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STUDYING THE ROLE OF *CAT*8 TRANSCRIPTIONAL ACTIVATOR IN REGULATION OF XYLOSE ALCOHOLIC FERMENTATION IN NON-CONVENTIONAL YEASTS

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Xylose is considered as semi-fermentative carbon source showing features of both fermentative and respiratory substrates. Being important carbon source for alcoholic fermentation, search for approaches which activate fermentative abilities of this pentose and simultaneously block its respiration is of great interest.

We pay attention to *CAT*8, the global transcriptional regulator involved in regulation of gluconeogenesis and utilization of alternative to glucose carbon sources in *Saccharomyces cerevisiae*. However, the functions of *CAT*8 homologue in the thermotolerant methylotrophic yeast *Ogataea* (*Hansenula) polymorpha* were not studied. It is known that *O. polymorpha* is promising organism for high-temperature alcoholic fermentation of lignocellulosic sugars, such as glucose, cellobiose and xylose, however, ethanol yield and productivity by the wild-type strains is very low.

Homologue of *S. cerevisiae CAT*8 gene was isolated from the sequenced strain *O. polymorpha* NCYC495 and used for construction of the deletion cassette. The strains with knock out in *CAT*8 gene were constructed on the background of the wild-type strain and available the best ethanol producer from xylose. Both types of deletion strains have defect in growth on gluconeogenic substrates (glycerol, ethanol) whereas growth on glucose and xylose was not affected. The mutants *cat8Δ* isolated from the wild-type strain did not show changes in ethanol production in glucose medium whereas accumulated 2-3 times more ethanol in the medium with xylose. The *cat8Δ* mutants isolated from the most advanced ethanol producer from xylose also did not show any differences in ethanol production in glucose medium whereas accumulated 25-30 % more ethanol in the medium with xylose. Maximal accumulation from xylose reached 12.5 g of ethanol per Liter at 45°C which exceeds ethanol accumulation in the wild-type strain NCYC495 near 25 times. Inversely, strain of *O. polymorpha* with overexpression of *CAT*8 accumulated less ethanol from xylose relative to the parental wild-type strain. Data on the expression of number of genes involved in xylose metabolism, glycolysis, gluconeogenesis, pentose phosphate pathway and respiration as well as on the specific activities of the corresponding enzymes will be provided. In order to clarify the function of *CAT*8 in other yeast species, cassette for deletion of *CAT*8 in *Pichia* (*Scheffersomyces*) *stipitis* have been constructed. Isolation of corresponding mutant is under way.

Summarizing, it could be concluded that the transcription regulator *CAT*8 is apparently involved in repression of xylose alcoholic fermentation pathway and consequently its damage strongly activates this process and could be useful for construction of the industrial xylose fermenting strains.