Development of Efficient Xylose Fermentation in *Saccharomyces cerevisiae*

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Hydrolysates from lignocellulosic biomasses are an interesting alternative substrate for ethanol production and contain different varieties of sugar components, being glucose and xylose the predominant monosaccharides. *Saccharomyces cerevisiae* ferment hexoses with great efficiency, but this yeast are unable to ferment xylose. Thus, the first challenge for an efficient alcoholic fermentation of xylose is the introduction of a heterologous enzyme that converts xylose into xylulose, like xylose isomerase, which is not dependent on redox potential. Using *S. c.* industrial and laboratory strains grown in different carbon sources (xylose, glucose or fructose) we determined the levels of sugar consumption by dinitrosalicylate, glucose oxidase-peroxidase and phloroglucinol methods. All industrial strains stopped growing after 24h, while the laboratory strain continued growing until reach the same cell concentration as the industrial strains after 48h in xylose medium. In face of theses results, the following experiments employed only one industrial strain and laboratory strain. As expected, the presence of glucose or fructose inhibited xylose consumption. After 24h of growth only in xylose, 30% of the xylose content was consumed, while in the media with fructose or glucose plus xylose the consumption was half and 6-fold lower, respectively and all fructose and glucose were consumed. Bioinformatic analyses of xylose isomerase and xyluloquinase sequences from bacteria genre *Xanthomonas,* Burkholderia and fungus *Piromyces* sp. and *Picchia stipitis* were perfomed based on the data banks of NCBI, with the aid of CLC Workbench, along with softwares clustalW. The results of sequence alignments of xylose isomerase and xyluloquinase showed some similarities between genomic and proteomic sequences of all strains analyzed suggesting that all of them are good candidates to improve xylose fermentation in *Saccharomyces cerevisiae.*