

An L-arabinose isomerase from *Acidothermus cellulolyticus* ATCC 43068: cloning, expression, purification, and characterization

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Abstract The *araA* gene encoding an L-arabinose isomerase (L-AI) from the acido-thermophilic bacterium *Acidothermus cellulolyticus* ATCC 43068 was cloned and overexpressed in *Escherichia coli*. The open reading frame of the L-AI consisted of 1,503 nucleotides encoding 501 amino acid residues. The recombinant L-AI was purified to homogeneity by heat treatment, ion-exchange chromatography, and gel filtration. The molecular mass of the enzyme was estimated to be approximately 55 kDa by sodium dodecyl sulfate-polyacrylamide gel electrophoresis. The purified enzyme was optimally active at 75°C and pH 7.5. It required divalent metal ions, either Mn²⁺ or Co²⁺, for both enzymatic activity and thermostability improvement at higher temperatures. The enzyme showed relatively high activity and stability at acidic pH. It exhibited over 90% of its maximal activity at pH 6.0 and retained 80% of activity after 12 h incubation at pH 6.0. Catalytic property study showed that the enzyme had an interesting catalytic efficiency. Its apparent K_m , V_{max} , and catalytic efficiency (k_{cat}/K_m) for D-galactose was 28.9 mM, 4.9 U/mg, and 9.3 mM⁻¹min⁻¹, respectively. The enzyme carried out the isomerization of D-galactose to D-tagatose with a conversion yield over 50% after 12 h under optimal conditions, suggesting its potential in D-tagatose production.

Keywords L-Arabinose isomerase · *Acidothermus cellulolyticus* · D-Tagatose · Purification · Characterization

Introduction

D-Tagatose is a hexoketose monosaccharide sweetener, which is an isomer of D-galactose and rarely found in nature (Kim 2004). D-Tagatose occurs naturally in small quantities in *Sterculia setigera* gum, and it is also found in dairy products (Troyono et al. 1992; Mendoza et al. 2005). The sweetness of D-tagatose is 92% that of sucrose when compared in 10% solutions, but with only 38% of the calories. It has been shown to have numerous health and medical benefits, including treatment of obesity (Donner et al. 1999), prevention of dental caries, regulation of intestinal flora (Kim 2004; Buemann et al. 2000), improvement of pregnancy and fetal development, and reduction of symptoms of type 2 diabetes, hyperglycemia, anemia, and hemophilia (Levin 2002; Oh 2007; Lu et al. 2008; Rosenplenter and Mende 2004; Kim 2004). Based on these properties, D-tagatose has attracted a great deal of attention in recent years as a low calorie sugar-substituting sweetener, an intermediate for synthesis of other optically active compounds, and an additive in detergent, cosmetic, as well as in pharmaceutical formulations (Oh 2007; Lu et al. 2008; Kim 2004).

Recently, there has been great interest in the biological manufacture of D-tagatose from D-galactose. Several enzymes involved in the biotransformation of D-tagatose have been investigated (Rollini and Manzoni 2005; Ishida and Kamiya 1997; Kim et al. 2006). L-Arabinose isomerase (L-AI, EC 5.3.1.4) is considered to have the most potential use for D-tagatose production, since it can catalyze the isomerization of D-galactose to D-tagatose and convert L-arabinose to L-ribulose, based on the similarity in config-

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uration of the substrates (Cheetham and Wootton 1993). A number of L-AIs have been identified from various microorganisms (Chouayekh et al. 2007; Jørgensen et al. 2004; Kim et al. 2002, 2003b; Kim and Oh 2005; Lee et al. 2004, 2005a, b; Nakamatu and Yamanaka 1969; Patrick and Lee 1968), while previous studies on the effect of reaction temperature on the conversion of D-galactose to D-tagatose by L-AIs showed that conversion increased as the incubation temperature was raised (Lee et al. 2004). At higher temperatures, the equilibrium of isomerization reaction shifted toward D-tagatose (Kim et al. 2002). Thus, L-AI with high activity and stability at higher temperatures would have the most potential for D-tagatose production.

To attain a thermostable enzyme for better manipulation, new thermotolerant organisms carrying the target enzyme need to be screened. The organism used as source of L-AI in this study is *Acidothermus cellulolyticus* ATCC 43068, an acidothermotolerant bacterium that thrives at an optimum condition of 55°C, pH 5.2 (Mohagheghi et al. 1986). Although L-AIs have been characterized from various microorganisms and the mechanism regarding isomerization has been suggested, L-AI has never been reported from *A. cellulolyticus*. The elucidation of the *A. cellulolyticus* genome sequence (NCBI accession number: NC_008578) in 2006 opened the door for genome scale research on this important microbial strain (Barabote et al. 2009). In this paper, we identified the L-AI in *A. cellulolyticus* ATCC 43068 (ACAI) and reported the gene cloning, expression, purification, and characterization of this L-AI. The feasibility of the recombinant enzyme used for D-tagatose production was assessed and discussed in comparison with previously described L-AIs.

