Journal of Industrial Microbiology and Biotechnology, vol. 40(9), 2013, pages 1039-1050

Time-based comparative transcriptomics in engineered xylose-utilizing Saccharomyces cerevisiae identifies temperature-responsive genes during ethanol production

Abstract

Agricultural residues comprising lignocellulosic materials are excellent sources of pentose sugar, which can be converted to ethanol as fuel. Ethanol production via consolidated bioprocessing requires a suitable microorganism to withstand the harsh fermentation environment of high temperature, high ethanol concentration, and exposure to inhibitors. We genetically enhanced an industrial Saccharomyces cerevisiae strain, sun049, enabling it to uptake xylose as the sole carbon source at high fermentation temperature. This strain was able to produce 13.9 g/l ethanol from 50 g/l xylose at 38 C. To better understand the xylose consumption ability during long-term, high-temperature conditions, we compared by transciptomics two fermentation conditions: high temperature (38 C) and control temperature (30 C) during the first 12 h of fermentation. This is the first long-term, time-based transcriptomics approach, and it allowed us to discover the role of heat-responsive genes when xylose is the sole carbon source. The results suggest that genes related to amino acid, cell wall, and ribosomal protein synthesis are down-regulated under heat stress. To allow cell stability and continuous xylose uptake in order to produce ethanol, hexose transporter HXT5, heat shock proteins, ubiquitin proteins, and proteolysis were all induced at high temperature. We also speculate that the strong relationship between high temperature and increased xylitol accumulation represents the cell's mechanism to protect itself from heat degradation.

Keywords

Bioethanol; Saccharomyces cerevisiae; Thermotolerant; Transcriptomics; Xylose