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AGT1, Encoding an α -Glucoside Transporter Involved in Uptake and Intracellular Accumulation of Trehalose in *Saccharomyces cerevisiae*

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The trehalose content in *Saccharomyces cerevisiae* can be significantly manipulated by including trehalose at an appropriate level in the growth medium. Its uptake is largely dependent on the expression of *AGT1*, which encodes an α -glucoside transporter. The trehalose found in a *tps1* mutant of trehalose synthase may therefore largely reflect its uptake from the enriched medium that was employed.

Most work on trehalose metabolism in yeast concerns factors governing its endogenous level (6, 14, 15). Trehalose synthase is a multimeric protein composed of four subunits encoded by *TPS1*, *TPS2*, *TSL1*, and *TPS3* (2, 18), of which only Tps1p catalyzing the formation of trehalose-6-phosphate from UDP-Glc and glucose-6-phosphate is essential for growth on rapidly fermentable carbon sources like glucose and fructose (8, 22). The molecular mechanism underlying this defect is not yet understood (21). The deletion of *TPS1* in principle results in the loss of trehalose accumulation. However, the existence of another functional pathway for trehalose synthesis in yeast has been postulated, based on data showing that trehalose accumulation is somehow related to maltose metabolism or constitutive maltose gene expression (5, 15) and on one report of a putative ADP-Glc-dependent trehalose synthase activity (17). However, most demonstrations in wild-type and *tps1* mutant strains have employed an enriched medium such as yeast extract-peptone (YEP), and our analysis of yeast extract from various commercial sources (Difco and BOKAR Diagnostic) by using ionic exchange chromatography with pulsed amperometric detection (4) shows it to contain ca. 1.5% trehalose by weight, which would result in a yield of 150 μ g of free trehalose per ml of YEP medium. Since *Saccharomyces cerevisiae* is known to show both a high- and a low-affinity trehalose uptake (13, 19, 20), we speculated that the trehalose accumulation of *tps1* mutant cells might be related to uptake from the medium, perhaps involving *AGT1*, a maltose-controlled gene encoding a transporter with broad specificity for α -glucosides, including trehalose (10).

Yeast mutant strains used in this work were derived from the prototrophic CEN.PK113-7D strain (the kind gift of K.-D. Entian and P. Kötter, Frankfurt, Germany), which possesses a *MAL2-8^c* dominant mutation. Culturing was carried out at

30°C in YEP medium (10 g of yeast extract and 10 g of Bacto Peptone per liter) or in mineral medium (MIN) prepared according to the method described in reference 23 and buffered at pH 5.8 by the addition of 10 g of succinic acid and 6 g of NaOH per liter. The carbon source was added to the media at a final concentration of 10 g \cdot liter⁻¹, and auxotrophic requirements, when required, were added at 100 mg \cdot liter⁻¹. The deletion of *TPS1* and *AGT1* was performed according to the PCR and short homolog fragment procedure of Wach et al. (24) by using the pUG6 plasmid bearing the *loxP-kanMX4-loxP* module (9) for *TPS1* and pUG6lacZ bearing *lacZ-kanMX4* (3) for *AGT1*. The oligonucleotides used to construct the deletion cassette were as follows: d-TPS1 (5'-ATGACTACGGATAA CGCTAAGGCGCAACTGACCTCGTCTTCAGCTGAAGC TTCGTACGC-3'), containing the sequence from nucleotide +1 (A of the start codon) to +40 of the *TPS1* open reading frame (ORF), and f-TPS1 (5'-TCAGTTTTTGGTGGCAGA GGAGCTTGTGAGCTGATGATGCATAGGCCACTAG TGGATCTG-3'), containing the complementary sequence from nucleotide +1445 to +1488 of the *TPS1* ORF, and S1-LAGT1 (5'-ATGAAAATATCATTTCATTGGTAAGCAA GAAGAAGGCTGCCTCAAAATTCGTACGCTGCAGGT CGAC-3'), containing the sequence from nucleotide +1 (A of the start codon) to +48 of the *AGT1* ORF, and S2-AGT1 (5'-TAATTCTCGCTGTTTTATGCTTGAGGACTGACT GATACTCTCATCAGCGCATAGGCCACTAGTGGATC TG-3'), containing the complementary sequence from nucleotide +1783 to +1830 of the *AGT1* ORF.

