

DESCRIPTION FOR THE GENERAL PUBLIC (IN ENGLISH)

Glucose is the most abundant sugar on the planet and its metabolism is well studied and understood. However, several aspects of glucose catabolism in eukaryotes, including that in yeasts, remain to be elucidated. Regulation of metabolism of the second most abundant sugar, xylose, is at the preliminary stage of research. Very few are known on the role of transcriptional activators and repressors in the regulation of glucose and xylose catabolism in yeasts. The role of transcription factors Gcr1, Gcr2, Mig1, Mig2, Znf1, Asg1, Ace2 and Swi5 in regulation of glucose catabolism and that of Cat8 in regulation of xylose catabolism was observed. The mechanisms of action of the mentioned proteins are not known in the most of the cases. In the current proposal, we plan to delete and overexpress genes coding for several putative transcriptional factors in the non-conventional thermotolerant yeast *Ogataea (Hansenula) polymorpha* and to study effects of these genetic changes on metabolism and fermentation of glucose and xylose. Expression of the relevant structural genes involved in glucose and xylose catabolism and concentration of intracellular and extracellular metabolites will be determined in the constructed strains. Binding of the transcription factors with target promoters will be studied. The project will utilize modern methods of molecular genetics, biochemistry and analytical chemistry. Successful fulfillment of the project is prerequisite for understanding mechanisms of the regulation of glucose and xylose metabolism in yeasts and could be used for ruling these processes.