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Title	Functional reassignment of Cellvibrio vulgaris EpiA to cellobiose 2-epimerase and an evaluation of the biochemical functions of the 4-O-beta-d-mannosyl-d-glucose phosphorylase-like protein, UnkA
Author(s)	Saburi, Wataru; Tanaka, Yuka; Muto, Hirohiko; Inoue, Sota; Odaka, Rei; Nishimoto, Mamoru; Kitaoka, Motomitsu; Mori, Haruhide
Citation	Bioscience biotechnology and biochemistry, 79(6), 969-977 https://doi.org/10.1080/09168451.2015.1012146
Issue Date	2015-06-04
Doc URL	http://hdl.handle.net/2115/62061
Rights	This is an Accepted Manuscript of an article published by Taylor & Francis in Bioscience biotechnology and biochemistry on [date of publication], available online: http://www.tandfonline.com/doi/abs/10.1080/09168451.2015.1012146?journalCode=tbbb20
Type	article (author version)
File Information	70427(mori).pdf

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Running title: Characteristics of *C. vulgaris* CE and MGP

Functional Reassignment of *Cellvibrio vulgaris* EpiA to Cellobiose 2-Epimerase and an Evaluation of the Biochemical Functions of the 4-*O*-β-D-Mannosyl-D-glucose Phosphorylase-like Protein, UnkA.

Wataru SABURI,[1] Yuka TANAKA,[1] Hirohiko MUTO,[1] Sota INOUE,[1] Rei ODAKA,[1] Mamoru NISHIMOTO,[2] Motomitsu KITAOKA[2] and Haruhide MORI[1,†]

[1]*Research Faculty of Agriculture, Hokkaido University, N-9, W-9, Sapporo 060-8589, Japan*

[2]*National Food Research Institute, National Agriculture and Food Research Organization, 2-1-12 Kannondai, Tsukuba, Ibaraki 305-8642, Japan*

Received November 17, 2014; Accepted December 26, 2014

[†]To whom correspondence should be addressed. Tel/Fax: +81-11-706-2497; E-mail: hmori@chem.agr.hokudai.ac.jp

Abbreviations: BSA, bovine serum albumin; CE, cellobiose 2-epimerase; Glc-Man, β-D-glucosyl-(1→4)-D-mannose; HEPES, 4-(2-hydroxyethyl)piperazine-1-ethanesulfonic acid; β-mannanase, mannan endo-1,4-β-mannosidase; Man1*P*, α-D-mannose 1-phosphate; Man-Glc, β-D-mannosyl-(1→4)-D-glucose; MGP, 4-*O*-β-D-mannosyl-D-glucose phosphorylase; MES, 4-morpholineethanesulfonic acid

The aerobic soil bacterium *Cellvibrio vulgaris* has a β-mannan-degradation gene cluster, including *unkA*, *epiA*, *man5A*, and *aga27A*. Among these genes, *epiA* has been assigned to encode an epimerase for converting D-mannose to D-glucose, even though the amino acid sequence of EpiA is similar to that of cellobiose 2-epimerases (CEs). UnkA, whose function currently remains unknown, shows a high sequence identity to 4-*O*-β-D-mannosyl-D-glucose phosphorylase. In this study, we have investigated CE activity of EpiA and the general characteristics of UnkA using recombinant proteins from *Escherichia coli*. Recombinant EpiA catalyzed the epimerization of the 2-OH group of sugar residue at the reducing end of cellobiose, lactose, and β-(1→4)-mannobiose in a similar manner to other CEs. Furthermore, the reaction efficiency of EpiA for β-(1→4)-mannobiose was 5.5×10^4-fold higher than it was for D-mannose. Recombinant UnkA phosphorolyzed β-D-mannosyl-(1→4)-D-glucose and specifically utilized D-glucose as an acceptor in the reverse reaction, which indicated that UnkA is a typical 4-*O*-β-D-mannosyl-D-glucose phosphorylase.

Key words: *Cellvibrio vulgaris*; cellobiose 2-epimerase; 4-*O*-β-D-mannosyl-D-glucose phosphorylase; β-mannan; substrate specificity

β-Mannan is one of the major polysaccharides included in the hemicellulose found in all plant cell walls. The main chain of β-mannan is formed exclusively of β-(1→4)-linked D-mannosyl residues, whereas that of glucomannan is formed of a combination of β-(1→4)-linked D-mannosyl and D-glucosyl residues.[1)] Galactomannan has branches composed of single α-(1→6)-linked D-galactosyl residues, which branch out from its β-mannan backbone. Some glycosyl residues in the main chain of β-mannan are acetylated at the 2-OH or 3-OH position.

Several microbial enzymes have been reported to degrade β-mannan. For example, mannan endo-1,4-β-mannosidase (β-mannanase, EC 3.2.1.78) hydrolyzes the internal β-(1→4)-mannosidic linkages to produce oligosaccharides. α-Galactosidase (EC 3.2.1.22) and acetyl mannan esterase (EC 3.1.1.6) remove the galactosyl branches and acetyl groups, respectively, which enhances the degradation of β-mannan.[1-3)] The resulting oligosaccharides are then hydrolyzed to monosaccharides by β-mannosidase (EC 3.2.1.25) and β-glucosidase (EC 3.2.1.21). Senoura *et al.*[4)] found a new pathway for the degradation of β-mannan in *Bacteroides fragilis*, which was composed of several steps, including (1) the hydrolysis of β-mannan to β-(1→4)-mannobiose by β-mannanase; (2) the epimerization of β-(1→4)-mannobiose to β-D-mannosyl-(1→4)-D-glucose (Man-Glc) by cellobiose 2-epimerase (CE, EC 5.1.3.11); and (3) the phosphorolysis of Man-Glc to D-mannose 1-phosphate (Man1*P*) and D-glucose by 4-*O*-β-D-mannosyl-D-glucose phosphorylase (MGP, EC 2.4.1.281). Similar mannan degradation systems have been found in the other CE producing bacteria, including *Ruminococcus albus* and *Rhodothermus marinus*.[5,6)] In *R. albus*, β-(1→4)-mannooligosaccharides longer than β-(1→4)-mannobiose are phosphorolyzed to β-(1→4)-mannobiose and Man1*P* by the intracellular β-1,4-mannooligosaccharide phosphorylase (RaMP2) (EC 2.4.1.319).[5)]

