

Assessing Non-Conventional Yeasts for Bioethanol Production: *Meyerozyma* and *Lodderomyces* Bio-Prospecting Potential

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Sachharomyces cerevisiae
Saccharomyces cerevisiae

its inability to utilize xylose is a limiting factor for the overall efficiency of the process. Henceforth, we look forward to

Meyerozyma *Lodderomyces*, as were identified by ITS sequencing. Fermentation of mixed sugar

Meyerozyma
Lodderomyces respectively with an efficiency of about 65%. Strains were tolerant to inhibitors like 5-hydroxymethyl furfural and furfural at concentrations commonly found in pre-treated hydrolysates. This is the first report elucidating

Meyerozyma *Lodderomyces*

Keywords: Non-conventional; Mixed sugar; Fermentation process

Introduction

The ever surging costs of fossil fuels and the resulting greenhouse effects have necessitated the need to search for alternative cheaper and eco-friendly biofuel resources as an approach to reduce global warming [1, 2]. One such method for the low-cost production of bioethanol is to make use of the lignocellulose biomass as they contain carbohydrates that must be first hydrolysed into simple sugars and then fermented into ethanol. The derivation of higher value added products like fine chemicals or bio-fuel from lignocellulose biomass generally requires a multi-step processing that includes (i) pre-treatment (chemical, biological or mechanical etc.) (ii) Enzymatic hydrolysis (iii) fermentation process.

Saccharomyces cerevisiae has undoubtedly been the paradigm for eukaryotic research. The yeast, being the workhorse of fermentation industry, has dominated alcoholic fermentations owing to its high tolerance to ethanol and also to organic acids, complemented with the exceptional ability to flourish even at low pH and limited oxygen availability [3-5]. Production of bioethanol using lignocellulosic biomass cannot be economically feasible if only the glucose present in the hydrolysate is converted to ethanol owing to the fact that lignocellulosic biomass consisting of ~30 to 45% glucan and ~20 to 35% xylan, which on subsequent pre-treatment and enzymatic hydrolysis, is converted to glucose and xylose, respectively. Despite the presence of gene homologs in the genome of *S. cerevisiae* encoding the necessary enzymes for xylose metabolism i.e. xylose reductase (XR), xylitol dehydrogenase (XDH) and xylulokinase (XKS), it cannot natively utilize xylose hydrolysed from plant biomass. Also, during pre-treatment and hydrolysis of lignocellulose biomass, different monomeric sugars along with a wide range of inhibitory substances are produced which limit microbial fermentation.

Two possible approaches to overcome this problem could be 1. To genetically engineer *S. cerevisiae*, 2. To use non-conventional microorganisms. Industrial strains of *S. cerevisiae* have been engineered worldwide in different ways. However, xylose fermentation in engineered *S. cerevisiae* brings with it the issue of co-factor imbalance followed by low metabolic flux. Thus, a highly promising alternative to engineering industrial friendly model hosts to efficiently utilize

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