The gene encoding the cyclodextrin glycosyltransferase (CGTase) of *Paenibacillus pabuli* US132, previously described as an efficient antistaling agent and good candidate for cyclodextrins production, was cloned, sequenced, and expressed in *Escherichia coli*. Sequence analysis showed that the mature enzyme (684 amino acids) was preceded by a signal peptide of 34 residues. The enzyme exhibited the highest identity (94%) to the β-CGTase of *Bacillus circulans* no. 8. The production of the recombinant CGTase, as active form, was very low (about 1 U/mL) in shake flasks at 37°C. This production reached 22 U/mL after 22 hours of induction by mainly shifting the postinduction temperature from 37 to 19°C and using 2TY instead of LB medium. High enzyme production (35 U/mL) was attained after 18 hours of induction in fermentor using the same culture conditions as in shake flask. The recombinant enzyme showed $V_{\text{max}}$ and $K_m$ values of $253 \pm 36 \mu$mol of β-cyclodextrin/mg/min and $0.36 \pm 0.18$ g/L, respectively.

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1. INTRODUCTION

Cyclodextrin glycosyltransferases (CGTases; E.C.2.4.1.19) are starch degrading enzymes which generate cyclic oligosaccharides termed cyclodextrins (CDs). These oligosaccharides exist as three major types commonly known as α-CD, β-CD, and γ-CD having 6, 7, and 8 glucose residues, respectively. They have torus-shaped structures able to encapsulate a wide range of molecules, thereby modifying their physical and chemical properties. Consequently, CDs are extensively used in pharmaceutical, chemical, agricultural, cosmetic, and food industries [1, 2].

CGTases belong to the glycoside hydrolase family 13 (α-amylase family) [3]. Members of this family contain a catalytic $(\beta/\alpha)_8$ barrel and use an α-retaining mechanism but they display a variety of reaction specificities [4]. Whereas α-amylases typically catalyze starch hydrolysis reaction, CGTases catalyze mainly three transglycosylation reactions (cyclization, coupling, and disproportionation) besides a weak hydrolytic activity [5]. Both α-amylases and CGTases share three domains (A, B, and C) while CGTases possess two additional domains (D and E). Domains A and B form the catalytic core, domains C and E are involved in substrate binding whereas domain D has unknown precise function [6, 7].

Understanding the enzymatic features has been explored by cloning, sequencing, and comparing various cgtase genes [8–11]. The sequence data analysis has revealed the key amino acids residues that determine the reaction mechanism and product specificity, thereby enhancing genetic engineering techniques to provide modified CGTases [7, 12, 13].

*E. coli* is frequently adopted as host strain for heterologous protein expression since it is well characterised with various expression systems. However, the formation of inclusion bodies remains a significant barrier for expression of heterologous proteins in *E. coli*. Refolding of inclusion bodies into soluble and active form needs high cost and tedious jobs. Hence, maximizing the yield of soluble and active recombinant proteins in vivo by altering the culture conditions is an attractive alternative [14]. However, no universal approach has been established to minimize the formation of inclusion bodies and some empirical conditions must be screened on an individual basis. To date, there are only a few reports that succeeded the overproduction of
CGTase in *E. coli* by varying fermentation conditions [15–17].

In a previous study, the CGTase of *Paenibacillus pabuli* US132 was reported as good candidate for cyclodextrins production and efficient antistaling agent [18]. In this work, we described the molecular cloning of the US132 cgtase gene as well as the amino acid sequence inspection and the comparison with other related CGTases. We also reported the production enhancement of the recombinant active enzyme in *E. coli* by varying mainly the cultivation conditions.

