CLONING OF SUCROSE ISOMERASE ENCODING GENE FROM KLEBSIELLA SINGAPORENSIS ISB-36 AND ITS EXPRESSION IN PICHIA PASTORIS

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SUMMARY

Given potential health benefits including low glycemic index, tooth friendly, suitable to infants, elderly and diabetic patients, isomaltulose was considered as a promising alternative sweetener to sucrose. Due to the presence of liposaccharide endotoxin in *Serratia plymuthica* CBS 574.44, a Gram-negative bacterium, and minute amount of formaldehyde carried over, purification of isomaltulose requires rigorous controls in industry. To reduce the cost associated with product purification, here we propose the use of recombinant enzyme in isomaltulose production. The mature gene coding for sucrose isomerase synthase (*K.SI36.Pall*) from *Klebsiella singapurensis* ISB 36, which isolated from woodborer in Vietnam, was expressed in *Pichia pastoris* X33. The nucleotide sequence of *K.SI36.Pall* gene was similar to AY040843.1 of *Klebsiella* sp. LX3 except one nucleotide C to T in AY040843.1 replaced by T1025 in *K.SI36.Pall*. This leads to single amino acid difference in deduced protein sequence (from 342Ser to 342Phe). Furthermore, the addition of two amino acids (Glu and Phe) was observed at N-terminus. The calculated molecular weight of sucrose isomerase from *K.SI36.Pall* was 67.46 kDa and the pl was 6.55. There was one potential glycosylation site at 466Asn. The maximum sucrose isomerase activity in the culture broth reached 36.6 U.mL⁻¹ in 1 L shake-flask. The purified recombinant enzyme was most active at 40°C and pH 7.0. At the optimum condition, within 6 hours, the enzyme converted 94% of sucrose in a 40% sucrose solution into isomaltulose. This was the first study on the expression of sucrose isomerase synthase gene in *P. pastoris*, and the results showed the efficient conversion of sucrose isomerase recombinant.

Keywords: food sweetener, isomaltulose, Klebsiella, Pichia pastoris, recombinant enzyme, sucrose isomerase.

INTRODUCTION

Although playing the most important role in the food industry as a natural sweetener, sucrose, or table sugar, may cause negative effects, such as obesity, dental caries, heart diseases and is not suitable for people with diabetes (Lina et al., 2002). Isomaltulose, a structural isomer of sucrose has been found as a promising alternative. Unlike other sucrose substitutes, isomaltulose can be assimilated by the human body and served as the source of energy (Tiefenbacher, 2017). It is tooth-friendly, promoting the growth of intestine bifidobacteria, causing low glycemic response and suitable for diabetic patients, elderly and infants (Lina et al., 2002). In the food industry, isomaltulose is the precursor for the production of isomalt through hydrogenation (BeMiller, 2019).

In nature, isomaltulose occurs in small amounts in sugar cane syrup and honey (O’Donnell, Kearsley, 2012). It can be produced from sucrose by enzymatic rearrangement. The enzyme responsible for the process is termed as sucrose isomerase (EC 5.4.99.110) which catalyzes the conversion of sucrose (α-D-glucopyranosyl-(1-2)-β-D-fructofuranoside) into isomaltulose (6-O-alpha-D-glucopyranosyl-D-fructofuranose) and various amounts of D-glucose, D-fructose, and trehalulose (1-O-alpha-D-glucopyranosyl-beta-D-fructose) (Véronèse, Perlot, 1998; Véronèse, Perlot, 1999; Xu et al., 2013). Many bacterial species sucrose isomerase producing has been reported, including *Serratia plymuthica*, *Erwinia rhapontici*, *Enterobacter* sp., *Klebsiella singapurensis*, *Rautella planticola*, *Enterobacter* sp., *Pantoaea dispersa*, and *Pseudomonas mesoacidophila* (Goulter et al., 2012;
Mu et al., 2014a). Several of sucrose isomerase coding genes have been cloned, expressed and characterized (Cha et al., 2009; Park et al., 2010; Mu et al., 2014b). In general, sucrose isomerases are functioning in near-neutral pH and are thermolabile. For example, Pall from Klebsiella sp. LX3 expressed in Escherichia coli DH5α demonstrated the highest activity at pH 6.0 and 35°C. The half-life of the enzyme was merely 1.8 min at 50°C (Zhang et al., 2002). Surface display may alter the properties of sucrose isomerase. Sucrose isomerase from Enterobacter sp. FMB-1 expressed in E. coli was the most active at pH 6.0, while the surface-displayed enzyme in Saccharomyces cerevisiae showed the highest activity at pH 7.0. The latter was also slightly more stable to the effect of temperature than the one expressed in E. coli (Lee et al., 2011a; Wei et al., 2013).

