Increased production of isobutanol from xylose through metabolic engineering of Saccharomyces cerevisiae overexpressing transcription factor Znf1 and exogenous genes

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Abstract

To improve isobutanol production from xylose, *S. cerevisiae* was engineered to overexpress Znf1, xylose reductase (XR), xylitol dehydrogenase (XDH), xylulokinase, and isobutanol-pathway enzymes. Using a 5 L bioreactor with added $FeSO_4 \cdot 7H_2O$, the engineered strain produced 14.81 ± 0.40 g/L isobutanol from 10% xylose, corresponding to 155.88 mg/g consumed and a 264.75% yield improvement. Proteomic and transcriptomic analyses confirmed pathway activation and increased tolerance to lignocellulosic inhibitors.

Winpact Model: FS-05

Introduction

Biorefinery utilization of xylose remains challenging in *S. cerevisiae*. The transcription factor Znf1 has been shown to enhance non-fermentable carbon source metabolism. Coupling Znf1 overexpression with expression of xylose-pathway and isobutanol-production genes could improve yields. This study aimed to engineer *S. cerevisiae* and optimize fermentation conditions for scalable isobutanol production in a 5 L bioreactor.

Materials and Methods

Biorefinery utilization of xylose remains challenging in *S. cerevisiae*. The transcription factor Znf1 has been shown to enhance non-fermentable carbon source metabolism. Coupling Znf1 overexpression with expression of xylose-pathway and isobutanol-production genes could improve yields. This study aimed to engineer *S. cerevisiae* and optimize fermentation conditions for scalable isobutanol production in a 5 L bioreactor.

Results

- Isobutanol titer reached 14.81 ± 0.40 g/L (155.88 mg/g xylose) with $FeSO_4$ supplementation.
- Yield improved by ~264.75% compared to control.
- Proteomics indicated activation of valine biosynthesis, Ehrlich pathway, iron–sulfur cluster pathways.
- Transcriptomics confirmed Znf1-mediated upregulation of key genes in xylose utilization and stress tolerance.

References

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