2. MATERIALS AND METHODS

2.1. Bacterial strains, plasmids, and culture media

*Paenibacillus pabuli* US132 strain, previously isolated [18], was used as source of chromosomal DNA. *E. coli* DH5α (F

sup

E44 φ80

lacZΔ M15 Δ(lacZYA-argF) U169 endA1 recA1 hsdR17 (rK, mK) deoR thi-1 λ-gyrA96 relA1) was used for all plasmid constructions. *E. coli* ER2566 (F

lacI

fhu

A2 [lon] ompT lacZ:T7 gene1 gal sulA1 Δ(mcrC- mrr)114;IS10 R(mcr-73 miniTn10-TetS)2 R(zgb-210;Tn10) (TetS) endA1 [dcm]) and *E. coli* JM109 (F

traD36 proA

B r lac proAB e114 (McrA-) recA1 endA1 gyrA96 thi-1 hsdR17 (rK mK) supE44 relA1) were used for protein expression. The plasmids pSJ8 and pSJ9 (this work) carrying the cgtase US132 gene, derived from pCR2.1 (Invitrogen) and pTrc99a vector [19], respectively. *E. coli* recombinant strains were grown on LB, M9, 2TY [20], or M9ZB medium [16] containing 100 μg/mL ampicillin. *Paenibacillus pabuli* US132 strain was grown as previously described [18].

2.2. Cloning of the US132 cgtase gene and sequence analysis

To amplify an internal cgtase gene fragment, we used the highly conserved aa regions previously reported for CGTase enzymes as members of the α-amylase family [4, 21]. Furthermore, we aligned several cgtases DNA sequences and we located the corresponding CGTases conserved regions. Hence, a degenerate pair of primers, S209 (5′-GAYTTTGGCRRCCCAACYCAT-3′) and S211 (5′-ATCATGATTGTACRATRAA-3′), corresponding respectively to the conserved regions I (DFAPNH) and IV (FIDNHD), were designed. The chromosomal DNA isolated from *Paenibacillus pabuli* US132 strain was used as template for gene amplification by *Pfu* DNA polymerase (Fermentas). The PCR parameters were 94°C for 120 seconds followed by 35 cycles of 94°C for 30 seconds, 50°C for 45 seconds, and 72°C for 120 seconds. The PCR product was purified using Wizard SV Gel and PCR Clean-Up System (Promega). To amplify the entire US132 cgtase gene, we have conceived two primers, S260 (5′-TCCATAATTTTCCTTACGAT-3′) and S262 (5′-GGTACGTATCTCAGG-3′), flanking the closely matching cgtase gene (accession no. L25256). The resulting PCR fragment was cloned into the pCR2.1 vector to give pSJ8 plasmid harboring the US132 cgtase gene under the control of the IPTG inducible T7 promoter. The pSJ8 was digested with *Hind*III and *EcoRV* and the resultant cgtase gene was subcloned in the pTrc99a, under the control of the Trc promoter (IPTG inducible), to give pSJ9 plasmid. Nucleotide sequences of the US132 cgtase gene carried by three independent pSJ8 plasmids obtained from different PCR reactions were determined. DNA sequencing was carried out using the BigDye Terminator v3.1 Cycle Sequencing Kit and the automated ABI Prism3100-Avant Genetic Analyser (Applied Biosystems). Sequence analysis and comparison were performed with BioEdit and CLUSTAL W programs. Homology search was performed using BLAST search algorithm. For the promoter determination, the prokaryotic promoter prediction program NNPP2.2A (http://www.fruitfly.org/cgi-bin/seqtools/promoter.pl) was used. The US132 cgtase sequence was submitted to the EMBL data bank under Accession no. AM748796.

2.3. Heterologous expression and recombinant US132 CGTase purification

The heterologous expression of the US132 CGTase was investigated using different recombinant strains (DH5α/pSJ8, ER2566/pSJ8, DH5α/pSJ9, ER2566/pSJ9 or JM109/pSJ9), various temperature cultivation (37°C or 19°C during all operating time and 37°C followed by a shift to 19°C after IPTG induction) and different medium composition (LB, M9, 2TY or M9ZB). An overnight culture of the studied strain, cultivated at 37°C, was used to inoculate 50 mL of basal medium (in 250 mL shake flask) with an initial OD

600 nm

of 0.1. Protein expression was induced by addition of different IPTG concentration (16–240 μg/mL) at OD

600 nm

between 0.8 and 1. Effects of the postinduction time on the US132 CGTase production were also investigated. All experiments were performed at least twice.