Materials and methods

Materials

Taq Plus (Taq DNA polymerase + Pfu DNA polymerase) DNA polymerase, deoxynucleoside triphosphate, and chemicals for polymerase chain reaction (PCR) were obtained from Sangong (Shanghai, China), and the pMD19-T Simple vector, restriction endonuclease, and T4 DNA ligase were obtained from Takara (Dalian, China). The pET-22b(+) vector was purchased from Novagen (Darmstadt, Germany); electrophoresis reagents and all chemicals used for enzyme assays and characterization were obtained from Sigma (St. Louis, MO, USA). Oligonucleotides were synthesized by Sangong (Shanghai, China).

Bacterial strains and culture conditions

Acidothermus cellulolyticus (ATCC 43068) was obtained from the American Type Culture Collection (ATCC),

Manassas, VA, USA. *A. cellulolyticus* was grown in an ATCC medium (ATCC medium: 1473 LPBM acidothermophile medium, pH 5.2) at 55°C. *Escherichia coli* JM109 and *E. coli* BL21 were respectively used as hosts for cloning and expression. Strains were grown in Luria-Bertani (LB) medium with ampicillin (50 µg/ml) in a rotary shaker at 37°C. The plasmid pMD19-T Simple vector was used as a cloning and sequencing vector, and pET-22b(+) was used for expression.

Cloning and expression of the *araA* gene from *A. cellulolyticus* ATCC 43068

The genomic DNA of *A. cellulolyticus* ATCC 43068 was prepared with the method described by Saito and Miura (1963). The whole genome of this strain was sequenced and released in GenBank (NCBI accession number: NC_008578), which revealed that there is a putative *araA* gene encoding an L-AI in the genome (NCBI gene ID: 4485651, protein ID: YP_872632). Based on the putative gene, two primers were designed as follows: Primer 1, 5'-TATATAAGCTTTTCAC CACGGCCGCGATGC-3' and Primer 2, 5'-TTATCCATAT GACCGACCTGCCCTATCCG-3'. PCR amplification was performed by Taq Plus DNA polymerase for 30 cycles consisting of 94°C for 30 s, 58°C for 1 min, and 72°C for 1 min, followed by a final extension step of 10 min at 72°C. A DNA fragment about 1,500 bp was amplified and then sequenced by Sangong (Shanghai, China). Sequence analysis showed that it contains a 1,503-bp open reading frame encoding an L-AI. An expression plasmid (pET-ACAI) was constructed by ligation of gene *araA*, digested by *NdeI* and *HindIII*, into the corresponding restriction sites of the pET-22b(+) plasmid and transformed into *E. coli* BL21(DE3) competent cells. The transformed strain was cultured in LB medium supplemented with 0.05 mg/ml ampicillin at 37°C. When the culture reached an optical density of 0.6 at 600 nm, isopropyl-β-D-thiogalactopyranoside was added to a final concentration of 0.4 mM, and the cells were grown for an additional 6 h and harvested by centrifugation at 10,000×g, 4°C for 15 min.

Purification of ACAI

The centrifuged cells were resuspended in 50 mM Tris-HCl buffer (pH 8.0) and disrupted by sonication. The lysates were centrifuged (12,000×g, for 20 min at 4°C) to remove cell debris, and the supernatants were heated at 70°C for 15 min. The supernatants were collected as crude extract and heated at 70°C for 15 min. After centrifugation (12,000×g, 20 min, 4°C), the supernatant was loaded onto a Q-Sepharose column (3.5×15 cm; GE Healthcare, Sweden), pre-equilibrated with 20 mM Tris-HCl buffer (pH 8.0). Elution was performed with a linear gradient of

NaCl (0 to 1 M) at a flow rate of 2 ml/min. Protein fractions containing L-AI activity were pooled, concentrated, and passed through a Superdex 200 column (HiLoad 10/300 prep grade; GE Healthcare, Sweden), pre-equilibrated with 20 mM Tris–HCl buffer (pH 7.5) containing 150 mM NaCl, at a flow rate of 0.5 ml/min. All purification steps were carried out using an Äkta Purifier System (GE Healthcare, Sweden) at 4°C. The purified enzymes were dialyzed against 10 mM Tris–HCl (pH 7.5) and analyzed by 12% sodium dodecyl sulfate-polyacrylamide gel electrophoresis (SDS-PAGE).

Enzyme assay and protein determination

L-AI activity was measured by the determination of the amount of produced ketose (D-tagatose). The reaction mixture of 1 ml contained D-galactose (50 mM), MnCl₂ (1 mM), CoCl₂ (0.5 mM), Tris–HCl buffer (50 mM, pH 7.5), and 100 µl of enzyme preparation at a suitable dilution. The reaction mixture was incubated at 75°C for 30 min, followed by cooling samples on ice to stop the reaction. The generated D-tagatose was determined by the cysteine-carbazole sulfuric acid method, and the absorbance was measured at 560 nm (Dishe and Broenfreund 1951). One unit of L-AI activity was defined as the amount of enzyme catalyzing the formation of 1 µmol D-tagatose per minute.

Protein concentration was measured by the method of Lowry using bovine serum albumin as a standard (Lowry et al. 1951). During chromatographic purification steps, the protein concentration was estimated by observing the absorbance at 280 nm.

