±0.21 (3)	1.39 (1)	1.36±0.10 (2)	1.20±0.33 (3)	nd
YSH642 <i>gpd1gpd2</i>	1.57±0.24 (3)	nd	1.35±0.46 (2)	2.04±0.44 (3)	nd	nd

( ) number of independent assays  
nd not determined





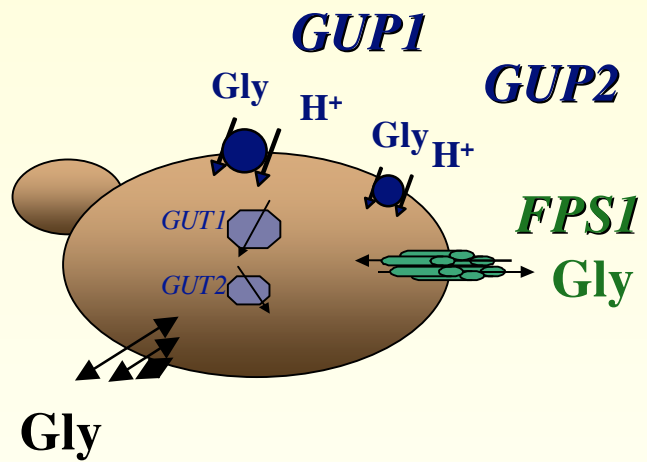
# Cells under glucose repression



## Induced cells

Growth on

ethanol  
glycerol

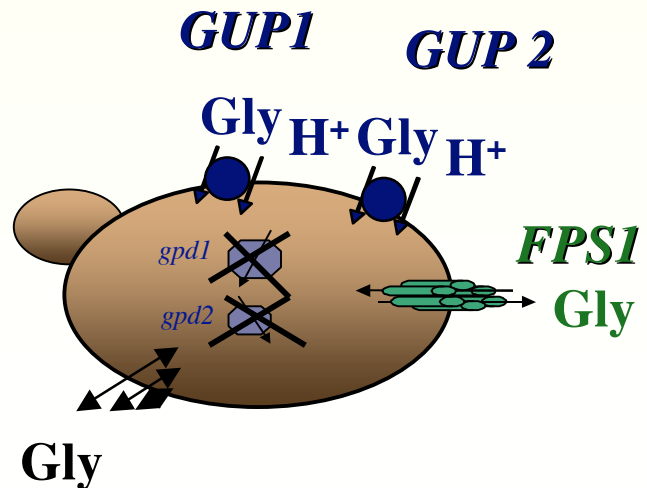


## Induced cells

Growth on

heavy salt stress  
with or without  
externally added

glycerol



## **Synthesis of results**

*GUP1* and *GUP2* mRNAs are always present regardless the carbon and energy source (fermentable or not fermentable)

*GUP1* mRNA levels are not affected by carbon and energy source or salt stress

Transcription of *GUP2* is increased with the inability to synthesize glycerol

*GUP2* mRNA levels increase with salt stress together with, apparently, the simultaneous presence of glycerol

## **Conclusions**

**Expression of *GUP1* and *GUP2* are regulated by post-transcriptional mechanisms**

***GUP2* transcription:**

**differently regulated from *GUP1***

***GPD1* and *GPD2* involved**

**involved in salt stress response**