Amplifications were carried out with Expand high-fidelity polymerase (Boehringer, Mannheim, Germany) according to standard procedures, and the amplified fragments (5 μ g) were used for gene disruption as described in reference 9. For the deletion of *ATH1*, a 4.4-kb fragment bearing the full gene was amplified by using a pair of primers (ATH1-250 [5'-CGTATC ACGACAAACCAACAGCC-3] and ATH1-500 [5'-CAAACC CTACTGACGAGAGAAG]) and genomic DNA from CEN. PK113-7D as a template. The PCR fragment cloned into the pGEM-T vector (Promega) was digested with *EcoRV-HpaI*, which was replaced by a 1.5-kb *EcoRV-SmaI kanMX4* frag-

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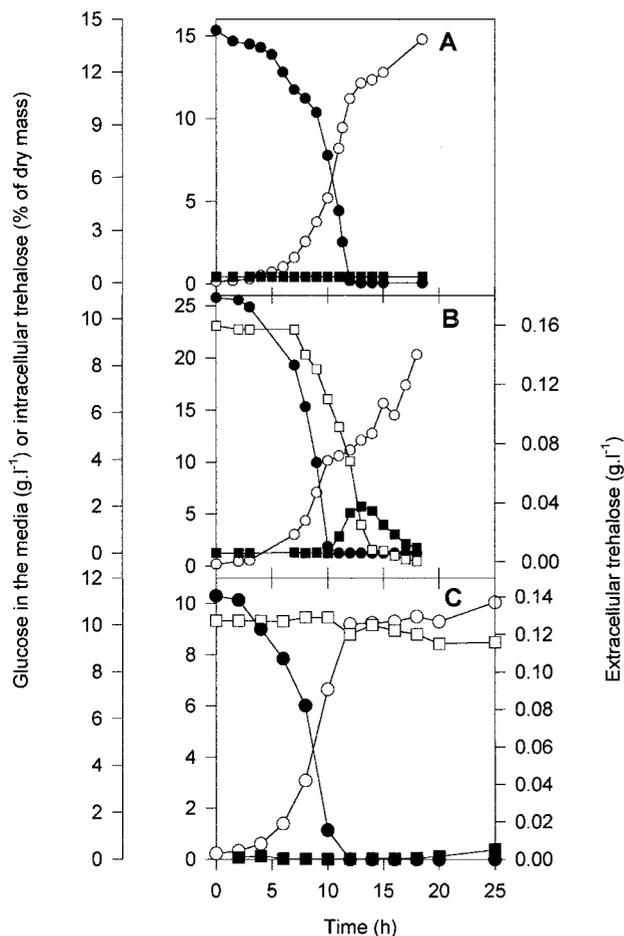


FIG. 1. Patterns of extracellular and intracellular trehalose levels during growth of wild-type CEN.PK113-7D (A and B) and RWY13 ($\Delta agt1$) [C] on galactose-MIN without (A) or with 0.15 g of trehalose \cdot liter⁻¹ (B and C). Shown are the optical densities at 660 nm (○), the level of glucose in the media (□), the level of extracellular trehalose (●), and the level of intracellular trehalose (■).

ment from pFAkanMX4 (24). This construct was cut with *ScaII* and *SpeI*, and the 3.45-kb fragment was gel purified and used for transformation (7). For the deletion of *NTH1*, a 1.2-kb *StuI-SnaBI* of plasmid pTZ18RNTH1 (12) was replaced by a

1.4-kb *EcoRV-SmaI kanMX* module from pFAkanMX4 to yield p Δ ATH1. This plasmid was cut with *PvuII-AlfII*, and the 3.6-kb fragment was used for transformation. Gene disruption was verified either by PCR (24) or by Southern blotting. The $\Delta agt1 \Delta tps1$ and $\Delta nth1 \Delta ath1$ double mutants were obtained by the crossing of haploid mutant strains. The correct $\Delta agt1 \Delta tps1$ mutant was characterized by its inability to grow on YEP-dextrose and its ability to turn dark blue on maltose due to the expression of *AGT1-lacZ*. The correct $\Delta nth1 \Delta ath1$ mutant was obtained from a typical tetrad as the only one lacking both acid and neutral trehalase activity. The level of intracellular trehalose was determined by the procedure described previously (16).