Effect of temperature and pH

The optimum temperature of enzyme activity was measured by assaying the enzyme samples over the range of 40–90°C for 30 min. Three buffer systems, sodium acetate (50 mM, pH 4.0–5.0), sodium phosphate (50 mM, pH 6.0–7.0), and Tris–HCl (50 mM, pH 7.5–9.0), were used for measuring the optimum pH of enzyme activity. The thermal stability of the enzyme was studied by incubating the enzyme in Tris–HCl buffer (50 mM, pH 7.5) with or without added Mn²⁺ and Co²⁺ ions (1 mM) at 75°C. At given time intervals, samples were withdrawn, and the residual activity was measured under standard assay conditions. To determine the pH stability, the enzyme was incubated at pH 6.0, 7.5, and 8.0 at room temperature (approximately 25°C) for up to 48 h, and the remaining enzyme activity was measured at time intervals under standard assay conditions.

Effect of various metallic ions

Before studying the effects of various metallic ions on ACAI activity, the enzyme solution was dialyzed against

50 mM Tris–HCl buffer (pH 7.5) containing 10 mM ethylenediamine tetraacetic acid (EDTA) for 48 h at 4°C. Subsequently, the enzyme was dialyzed against 50 mM EDTA-free Tris–HCl buffer (pH 7.5). Enzyme activity was then assessed as described above in the presence of the following ions at 1 mM: Co²⁺, Mn²⁺, Mg²⁺, Fe²⁺, Ca²⁺, Ba²⁺, Ni²⁺, Zn²⁺, and Cu²⁺, respectively. The activity without any metal ion addition was set to 100%. The measured activities were compared with the activity of the enzyme without metal ion addition under the same conditions.

Determination of kinetic parameters

Kinetic parameters of ACAI were determined in 50 mM Tris–HCl buffer (pH 7.5), 1 mM Mn²⁺, 0.5 mM Co²⁺, and 1–800 mM substrate (D-galactose). The samples were incubated at 75°C for 20 min. The enzyme reaction was stopped by chilling on ice, and the amount of D-tagatose was determined by the cysteine-carbazole sulfuric acid method. Kinetic parameters, such as K_m (mM) and V_{max} (U/mg protein) for substrates were obtained using the Lineweaver–Burk equation. All assays were performed in triplicate at least two separate times. The kinetic data presented represent averages of statistically relevant measurements with their associated standard deviations.

Analysis of the isomerization of D-galactose to D-tagatose by ACAI

The conversion mixture (10 ml) contained 50 mM of D-galactose, 0.5 mM Co²⁺, 1 mM Mn²⁺, and 1.0 mg of purified enzyme (19.29 U) in 50 mM Tris–HCl buffer (pH 7.5). The study of the kinetic conversion of D-galactose was investigated until 36 h at 70°C, 75°C, and 80°C. Samples were taken periodically, and the concentration of the generated D-tagatose was determined by the cysteine-carbazol-sulfuric acid method.

Results

Cloning and sequence analysis of the *araA* gene encoding an L-AI

The DNA sequence analysis of *araA* revealed an open reading frame of 1,503 bp, encoding a polypeptide of 501 amino acid residues with a calculated isoelectric point of pH 5.63 and molecular mass of 54,768 Da. It shows 100% identity with the nucleotide sequence corresponding to the putative *araA* gene (NCBI Gene ID: 4485651) from *A. cellulolytica* ATCC 43068 whole genome (GenBank accession number: NC_008578), suggesting a perfect conservation of the gene among *A. cellulolytica* strains. A homology

search revealed that the deduced *araA* gene product ACAI showed 55% amino acid identity with L-AI from *Geobacillus stearothermophilus* (AAD45718); 54% identity with L-AIs from *Bacillus stearothermophilus* (AAD45718), *Thermus* sp. (AY225311), and *Alicyclobacillus acidocaldarius* (AAY68209); 53% identity with L-AI from *Thermotoga neapolitana* (AY028379); 52% identity with L-AI from *Thermotoga maritime* (NP_228089); and 51% identity with L-AI from *E. coli* (AAA23463). Four highly conserved residues, E303, E333, H350, and H450, which are considered to be crucial for the catalytic activity of L-AI (Manjasetty and Chance 2006), were found in four conserved regions (Fig. 1).

Expression and purification of the *araA* gene

E. coli expressed recombinant L-AI exhibited a strong protein band of close to 55 kDa on SDS-PAGE, compared to that of the control *E. coli* BL21(DE3), which was in agreement with the predicted molecular mass for the L-AI protein (Kim et al. 2002; Kim and Oh 2005; Lee et al. 2004, 2005b; Patrick and Lee 1968; Poonperm et al. 2007; Prabhu et al. 2008; Rhimi and Bejar 2006). Recombinant ACAI was purified to electrophoretical homogeneity by heat treatment followed by ion-exchange chromatography and gel filtration with a yield of 27% (Table 1). The molecular mass of the purified enzyme was estimated to be approximately 55 kDa by SDS-PAGE (Fig. 2). The purified enzyme exhibited L-AI activity, which strongly supported the assumption that the putative *araA* gene in *A. cellulolyticus* ATCC 43068 corresponded to that of L-AI protein.

Effect of temperature, pH, and metal ions on ACAI activity

The temperature dependence of the recombinant enzyme was determined in the presence of Mn^{2+} (1 mM) and Co^{2+} (0.5 mM) after 30 min of incubation at various temperatures. The optimum temperature of the L-AI from *A. cellulolyticus* was 75°C. Investigation of pH effect on ACAI activity showed that the enzyme was optimally active at pH 7.5, while more than 90% of its maximum activity was maintained at the acidic pH of 6.0.