Centeno *et al.*[7)] reported that a gene cluster belonging to the aerobic soil bacterium *Cellvibrio mixtus* (same strain as *Cellvibrio vulgaris*) was involved in the degradation of β-mannan. This gene cluster is comprised of four genes, including *unkA*, *epiA*, *man5A*, and *aga27A*. *man5A* encodes β-mannosidase, which liberates D-mannose from the non-reducing end of β-(1→4)-mannooligosaccharides.[8)] *aga27A* encodes α-galactosidase, which exhibits hydrolytic activity towards the α-(1→6)-galactosidic linkages in galactomannan.[7)] EpiA has been assigned as an

epimerase, which is involved in the conversion D-mannose to D-glucose. However, the amino acid sequence of EpiA shows a high sequence identity (32–42%) to those of several other reported CEs.[9-16] UnkA, whose function currently remains unknown, has been classified into Glycoside hydrolase family 130 based on its amino acid sequence.[17] Glycoside hydrolase family 130 contains MGP, β-1,4-mannooligosaccharide phosphorylase and β-1,4-D-mannosyl-*N*-acetyl-D-glucosamine phosphorylase (EC 2.4.1.320).[18] The sequence identity of UnkA to other MGPs is high (57–66%), whereas that to *R. albus* β-1,4-mannooligosaccharide phosphorylase and *Bacteroides thetaiotaomicron* β-1,4-D-mannosyl-*N*-acetyl-D-glucosamine phosphorylase were low (21 and 17%, respectively). Both EpiA and UnkA are thought to be intracellular enzymes because they are predicted to have no signal peptide by SignalP 4.1 server.[19] These sequence data suggest that EpiA and UnkA may have CE and MGP activities, and that they could therefore be involved in the intracellular metabolism of the β-mannan found in *B. fragilis*.[4] In this study, we have investigated the biochemical characteristics of EpiA and UnkA using recombinant proteins from *Escherichia coli*.

Results and Discussion

Reaction of recombinant EpiA with disaccharide substrates

Recombinant EpiA was produced in *E. coli*, and 37.9 mg of purified protein was obtained from 1.0 L of culture broth. The resulting recombinant EpiA was incubated with cellobiose, lactose, and β-(1→4)-mannobiose to investigate its CE activity. As shown in Fig. 1a–c, the epimerized products of these substrates were detected by HPLC analysis. The reaction products were then hydrolyzed under acidic conditions and the hydrolysates was subjected to HPLC analysis, which showed that D-glucose and D-mannose were detected as the reaction products from cellobiose and β-(1→4)-mannobiose, and D-galactose and D-mannose were detected as the reaction products from lactose (Fig. 1d–f). The results of the reactions with cellobiose and β-(1→4)-mannobiose suggested that Glc-Man or Man-Glc was produced in the reactions. On the other hand, the result of the reaction with lactose clearly indicated that D-glucose residue at the reducing end of lactose was epimerized to D-mannose residue. Because EpiA had epimerization

activity toward the 2-OH group of the sugar residue at the reducing end, the reaction products from cellobiose and β-(1→4)-mannobiose were thought to be Glc-Man and Man-Glc, respectively. Recombinant EpiA did not act on any of the other disaccharides tested (i.e., maltose, isomaltose, sophorose, laminaribiose, gentiobiose, and β-(1→4)-xylobiose) (data not shown).

Kinetic analysis of recombinant EpiA

Recombinant EpiA exhibited its highest activity towards the disaccharide substrate β-D-glucosyl-(1→4)-D-mannose (Glc-Man) at pH 8.0 and a temperature of 40°C (Fig. 2), which was similar to the results obtained using D-mannose as a substrate.[7)] EpiA retained over 90% of its activity at pH values in the range of 5.2 to 10.0 and temperatures below 40°C following the pH (at 4°C for 24 h) and heat (at pH 8.0 for 30 min) treatment processes, respectively (Fig. 2).

The epimerization activities of EpiA towards several disaccharide substrates were compared with its activity towards D-mannose based on their kinetic parameters that determined from reaction rates at various substrate concentrations by non-linear regression to the Michaelis-Menten equation (Fig. 3). Recombinant EpiA showed a significant preference for disaccharides over D-mannose, and showed 1.4×10^{3}–5.5×10^{4}-fold higher k_{cat}/K_m values for the disaccharide substrates than it did for D-mannose (Table 1). The k_{cat}/K_m value for β-(1→4)-mannobiose was the highest of the disaccharide substrates tested, and was 16- and 39-fold higher than those for cellobiose and lactose, respectively. EpiA exhibited weak epimerization activity to β-(1→4)-mannotriose. Reaction rate to 5 mM β-(1→4)-mannotriose was $0.138 \pm 0.010\ s^{-1}$, which was 0.24% of that to 5 mM β-(1→4)-mannobiose ($57.9 \pm 3.3\ s^{-1}$). EpiA had high epimerization activity to β-(1→4)-linked disaccharides, and β-(1→4)-mannobiose is the best substrate of β-(1→4)-linked disaccharides as other reported CEs.[4,13,16,20)] EpiA was consequently designated as *Cv*CE.

Enzymatic characterization of UnkA

Recombinant UnkA was produced in *E. coli*, which gave 168 mg of purified protein from 1.0 L of culture broth. The resulting recombinant UnkA showed phosphorolytic activity towards 2 mM Man-Glc in the presence of 100 mM sodium phosphate buffer (pH 8.0), and the specific activity toward these substrates was 24.7 U/mg. The highest activity was obtained at pH 8.0 and a temperature of 45°C (Fig. 4). Furthermore, greater than 90% of the initial activity of UnkA was retained at pH values in the range of 3.9–10.6 and temperatures below 37°C after the pH (at 4°C for 24 h) and heat (at pH 8.0 for 20 min) treatment processes, respectively.

Recombinant UnkA was incubated with Man-Glc, β-(1→4)-mannobiose, β-(1→4)-mannotriose, epimerized product of β-(1→4)-mannotriose by *Cv*CE, cellobiose, and lactose. It exhibited phosphorolytic activity only towards Man-Glc (Fig. 5). The spectrophotometric analysis of phosphorolysis of cellobiose and lactose revealed that the activities to these oligosaccharides were ≤0.07 U/mg, indicating that -1 subsite of UnkA is highly specific to mannosyl residue. The acceptor specificity of the recombinant UnkA was investigated based on its synthetic activity towards 10 mM Man1*P* and a variety of different sugars, including D-glucose, D-mannose, D-allose, D-galactose, D-xylose, 1,5-anhydro-D-glucitol, 2-deoxy-D-glucose, 3-deoxy-D-glucose, 6-deoxy-D-glucose, D-glucosamine, *N*-acetyl-D-glucosamine, D-fructose, L-arabinose, D-glucitol, methyl α-D-glucoside, methyl β-D-glucoside, *N,N'*-diacetylchitobiose, maltose, cellobiose, and β-(1→4)-mannobiose. UnkA exhibited synthetic activity towards D-glucose, 6-deoxy-D-glucose, and D-xylose (Table 2). A comparison of the $k_{cat(app)}/K_{m(app)}$ values of UnkA for 6-deoxy-D-glucose and D-xylose with the $k_{cat(app)}/K_{m(app)}$ value of UnkA for D-glucose revealed that they were 5.1- and 34-fold lower, respectively. This result indicates that UnkA has a high specificity for D-glucose in its +1 subsite (acceptor binding site) than it does for 6-deoxy-D-glucose or D-xylose, which is similar to the results observed for several other MGPs.[5,6] Based on these results, UnkA was designated as *Cv*MGP.