Industrially, isomaltulose is produced from food-grade sucrose by using the formalddehyde-inactivated cells of Protaminobacter rubrum (=Serratia plymuthica) CBS 574.44 as biocatalyst and followed by purification and crystallization (Krastanov, Yoshida, 2003; Kawaguti, Sato, 2010; Goultier et al., 2012; Mu et al., 2014b). Although S. plymuthica is a nonpathogenic species, due to the presence of liposaccharide endotoxin in the cell wall and formalddehyde used for bacterial inactivation, the purification step should be carried out with rigorous monitoring (Orsi, Sato, 2016). In this study, we propose a new approach, whereas isomaltulose be produced from sucrose using recombinant enzyme expressed extracellularly by Pichia pastoris. The conversion mixture is expected to be free from endotoxin and formalddehyde, and thus reduces the cost for recovery.

MATERIALS AND METHODS

Microorganism

Strain Klebsiella singaporensis ISB-36 demonstrating sucrose isomerase activity was previously isolated from the excrement of woodborer Colosternomallinosa sulphurea Heller on Anisoptera costata Korth collected in Bạc Bằng forest station at Bến Cát, Bình Dương, Vietnam (Nguyễn Thanh Thụy et al., 2013). The strain was identified as K. singaporensis as it shared 100% nucleotide homology with the rpoB sequence JX425353 of LMG 23571, the type strain of K. singaporensis (JX425353.1).

Cloning and expression

A gene coding for mature sucrose isomerase without sequence for signal peptide (K.SI36.Pall) was isolated by PCR amplification reaction from K. singaporensis ISB-36 using primer pair SI12-EcoRI (AGC TGA ATT CGC ACC ATC CTT GAA TCA G) and SI13-XbaI-R (TTG TTC_TAG_ATT ACC GCA GCT TAT ACA C) designed based on the GenBank sequence AAK82938 encoding sucrose isomerase of K. singaporensis LX3 (K.LX3.Pall). The location of cleavage sites for signal peptide sequence was predicted using SignalP 4.1 (http://www.cbs.dtu.dk/services/SignalP/). For PCR, HF-Phusion DNA polymerase (Thermofisher, United States) was used. The amplified product was digested with EcoRI and XbaI (Fermentas, United States), purified using GeneJET Gel Extraction kit (Fermentas, United States), and ligated to pPICZαA (Invitrogen, United States) previously digested with the same enzymes using T4 ligase (Fermentas, United States). The ligation product was transformed into E. coli DH5α (Invitrogen, United States) by heat shock and spread on LB low-salt agar (0.5% yeast extract, 1% tryptone, 0.5% NaCl, 1.5% agar, pH 7.0) supplemented with 50 mg/L zeocin (Invitrogen) and incubated at 37°C. After 24 h, colonies were picked, grown in liquid LB-zeocin and the plasmids were extracted, digested with EcoRI and XbaI to examine the presence of the heterologous inserts.

The pPICZαA containing K.SI36.Pall gene from K. singaporensis ISB-36 was opened with MssI (Fermentas, United States) and transformed into P. pastoris X33 (Invitrogen, United States) using a Micropulser Electroporator (BioRad, United States) according to the manufacturer’s instructions. The transformants were selected usingYPD-zeocin agar (1% yeast extract, 2% bacto peptone, 2% glucose, 1.5% agar, 100 mg/L zeocin). Purified transformants were grown in expression medium BMM with methanol as the sole carbon source (100 mM potassium phosphate, pH 6.0, 1.34% yeast nitrogen base (YNB, Difco), 0.4 ppm biotin, 0.5% methanol).

