

Expression of trehalose synthase gene from *Pseudomonas putida* P06 in *Pichia pastoris*

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Abstract: The trehalose synthase (TreS) gene from *Pseudomonas putida* P06 was successfully ligated with pPICZaA expression vector by the EcoRI and XbaI and was transformed into *Pichia pastoris* GS115 by electrotransformation. The trehalose synthase gene was fused to the genome of *Pichia pastoris* GS115 and was controlled by AOX1 promoter. The TreS protein was successfully expressed intracellularly. SDS-PAGE results illustrated that a specificity protein band was observed at about 76 kDa. The cell lysates could convert 60% maltose into trehalose at 50°C and pH 7.5 in 10% maltose substrate for 24 h. The *Pichia pastoris* exogenous gene expression host is safer to produce endotoxin free TreS than *E. coli*.

Keywords: Trehalose synthase, *Pseudomonas putida* P06, *Pichia pastoris*, cloning and expression.

INTRODUCTION

Trehalose is a non-reducing disaccharide, two glucose molecules linked by an α , α -1, 1- glycosidic bond. Trehalose is widely synthesised in organisms, including microorganisms, plants and animals (Elbein et al., 2003). Trehalose has many good features, such as thermostability and pH-stability. It can effectively prevent protein and cell membrane damage in extreme conditions, including dehydration, desiccation, heat, oxidation and cold. With the development of trehalose application, it has been used in food, cosmetics, pharmaceuticals, agricultural industries (Elbein et al., 2003; Satpathya et al., 2004).

The benefits of trehalose have been recognized by researchers for many years, and the new application study is also expanding, but the scale-up industrial production of trehalose is still limited. Recently, the pathway of converting maltose into trehalose by trehalose synthase has been considered to be a very good method, because the process is simple and can be controlled easily. Moreover, the most important factor is that maltose as a substrate is low cost. Several trehalose synthase producing strains have been screened, identified and have been expressed in *Escherichia coli*, *Pseudomonas stutzeri* CJ38 (Lee et al., 2005), *Corynebacterium glutamicum* ATCC13032 (Kim et al., 2010), *Arthrobacter aureus* CGMCC 1.1892 (Wu et al., 2009), *Meiothermus ruber* CBS-01 (Zhu et al., 2010), *Mycobacterium smegmatis* (Pan et al., 2004), *Pseudomonas putida* (Ma et al., 2006) and *Thermobifida fusca* (Wei et al., 2004). The expression of trehalose synthase in *Pichia pastoris* was not reported so far. In the present study, the trehalose synthase gene from *Pseudomonas putida* P06 was cloned

and expressed in *Pichia pastoris* GS115, in order to produce endotoxin free trehalose synthase.

MATERIAL AND METHODS

Strains and plasmids

Pseudomonas putida P06 was preserved in Key Laboratory of Shandong Microbial Engineering in China. *Pichia pastoris* GS115 was used for expressing the TreS protein. Plasmid pPICZaA as the expression vector of TreS was adopted in *Pichia pastoris* GS115. *Escherichia coli* DH5a was exploited to manipulate TreS gene.

Gene cloning and expression vector construction

The sequence of the open reading frame (gi = 1042893, NCBI) annotated as TreS in GenBank. TreS gene was cloned from the total DNA of *Pseudomonas putida* P06 using polymerase chain (PCR) reaction amplification with sense primer pTreSF 5'-CGGAATTCATGACCCAGCC-CGACC-3' and antisense primer pTreSR 5'-GCTCTAGATCAAACATGCCCGCTGC-3', (the EcoRI and XbaI restriction site is italicized, respectively). The PCR procedure with *pfu* DNA polymerase was performed through 30 cycles (30 s at 95°C, 30 s at 54°C, 2.5 min at 72°C), followed by a final extension for 10 min at 72°C. The PCR product was purified and digested by the EcoRI and XbaI restriction enzyme, and ligated with pPICZaA expression vector by the same restriction enzyme. The recombinant pPICZaA-TreS plasmid was first transformed into *E. coli* DH5a, and the marker positive colonies were selected from LB agar medium containing 25 μ g/ml zeocin for sequence analysis.