The kinetic parameters of *Cv*MGP for the phosphorolysis and synthesis of Man-Glc were determined from its reaction rates at various substrate concentrations. In a similar manner to that observed in several other MGPs,[5,6] the phosphorolysis and synthesis of Man-Glc by recombinant *Cv*MGP obeyed a sequential bi-bi mechanism, involving the formation of a ternary

complex composed of the enzyme and two substrates (Fig. 6). The kinetic parameters of the recombinant *Cv*MGP were as found to be k_{cat} = 48.7 ± 0.29 s^{-1}, K_{mA} = 0.653 ± 0.035 mM, K_{mB} = 0.779 ± 0.017 mM, and K_{iA} = 2.42 ± 0.11 mM (A, Pi; B, Man-Glc) for the phosphorolysis; and k_{cat} = 97.9 ± 9.5 s^{-1}, K_{mA} = 0.685 ± 0.013 mM, K_{mB} = 11.3 ± 3.7 mM, and K_{iA} = 0.792 ± 0.32 mM (A, Man1*P*; B, D-glucose) for the synthesis.

Metabolic pathway of β-mannan in C. vulgaris

In this study, we have clearly shown that EpiA (*Cv*CE) and UnkA (*Cv*MGP) are CE and MGP enzymes, respectively. Considering the functions of these enzymes, *C. vulgaris* probably degrades β-(1→4)-mannobiose through epimerization and phosphorolysis pathways in the same way as *B. fragilis*,[4] *R. albus*,[5] and *R. marinus*[6] (Fig. 7). D-Mannose could be produced intracellularly through the β-mannosidase (Man5A)-catalyzed hydrolysis of β-(1→4)-mannooligosaccharides. It could be subsequently metabolized *via* D-glucose as postulated by Centeno *et al*.,[7] although the epimerization activity of *Cv*CE towards D-mannose is very low. Alternatively, D-mannose could be converted to D-fructose 6-phosphate through sequential reactions with hexokinase (EC 2.7.1.1) and mannose-6-phosphate isomerase (EC 5.3.1.8) to allow for further metabolism through glycolysis. Man5A shows 670-fold higher k_{cat}/K_m values for β-(1→4)-mannotriose and β-(1→4)-mannotetraose than it does for β-(1→4)-mannobiose.[8] The substrate chain-length preference observed in these cases is similar to that of *R. albus* β-1,4-mannooligosaccharide phosphorylase.[5] The low activity of these enzymes towards β-(1→4)-mannobiose therefore suggests that the reactions of CE and MGP are particularly important to the metabolism of this oligosaccharide. *Cv*CE has weak epimerization activity to β-(1→4)-mannotriose. However the epimerization of this oligosaccharide unlikely occurs in the metabolism, because β-(1→4)-mannotriose could be rapidly degraded to (1→4)-mannobiose and D-mannose by Man5A. Compared with an obligatory anaerobe *R. albus*, *C. vulgaris*, which is an aerobic bacterium, more efficiently generates the ATP required for the phosphorylation of monosaccharides. Consistent with differences in the availability of oxygen to these bacteria, in that *C. vulgaris* uses β-mannosidase to release "free" D-mannose to facilitate the degradation of

β-(1→4)-mannooligosaccharide, whereas *R. albus* uses phosphorylase to allow for the direct release of a sugar phosphate.

Experimental

Bacterial strain. C. vulgaris NCIMB8633 was purchased from NCIMB (Aberdeen, UK). This bacterium was aerobically cultured according to supplier's instruction.

Preparation of recombinant Cv*CE.* The *Cv*CE gene was amplified by PCR with the following primers 5′-AAACATATGAACGCCGCCATGCTTCCTTCA-3′ (sense, *Nde*I site underlined) and 5′-AAAGAATTCTTAAACCAAATCCTTCATTA-3′ (antisense, *Eco*RI site underlined), and then cloned into the *Nde*I and *Eco*RI sites of pET23a (Novagen, Darmstadt, Germany). Primestar HS DNA polymerase (Takara Bio, Otsu, Japan) was used for the PCR process. Genomic DNA of *C. vulgaris*, which was prepared using a Bacteria Genomic Prep Mini Spin Kit (GE Healthcare, Uppsala, Sweden), was used as template. The DNA sequence of the inserted region was analyzed using an Applied Biosystems 3130 Genetic Analyzer (Life Technologies, Carlsbad, CA, USA). *E. coli* BL21 (DE3), which had been transformed with the *Cv*CE expression vector, was cultured in 1 L of Luria-Bertani medium containing 100 μg/mL of ampicillin at 37°C until the A_{600} value reached 0.5. Production of the recombinant protein was induced by the addition of 1 mL of 0.1 M isopropyl β-D-thiogalactoside to the culture medium (final concentration, 0.1 mM), and the resulting mixture was incubated with vigorous shaking at 18°C for 16 h. Bacterial cells, which had been harvested by centrifugation at 6,000 ×*g* for 10 min at 4°C, were suspended in 30 mL of 10 mM sodium phosphate buffer (pH 7.0) and disrupted by sonication. The cellular debris was removed by centrifugation at 8,000 ×*g* for 10 min at 4°C, and the resulting supernatant was applied to a Toyopearl DEAE-650M column (2.8 I.D. × 6.5 cm, Tosoh, Tokyo), which had been equilibrated with 10 mM sodium phosphate buffer (pH 7.0). The adsorbed protein was eluted with a linear gradient of NaCl from 0 to 0.5 M (total elution volume, 400 mL). Ammonium sulfate was added to the pooled fractions up to 30% saturation, and the sample was applied to a Toyopearl Butyl-650M column (1.6 I.D. × 2.0 cm,

Tosoh), which had been equilibrated with 10 mM sodium phosphate buffer (pH 7.0) containing 30% saturation ammonium sulfate. The adsorbed protein was eluted with a descending linear gradient of ammonium sulfate from 30 to 0% saturation (total elution volume, 200 mL). The collected fractions were dialyzed against 5 mM sodium phosphate buffer (pH 7.0), and applied to a hydroxyapatite Bio-Gel HTP column (2.8 I.D. × 2.0 cm, Bio-Rad, Hercules, CA, USA). Non-adsorbed fractions were collected (contaminant protein was adsorbed on the resin). Purified recombinant *Cv*CE was mixed with an equal volume of glycerol and stored at –20°C.

Preparation of recombinant Cv*MGP*. The *Cv*MGP gene was inserted into pET23a as described above. Primers 5′-TTGACATATGAGTAGTTTTAAAGAAAAAGC-3′ (sense, *Nde*I site underlined) and 5′-CGTTGAATTCTTAAACCAAATCCTTCATTA-3′ (antisense, *Eco*RI site underlined) were used for the PCR process. The production of recombinant *Cv*MGP was carried out in the same fashion as that of the recombinant *Cv*CE, and the recombinant protein was extracted from bacterial cells using a 20 mM 4-morpholineethanesulfonic acid (MES)-NaOH buffer (pH 6.5) solution by sonication. The cell-free extract was subjected to purification by Toyopearl DEAE-650M column chromatography (2.8 I.D. × 25 cm), where the adsorbed protein was eluted using the conditions described above (equilibrium buffer, 20 mM MES-NaOH buffer, pH 6.5). The pooled fractions were further purified by Toyopearl Butyl-650M column chromatography (2.8 I.D. × 12 cm), where a 20 mM MES-NaOH buffer (pH 6.5) solution containing a 30% saturation of ammonium sulfate was used to equilibrate the column. The adsorbed protein was eluted according to the procedure described above. Purified recombinant *Cv*MGP was dialyzed against a 20 mM MES-NaOH buffer (pH 6.5) solution and stored at –80°C.