Sucrose isomerase activity assay

Sucrose isomerase activity was routinely determined based on the formation of reducing sugar (isomaltulose) from the non-reducing precursor (sucrose) using DNS assay (Ghose, 1987). Since D-glucose, D-fructose, trehalulose can be the by-product of the enzymatic rearrangement, the conversion products were assessed by HPLC. Enzymatic
reactions were carried out in 20% of sucrose solution in 20 mM sodium phosphate buffer, pH 7.0. The reaction was performed in 1.5 mL microtubes at desired temperatures. After 30 min, sucrose isomerase was inactivated by heating at 100°C for 10 min and then the amount of reducing sugar was determined by DNS method. One unit of sucrose isomerase is determined as the amount of enzyme required for conversion of sucrose into 1 µmol of reducing sugar per min at a given testing condition. The assay was carried out in triplicate and the mean value was given.

For HPLC analyses, reverse-phase column Cosmosil ODS 5C18MSII (Nacalai Tesque, United States) was used. Fractions were eluted with water at the rate of 0.6 mL/min at 25°C and detected by a RID 6A Refractive Index Detector (Shimadzu, Japan). Sugar standards, including D-glucose, D-fructose, sucrose (Sigma, United States), and isomaltulose (Wako pure Chemical Industries, Japan) were used.

**Enzyme production and purification**

The yeast *P. pastoris* X33 harboring *K.SI36.PalI* gene was grown in 50 mL of BMG (100 mM potassium phosphate, pH 6.0, 1.34% YNB, 0.4 ppm biotin, 1% glycerol) at 28°C with shaking at 150 rpm for 24 h. The cells were harvested by centrifugation and reinoculated in 200 mL expression medium BMM and incubated at the same condition. For remaining inducing state for the recombinant enzyme synthesis, 0.5% methanol was added every 24 h. After 96 h, the fermentation broth was centrifuged at 6000 × g for 30 min at 4°C and cells were discarded. The obtained supernatant was concentrated using Viva flow 200, 30 kDa MWCO (Sartorius, Germany). The enzyme was further purified using Superdex 200 (GE Healthcare, United States) gel filtration. Sample of 5 mL was loaded into XK 26/40 column (GE Healthcare, United States) and eluted with 20 mM sodium phosphate buffer, pH 7.0 at the rate of 1 mL/min with column temperature maintained at about 10°C. Fractions of 5 mL were collected and tested for sucrose isomerase activity.

**Effect of pH and temperature**

Purified sucrose isomerase was used to assess the effect of pH and temperature on the activity and the stability of the enzyme. Testing the enzyme activity at different temperatures (20-80°C) was carried out in 20 mM sodium phosphate buffer, pH 7.0. For testing the effect of pH, following buffer systems (50 mM) were used: pH 4, 5, 6 - citrate-phosphate; pH 7, 8 - sodium phosphate; pH 9, 10 - glycine sodium hydroxide. To determine thermostability, enzyme was incubated at 40, 50, 60°C, pH 7.0 and the remaining activity was measured at different time intervals. Similarly, for assessing the pH stability, the enzyme was incubated at different pHs, but the temperature was kept at 40°C.

**Enzyme kinetic**

Conversion kinetics were studied using sucrose substrate concentrations of 20 and 40%. An initial sucrose isomerase activity of 10 U.mL⁻¹ was measured and the reaction was carried out at pH 7.0, 40°C in a volume of 5 mL. Samples collected at different time intervals were heat-treated (100°C, 10 min) then analyzed by DNS and HPLC.