Batch fermentation was carried out in a 7 L fermentor INFORS AG CH-4103 (Bottmingen, Switzerland) containing 4.5 L of 2TY medium. The fermentor was inoculated, with an initial OD

600 nm

of 0.1, by an overnight culture of the ER2566/pSJ8 strain grown at 37°C in 2TY broth. The pH, aeration and agitation were maintained constant at 7.4, 1.5 vvm and 500 rpm, respectively, during all cultivation. The temperature was shifted from 37°C to 19°C after induction with 16 mg/L of IPTG when OD

600 nm

reached 0.8–1.

The CGTase extract was prepared from the periplasm by the modified osmotic-shock procedure of Ausubel et al. [22]. Cells were harvested by centrifugation at 8000 × g for 10 minutes and the pellets were suspended in 30 mM Tris-HCl buffer (pH 8) containing 20% sucrose and 1 mM EDTA. After agitation for 10 minutes at 25°C, cells removed by centrifugation were rapidly suspended in ice-cold water, incubated for 10 minutes at 0°C and clarified by centrifugation at 12000 × *g* for 30 minutes. The supernatant was recovered as periplasmic fraction and used for CGTase assay. Residual cells were sonicated at 4°C for 6 minutes (pulsations 3s, amplify 90) using a Vibra-Cell 72405 Sonicator and insoluble fraction (cells debris) was recovered by centrifugation at 12000 × *g* for 30 minutes.

For the purification of the recombinant US132 CGTase, the ER2566/pSJ8 periplasmic fraction was heat-treated at 60°C for 15 minutes in presence of 10 mM calcium followed
by centrifugation at 16000 × g for 30 minutes at 4°C. The supernatant was then purified using hydrophobic interaction chromatography and starch adsorption as previously described for the native enzyme [18].

2.4. CGTase assay and kinetic parameters determination

The CGTase activity, determined as dextrinisation activity, was monitored at 60°C for 10 min as described in a previous work [18].

The kinetic parameters (Km and Vmax) were determined by incubating the purified CGTase at 60°C in 50 mM sodium acetate buffer (pH 6.5) and using various concentrations of soluble starch ranging from 0.4 to 1.6 g/L. Samples were taken at regular time intervals and the reaction was stopped by boiling for 5 minutes. The amount of generated β-CDs was detected according to a phenolphthalein method [23]. The initial speed was calculated for each substrate concentration and then represented according to the Lineweaver-Burk method [24]. The Km and Vmax were determined graphically using Hyper32 program (http://homepage.ntlworld.com/john.easterby/hyper32.html).

3. RESULTS AND DISCUSSION

3.1. Identification of the P. pabuli US132 cgtase gene

To clone the US132 cgtase gene, an internal PCR fragment of about 600 bp was firstly amplified using US132 genomic DNA and two primers corresponding to the conserved regions I and IV in CGTases as described in Materials and Methods section. The nucleotide sequence of this internal fragment (582 bp) showed the highest homology (95% identity) with homologous region of the putative Bacillus Q cgtase gene (accession no. L25256). This result incited us to conceive two primers from the 5’ and 3’ flanking regions of the Bacillus Q cgtase gene in order to amplify the entire US132 cgtase gene using the chromosomal DNA of P. pabuli US132 as template. The PCR amplification, using Pfu DNA polymerase, gave a nucleotide fragment of approximately 2400 bp. The cloning of this fragment in pCR2.1 vector, under the control of the T7 promoter, provided pSJ8 plasmid and conferred starch degrading activity for E. coli host strains.