Protein assay. The concentrations of protein in the fractions collected by column chromatography were measured using a UV method (A_{280}),[21] assuming that an extinction coefficient of 1.00 mg/mL of protein was equal to 1.00. The concentration of the purified enzyme was determined from the amino acid concentrations of the acid hydrolysate (6 M HCl at

110°C for 24 h), which were measured by the ninhydrin colorimetric method using a JLC-500/V amino acid analyzer (JEOL, Tokyo, Japan).[22)]

Analysis of reaction products of Cv*CE.* A reaction mixture (1 mL) containing 6.4 μM recombinant *Cv*CE, 100 mM substrate, and 10 mM sodium phosphate buffer (pH 8.0) was incubated at 37°C for 48 h. β-(1→4)-Mannobiose (Megazyme, Wicklow, Ireland), cellobiose (Sigma, St. Louis, MO, USA), and lactose (Nacalai Tesque, Kyoto, Japan) were used as substrates. The enzyme reaction was stopped by heating the sample at 100°C for 3 min. The reaction products were purified by HPLC under the following conditions: column, Sugar SP0810 (8.0 I.D. × 300 mm, Shodex, Tokyo); column temperature, 80°C; eluent, water; flow rate, 0.8 mL/min; and detection method, refractive index. The purified reaction product (40 μg) was hydrolyzed in 2 M trifluoroacetic acid at 100°C for 3 h. The reaction mixture was evaporated to dryness to give a residue, which was dissolved in 25 μL of water. The resulting solution was then analyzed by HPLC as follows: injection volume, 5 μL; columns, two tandem Sugar SP0810 columns, column temperature, 70°C; eluant, water; flow rate, 0.5 mL/min; and detection method, pulsed amperometry. D-Mannose (Wako Pure Chemical Industries, Osaka, Japan), D-glucose (Wako Pure Chemical Industries), and D-galactose (Nacalai Tesque) were used as standards.

Substrate specificity of Cv*CE.* A reaction mixture (5 μL), containing 13.8 μM recombinant *Cv*CE, 40 mM substrate, and 20 mM sodium phosphate buffer (pH 8.0) was incubated at 37°C for 24 h. Several substrates were tested, including maltose (Nihon Shokuhin Kako, Tokyo), gentiobiose (Nacali Tesque), lactose, isomaltose (Seikagaku, Tokyo), cellobiose, sophorose (Sigma), β-(1→4)-mannobiose, laminaribiose (Megazyme), and β-(1→4)-xylobiose (Wako Pure Chemical Industries). One microlitre of the reaction mixture was spotted onto a TLC plate (Silica Gel 60 F_{254}, Merck, Darmstadt, Germany), and the plate was developed using a 2:2:1 (v/v/v) mixture of 2-propanol/1-butanol/water. The developed TLC plate was visualized by

spraying it with a detection reagent composed of a 100:2:1 (v/v/v) mixture of acetic acid/sulfuric acid/anisaldehyde followed by heating.

Enzyme assay of Cv*CE.* CE activity was assayed based on the epimerization of Glc-Man to cellobiose. Glc-Man was prepared from α-D-glucose 1-phosphate and D-mannose through the reverse reaction of *R. albus* cellobiose phosphorylase.[23] A reaction mixture (50 μL) containing enzyme, 10 mM Glc-Man, 42 mM sodium phosphate buffer (pH 8.0), and 0.2 mg/mL bovine serum albumin (BSA) was incubated at 37°C for 10 min. The reaction was then terminated by heating the sample at 100°C for 3 min, and the amount of cellobiose produced by the reaction was measured as described previously.[24] Briefly, cellobiose was phosphorolyzed with cellobiose phosphorylase, and the resulting D-glucose was measured using a Glucose CII-Test (Wako Pure Chemical Industries). This enzyme assay method was used to investigate effects of pH and temperature.

Epimerization activity to β-(1→4)-mannotriose was determined from the amount of D-glucose liberated from the epimerization product by the enzymatic degradation. A reaction mixture (50 μL) containing 641 nM *Cv*CE, 5 mM β-(1→4)-mannotriose (Megazyme), 40 mM sodium phosphate buffer (pH 8.0), and 0.2 mg/mL BSA was incubated at 37°C for 10 min. The reaction was stopped by heating the sample at 100°C for 5 min. The sample was mixed with 100 μL of the enzyme mixture, containing 1.3 μg/mL *R. albus* MGP (RaMP1), 0.65 mg/mL RaMP2, and 50 mM sodium phosphate buffer (pH 7.0), and 20 μL of D-glucose quantification reagent described previously.[20] After incubation of the sample at 37°C for 30 min, A_{505} was measured. As standard, 0-0.5 mM D-glucose was used.

The kinetic parameters for the epimerization reactions of D-mannose, β-(1→4)-mannobiose, lactose, and cellobiose were determined experimentally. The rates of reaction were determined at various substrate concentrations and the resulting data were fitted to the Michaelis-Menten equation using the version 7.0.2 of the Grafit program (Erithacus Software, East Grinstead, UK) to calculate kinetic parameters. For the reaction with D-mannose, 50 μL of a reaction mixture containing 9.22 μM recombinant *Cv*CE (from which the glycerol had been removed by dialysis),

50–500 mM D-mannose and 12 mM sodium phosphate buffer (pH 8.0) was incubated at 37°C for 2 h. The reaction was stopped by the addition of 25 μL of 0.1 M HCl, and the resulting mixture was immediately heated at 100°C for 3 min. The pH of the mixture was then adjusted to 8.0 by adding 50 μL of 200 mM sodium phosphate buffer (pH 8.0). The amount of D-glucose produced by this reaction was determined with a D-glucose determination kit (Roche, Darmstadt, Germany). For the reaction with lactose and cellobiose, 100 μL of a reaction mixture containing 86.5 nM recombinant *Cv*CE, 5–40 mM substrate, and 12 mM sodium phosphate buffer (pH 8.0) was incubated at 37°C for 20 min. The enzymatic reaction was then stopped by the addition of 50 μL of 0.1 M HCl, and the resulting mixture was immediately heated at 100°C for 3 min. The progress of the reaction (product formation) was measured by HPLC using two tandem Sugar SP0810 columns as described above. Authentic Glc-Man[23)] and epilactose[25)] were used as standards. The kinetic parameters for β-(1→4)-mannobiose were determined as previously reported.[20)] A reaction mixture (50 μL) containing 8.01 nM recombinant *Cv*CE, 1.0–15 mM β-(1→4)-mannobiose, and 40 mM sodium phosphate buffer (pH 8.0) was incubated at 37°C for 10 min. The enzymatic reaction was then terminated by the addition of 20 μL of 0.1 M HCl, and the resulting mixture was immediately heated at 100°C for 3 min. The sample was neutralized with 20 μL of 0.1 M NaOH, and the resulting Man-Glc was quantified using a colorimetric quantification method.[20)]