**RESULTS**

**Cloning and sequence analysis of *K.SI36.PalI* gene**

The PCR amplification of *K.SI36.PalI* gene from genomic DNA of *K. singaporensis* ISB36 using primers SI12-EcoRI and SI13-XbaI yielded in a fragment of about 1700 bp (Figure 1(a)). After ligating with *pPICZαA* and transforming into *E. coli* DH5α, the insert was sequenced using the primers *α* and 3’-*AOX1*. The closest GenBank sequence was AAK82938 of *K. singaporensis* LX3 with 99.94% similarity (differ 1 nucleotide over 1713 nucleotides in mature gene). There was a nucleotide substitution leading to the alteration from Ser at the amino acid position 342 of *K. singaporensis* LX3 to Phe. In our construct, the native 28 amino acid signal peptide sequence was replaced by the α-factor sequence of the plasmid. The PCR amplification of the mature gene sequence was AAK82938 of *K. singaporensis* LX3 with 99.94% similarity (differ 1 nucleotide over 1713 nucleotides in mature gene). There was a nucleotide substitution leading to the alteration from Ser at the amino acid position 342 of *K. singaporensis* LX3 to Phe. In our construct, the native 28 amino acid signal peptide sequence was replaced by the α-factor sequence of the plasmid. The mature sequence of the *K.SI36.PalI* gene was expected to differ from *K. singaporensis* LX3 also by two amino acid (Glu and Phe) introduced with the primer (*EcoRI recognition site*) at the N-terminus. The predicted protein would have 572 amino acids and with estimated molecular weight of 67.46 kDa, pI of 6.55. The enzyme was expected to have a low level of glycosylation as there was only one potential glycosylation site at 466Asn identified.

After transformation to *P. pastoris* X33, 24 yeast clones were selected and tested for sucrose isomerase activity. All selected clones expressed sucrose isomerase activity after 72 h of cultivation. The mean activity was 13.4 U.mL⁻¹ and the maximum activity obtained was 32 U.mL⁻¹ (Figure 2).
Figure 1. Cloning of K.SI36.Pall gene from K. singaporensis ISB36. (a): PCR product amplified with primers SI12-EcoRI and SI13-XbaI-R. (b): pPICZαA containing K.SI36.Pall gene (1) before and (2) after digestion with EcoRI and XbaI; (c): P. pastoris clones growing on YPD-zeocin agar.

Figure 2. Screening of P. pastoris X33 clones containing K.SI36.Pall gene for sucrose isomerase activity.

Fermentation and purification of the enzyme

Based on initial screening, clone X33.SI36#7 was selected from top high sucrose isomerase activity (#19, #6, #7 and #24) for enzyme expression and characterization. The yeast was cultivated in a 2 L fermentor with pH maintained at 5.0 and dissolved oxygen above 10%. After 96 h, wet biomass reached 90 g.L⁻¹ and extracellular protein concentration was 10 µg.mL⁻¹. Sucrose isomerase activity of the culture supernatant was 36.6 U.mL⁻¹. After 10-fold concentration, the activity of 300.8 U.mL⁻¹ was achieved. After gel-filtration purification, the sucrose isomerase activity was 46.5 U.mL⁻¹. SDS-PAGE indicated the presence of one protein band just below the 66.2 kDa marker protein, slightly smaller than the predicted size (67.46 kDa). The absence of the smear zone above the band indicated a low level of glycosylation (Figure 3).
Effect of temperature

Sucrose isomerase of *K. singaporensis* ISB36 expressed in *P. pastoris* X33 showed maximum activity at 40°C. At higher temperatures, the enzyme rapidly lost the function. At 50°C and 60°C the activity was only 20% and 7% of that at 40°C, respectively. The enzyme was thermostable with the half-life less than 10 min at 50°C, and less than 1 h at 40°C. The data obtained by this study agree well with the previous reports. Enzyme sucrose isomerase synthase from *K. singaporensis* LX3 (*K.LX3.Pali*) was most active at 35-40°C and at 50°C and 60°C, the activity was only 47% and 6% of the optimum (Zhang et al., 2002). Similarly, sucrose isomerase from *Enterobacter* sp. FMB-1 has an optimum temperature of 45°C and lost activity at 60°C (Lee et al., 2011b).

Effect of pH

The enzyme had no activity outside the pH 5.0 to pH 10.0 range (Figure 5) and it functioned best at pH 7.0. At pH 6.0 or pH 8.0, the activity of the enzyme reduced by 35%. At low temperature, the enzyme was rather stable at different pHs after 72 h of incubation at 4°C in the buffers with pH 5.0 and pH 7.0, the residual activity of the enzyme detected was 75% and 80%, respectively. At the temperature optimum (40°C), the enzyme lost activity rapidly when incubated in the buffer with pH 5.0 and with a lesser extent at pH 6.0 and pH 7.0.