To determine the effect of metal ions, ACAI activity was measured in the presence of various metal ions. The enzyme had a requirement for metal ion for activity stimulation. Its activity was significantly activated by the addition of 1.0 mM Mn^{2+} (4.5-fold) and 0.5 mM Co^{2+} (5.5-fold). The full activity (6.1-fold) was achieved when both of Mn^{2+} and Co^{2+} were added at the concentration of 1 and 0.5 mM, respectively. Compared to Mn^{2+} and Co^{2+} , other metal ions, such as Mg^{2+} , Ni^{2+} , and Ba^{2+} , were poor activators (data not shown). Fe^{2+} , Ca^{2+} , and Zn^{2+} had no

effect on ACAI activity, while Cu^{2+} inhibited the enzyme up to approximately 30%.

Effect of temperature, pH, and metal ions on ACAI stability

The ACAI was perfectly stable at 65°C, and no significant activity decrease was observed after 2 h incubation without metal ion addition. At higher temperatures (>65°C), the thermostability of ACAI was proved to be metal-dependent. In the absence of metallic ions, the enzyme was inactivated up to 50% activity under the same conditions (Fig. 3a), while the enzyme maintained 90% and 76% activity after 2 h incubation at 75°C in the presence of 1 mM Co^{2+} and 1 mM Mn^{2+} , respectively. The pH stability of ACAI was measured at pH ranging from 6.0 to 8.0 at room temperature (approximately 25°C). The enzyme showed relatively high stability at acidic pH, since 80% and 70% of its activity were retained after 12 and 24 h of incubation at pH 6.0, respectively (Fig. 3b).

Kinetic studies of ACAI for D-galactose

On the basis of the Lineweaver–Burk plots, the kinetic parameters of ACAI for D-galactose were determined under optimal temperature and pH conditions (75°C, pH 7.5). The apparent K_m , V_{max} , and catalytic efficiency k_{cat}/K_m of ACAI using D-galactose as a substrate were 28.9 mM⁻¹, 4.9 μmol min⁻¹mg⁻¹, and 9.3 min⁻¹mM⁻¹, respectively.

Production of D-tagatose by ACAI at different temperatures

The isomerization of D-galactose (50 mM) to D-tagatose by ACAI at 70°C, 75°C, and 80°C (pH 7.5) demonstrated that the isomerization reaction of D-galactose to D-tagatose reached equilibrium after 12 h incubation, and the conversion ratio was 45%, 53%, and 43% at 70°C, 75°C, and 80°C, respectively (Fig. 4). The production of D-tagatose from D-galactose was further proved by high-performance liquid chromatography analysis, and no by-product was observed.

Discussion

Based on the analysis of the genome sequence of *A. cellulolyticus* ATCC 43068, an isomerase-encoding gene (*araA*) was proposed as an L-AI. The identified *araA* gene was cloned from *A. cellulolyticus* ATCC 43068, overexpressed in *E. coli*, and it was confirmed that the gene product ACAI exhibited L-AI activity for D-tagatose production. Sequence analysis showed that ACAI had higher identity to thermophilic L-AIs than mesophilic L-AIs, and the content of hydrophobic amino acid of ACAI was also higher than mesophilic L-AIs, indicating that

Fig. 1 Multiple sequence alignment of L-arabinose isomerase (L-AI) from *Escherichia coli* (ECAI), *Alicyclobacillus acidocaldarius* (AAAI), *Bacillus stearothermophilus* (BSAI), *Thermus* sp. (TSAI), *Geobacillus stearothermophilus* (GSAI), *Thermotoga maritima* (TMAI), and *Thermotoga neapolitana* (TNAI). The alignment was performed using ClustalW program. Amino acid residues that are identical in all the displayed sequences are marked by *asterisks*; strongly conserved or weakly conserved residues are indicated by *colons* and *dots*, respectively. The residues involved in the active site of L-AI from *E. coli* are indicated with *arrows*