The nucleotide sequence analysis of the fragment containing the US132 cgtase gene revealed the presence of a single open reading frame (ORF) with two potential initiation ATG codons (Figure 1). A putative Shine-Dalgarno site (5’-AGAAGGTGG-3’), exhibiting a good rationally complementarity with the 3’ end of the US132 16S rRNA gene [18], was 7 bases upstream the first ATG codon. Consequently, this latter is most likely the true initiator codon. Thus, the US132 cgtase ORF, consisted of 2157 bp, encoded a protein having 718 amino acids. By using the promoter prediction program, a potential −10 region (5’-TGTGCA-3’) and −35 region (5’-TTGCGG-3’) were found at 101 and 124 bp upstream the initiator codon, respectively. The first 34 amino acids are considered as signal peptide according to the SignalP server (http://www.cbs.dtu.dk/services/signalP). Therefore, the mature enzyme was consisted of 684 amino acids with an estimated molecular mass of about 74.3 kDa.

The alignment of the mature US132 CGTase sequence to the data bank showed 93, 92, 74, and 73% identity with the CGTases of Bacillus sp. (accession no. CAA46901), Bacillus licheniformis (accession no. CAA33763), Bacillus circulans strain 251 (accession no. CA55023), and Bacillus sp.1011 (accession no. 1175A), respectively. The highest homology (97% similarity and 94% identity) was found with the CGTase of Bacillus circulans strain no. 8 (accession no. 1CGT). The alignment showed a difference of 39/684 amino acids which does not radically affect the product specificity. Indeed, both enzymes are specific for the β-CD production and are classified as β-CGTases since they generated a mixture of CDs composed of α-, β-, and γ-CD 20:58:13 and 10:64:20 ratios for the CGTase of strain US132 and B. circulans strain no. 8 [25], respectively. However, as far as we know, no data was available concerning biochemical properties of the CGTase of B. circulans strain no. 8 (pH, thermostability, thermostability) allowing the comparison of these two enzymes.

From the multiple sequence alignment (Figure 2), the five structural domains (A, B, C, D, and E) [11, 26] could be identified in the US132 CGTase. Furthermore, four highly conserved regions labelled I–IV and located in the catalytic domain were found. These conserved regions would constitute the active center of the enzyme since it contained the three catalytic residues Asp229, Glu257, and Asp328 referring to the CGTase of B. circulans strain no. 8 numbering. The conserved amino acids in the acceptor binding site, namely Lys47, Tyr89, Asn94, Phe183, Asn193, Leu194, Tyr195, Asp196, Phe259, Phe283, and Asp371, reported as the main determinants for cyclization reaction [12, 27], were also identified.

3.2. Production enhancement of the active recombinant US132 CGTase

The purification of the US132 CGTase from the native strain (Paenibacillus pabuli) was extremely hampered by the viscosity of the crude supernatant, probably due to the presence of polysaccharides of unknown nature (data not shown). In the aim to overcome this problem and also to overproduce the US132 CGTase, we have tested the enzyme production from the initial recombinant E. coli strain (DH5α/pSJ8). This study showed that this latter strain, cultivated in LB medium at 37°C and induced by 16 µg/mL IPTG for 18 hours, exhibited a very low activity of about only 0.3 U/mL. For this reason, we have studied the effect of several parameters on the production enhancement of the active recombinant CGTase.

3.2.1. Effect of the association promoter/host strain

Using the same culture conditions (LB medium, 37°C and induction by 16 µg/mL IPTG for 18 hours), the association E. coli ER2566/pSJ8 increased the production of the active recombinant enzyme by 3-fold (Table 1) since the ER2566...
production of the active enzyme at low cultivation temperature could be explained: (i) the reduction of the high rate of protein synthesis, which prevents misfolding [14], (ii) the enhancement of chaperones expression, which allows correct protein folding [30].

Based on all obtained data, we retained for further investigation the strain *E. coli* ER2566/pSJ8 and a culture temperature at 37°C followed by a shift to 19°C after induction.