*Enzyme assay of Cv*MGP. MGP activity was determined by measuring the phosphorolytic velocity towards 2 mM Man-Glc. A reaction mixture (50 μL) containing enzyme, 2 mM Man-Glc, 100 mM sodium phosphate buffer (pH 8.0), 4 mM 4-(2-hydroxyethyl)piperazine-1-ethanesulfonic acid (HEPES)-NaOH buffer (pH 6.5), and 0.2 mg/mL BSA was incubated at 37°C for 10 min. The enzymatic reaction was then terminated by adding 100 μL of 2 M Tris-HCl buffer (pH 7.0) and immediately heating the resulting mixture at 100°C for 3 min. The liberated D-glucose was measured using a Glucose CII test.

The acceptor specificity of the recombinant *Cv*MGP in the reverse reaction was investigated by measuring its synthetic activity towards 10 mM Man1*P* and various acceptor substrates. A

reaction mixture (20 μL) containing recombinant *Cv*MGP (10 nM for D-glucose and 300 nM for the other substrates), 10 mM Man1*P*, 10 mM acceptor, 104 mM HEPES-NaOH buffer (pH 8.0), and 0.2 mg/mL BSA was incubated at 37°C for 10 min. The enzymatic reaction was stopped by heating the sample at 80°C for 5 min, and the amount of inorganic phosphate generated by the reaction was measured according to the method published by Lowry and Lopez.[26)] Man1*P* (dicyclohexylamine salt) was prepared according to the method of Liu *et al*.[27)] Several acceptor substrates were tested, including D-glucose, D-mannose, D-allose (Wako Pure Chemical Industries), D-galactose, D-xylose (Wako Pure Chemical Industries), 1,5-anhydro-D-glucitol (Wako Pure Chemical Industries), methyl α-D-glucoside (Wako Pure Chemical Industries), methyl β-D-glucoside (Wako Pure Chemical Industries), 6-deoxy-D-glucose (Sigma), cellobiose, *N*,*N'*-diacetylchitobiose (Sigma), 2-deoxy-D-glucose (Tokyo Chemical Industries, Tokyo), D-glucosamine (Tokyo Chemical Industries), D-fructose (Nacalai Tesque), D-glucitol (Nacalai Tesque), *N*-acetyl-D-glucosamine (Nacalai Tesque), 3-deoxy-D-glucose (Carbosynth, Berkshire, UK), L-arabinose (Kanto Chemical, Tokyo), maltose, and β-(1→4)-mannobiose. The apparent kinetic parameters for the acceptor substrates were calculated by fitting the reaction rates at various concentrations of the acceptor substrates (1.25–25 mM) and 10 mM Man1*P* to the Michaelis-Menten equation.

Kinetic parameters for phosphorolysis and synthesis of Man-Glc were determined from the reaction rates at various substrate concentrations by fitting the results to the following equation for a sequential bi bi mechanism[28)] using version 7.0.2 of the Grafit program:

$$v = k_{cat}[A][B]/(K_{iA}K_{mB} + K_{mB}[A] + K_{mA}[B] + [A][B])$$

(For phosphorolysis, A = inorganic phosphate, B = Man-Glc; for synthesis, A = Man1*P*, B = D-glucose)

The phosphorolysis of Man-Glc was carried out in a 50 μL reaction mixture containing 13–38 nM recombinant *Cv*MGP, 0.5–10 mM sodium phosphate buffer (pH 8.0), 0.25–1.5 mM Man-Glc, 104 mM HEPES-NaOH buffer (pH 8.0), and 0.2 mg/mL BSA. The reaction rates for the synthesis of Man-Glc were determined from the amount of inorganic phosphate liberated by the

reaction using a reaction mixture (20 μL) consisting of 5.0 nM recombinant *Cv*MGP, 0.5–2.0 mM Man1*P*, 5.0–40 mM D-glucose, 104 mM HEPES-NaOH buffer (pH 8.0), and 0.2 mg/mL BSA. The enzymatic reactions and processes involved in the subsequent quantification of the reaction products were carried out as described above.

Effects of the pH and temperature on the activity and stability. The optimum pH values for *Cv*CE and *Cv*MGP were investigated based on the enzyme activities at various pH values. The reaction buffer for *Cv*CE was changed to Britton-Robinson buffer (pH 6.0–9.5). Sodium citrate buffer (pH 3.0–6.0), MES-NaOH buffer (pH 6.0–7.0), HEPES-NaOH buffer (pH 7.0–8.5), and glycine-NaOH buffers (pH 8.5–10.5) were used as the reaction buffers for *Cv*MGP. The optimum temperatures for *Cv*CE and *Cv*MGP were determined from the activities at various temperatures. The stable pH and temperature ranges were evaluated by measuring the residual activities of the enzymes after the pH and heat treatment processes, respectively. Mixtures (100 μL) containing the enzyme and 100 mM Britton-Robinson buffer (pH 3.0–12.5) were incubated at 4°C for 24 h to determine the enzyme stability as a function of pH. The stability of the enzyme as a function of temperature was investigated as follows: For *Cv*CE, mixtures (30 μL) containing enzyme, 67 mM sodium phosphate buffer (pH 8.0), and 0.33 mg/mL BSA were incubated at 20–50°C for 30 min, whereas mixtures (100 μL) containing enzyme, 20 mM HEPES-NaOH buffer (pH 8.0), and 1 mg/mL BSA, were incubated at 20–50°C for 20 min for *Cv*MGP. The enzyme was considered stable under conditions that allowed for the retention of ≥90% of the enzymes initial activity prior to the treatment.

Analysis of substrate specificity of CvMGP in the phosphorolysis. A reaction mixture (5 μL) containing 189 nM *Cv*MGP, 5 mM substrate, 5 mM sodium phosphate buffer (pH 8.0), and 0.25 mg/mL BSA was incubated at 37°C for 4 h. One microlitre of the reaction mixture was analyzed by TLC in which the plate was developed two times using a 12:3:4 (v/v/v) mixture of 2-propanol/1-butanol/water and the chromatogram was visualized as described above. Man-Glc, β-(1→4)-mannobiose, β-(1→4)-mannotriose, epimerized β-(1→4)-mannotriose by *Cv*CE,

cellobiose, and lactose were tested as substrate. The epimerized β-(1→4)-mannotriose was prepared as follows: a reaction mixture (25 μL) containing 1.3 μM *Cv*CE, 10 mM β-(1→4)-mannotriose, 20 mM sodium phosphate buffer (pH 8.0), and 0.4 mg/mL BSA was incubated at 37°C for 20 h. The reaction was stopped by heating the sample at 100°C for 3 min, and the reaction mixture was desalted with Amberlite MB-4 (Roam and Haas, Philadelphia, PA, USA). Resulting sample was used as the substrate of *Cv*MGP.