ACAI	—MTDLPYPEYECWFLTGSQHLYGEDVLSAVARQSAIVEALN—AAGLPVRLVWPKVLTDA	58
ECAI	—MTIFD—NVEYWFVIGSQHLYGPETLRQVTAQAEHVNALNTEAKLPCKLVLKPLGTTT	58
AAAI	MMLSLR—PYEFWFVITGSQHLYGEEALKQVEEHSRIMVNEWRNDSVFPFPLVFKSVVITP	57
BSAI	—MLSLR—PYEFWFVITGSQHLYGEEALKQVEEHSRIMVNEWRNDSVFPFPLVFKSVVITP	57
TSAI	—MLSLR—PYEFWFVITGSQHLYGEEALKQVEEHSRIMVNEWRNDSVFPFPLVFKSVVITP	57
GSAI	MMLSLR—PYEFWFVITGSQHLYGEEALKQVEEHSRIMVNEWRNDSVFPFPLVFKSVVITP	58
TMAI	—MTDLK—QYEFWFLVGSQLYGLETLKKVEQASKIVDSLNDPFPFSKIVLKPVLKSS	57
TNAI	—MTDLK—QYEFWFLVGSQLYGLETLKKVEQASRIVEALNDPFPFSKIVLKPVLKNS	57
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ACAI	TGIRRMCEASATDACIGVIAWMHTFSPAKAWINGLLALRKLPLHLHTQANLTPWSTID	118
ECAI	DEITAIICRDANYDDPCAGLVVWLHTFSPAKMWINGLTMLNKPILLQFHTQFNAALPWDSID	117
AAAI	EEIRRVCLEANASEQCAGVITWMHTFSPAKMWIGGLELRKPLHLHTQFNRIIPWDSID	118
BSAI	EEIRRVCLEANASEQCAGVITWMHTFSPAKMWIGGLELRKPLHLHTQFNRIIPWDSID	117
TSAI	EEIRRVCLEANASEQCAGVITWMHTFSPAKMWIGGLELRKPLHLHTQFNRIIPWDSID	117
GSAI	EEIRRVCLEANASEQCAGVITWMHTFSPAKMWIGGLELRKPLHLHTQFNRIIPWDSID	118
TMAI	SEITEIFEKANADPKCAGVIVMHTFSPKMWIRGLSINKKPLHLHTQYNYREIPWDTID	117
TNAI	AEIREIFEKANAEPKCAGVIVMHTFSPKMWIRGLSINKKPLHLHTQYNYREIPWDTID	117
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ACAI	MDFMNLNQAAGHGREFYVAARLAI PRKIVTGHFSDPVDVRIAAWQRAAGLADLRSTR	178
ECAI	MDFMNLNQTAAHGREFGFI GARMRQQAHVVTGHWQDKQAHERIGSWMRQAVSKQDTRHLK	177
AAAI	MDFMNLNQAAGHGREYGF I GARMGVARKVVVGHWEDPVSRYERLAKWMRTAVAFESRHLK	178
BSAI	MDFMNLNQAAGHGREYGF I GARMGVARKVVVGHWEDPEVRYERLAKWMRTAVAFESRNLK	177
TSAI	MDFMNLNQAAGHGREYGF I GARMGVARKVVVGHWEDPEVRYERLAKWMRTAVAFESRHLK	177
GSAI	MDFMNLNQAAGHGREYGF I GARMGVARKVVVGHWEDPEVRYERLAKWMRTAVAFESRNLK	178
TMAI	MDYMNLNQAAGHGREHGF I HARMRLPRKVVVGHWEKEVREKIAKWMRVACAIQDGRMCQ	177
TNAI	MDFMNLNQAAGHGREHGF I HARMRLPRKVVVGHWEDREVREKIAKWMRVACAIQDGRGTGQ	177
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ACAI	LVRFGDMRNVAVTDGDRVEAQIRLSA IETYGVIDLGVRVDAVAESDVALVDRLADY	238
ECAI	VCRFGDNMREVAVTDGDRVAAQIKFGFSVNTWAVGDLVQVNSISDGDVNALVDEYESC	237
AAAI	VARFGDNMREVAVTEGDKVGAQIQFGWSVNGYIGDLVQYIRDVSEKINELLEEAEL	238
BSAI	VARFGDNMREVAVTEGDKVGAQIQFGWSVNGYIGDLVQYIRDVSEKINELLEEAEL	237
TSAI	VARFGDNMREVAVTEGDKVGAQIQFGWSVNGYIGDLVQYIRDVSEKINELLEEAEL	237
GSAI	VARFGDNMREVAVTEGDKVGAQIQFGWSVNGYIGDLVQYIRDVSEKINELLEEAEL	238
TMAI	IVRFGDNMREVAVTEGDKVGAQIQFGWSVNGYIGDLVQYIRDVSEKINELLEEAEL	237
TNAI	IVRFGDNMREVAVTEGDKVGAQIQFGWSVNGYIGDLVQYIRDVSEKINELLEEAEL	237
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ACAI	DMAPELTIGGARHESLRYAAKLELALRSFLHDGRFTAFTNFEDLGLRQLPGLAVQRLM	298
ECAI	TMTPATQIHGEKRNVLAAARIELGMKRFLEQGFHAFATTTFEDLHGMKQLPGLAVQRLM	297