Screening the high-level expression transformants

The correct sequencing of pPICZaA-TreS was linearized with BstXI. The *Pichia pastoris* GS115 competent cells

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were prepared by pretreating *Pichia pastoris* with lithium acetate and 1% dithiothreitol to mix with linearized recombinant plasmid in 0.2 cm electroporation cuvette for electroporation at 1.5kv and 5 ms. After pre-incubation for 3 h at 30°C in 1M sorbitol, the competent cells, which were pre-incubated for 3h at 30°C, were plated on YPDS medium (peptone 2%, yeast extract 1%, glucose 2%, sorbitol 1M and agar 2%) with 100µg/ml zeocin to screen positive colonies that integrated TreS gene in 5'AOX zone of *Pichia pastoris* GS115 for 2-3 days. Then *Pichia pastoris* positive transformants were coated on YPDS plates containing 500 µg/mL, 1000 µg/mL, and 2000 µg/mL zeocin. Multicopy transformants were screened from the YPDS plates (2000 µg/mL zeocin) and the TreS was highly expressed. After positive transformants were screened, the transformants were cultivated for 18h at 30°C, 250rpm centrifugal in BMGY medium containing peptone 2%, yeast nitrogen base 1.34%, yeast extract 1%, biotin 4×10⁻⁵% and glycerol 1%, the pH was adjusted at 6.0. The cells were then centrifuged (250 rpm) and were developed for 72 h at 30°C, in BMMY medium containing yeast extract 1%, peptone 2%, yeast nitrogen base 1.34%, biotin 4×10⁻⁵%, 0.5% methanol (v/v), the pH was adjusted at 6.0. In order to maintain the continuous induction, the absolute methanol was added to the shake flask every 24h during the incubation period. The methanol concentration in fermentation liquid was controlled in 0.5%. The cell precipitate was harvested by centrifugation after the fermentation, then the TreS activity of the clear supernatant and the cell lysates were analyzed. The protein band was analyzed by SDS-PAGE.

RESULTS

TreS gene cloning and expression vector construction

According to the TreS ORF sequence of *Pseudomonas putida* P06, using the primer pairs (pTreSF and pTreSR), the TreS gene was cloned from *Pseudomonas putida* P06 by PCR and the band was clearly visible (fig. 1) on the agarose gel electrophoresis.

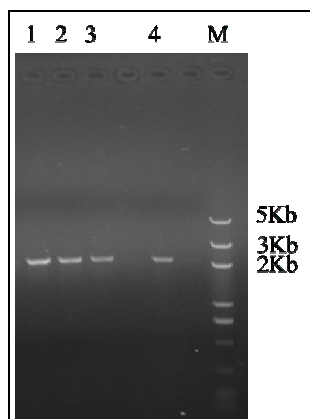


Fig. 1: Amplification of TreS from chromosomal DNA of *P. putida* P06 by PCR Lanes 1-4, target sequence of *P. putida*; LaneM, Trans2K™ Plus DNA Marker

The PCR product was recovered from the gel and ligated to pPICZαA after double restriction enzyme digestion of EcoRI and XbaI. The target sequence was cloned into plasmid pPICZαA and sequenced. Sequence analysis illustrated that target sequence was 100% matched with the gene from *Pseudomonas putida* P06. The recombinant expression vector pPICZαA-TreS was transformed into the *E. coli* DH5α strain for cloning and the positive clone bacteria was picked from LB solid medium with 25µg/ml zeocin for colony PCR template (the positive clone strains were obtained). The positive clone strains were then activated, and their plasmids were extracted and digested by EcoRI and XbaI, following the verification by agarose gel electrophoresis as shown in fig. 2.

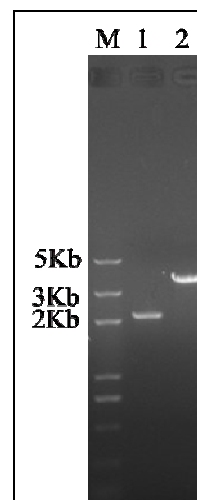


Fig. 2: The double digest results of target gene and the plasmid Lane 1, double digest of TreS target gene; Lane 2, double digest of pPICZαA plasmid ; LaneM, Trans2K™ Plus DNA Marker

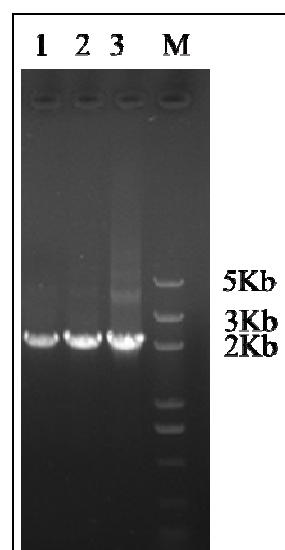


Fig. 3: PCR of positive transformants Lane1-3: PCR amplified DNA product of positive transformants; laneM: Trans2K™ Plus DNA Marker

TreS encoded protein expression in *Pichia pastoris* GS115

The TreS gene with no signal peptide sequences was integrated into pPICZ α A vector and connected with the α -factor signal for the enzyme secretion. Binding sites located in the cleavage site (Kex2). High tolerance (2000 μ g/mL zeocin) strains were selected, the TreS gene was analyzed by PCR. The band of approximately 2.1Kb revealed that the TreS gene got integrated into the genome of *Pichia pastoris* GS115, as shown in fig.3.