### 3.2.3. Effect of medium composition and postinduction time

The composition of growth medium could have significant metabolic effects on both cells growth and protein production [31]. To investigate the effect of this parameter, the strain *E. coli* ER2566/pSJ8 was cultivated in 2TY, M9ZB, and M9 besides LB medium used in all previous experiences. The US132 CGTase production monitored after 18 hours of induction showed that the use of M9ZB and 2TY medium increased the production by about 1.1-fold (16.5 U/mL) and 1.3-fold (20 U/mL), respectively, in comparison to that obtained by LB broth. However, the use of M9 medium decreased the production to attain only 8 U/mL. The enhancement of the US132 CGTase production was likely correlated with cell density since the OD_{600nm} reached about 3.7, 4.8, 6, and 2 for the LB, M9ZB, 2TY, and M9 medium, respectively (Figure 4). Moreover, this difference in the production level of the recombinant active enzyme, using different medium, could be also influenced by the growth phase at which induction took place on.

Otherwise, extensive attempts to improve the enzyme production using different IPTG concentrations and stress additives (sorbitol, mannitol, and ethanol) did not increase the US132 CGTase production (data not shown) as reported for other recombinant proteins [16, 28, 32].

The effect of postinduction time on the US132 CGTase production was examined by analysis of samples taken, from ER2566/pSJ8 culture performed in 2TY medium, at different times after IPTG addition. Following the IPTG induction, the culture temperature is shifted from 37 to 19°C. The evolution of both cell growth and active enzyme production (Figure 5) showed that the CGTase production reached its maximum (22 U/mL) after 22 hours of induction when cells are at full stationary phase. When culture attained the lysis phase the production of the active enzyme decreased by about 27% probably due to the proteases release.

### 3.2.4. Batch fermentation scale

The fermentation, using the ER2566/pSJ8, was scaled up in 7L fermentor strain under the conditions previously
Table 3: Purification steps of the recombinant US132 CGTase.

| Purification step       | Total activity (U) | Total protein (mg) | Specific activity (U/mg) | Yield (%) | Purification (fold) |
|-------------------------|-------------------|-------------------|--------------------------|-----------|---------------------|
| Crude extract           | 7000              | 35                | 200                      | 100       | —                   |
| Heat treatment          | 6650              | 14.8              | 450                      | 95        | 2.2                 |
| HIC*                    | 4340              | 1.55              | 2800                     | 62        | 14                  |
| Starch adsorption       | 1400              | 0.28              | 5000                     | 20        | 25                  |

HIC: Hydrophobic Interaction Chromatography.

Figure 1: Nucleotide and deduced amino acid sequences of the CGTase of *Paenibacillus pabuli* US132. The putative ribosome-binding site (RBS) is double underlined. The putative promoter regions (−10 and −35) are shaded. The two possible initiator codons are boxed. The underlined amino acid sequence was the predicted signal peptide and the vertical arrow indicated the possible signal peptide cleavage site. Full nucleotide and amino acid sequences data reported in this paper were submitted to the GenBank under the accession number AM748796.
optimised: 2TY medium and temperature shift from 37 to 19°C after IPTG induction. Interestingly, the production of the US132 CGTase in fermentor reached a maximum (35 U/mL) after only 18 hours of induction while this maximum (22 U/mL) was obtained after 22 hours in Erlenmeyer. It should be mentioned that the cell density obtained in the two cases was almost the same (about OD_{600nm} = 6). This finding suggests that the improvement of the active enzyme production was not only related to the cell growth but it could also depend on the stability of fermentation parameters (pH and pO₂), which probably affect translation and correct folding of recombinant proteins as well as proteolysis according to Makrides [28].

3.3. Purification and kinetics parameters determination of the recombinant US132 CGTase

For the purification of the recombinant US132 CGTase, we have used the periplasmic fraction of the ER2566/pSJ8 strain cultivated in the fermentor in the cultivation conditions described above. This periplasmic fraction was firstly...
heat-treated at 60°C in order to remove *E. coli* thermolabile proteins. The extract was then purified using hydrophobic interaction chromatography (HIC) and starch adsorption as described for the native enzyme [18]. The recombinant enzyme was purified to homogeneity 25-fold with a yield of 20% (Table 3, Figure 6). This recombinant US132 CGTase retained the same biochemical properties (data not shown) as the native enzyme (thermoactivity, thermostability, pH stability, CDs production) [18].