The phosphorolytic activity of *Cv*MGP to cellobiose and lactose was measured based on the amount of D-glucose liberated. A reaction mixture (50 μL) containing 151 nM *Cv*MGP, 2 mM cellobiose or lactose, 100 mM sodium phosphate buffer (pH 8.0), and 0.2 mg/mL BSA was incubated at 37°C for 10 min. D-Glucose liberated was measured as described above.

Acknowledgments

Part of this work was supported by JSPS KAKENHI with a Grants-in-Aid for Young Scientists (B) (Grant No 26850059). We would like to thank Tomohiro Hirose of the Instrumental Analysis Division, Equipment Management Center, Creative Research Institute, Hokkaido University, and the staff of the DNA Sequencing Facility of the Research Faculty of Agriculture, Hokkaido University for amino acid and DNA sequence analyses, respectively.

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Figure legends

Fig. 1. HPLC analysis of the products resulting from the reaction of recombinant EpiA (*Cv*CE) with various disaccharide substrates.

Panels, a, b, and c show the HPLC chromatograms of reaction mixtures with β-(1→4)-mannobiose, cellobiose, and lactose, respectively. S and P indicate substrate and product, respectively. The glycerol in this figure was from the enzyme solution. Reaction products from β-(1→4)-mannobiose, cellobiose, and lactose, were hydrolyzed with trifluoroactetic acid, and analyzed by HPLC (panels d, e, and f, respectively).

Fig. 2. Effects of pH and temperature on activity and stability of EpiA (*Cv*CE).

Epimerization activity of EpiA (*Cv*CE) was measured using 10 mM Glc-Man as substrate. a, pH activity profile. Epimerization activity was measured at indicated pH values at 37°C. b, pH stability. Residual activity was measured after incubation at indicated pH values at 4°C for 24 h. c, Temperature activity curve. Activity was measured at indicated temperatures at pH 8.0. d, Temperature stability. Residual activity was measured after incubation at indicated temperatures at pH 8.0 for 30 min. Error bars indicate standard deviation from three independent experiments.

Fig. 3. [s]-*v* plots for epimerization of EpiA (*Cv*CE) towards various substrates.

a, β-(1→4)-Mannobiose (closed circles); b, cellobiose (open circles) and lactose (closed triangles); and c, D-mannose (open triangles). Error bars indicate standard deviation from three independent experiments.

Fig. 4. Effects of pH and temperature on activity and stability of UnkA (*Cv*MGP).

Phosphorolytic activity of UnkA (*Cv*MGP) was measured using 2 mM Man-Glc as substrate. a, pH activity profile. Epimerization activity was measured at indicated pH values at 37°C. Closed circles, sodium citrate buffer (pH 3.0–6.0); open circles, MES-NaOH buffer (pH 6.0–7.0); closed triangles, HEPES-NaOH buffer (pH 7.0–8.5); and open triangles, glycine-NaOH buffers (pH 8.5–10.5). b, pH stability. Residual activity was measured after incubation at

indicated pH values at 4°C for 24 h. c, Temperature activity curve. Activity was measured at indicated temperatures at pH 8.0. d, Thermal stability. Residual activity was measured after incubation at indicated temperatures at pH 8.0 for 20 min. Error bars indicate standard deviation from three independent experiments.

Fig. 5. Specificity of UnkA (*Cv*MGP) in the phosphorolytic reaction.

Plus and minus mean the reaction with and without the enzyme, respectively. S1, Man1*P*; S2, D-glucose; MG, Man-Glc; M2, β-(1→4)-mannobiose; M3, β-(1→4)-mannotriose; M3E, epimerized β-(1→4)-mannotriose by EpiA (*Cv*CE); C, cellobiose; and L, lactose.

Fig. 6. Double reciprocal plots for phosphorolysis and synthesis of Man-Glc catalyzed by UnkA (*Cv*MGP).

a, Double reciprocal plots for phosphorolysis of Man-Glc. The concentrations of Man-Glc ware 0.25 mM (closed circles), 0.50 mM (open circles), 0.75 mM (closed triangles), 1.0 mM (open triangles), and 1.5 mM (closed squares). b, Double reciprocal plots for synthesis of Man-Glc. Concentrations of D-glucose were 5.0 mM (closed circles), 10 mM (open circles), 20 mM (closed triangles), 30 mM (open triangles), and 40 mM (closed squares). Error bars indicate standard deviation from three independent experiments.

Fig. 7. Metabolic pathway of β-(1→4)-mannooligosaccharides in *C. vulgaris*.

HK, hexokinase; GPI, glucose phosphate isomerase; PMM, phosphomannomutase; PMI, mannose 6-phosphate isomerase.