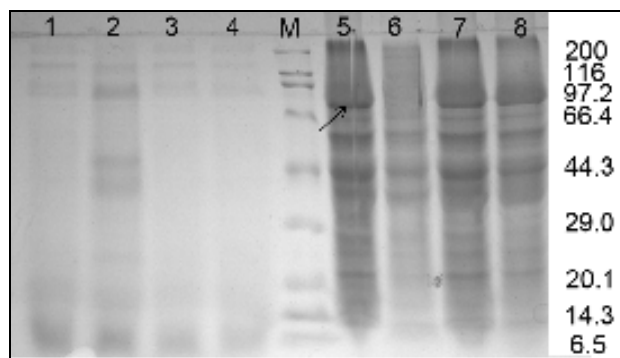


Fig. 4: SDS-PAGE (10%) of TreS (extracellular and intracellular) LaneM, Protein Markers (Broad); Lane1, 3, 4, SDS-PAGE of extracellular recombinant TreS; Lane5, 7, 8: SDS-PAGE of intracellular recombinant TreS; Lane2, 6, SDS-PAGE of extracellular and intracellular blank control

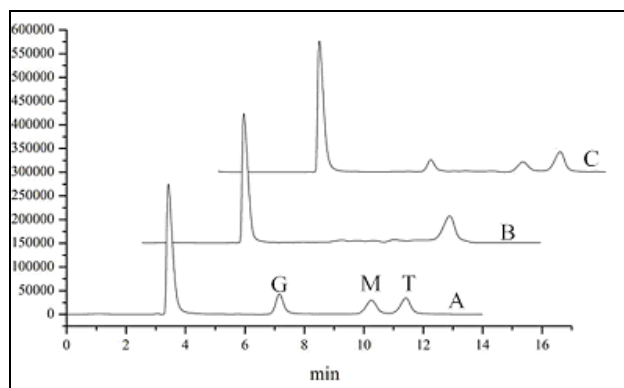


Fig. 5: HPLC chromatograms results of the samples A: The enzyme assay in intracellular contents; B: The enzyme assay in extracellular contents; C: the standard substances. M: maltose (10.3min); G: glucose(7.2min); T: trehalose(11.5min).

The recombinant *Pichia pastoris* GS115 expressing TreS was induced by absolute methanol in shake flask for 72 h. The yeast cells were centrifugated (6000 \times g) for 10 min at 4 $^{\circ}$ C to obtain the pellet. The wet cell pellet of 100 g (the cell dry weight of per liter liquid) was suspended in 10 mmol/L phosphate buffered solution (Na $^{+}$, pH7.5) and the volume was made up to 1000mL. The cell suspension was cyclically disrupted twice by high-pressure homogenizer

(APV-2000, Germany) at 1300 bar. More than 95% cells were disrupted as observed after methylene blue staining. The fermentation supernatant and the cell lysates were used to convert maltose and SDS-PAGE, respectively. The SDS-PAGE analysis showed (fig. 4) that an recombinant intracellular protein of about 76 kDa (in accordance to the predicted value), was expressed. No specific protein was detected in supernatant. In order to further prove the TreS location (intracellular and extra cellular), the culture medium supernat or the cell homogenates was mixed with the final concentration of 10% maltose solution of pH 7.5 at 50 $^{\circ}$ C for 24h, then boiled the mixed solution for 10 min to analyze the content of trehalose. Accordingly, there was no trehalose production in extracellular mixed reaction solution, rather trehalose was found intracellular (fig. 5).

DISCUSSION

We have demonstrated that trehalose synthase gene from *Pseudomonas putida* P06 was inserted into expression vector and expressed as target recombinant enzyme. Although, trehalose synthase with activity can accumulate in cells, but the trehalose synthase could not be secreted into the culture medium. Genes encoding the trehalose synthase from other species have been used to express and encode for recombinant enzyme, but it could only be expressed in *Escherichia coli* system. And recent data is not available regarding to exogenous trehalose synthase gene expression in *Pichia pastoris* GS115. However *Pichia pastoris* expression system has been used widely (Lee et al., 2007; Yu et al., 2009; Tang et al., 2012). Gene of trehalose synthase from *Pseudomonas putida* P06 has been expressed for the first time in *Pichia pastoris* GS115. The *Pichia pastoris* as a host strain may be more safe than the *E.coli* system, because of endotoxin problem associated with in *E. coli*.