AAAI	DIVPAGRQDGPVRESIREQARIELGLKAFKLDGNGFAAFTTTFEDLHGMKQLPGLAVQRLM	298
BSAI	DIVPAGRQDGPVRESIREQARIELGLKAFKLDGNGFAAFTTTFEDLHGMKQLPGLAVQRLM	297
TSAI	DIVPAGRQDGPVRESIREQARIELGLKAFKLDGNGFAAFTTTFEDLHGMKQLPGLAVQRLM	298
GSAI	DIVPAGRQDGPVRESIREQARIELGLKAFKLDGNGFAAFTTTFEDLHGMKQLPGLAVQRLM	297
TMAI	IMP——EDEYSLKAIREQAKIEIALREFLKEKNVAGFTTTFEDLHDLPLPGLAVQRLM	293
TNAI	IMP——EDEYSLKAIREQAKMIEIALREFLKEKNIAFTTTFEDLHDLPLPGLAVQRLM	293
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ACAI	ADGFGFAGEGDWKTAALLVRAVKTMSRGLPGGTSFMEDYTYHLEPSSRGLVLAHMLVCP	358
ECAI	QQGYGFAEGEDWKTAAALLRIMKVMSTGLQGGTSFMEDYTYHFEKGNLVLGSHMLVCP	357
AAAI	AEGYFGGEGDWKTAALVRLMKVMADGK—GTSFMEDYTYHFEKGNELVLAHMLVCP	356
BSAI	AEGYFGGEGDWKTAALVRLMKVMADGK—GTSFMEDYTYHFEKGNELVLAHMLVCP	355
TSAI	AEGYFGGEGDWKTAALVRLMKVMADGK—GTSFMEDYTYHFEKGNELVLAHMLVCP	355
GSAI	AEGYFGGEGDWKTAALVRLMKVMADGK—GTSFMEDYTYHFEKGNELVLAHMLVCP	356
TMAI	EEGYGFAEGDWKAAGLVRAIKVMGTSLPGGTSFMEDYTYHLEPSSRGLVLAHMLVCP	353
TNAI	EEGYGFAEGDWKAAGLVRAIKVMGAGLPGGTSFMEDYTYHLEPSSRGLVLAHMLVCP	353
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ACAI	↓	
ACAI	L TSA—TPRCEIHPLLMGGREDPVRLVFTADPAPAVIVGLCDMGRDLRLVANTADLVAPPE	417
ECAI	LAVEEKPILDVQHLGIGGKDDPARLIFNTQTGPATVASLIDLGDYRRLVNCIDTVKTHP	417
AAAI	IAAT—RPRIEVHPLSIGGKEDPARLVFDGGEAAVNASLIDLGHRFRLVNEVDVAVKPEH	415
BSAI	IAAT—RPRIEVHPLSIGGKEDPARLVFDGGEAAVNASLIDLGHRFRLVNEVDVAVKPEH	414
TSAI	IAAT—RPRIEVHPLSIGGKEDPARLVFDGGEAAVNASLIDLGHRFRLVNEVDVAVKPEH	414
GSAI	IAAT—RPRIEVHPLSIGGKEDPARLVFDGGEAAVNASLIDLGHRFRLVNEVDVAVKPEH	415
TMAI	IAKE—KPRIEVHPLSIGGKADPARLVFDGQEGPAVNASIVDMGNRFRLLVNNKVLVSPIER	412
TNAI	IAKE—KPRIEVHPLSIGGKADPARLVFDGQEGPAVNASIVDMGNRFRLLVNNRVLVSPIER	412
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ACAI	↓	
ACAI	PLRPLPVARAVWQHPPELKAATAAWIAGGPHHTALSTAVSAREIRDFAARMAGLELVLD	477
ECAI	SLPKLPVANALWKAQPDLTASEAWILAGGAHHTVFSHALNLDNRMQFAEMHDIETVVID	475
AAAI	DMPKLPVARILWKPRLPRLRDSAEAWILAGGAHHTCFSAVTTTEQLQDFAEMAGIECVVIN	475
BSAI	EMPKLPVARILWKPRLPRLRDSAEAWILAGGAHHTCFSAVTTTEQLQDFAEMAGIECVVIN	474
TSAI	EMPKLPVARILWKPRLPRLRDSAEAWILAGGAHHTCFSAVTTTEQLQDFAEMAGIECVVIN	474
GSAI	DMPKLPVARILWKPRLPRLRDSAEAWILAGGAHHTCFSAVTTTEQLQDFAEMAGIECVVIN	475
TMAI	KMPKLPVARILWKPRLPDKFRATTAWILAGGSHHTAFSTAVDVEYLIIDWAEALEIYVVID	472
TNAI	KMPKLPVARILWKPRLPDKFRATTAWILAGGSHHTAFSTAVDVEYLIIDWAEALEIYVVID	472
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ACAI	EHTALDAALDRLWAIEQTRASRPW	501
ECAI	NDTRLPAFKDALRWNEVY	495
AAAI	EHTSVSFKNELRWNEVFWRGR	497
BSAI	EHTSVSFKNELRWNEVFWRGR	496
TSAI	EHTSVSFKNELRWNEVFWRGR	496
GSAI	EHTSVSFKNELRWNEVFWRGR	497
TMAI	ENLDLEDFKKELRWNELYWGLLKR	496
TNAI	ENLDLENFKELRWNELYWGLLKR	496
	:: : . * * *	