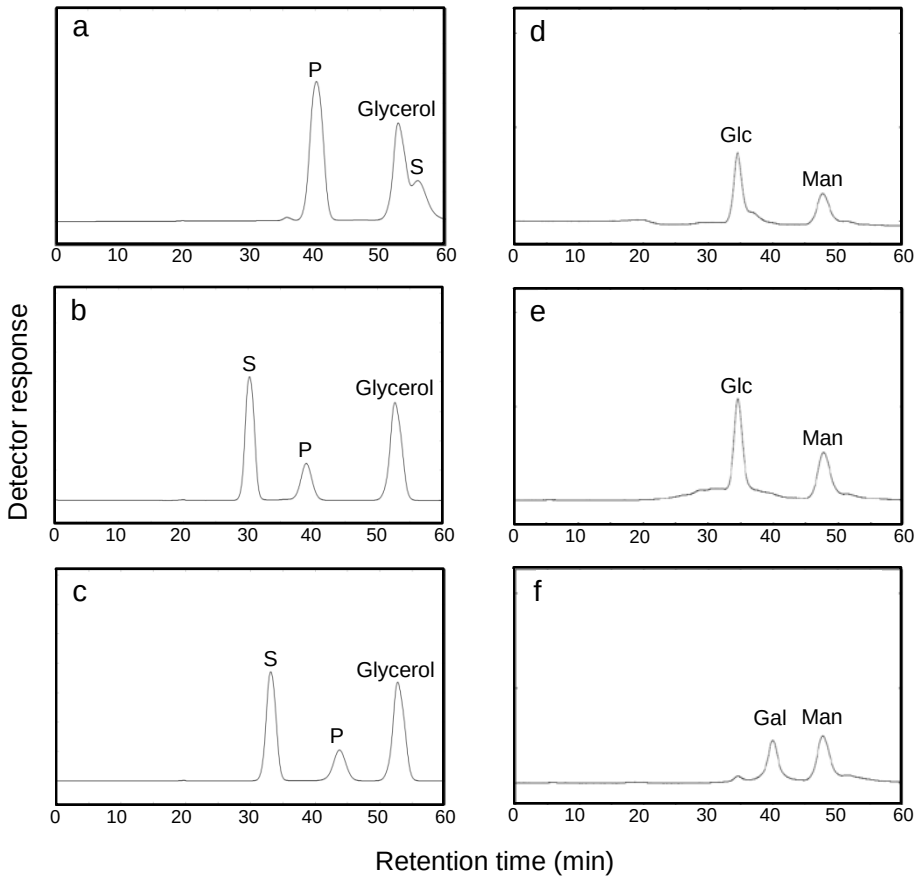


Fig. 1, Saburi *et al.*

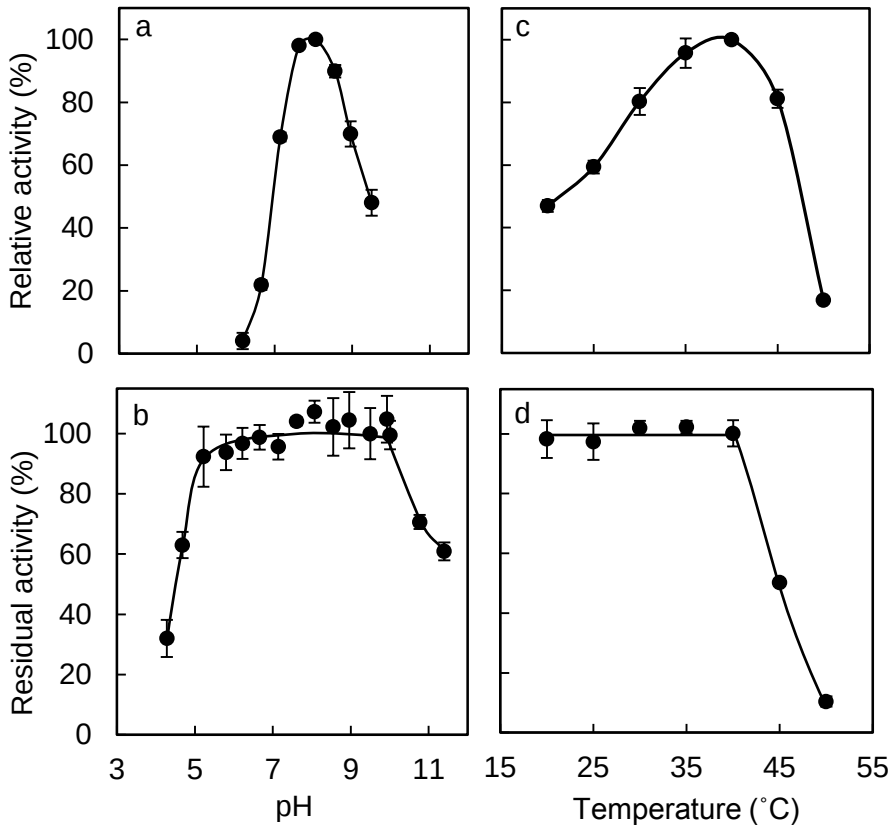
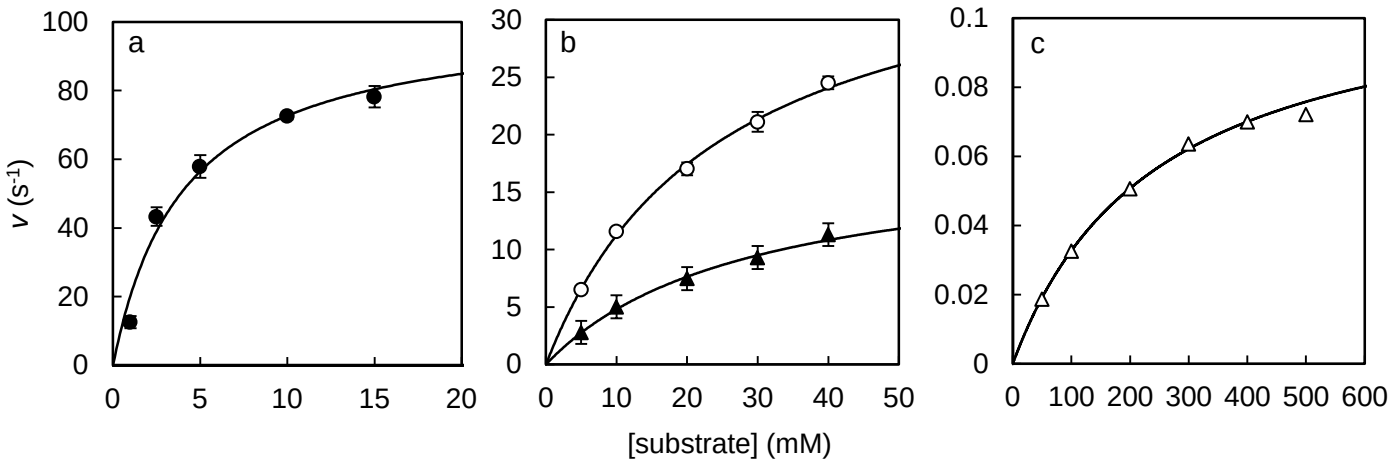


Fig. 2, Saburi *et al.*



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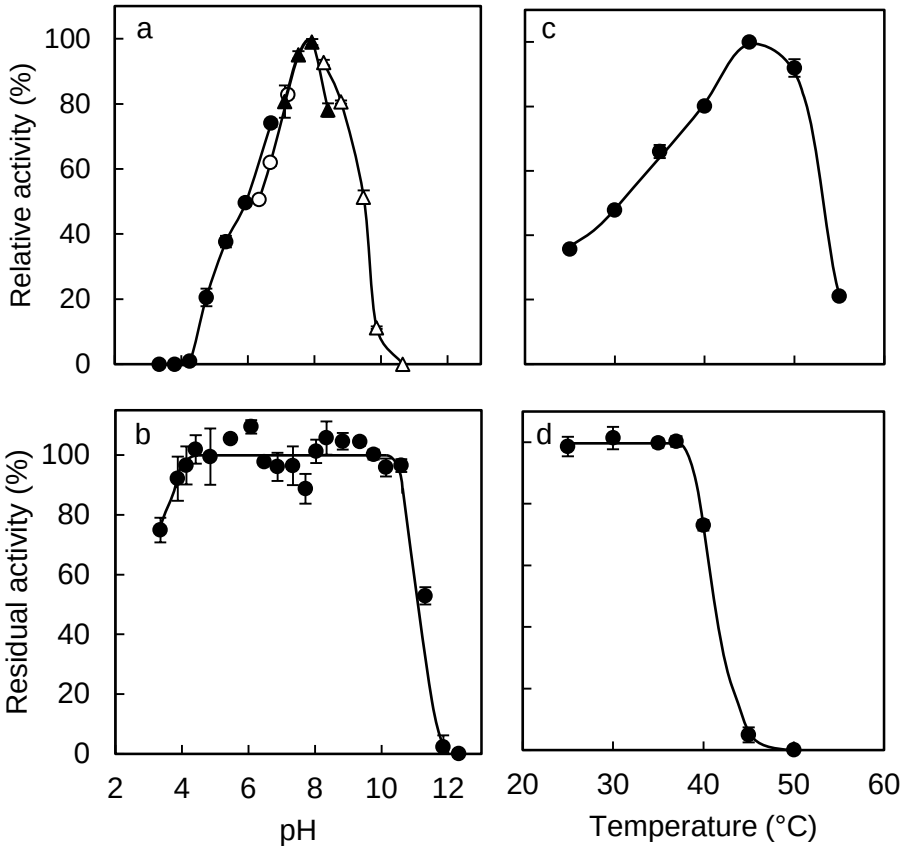