Nevertheless, recombinant protein gene was not expressed for extracellular product as expected. As per secreted protein mechanism (Damasceno et al., 2012), *Pichia pastoris* belongs to posttranslational translocation, target enzyme synthesis undergoes many mechanisms starting from gene to the complete protein synthesis. Even one of the factors such as gene dosage and codon bias may lead to improper enzyme synthesis. Thus, it needs to continue with the analysis the reasons regarding the recombinant protein gene expressed on intracellularly and not extracellularly.

The present research findings have demonstrated that the gene encoding for trehalose synthase from *Pseudomonas putida* P06 could be successfully expressed in *Pichia pastoris* system. The focused research regarding the TreS protein extracellular secretion will continue.

REFERENCES

- Damasceno LM, Huang CJ and Batt CA (2012). Protein secretion in *Pichia pastoris* and advances in protein production. *Appl. Microbiol. Biotechnol.*, **93**: 31-39.
- Elbein AD, Pan YT, Pastuazak I and Carroll D (2003). New insights on trehalose: A multifunctional molecule. *Glycobiology.*, **13**: 17-27.
- Kim TK, Jang JH, Cho HY, Lee HS and Kim YW (2010). Gene cloning and characterization of a trehalose synthase from *Corynebacterium glutamicum* ATCC13032. *Food Sci. Biotechnol.*, **19**: 565-569.
- Lee JC, Choi YJ, Lee PC, Kang S, Bok JD and Cho J (2007). Recombinant production of *Penicillium oxalicum* PJ3 phytase in *Pichia Pastoris*. *World J. Microbiol. Biotechnol.*, **23**: 443-446.
- Lee JH, Lee KH, Kim CG, Lee SY, Kim GJ, Park YH and Chung SO (2005). Cloning and expression of a trehalose synthase from *Pseudomonas stutzeri* CJ38 in *Escherichia coli* for the production of trehalose. *Appl. Microbiol. Biotechnol.*, **68**: 213-219.
- Ma Y, Xue L and Sun DW (2006). Characteristics of trehalose synthase from permeablized *Pseudomonas putida* cells and its application in converting maltose into trehalose. *J. Food Eng.*, **77**: 342-347.
- Pan YT, Edavana VK, Jourdian WJ, Edmondson R, Carroll IP and Elbein AD (2004). Trehalose synthase of *Mycobacterium smegmatis* purification, cloning, expression, and properties of the enzyme. *Eur. J. Biochem.*, **271**: 4259-4269.
- Satpathya GR, To'ro'ka Z, Balia R, Dwyre DM, Little E, Walker NJ, Tablin F, Crowe JH and Tsvetkova NM (2004). Loading red blood cells with trehalose: A step towards Biostabilization. *Cryobiology*, **49**: 123-136.
- Tang XS, Tang ZR, Wang SP, Feng ZM, Zhou D, Li TJ and Yin YL (2012). Expression, Purification and Antibacterial Activity of Bovine Lactoferrampin-Lactoferricin in *Pichia pastoris*. *Appl. Biochem. Biotechnol.*, **166**: 640-651.
- Wei YT, Zhu QX, Luo ZF, Lu FS, Chen FZ, Wang QY Huang K, Meng JZ, Wang R and Huang RB (2004). Cloning, expression and identification of a new trehalose synthase gene from *Thermobifida fusca* genome. *Acta. Bioch. Bioph. Sin.*, **36**: 477-484.
- Wu XL, Ding HB, Ming Y and Yu Q (2009). Gene cloning, expression and characterization of a novel trehalose synthase from *Arthrobacter aurescens*. *Appl. Microbiol. Biotechnol.*, **83**: 477-482.
- Yu HJ, Yan X, Shen WL, Hong Q, Zhang J, Shen YJ and Li SP (2009). Expression of methyl parathion hydrolase in *Pichia pastoris*. *Curr. Microbiol.*, **59**: 573-578.
- Zhu YM, Wei DS, Zhang J, Wang YF, Xu HY, Xing LX and Li MC (2010). Overexpression and characterization of a thermostable trehalose synthase from *Meiothermus ruber*. *Extremophiles*, **14**: 1-8.