The kinetic parameters were determined by incubating the purified recombinant US132 CGTase in presence of various soluble starch concentrations and using the Lineweaver-Burk method. The $V_{\text{max}}$ and $K_m$ values were evaluated to be $253 \pm 36 \mu$mol of $\beta$-cyclodextrin/mg/min and $0.36 \pm 0.18$ g/L, respectively. $K_m$ values determined, using also soluble starch as substrate, for CGTase from *Bacillus agaradhaerens* [33], *Bacillus circulans* E192 [34], *Bacillus firmus* [35], and *Bacillus* sp. TS1-1 [11] were 21.2, 5.7, 1.21, and 0.52 g/L, respectively. Since a small value of $K_m$ exhibited a high affinity for the substrate, the values shown above suggested that US132 CGTase was more specific towards starch than the other reported CGTases.
4. CONCLUSION

The molecular characterization of the gene encoding the US132 CGTase showed that the enzyme is a novel β-CGTase exhibiting 95% of identity with the β-CGTase from Bacillus circulans strain no. 8.

The production of the active US132 CGTase by E. coli DH5α under usual culture conditions (37°C and LB) was very low (0.3 U/mL) suggesting the formation of inclusion bodies. The investigation of different culture parameters showed that mainly the shift of the operating temperature from 37 to 19°C increased the production of the active CGTase to reach 22 U/mL. This production was further enhanced to reach 35 U/mL by using batch fermentation while the native strain produced only 18 U/mL.

The recombinant US132 CGTase, purified to homogeneity, shared the same biochemical properties with the native enzyme. The determination of the kinetic parameters (V_max and K_m) of this recombinant enzyme showed that the US132 CGTase had the highest affinity towards soluble starch in comparison to other reported CGTases.

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REFERENCES

[1] A. Biwer, G. Antranikian, and E. Heinze, "Enzymatic production of cyclodextrins," Applied Microbiology and Biotechnology, vol. 59, no. 6, pp. 609–617, 2002.

[2] E. M. M. Del Valle, "Cyclodextrins and their uses: a review," Process Biochemistry, vol. 39, no. 9, pp. 1033–1046, 2004.

[3] B. Henrissat, "A classification of glycosyl hydrolases based on amino acid sequence similarities," The Biochemical Journal, vol. 280, part 2, pp. 309–316, 1991.

[4] T. Kuriki and T. Imanaka, "The concept of the α-amylase family: structural similarity and common catalytic mechanism," Journal of Bioscience and Bioengineering, vol. 87, no. 5, pp. 557–565, 1999.

[5] B. A. van der Veen, J. C. M. Uitdehaag, B. W. Dijkstra, and L. Dijkhuizen, "Engineering of cyclodextrin glycosyltransferase reaction and product specificity," Biochimica et Biophysica Acta, vol. 1543, no. 2, pp. 336–360, 2000.

[6] D. Penninga, B. A. van der Veen, R. M. A. Knektel, et al., "The raw starch binding domain of cyclodextrin glycosyltransferase from Bacillus circulans strain 251," The Journal of Biological Chemistry, vol. 271, no. 51, pp. 32777–32784, 1996.

[7] R. D. Wind, R. M. Buitelaar, and L. Dijkhuizen, "Engineering of factors determining α-amylase and cyclodextrin glycosyltransferase specificity in the cyclodextrin glycosyltransferase from Thermoanaerobacterium thermosulfurigenes EM1," European Journal of Biochemistry, vol. 253, no. 3, pp. 598–605, 1998.

[8] L. Nitschke, K. Heeger, H. Bender, and G. E. Schulz, "Molecular cloning, nucleotide sequence and expression in Escherichia coli of the β-cyclodextrin glycosyltransferase gene from Bacillus circulans strain no. 8," Applied Microbiology and Biotechnology, vol. 33, no. 5, pp. 542–546, 1990.