Table 1 Purification of the recombinant L-arabinose isomerase

Purification step	Total Protein (mg)	Total activity (U)	Specific activity (U/mg)	Yield (%)	Purification fold
Crude extract	672	396	0.59	100	1
Heat treatment	75.6	322	4.26	81	7.2
Ion-exchange chromatography	27.3	206	7.55	52	12.8
Gel filtration	5.6	108	19.29	27	32.7

ACAI is much more hydrophobic than other mesophilic AIs. In addition, most of the amino acids in the conserved regions were hydrophobic. ACAI was characterized to be thermostable at high temperatures. This result is consistent with the fact that hydrophobic interactions are important for protein thermostability.

Generally, a major consideration in a biotransformation process is the development and/or improvement of suitable biological catalysts (Illanes 1999). It has been reported that thermotolerant enzymes, which can provide higher reaction rates and process yields, higher solubility of substrates and products, and fewer contamination problems, are an important aspect of biocatalytic processes (Poonperm et al. 2007; Kim 2004). The ACAI from *A. cellulolyticus* ATCC 43068 was optimally active at 75°C with Mn²⁺ and Co²⁺ additions and perfectly stable below 65°C without metal ion addition, suggesting that this enzyme is remarkably thermostable.

On the other hand, industrial application requires a slightly acidic pH range to reduce browning reaction and

the formation of by-products (Kim 2004). Therefore, thermostable L-AIs with high activity and stability at a moderately low pH will be interesting (Lee et al. 2005b). ACAI from *Acido-thermophile* bacterium *A. cellulolyticus*

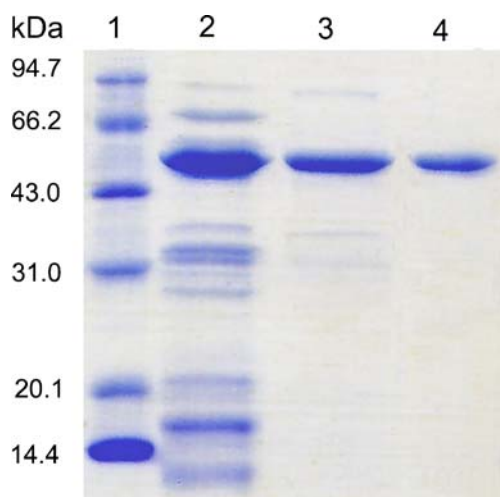


Fig. 2 Sodium dodecyl sulfate-polyacrylamide gel electrophoresis (SDS-PAGE) analysis of recombinant ACAI from each purification step. *Lanes:* 1, molecular standard marker (20 µg/ml); 2, cell extract after heat treatment (µg/ml); 3, sample from lane 2 after Q-sepharose ion exchange (89.6 µg/ml); 4, sample from lane 3 after Superdex 200 gel filtration (37.3 µg/ml). The volume loaded on SDS-PAGE for each sample was 15 µl

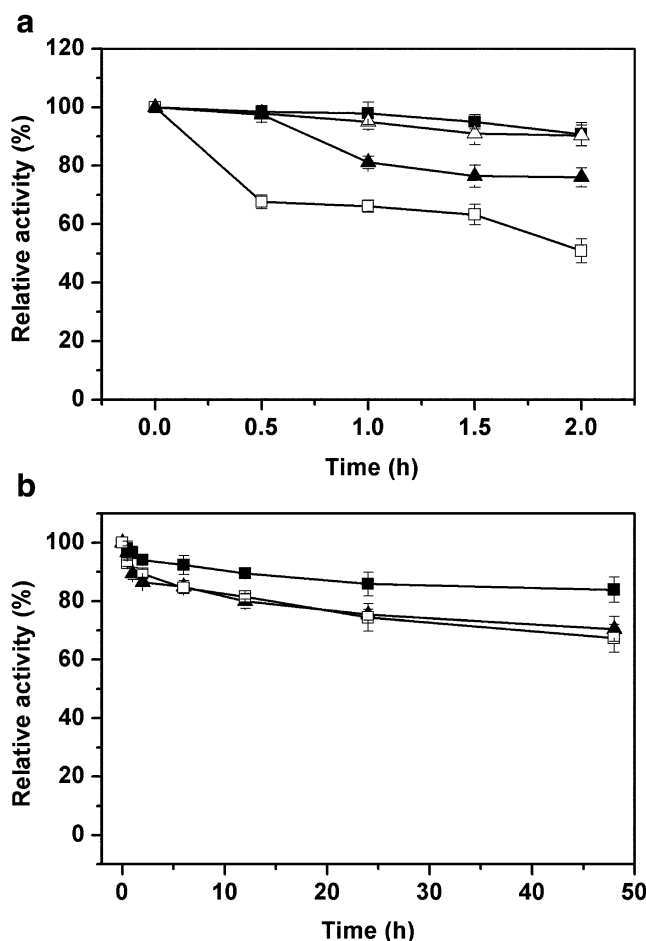


Fig. 3 Effect of temperature (a) and pH (b) on ACAI stability. **a** The thermal stability profiles of the purified ACAI. *Closed squares:* thermal stability at 65°C in the absence of metallic ions; *open squares:* thermal stability at 75°C in the absence of metallic ions; *closed triangles:* thermal stability at 75°C in the presence of 1 mM Mn²⁺; *open triangles:* thermal stability at 75°C in the presence of 1 mM Co²⁺. **b** The pH stability profiles of the purified ACAI. *Closed squares:* pH 8.0; *open squares:* pH 7.5; *closed triangles:* pH 6.0. Residual activity was measured under standard conditions (75°C, pH 7.5). Activity measured with non-incubated enzyme was set to 100%

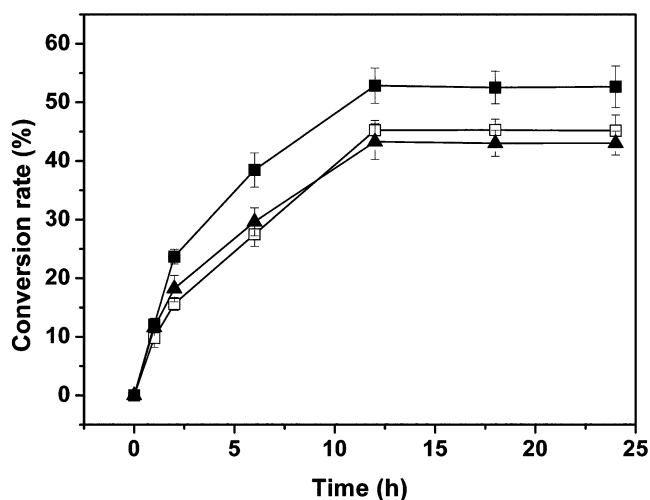


Fig. 4 Conversion of D-galactose to D-tagatose by ACAI at different temperatures. *Open squares*: conversion curve at 70°C; *closed squares*: conversion curve at 75°C; *closed triangles*: conversion curve at 80°C