Reaction kinetic

The conversion of sucrose into isomaltulose by recombinant sucrose isomerase was rapid and efficient. After 2 h of incubation with 10 U/mL sucrose isomerase, 60% of sucrose in the 40% sucrose solution was converted into isomaltulose and after 6 h, the conversion was nearly complete (94%) (Figure 6). HPLC analysis indicated the presence of a minor amount of D-glucose, D-fructose, and trehalulose (4-5% in total, data not shown).
Figure 4. The effect of temperature on sucrose isomerase activity. (a): activity at different temperatures; (b): thermostability of the enzyme.

Figure 5. The effect of pH on sucrose isomerase activity. (a): activity at different pHs; (b): the stability of enzyme at different pHs.

Figure 6. Kinetic of isomerization at different initial sucrose concentrations.
CONCLUSION

With one amino acid substitution, sucrose isomerase obtained from *K. singaporensis* ISB36 was nearly identical to the previously studied of *K. singaporensis* LX3 (Zhang et al., 2002; Zhang et al., 2003). The enzyme expressed in *P. pastoris* demonstrated similar properties with the enzyme expressed in *E. coli* in terms of pH, temperature optima and stability. The recombinant enzyme could efficiently convert sucrose into isomaltulose with a minor amount (less than 5%) of by-products. This is the first report on the expression of sucrose isomerase using *P. pastoris* system. The use of recombinant sucrose isomerase could reduce the risk associated with endotoxin and formaldehyde in isomaltulose production.

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REFERENCES

BeMiller JN (2019) Oligosaccharides. In Carbohydrate Chemistry for Food Scientists: 49–74.

Cha J, Jung JH, Park SE, Cho MH, Seo DH, Ha SJ, Park CS (2009) Molecular cloning and functional characterization of a sucrose isomerase (isomaltulose synthase) gene from *Enterobacter* sp. FMB-1. *J Appl Microbial* 107(4): 1119–1130.

Ghose TK (1987) Measurement of cellulase activities. *Pure Appl Chem*59(2): 257–268.

Goulter KC, Hashimi SM, Birch RG (2012) Microbial sucrose isomerases: Producing organisms, genes and enzymes. *Enzyme Microb Technol* 50(1): 57–64.

Kawaguti HY, Sato HH (2010) Isomaltulose production by free cells of *Serratia plymuthica* in a batch process. *Food Chem* 120(3): 789–793.

Krstanov A, Yoshida T (2003) Production of palatinose using *Serratia plymuthica* cells immobilized in chitosan. *J Ind Microbiol Biotechnol* 30(10): 593–598.

Lee GY, Jung JH, Seo DH, Hansin J, Ha SJ, Cha J, Park CS (2011a) Isomaltulose production via yeast surface display of sucrose isomerase from *Enterobacter* sp. FMB-1 on *Saccharomyces cerevisiae*. *Bioresour Technol* 102(19): 9179–9184.

Lina BR, Jonker D, Kozianowski G (2002) Isomaltulose (Palatinose 1): a review of biological and toxicological studies. *Food and Chemical Toxicol* 40: 1375–1381.

Mu W, Li W, Wang X, Zhang T, Jiang B (2014a) Current studies on sucrose isomerase and biological isomaltulose production using sucrose isomerase. *Appl Microbiol Biotechnol* 98(15): 6569–6582.

Mu W, Li W, Wang X, Zhang T, Jiang B (2014b) Current studies on sucrose isomerase and biological isomaltulose production using sucrose isomerase. *Appl Microbiol Biotechnol* 98(15): 6569–6582.

Nguyễn Thanh Thùy, Nguyễn T Hoa Mai, Đinh T Mỹ Hàng, Vũ Nguyên Thành (2013) Công nghệ sản xuất isomaltulose từ sucrose sử dụng vi khuẩn *Enterobacter* sp. ISB-25. *Tạp chí Khoa học và Công nghệ* 51(2): 173–184.

O’Donnell K, Kearsley M (2012) Sweeteners and sugar alternatives in food technology. John Wiley & Sons.

Orsi DC, Sato HH (2016) Isomaltulose production using free and immobilized *Serratia plymuthica* cells. *Afr J Biotechnol* 15(20):835–842.