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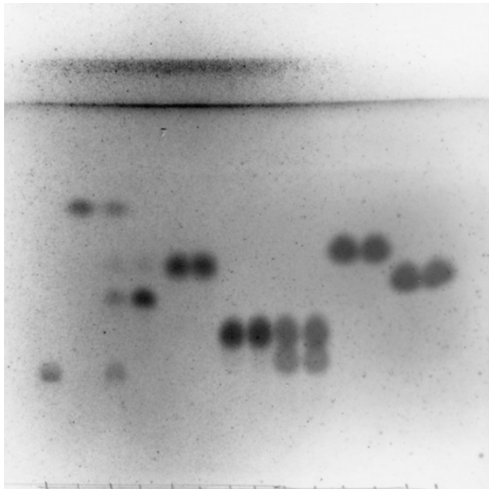

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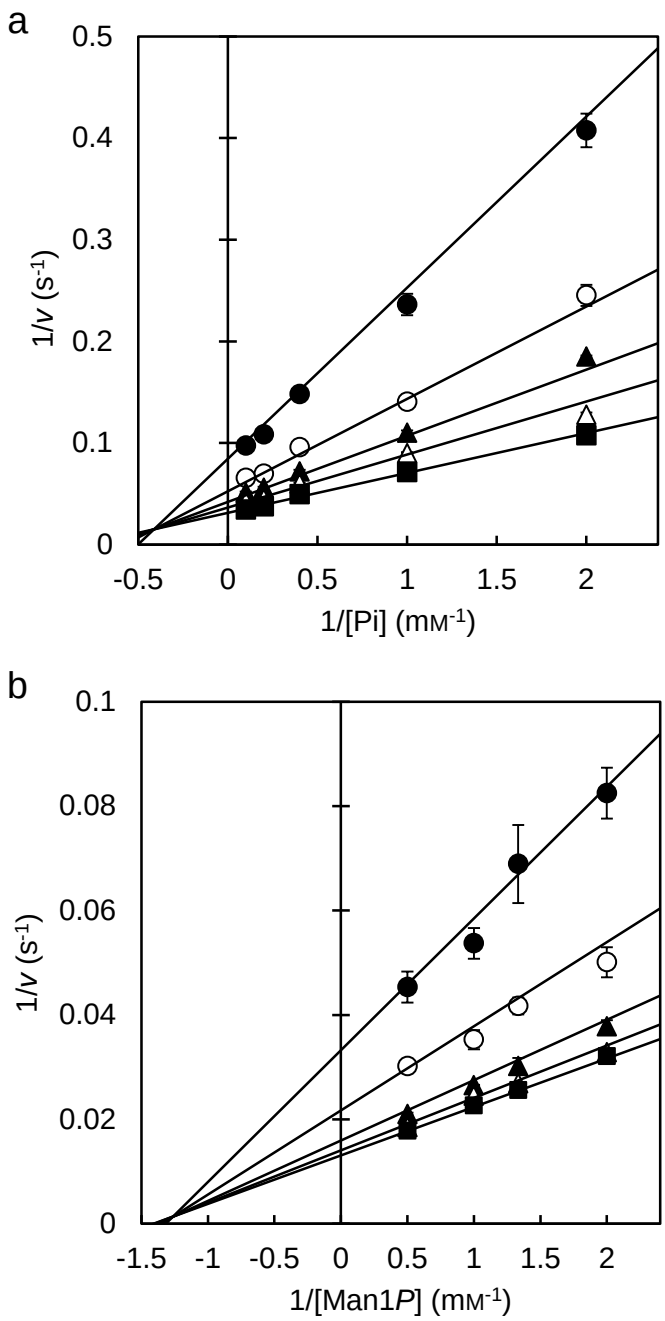

Fig. 6, Saburi *et al.*

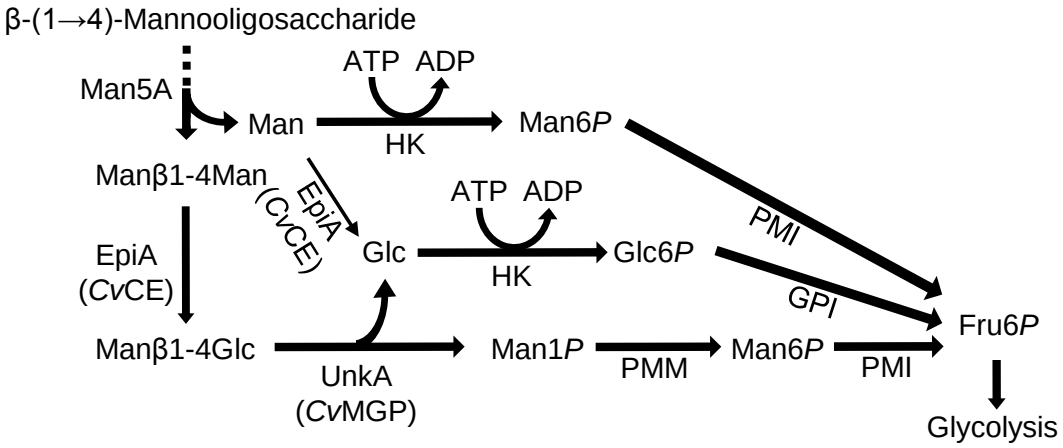

Fig. 7, Saburi *et al.*

Table 1. Kinetic Parameters of Recombinant EpiA (*Cv*CE).

Substrate	k_{cat} (s^{-1})	K_m (mM)	k_{cat}/K_m ($mM^{-1}s^{-1}$)
β-(1→4)-Mannobiose	102 ± 5	4.03 ± 0.72	25.3
Cellobiose	38.8 ± 1.0	24.5 ± 0.8	1.58
Lactose	18.6 ± 1.7	28.7 ± 6.3	0.648
D-Mannose	0.113 ± 0.003	245 ± 10	4.61×10^{-4}

Each value represents the mean ± standard deviation of three independent experiments.

Table 2. Apparent Kinetic Parameters of Recombinant UnkA (*Cv*MGP) for Various Acceptor Substrates.

Substrate	$k_{cat(app)}$ (s^{-1})	$K_{m(app)}$ (mM)	$k_{cat(app)}/K_{m(app)}$ ($mM^{-1}s^{-1}$)
D-Glucose	91.3 ± 3.4	14.1 ± 1.5	6.48
6-Deoxy-D-glucose	48.1 ± 6.7	37.5 ± 5.1	1.28
D-Xylose	8.63 ± 1.05	45.6 ± 8.6	0.189

Each value represents the mean ± standard deviation of three independent experiments.