ATCC 43068 exhibits high activity and stability at a broad pH range of 6.0–8.0. Although the ACAI showed maximum activity at pH 7.5, it maintained more than 90% of its maximum activity at pH 6.0, and no significant activity decrease was observed after 48 h incubation at pH 6.0. Generally, the isomerization of D-galactose to D-tagatose reached equilibrium after 12 h of incubation. Indeed, the ACAI retained more than 80% of its maximum activity after 12 h incubation at pH 6.0, making ACAI a good candidate for industrial applications at acidic pH (approximately 6) values.

The majority of L-AIs are metalloproteins involving metal ions for their optimal activity and thermostability (Rhimi and Bejar 2006). It was reported that mesophilic

and thermophilic L-AIs require Mn^{2+} as a cofactor to enhance the isomerization reaction rate (Patrick and Lee 1968), while the hyperthermophilic L-AIs require Co^{2+} (Kim et al. 2002; Lee et al. 2004). The ACAI required a divalent metal ion, either Mn^{2+} or Co^{2+} , for both enzymatic activity and thermostability improvement at high temperature. The addition of 1 mM Mn^{2+} plus 0.5 mM Co^{2+} greatly improved its activity (6.1-fold). The thermostability of ACAI at higher temperatures ($\geq 65^\circ C$) was proved to be metal-dependent. In the absence of metallic ions, the enzyme was inactivated up to 50% activity after 2 h incubation at 75°C (Fig. 3a). While in the presence of 1 mM Co^{2+} and 1 mM Mn^{2+} , the activity increased by 40% and 26%, respectively, after 2 h of incubation at 75°C compared to that in the absence of metallic ions (Fig. 3a). These results suggested the both of Mn^{2+} and Co^{2+} ions played important roles in the enzyme stabilization at high temperatures and in the isomerization reaction.

Although L-AIs catalyzes the reversible isomerization of both L-arabinose to L-ribulose and D-galactose to D-tagatose, respectively, L-arabinose is the preferred substrate of L-AI (Oh 2007), which limits the industrial application for D-tagatose production. ACAI catalyzes the isomerization of L-arabinose to L-ribulose (data not shown), also showed high substrate affinity towards D-galactose. Compared with other L-AIs, ACAI exhibits a high catalytic efficiency (k_{cat}/K_m ; $9.3 \text{ min}^{-1} \text{ mM}^{-1}$; Table 2), which makes it potential for D-tagatose production. This enzyme efficiency was related to the high yield of D-tagatose production which reached 53% after 12 h at 75°C. Structural and mechanistic studies, to clarify the reason for substrate choosing of ACAI, are presently under way.

Table 2 Comparison of L-arabinose isomerase kinetic constants from various microbial origins

Bacteria	Substrate	V_{max} ($U \text{ mg}^{-1}$)	K_m (mM)	k_{cat}/K_m ($\text{min}^{-1} \text{ mM}^{-1}$)	References
<i>Escherichia coli</i>	D-galactose	NR	NR	NR	(Yoon et al. 2003)
<i>Bacillus licheniformis</i>	D-galactose	NR	NR	NR	(Prabhu et al. 2008)
<i>Bacillus halodurans</i>	D-galactose	1.3	167	0.4	(Lee et al. 2005a)
<i>Geobacillus stearothermophilus</i> T6	D-galactose	9	120	4.3	(Kim et al. 2003a)
<i>Lactobacillus plantarum</i>	D-galactose	7	69.7	1.6	(Chouayekh et al. 2007)
<i>Thermus</i> sp. IM6501	D-galactose	NR	NR	NR	(Kim et al. 2003b)
<i>Thermoanaerobacter mathranii</i>	D-galactose	NR	NR	NR	(Jørgensen et al. 2004)
<i>Alicyclobacillus acidocaldarius</i>	D-galactose	7.5	129	3.3	(Lee et al. 2005b)
<i>Geobacillus thermodenitrificans</i>	D-galactose	6.9	408	0.5	(Kim and Oh 2005)
<i>Bacillus stearothermophilus</i> US100	D-galactose	8.9	57	8.5	(Rhimi and Bejar 2006)
<i>Thermotoga neapolitana</i>	D-galactose	14.3	116	3.2	(Kim et al. 2002)
<i>Thermotoga maritima</i>	D-galactose	8.9	60	8.5	(Lee et al. 2004)
<i>Acidothermus cellulolyticus</i> ATCC 43068	D-galactose	4.9	28.9	9.3	This study

NR not reported

The L-AI from *A. cellulolytica* ATCC 43068 was characterized to be thermostable, active, and stable at acidic pH, and be efficient for D-tagatose biotransformation, which makes it a good candidate to produce D-tagatose in ideally industrial condition.

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