Xylose-utilization of recombinant *S. cerevisiae* containing XYL1, XYL2 and XYL3 isolated from *Pichia stipitis*

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Lignocellulosic biomass is the most abundant source of bioethanol in the world. *Saccharomyces cerevisiae* is effective for industrial scale production of ethanol, but it cannot utilize xylose as the sole carbon source which are present in high amounts in lignocellulosic biomass. Therefore, many research groups have tried to produce ethanol by introduction of metabolism of xylose fermentation into *S. cerevisiae*. *Pichia stipitis* is a good candidate for the development of a recombinant *S. cerevisiae* for ethanol production through the xylose utilization.

Our objective in the present research was to construct the recombinant *S.cerevisiae* capable of xylose utilization, which contain xylose reductase (XR), xylitol dehydrogenase (XDH) and xylulokinase (XK) from *Pichia stipitis*. Plasmid pYES2.0 was used for the overexpression of XR, XDH and XK in *S. cerevisiae*. The ORF of XYL1, XYL2 and XYL3 were isolated from genomic DNA of *P. stipitis* CBS5773. In addition optimize fermentation for improving ethanol productivity.