

*Heterologous secretory expression of β -glucosidase from *Thermoascus aurantiacus* in industrial *Saccharomyces cerevisiae* strains*

Izat Smekenov, Marzhan Bakhtambayeva, Kudaybergen Bissenbayev, Murat Saparbayev, Sabira Taipakova & Amangeldy K. Bissenbayev

Brazilian Journal of Microbiology

ISSN 1517-8382

Braz J Microbiol

DOI 10.1007/s42770-019-00192-1



Your article is protected by copyright and all rights are held exclusively by Sociedade Brasileira de Microbiologia. This e-offprint is for personal use only and shall not be self-archived in electronic repositories. If you wish to self-archive your article, please use the accepted manuscript version for posting on your own website. You may further deposit the accepted manuscript version in any repository, provided it is only made publicly available 12 months after official publication or later and provided acknowledgement is given to the original source of publication and a link is inserted to the published article on Springer's website. The link must be accompanied by the following text: "The final publication is available at link.springer.com".



Heterologous secretory expression of β -glucosidase from *Thermoascus aurantiacus* in industrial *Saccharomyces cerevisiae* strains

Izat Smekenov^{1,2} · Marzhan Bakhtambayeva^{1,2} · Kudaybergen Bissenbayev^{2,3} · Murat Saparbayev⁴ · Sabira Taipakova^{1,2} · Amangeldy K. Bissenbaev^{1,2}

Received: 27 November 2018 / Accepted: 14 November 2019
© Sociedade Brasileira de Microbiologia 2019

Abstract

The use of plant biomass for biofuel production will require efficient utilization of the sugars in lignocellulose, primarily cellobiose, because it is the major soluble by-product of cellulose and acts as a strong inhibitor, especially for cellobiohydrolase, which plays a key role in cellulose hydrolysis. Commonly used ethanologenic yeast *Saccharomyces cerevisiae* is unable to utilize cellobiose; accordingly, genetic engineering efforts have been made to transfer β -glucosidase genes enabling cellobiose utilization. Nonetheless, laboratory yeast strains have been employed for most of this research, and such strains may be difficult to use in industrial processes because of their generally weaker resistance to stressors and worse fermenting abilities. The purpose of this study was to engineer industrial yeast strains to ferment cellobiose after stable integration of *tabg11* gene that encodes a β -glucosidase from *Thermoascus aurantiacus* (TaBg11). The recombinant *S. cerevisiae* strains obtained in this study secrete TaBg11, which can hydrolyze cellobiose and produce ethanol. This study clearly indicates that the extent of glycosylation of secreted TaBg11 depends from the yeast strains used and is greatly influenced by carbon sources (cellobiose or glucose). The recombinant yeast strains showed high osmotolerance and resistance to various concentrations of ethanol and furfural and to high temperatures. Therefore, these yeast strains are suitable for ethanol production processes with saccharified lignocellulose.

Keywords *Thermoascus aurantiacus* · *Saccharomyces cerevisiae* · β -Glucosidase · Cellobiose · Industrial strains · Ethanol

Responsible Editor: Eleni Gomes.

Electronic supplementary material The online version of this article (<https://doi.org/10.1007/s42770-019-00192-1>) contains supplementary material, which is available to authorized users.

✉ Amangeldy K. Bissenbaev
Amangeldy.Bisenbaev@kaznu.kz

¹ Department of Molecular Biology and Genetics, Faculty of Biology and Biotechnology, Al-Farabi Kazakh National University, Almaty, Kazakhstan 050040

² Scientific Research Institute of Biology and Biotechnology Problems, Al-Farabi Kazakh National University, Almaty, Kazakhstan 050040

³ Nazarbayev Intellectual School, Almaty, Kazakhstan 050044

⁴ Gustave Roussy Cancer Campus, CNRS UMR8200, Université Paris-Sud, F-94805 Villejuif Cedex, France

Introduction

Biofuels are expected to become some of the major sources of renewable energy and mainly include cellulosic ethanol, bio-diesel, and biogas. Significant attention has been diverted to ethanol from abundant renewable lignocellulosic feedstocks because of the low cost and good availability of ethanol [1, 2]. However, this is a very costly process owing to the robust and complex structure of lignocelluloses, which requires multistep operations, including pre-treatment, enzymatic hydrolysis, and fermentation. Upon hydrolysis, lignocelluloses yield a mixture of monomeric hexoses (glucose and galactose) and pentoses (xylose and arabinose). To develop an inexpensive process, a different metabolic engineering strategy has been employed in attempts to enable *Saccharomyces cerevisiae* to simultaneously ferment all available sugars in biomass hydrolysates (Fig. S1). For more efficient conversion of xylose to ethanol, either xylose reductase/xylytol dehydrogenase (XR/