AMINOACID RESIDUES INVOLVED IN THE ACTIVE SUGAR-H^+ SYMPORT MEDIATED BY THE *AGT1* PERMEASE OF *SACCHAROMYCES CEREVISIAE*

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S. cerevisiae is widely used in industrial applications such as baking, brewing and production of fuel ethanol. Sugar transport into the cells is the first step in their metabolism, and is also the rate-limiting step for fermentation. In this yeast the *AGT1* gene encodes for an active α-glucoside- H^+ symporter with high affinity for sucrose and trehalose, and lower affinity for maltose and maltotriose. Aiming to identify amino acids involved in the active H^+ co-transport and/or substrate specificity, in order to improve the fermentation process were these sugars are used, mutant *AGT1* permeases were generated by site direct mutagenesis of three charged residues present in transmembrane helices (Glu-120, Asp-123, Arg-504). Each mutant permease was expressed in an *agt1*-? *S. cerevisiae* strain, and its functionality assayed through growth on maltotriose. Of these three residues, substitution of Arg-504 by alanine totally abolished sugar transport, while substitution of Glu-120 affected maltotriose utilization by the yeast cells. The substitution of Asp-123 by glycine yielded a mutant permease with significantly lower maltotriose consumption rates, when compared with the wild-type *AGT1* transporter. Thus, our results indicate that Arg-504, and probably also Glu-120 and Asp-123, are amino acid residues involved in the active sugar-H^+ symport activity mediated by the *S. cerevisiae AGT1* permease.

Key words: AGT1, permease, *Saccharomyces*.

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