

## **Identification of Protein Kinase(s) Involved in Phosphorylation of H<sup>+</sup>-ATPase of Plasma Membrane of Yeast Cells.**

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The plasma membrane H<sup>+</sup>-ATPase of yeast cells is a very important enzyme considered as essential for nutrient uptake by a secondary active transport system as well as for internal pH control. The activation of the enzyme induced by glucose causes a change in kinetic parameters leading to a reduction in the K<sub>m</sub> for ATP and an increase in the V<sub>max</sub> of ATP hydrolysis. These changes seem to be the result of phosphorylation of two different sites in the C-terminal domain of the enzyme. It has been shown that activation of the enzyme, induced by sugar, is clearly dependent on the metabolism of calcium. (Trópia *et al. Biochem. Biophys. Res. Comm.* 343: 1234-1242, 2006), and requires the participation of phospholipase C, protein C kinase, besides the involvement of a glucose sensor Snf3p and G protein Gpa2p. However, it has not yet been identified the protein kinase(s) involved in H<sup>+</sup>-ATPase phosphorylation. In this work, we show results of a screening with yeast strains presenting single deletions in genes encoding for all protein kinases. By measuring sugar induced extracellular acidification, we identified potential protein kinases that may be important candidates to the mechanism of H<sup>+</sup>-ATPase phosphorylation.

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