[9] Q. Qi and W. Zimmermann, "Cyclodextrin glucanotransferase: from gene to applications," Applied Microbiology and Biotechnology, vol. 66, no. 5, pp. 475–485, 2005.

[10] K. Hirano, T. Ishihara, S. Ogasawara, et al., "Molecular cloning and characterization of a novel γ-CGTase from alkalophilic Bacillus sp,” Applied Microbiology and Biotechnology, vol. 70, no. 2, pp. 193–201, 2006.

[11] K. Rahman, R. Md. Ilias, O. Hassan, N. A. Nik Mahmood, and N. A. Abdul Rashid, "Molecular cloning of a cyclodextrin glucanotransferase gene from alkalophilic Bacillus sp. TS1-1 and characterization of the recombinant enzyme," Enzyme and Microbial Technology, vol. 39, no. 1, pp. 74–84, 2006.

[12] B. A. van der Veen, H. Leemhuis, S. Kralj, J. C. M. Uitdehaag, B. W. Dijkstra, and L. Dijkhuizen, "Hydroporphic amino acid residues in the acceptor binding site are main determinants for reaction mechanism and specificity of cyclodextrin glycosyltransferase," The Journal of Biological Chemistry, vol. 276, no. 48, pp. 44557–44562, 2001.

[13] M. Takada, Y. Nakagawa, and M. Yamamoto, "Biochemical and genetic analyses of a novel γ-cyclodextrin glucanotransferase from an alkalophilic Bacillus clarkii 7364," The Journal of Biotechnology, vol. 133, no. 3, pp. 317–324, 2003.

[14] H. P. Sørensen and K. K. Mortensen, "Soluble expression of recombinant proteins in the cytoplasm of Escherichia coli," Microbial Cell Factories, vol. 4, article 1, pp. 1–8, 2005.

[15] C. L. Jeang, C. H. Wung, B. Y. Chang, S. S. Yeh, and D. W. Lour, "Characterization of the Bacillus macerans cyclodextrin glucanotransferase overexpressed in Escherichia coli; Proceedings of the National Science Council, Republic of China B, vol. 23, no. 2, pp. 62–68, 1999.

[16] M. H. Kim, J. K. Lee, H. K. Kim, C. B. Sohn, and T. K. Oh, "Overexpression of cyclodextrin glycosyltransferase gene from Brevibacillus brevis in Escherichia coli by control of temperature and mannitol concentration," Biotechnology Techniques, vol. 13, no. 11, pp. 765–770, 1999.

[17] H.-H. Jin, S. H. Nam, D.-H. Kweon, Y.-C. Park, and J.-H. Seo, "Effects of environmental factors on in vivo folding of Bacillus macerans cyclodextrin glycosyltransferase in recombinant Escherichia coli," Journal of Microbiology and Biotechnology, vol. 11, no. 1, pp. 92–96, 2001.

[18] S. Jemli, E. Ben Messaoud, D. Ayadi-Zouari, B. Naili, B. Khemakhem, and S. Bejar, "A β-cyclodextrin glycosyltransferase from a newly isolated Paenibacillus pabuli US132 strain: purification, properties and potential use in bread-making," Biochemical Engineering Journal, vol. 34, no. 1, pp. 44–50, 2007.

[19] E. Amann and J. Brosius, "‘ATG vectors’ for regulated high-level expression of cloned genes in Escherichia coli," Gene, vol. 40, no. 2–3, pp. 183–190, 1985.

[20] J. Sambrook, E. F. Fritsch, and T. Maniatis, Molecular Cloning: A Laboratory Manual, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY, USA, 2nd edition, 1989.

[21] Š. Janeček, "How many conserved sequence regions are there in the α-amylase family?" Biologia, vol. 57, supplement 11, pp. 29–41, 2002.