In agreement with the idea that the trehalose content can be manipulated by including trehalose in the growth medium, Fig. 1A shows that although there was a barely detectable level of trehalose in a wild-type strain (with a *MAL^c* mutation) cultivated on galactose-MIN, this level was significantly increased when the medium also contained 0.15 g of trehalose \cdot liter⁻¹ (Fig. 1B), but this accumulation was prevented by the deletion of *AGT1* (Fig. 1C). Table 1 shows that the maximal content of trehalose during the growth of a wild-type strain on YEP-galactose was about 10% of the dry mass and that this level dropped to 3.2% in the *tps1* isogenic strain. By contrast, in galactose-MIN, the content of the disaccharide in the wild-type strain reached ca. 1% and was not detectable in the *tps1* mutant. Both strains, however, were able to accumulate about 2% trehalose when the medium was initially supplemented with 0.15 g of trehalose \cdot liter⁻¹.

The use of varying exogenous trehalose concentrations shows that with 1 g \cdot liter⁻¹ (ca. 3 mM), a 9% intracellular concentration of trehalose can be attained even in galactose-MIN. For a cell sap of 2.4 ml per g of cell dry mass (1, 11), this content corresponds to 110 mM, suggesting an active uptake of trehalose. The accumulation of trehalose was largely abolished by the deletion of *AGT1*, with a residual internal trehalose concentration probably contributed by trehalose synthase activity, as indicated by its loss in the *agt1 tps1* double mutant. However, at a much higher exogenous trehalose concentration (10 g \cdot liter⁻¹ or 30 mM), its endogenous level was on the order of 1% in both the single (*agt1*) and the double (*agt1 tps1*) mutants. This latter result is in agreement with previous work showing the existence of a nonconcentrative low-level *K_m* uptake system for trehalose (13, 19). Since acid and neutral tre-

TABLE 1. Levels of trehalose in wild-type and isogenic mutant strains with *AGT1*, *TPS1*, *NTH1*, or *ATH1* deleted during growth on different media

Growth medium	% Trehalose in dry mass of yeast with genotype ^a				
	Wild type	<i>AGT1 tps1</i>	<i>agt1 TPS1</i>	<i>agt1 tps1</i>	<i>nth1 ath1 AGT1</i>
YEP + galactose	9.50	3.2	ND	0.0	ND
MIN + galactose	1.20	BD	ND	0.0	ND
+ trehalose (0.15 g \cdot liter ⁻¹) ^b	2.0	1.80	0.40	0.0	ND
+ trehalose (0.1 g \cdot liter ⁻¹)	1.28	ND	0.38	0.0	ND
+ trehalose (1.0 g \cdot liter ⁻¹)	8.80	ND	0.41	0.01	ND
+ trehalose (10 g \cdot liter ⁻¹)	12.9	ND	1.34	0.91	ND
MIN + glucose	0.39	ND	0.0	ND	2.0
+ trehalose (0.1 g \cdot liter ⁻¹)	1.28	ND	0.0	ND	3.80
+ trehalose (1.0 g \cdot liter ⁻¹)	8.80	ND	ND	ND	9.50
+ trehalose (4.0 g \cdot liter ⁻¹)	9.70	ND	ND	ND	11.10

^a Although the intracellular trehalose level was determined during growth, the only values reported were the maximal ones attained for each growth condition. BD, below detection; ND, not done.

^b Value of trehalose contained in YEP medium.

halases counteract the endogenous formation of trehalose (14), their influence on intracellular trehalose content was investigated by deleting the corresponding *NTH1* and *ATH1* genes. It is shown in Table 1 that the content of trehalose determined at the end of growth on glucose-MIN increased from 0.39% in a wild-type strain to 2% in cells lacking both trehalases. However, their absence had much less influence on the level of intracellular trehalose as its external concentration was increased, suggesting that yeast cells have a limiting capacity to store a maximum of 12 to 13% trehalose. Taken together, these results conclusively demonstrate that the accumulation of trehalose in yeast is mediated by at least two pathways: the first is via the endogenous UDP-Glc-linked trehalose synthase complex and the second is the uptake of exogenous trehalose via the high-affinity α -glucoside transporter encoded by *AGTI*.

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