Park JY, Jung JH, Seo DH, Ha SJ, Yoon JW, Kim YC, Park CS (2010) Microbial production of palatinose through extracellular expression of a sucrose isomerase from *Enterobacter* sp. FMB-1 in *Lactococcus lactis* MG1363. *Bioresour Technol* 101(22): 8828–8833.

Tiefenbacher KF (2017) Technology of main ingredients—sweeteners and lipids. In *Wafer and Waffle*: 123–225.

Veronese T, Perlot P (1998) Proposition for the biochemical mechanism occurring in the sucrose isomerase active site. *FEBS Lett* 441(3): 348–352.

Véronèse T, Perlot P (1999) Mechanism of sucrose conversion by the sucrose isomerase of *Serratia plymuthica* ATCC 15928. *Enzyme Microb Technol* 24(5–6): 263–269.

Wei Y, Liang J, Huang Y, Lei P, Du L, Huang R (2013) Simple, fast, and efficient process for producing and purifying trehalulose. *Food Chem* 138(2–3):1183–1188.

Xu Z, Li S, Li J, Li Y, Feng X, Wang R, Zhou J (2013) The structural basis of *Erwinia rhapontici* isomaltulose synthase. *PLoS ONE* 8(9).

Zhang D, Li N, Lok SM, Zhang LH, Swaminathan K (2003) Isomaltulose synthase (Pall) of *Klebsiella* sp. LX3: Crystal structure and implication of mechanism. *J Biol Chem* 278(37): 35428–35434.

Zhang D, Li X, Zhang LH (2002) Isomaltulose synthase from *Klebsiella* sp. strain LX3: Gene cloning and characterization and engineering of thermostability. *Appl Environ Microbiol* 68(6): 2676–2682.
TÁCH ĐÔNG GEN MÃ HÓA SUCROSE ISOMERASE TỪ KLEBSIELLA SINGAPORENSIS ISB-36 VÀ BIỂU HIỆN TRÊN PICHIA PASTORIS

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Tóm tắt

Với những lợi ích sức khỏe như chi số đường huyết thấp, không gây sâu răng, phù hợp với trẻ sơ sinh, người già và bệnh nhân tiểu đường, isomaltulose được coi là một chất ngày thay thế đầy hấp hối cho sucre. Do sự hiện diện của endotoxin liposaccharide trong Serratia plymuthica CBS 574.44, một vi khuẩn Gram âm, và formaldehyde tồn đọng, tính chất isomaltulose đối hồi được kiểm soát chặt chẽ trong công nghiệp. Để giảm chi phí tính chất sản phẩm, chúng tôi đề xuất sử dụng sucre isomerase tái hôp trong sản xuất isomaltulose. Gen trình thành mã hóa enzyme sucre isomerase (K.SI36.Pall) từ Klebsiella singaporesis ISB 36 phân lập từ ấu trùng xén tóc ở Việt Nam được biểu hiện trong Pichia pastoris X33. Gen K.SI36.Pall tương đồng với trình tự AY040843.1 của Klebsiella sp. LX3 ngoài trừ một nucleotide tại vị trí C663 trong AY040843.1, được thay bằng T663 trong trình tự của K.SI36.Pall. Điều này dẫn đến sự khác biệt một amino acid thành phần (342Ser thành 342Phe). Thêm vào đó, hai amino acid Glu và Phe được quan sát thấy ở đầu N. Khởi lượng phân tử tính toàn của sucre isomerase từ K.SI36.Pall là 67,46 kDa, pl là 6,55. Một vị trí glycosyl hóa tiềm năng tại 466Asn. Hoạt tính sucre isomerase trong canh đường đạt 36,6 U.mL⁻¹ trong bình tam giác 1 L. Enzyme tính chất hoạt động mạnh nhất ở pH 7,0 và 40°C. Ở điều kiện tối ưu, enzyme chuyển hóa 94% sucre trong dung dịch sucre 40% thành isomaltulose trong vòng 6 giờ. Đây là nghiên cứu đầu tiên về biểu hiện của sucre isomerase ở P. pastoris và kết quả đã cho thấy sự chuyển hóa hiệu quả của enzyme tái hôp.

Từ khóa: chất ngọt thực phẩm, isomaltulose, Klebsiella, Pichia pastoris, enzyme tái hôp, sucre isomerase.