

## Evaluation of *S. cerevisiae* promoters during growth on xylose

<u>L. Mande<sup>1</sup></u>; W.H. Van Zyl<sup>2</sup>; I. Ncube<sup>1</sup>; D.C. La Grange<sup>1</sup>



## Motivation

•Identify a promoter that is strongly induced during growth on xylose

• Increase production of recombinant enzymes

needed during the degradation of lignocelluloses

•Recombinant enzymes such as xylanases, betaglucosidase, cellulases etc





- S.cerevisiae has been used for years in the production of recombinant proteins
- > S.cerevisiae is a widely used organism
  - fast cell growth
  - tolerate high ethanol concentration
  - tolerate wide spectrum of inhibitors
  - well-characterised physiology & genetics
  - GRAS status



- Glucose is the most abundant sugar in nature (cellulose)
- S. cerevisiae is a Crabtree positive yeast
- Its produces ethanol on glucose under aerobic conditions (little biomass)
- High expression level of recombinant protein is linked to the amount of biomass obtained during fermentation (Ferndahl *et al.*, 2010)





- Xylose is the second most abundant sugar in nature and considered a waste in most industries
- S. cerevisiae cannot utilise xylose as a carbon source
- S.cerevisiae engineered to grow on xylose has been reported to produce more biomass on xylose
- Xylose is the more suitable carbon source in recombinant protein production









#### **Restriction map of the plasmids**



Figure 1. pPGK1 used as base for the construction of all episomal plasmids.





Figure 2. Engineered *S.cerevisiae* on xylose and SC –URA3 with glucose.



Growth of engineered and wild S.cerevisiae on xylose type S.cerevisiae on glucose DD600nm 0D600nm n Incubation Time Incubation Time (Hour)

Growth of engineered and wild type

Figure 3.Growth curve of the wild type and engineered yeast on glucose and on xylose



Transformants spotted on RBB-xylan plates with different carbon source





RBB-xylan xylose

RBB-xylan glucose

Figure 4. The RBB-xylan plates used to confirm xylanase activity



DNS ASSAY was done to determine the xylanase activity following the method by (Bailey *et al*, 1992)





Figure 5. Determination of the amount of xylanase enzyme produced using DNS assay

# Results and Discussion



Figure 6. Determination of the amount of xylanase enzyme produced using DNS assay



#### Construction of *fur1::LEU2* strains





## **FUTURE WORK**

Evaluation of episomal promoters during growth on xylose

Determine metabolic burden during growth on xylose in the bioreactor



## ACKNOWLEDGEMENT

➤ Many thanks Dr. La Grange

- Prof Ncube and Prof van Zyl
- ≻ Dr V. Mbazima
- Van Zyl lab (Stellenbosch University)
- Department of BMBT (University of Limpopo)
- RSES for financial assistance

## Thank you .....

![](_page_17_Picture_1.jpeg)

#### **Fur1 Disruption**

fur1::LEU2 allele was Isolated as 3.27kb from pDF1 plasmid

➤Ncol-Nsil restriction enzymes

Disrupted using the gene replacement method

![](_page_18_Figure_4.jpeg)

![](_page_20_Figure_1.jpeg)

(Aristidou and Pentila,2000)

#### **Transformation of integrated plasmids**

![](_page_21_Figure_1.jpeg)

#### Integrating expression cassettes

- PGK1p and PGK1t isolated from plasmid by restriction digest
- ➤ G418 isolated from plasmid by PCR
- 40bp URA3 overhangs added to expression cassette (target cassette to URA3-locus)
- Expression cassette cloned into pUC19

![](_page_22_Figure_5.jpeg)

![](_page_23_Picture_0.jpeg)

#### Transformation

![](_page_23_Figure_2.jpeg)

Rapid genomic DNA isolation, "Bust and Grab" method

#### Construction of the strain that grows on xylose

- S. cerevisiae Y294 (Matα leu 2-3, 112 ura 3-52,his 3,trp1-289)
- Transformation with pMJM121 with Synthetic codon optimised xylose isomerase
  - ➢ B. thetaiotaomicron XI
  - Selective marker (zeocin)
- Disruption cassette (gre3::Xyl3Hygromycin) was used to knock out GRE3 gene

#### RESULTS

![](_page_25_Figure_1.jpeg)

Figure 2: (A) Agarose gel electrophoresis of the PCR with XYN2 primers (B) Gel electrophoresis of PCR with promoter specific primer and XYN2 right primer