[22] F. S. Ausubel, R. Brent, R. E. Kingston, et al., Current Protocols in Molecular Biology, John Wiley & Sons, New York, NY, USA, 1987.

[23] D. A. Volkova, S. A. Lopatin, and V. P. Varlamov, "One-step affinity purification of cyclodextrin glucanotransferase from Bacillus sp. 1070," Biocatalysis, vol. 41, supplement 6, pp. 67–69, 2000.
[24] H. Lineweaver and D. Burk, “The determination of enzyme dissociation constants,” *Journal of the American Chemical Society*, vol. 56, no. 3, pp. 658–666, 1934.

[25] G. Parsiegla, A. K. Schmidt, and G. E. Schulz, “Substrate binding to a cyclodextrin glycosyltransferase and mutations increasing the γ-cyclodextrin production,” *European Journal of Biochemistry*, vol. 255, no. 3, pp. 710–717, 1998.

[26] R. D. Wind, W. Liebl, R. M. Buitelaar, et al., “Cyclodextrin formation by the thermostable α-amylase of *Thermoanaerobacterium thermosulfurigenes* EM1 and reclassification of the enzyme as a cyclodextrin glycosyltransferase,” *Applied and Environmental Microbiology*, vol. 61, no. 4, pp. 1257–1265, 1995.

[27] J. C. M. Uitdehaag, K. H. Kalk, B. A. van der Veen, L. Dijkhuizen, and B. W. Dijkstra, “The cyclization mechanism of cyclodextrin glycosyltransferase (CGTase) as revealed by a γ-cyclodextrin-CGTase complex at 1.8 Å resolution,” *The Journal of Biological Chemistry*, vol. 274, no. 49, pp. 34868–34876, 1999.

[28] S. C. Makrides, “Strategies for achieving high-level expression of genes in *Escherichia coli*,” *Microbiological Reviews*, vol. 60, no. 3, pp. 512–538, 1996.

[29] J. M. Vásquez-Bahena, J. Vega-Estrada, J. A. Santiago-Hernández, et al., “Expression and improved production of the soluble extracellular invertase from *Zymomonas mobilis* in *Escherichia coli*,” *Enzyme and Microbial Technology*, vol. 40, no. 1, pp. 61–66, 2006.

[30] M. Ferrer, T. N. Chernikova, M. M. Yakimov, P. N. Golyshin, and K. N. Timmis, “Chaperonins govern growth of *Escherichia coli* at low temperatures,” *Nature Biotechnology*, vol. 21, no. 11, pp. 1266–1267, 2003.

[31] N. Jacques, J. Guillerez, and M. Dreyfus, “Culture conditions differentially affect the translation of individual *Escherichia coli* mRNAs,” *Journal of Molecular Biology*, vol. 226, no. 3, pp. 597–608, 1992.

[32] J. G. Thomas and F. Baneyx, “Protein misfolding and inclusion body formation in recombinant *Escherichia coli* cells overexpressing heat-shock proteins,” *The Journal of Biological Chemistry*, vol. 271, no. 19, pp. 11141–11147, 1996.

[33] R. F. Martins and R. Hatti-Kaul, “A new cyclodextrin glycosyltransferase from an alkalophilic *Bacillus agaradhaerens* isolate: purification and characterisation,” *Enzyme and Microbial Technology*, vol. 30, no. 1, pp. 116–124, 2002.

[34] L. J. Bovetto, D. P. Backer, J. R. Villette, P. J. Sicard, and S. J. Bouquelet, “Cyclomaltodextrin glucanotransferase from *Bacillus circulans* E192. I. Purification and characterization of the enzyme,” *Biotechnology and Applied Biochemistry*, vol. 13, no. 1, pp. 48–58, 1992.

[35] B. N. Gawande, A. Goel, A. Y. Patkar, and S. N. Nene, “Purification and properties of a novel raw starch degrading cyclomaltodextrin glucanotransferase from *Bacillus firmus*,” *Applied Microbiology and Biotechnology*, vol. 51, no. 4, pp. 504–509, 1999.