A Novel Tripartite Aromatic Acids Transporter Is Essential for Terephthalate Uptake in Comamonas sp. Strain E6

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ABSTRACT

A novel type of aromatic acids transporter, which is similar to the tripartite tricarboxylate transporter (TTT), has been suggested to be involved in terephthalate (TPA) uptake by Comamonas sp. strain E6. This suggestion was based on the presence of the putative TPA-binding protein gene, tphC, in the TPA catabolic operon. The tphC gene is essential for growth on TPA, and similar to the genes encoding TTT-like substrate-binding proteins. Here we identified the two sets of E6 genes as tctBA and tpiBA, which encode TTT-like cytoplasmic transmembrane proteins. Disruption of tctA showed no influence on TPA uptake, but resulted in a complete loss of the uptake of citrate. This loss suggests that tctA is involved in citrate uptake. On the other hand, disruption of tpiA or tpiB demonstrated that both genes are essential for TPA uptake. Only when both tphC and tpiBA were introduced with the TPA catabolic genes into cells of a non-TPA degrading Pseudomonas strain, the resting cells of the transformant acquired the ability to convert TPA. From all these results, it was concluded that the TPA uptake system consists of the TpiA-TpiB membrane components and TPA-binding TphC. Interestingly, not only was the tpiA mutant of E6 unable to grow on TPA, or isophthalate, it also showed significant growth delays on o-phthalate and protocatechuate. These results suggested that the TpiA-TpiB membrane components are able to interact with multiple substrate-binding proteins. The tpiBA genes were constitutively transcribed as a single operon in E6 cells, whereas the transcription of tphC was positively regulated by TphR. TPA uptake by E6 cells was completely
inhibited by a protonophore, carbonyl cyanide \textit{m}-chlorophenyl hydrazone, indicating
that the TPA uptake system requires a proton motive force.
The uptake of substrates into the cells is the first important cellular event in the assimilation of aromatic acids for bacteria. To date, various types of transporters involved in the uptake of aromatic acids have been characterized. The major facilitator superfamily (MFS) transporters, which has twelve transmembrane α-helical spanners (TMSs), is the largest superfamily of secondary transporters (1). The aromatic acids/H⁺ symporter (AAHS) family within MFS has been extensively characterized for the following: PcaK of *Pseudomonas putida* PRS2000 for the uptake of protocatechuate (PCA) and 4-hydroxybenzoate (2), TfdK of *Cupriavidus necator* JMP134 for 2,4-dichlorophenoxy acetate uptake (3), BenK of *Acinetobacter bayl* for benzoate uptake (4), GenK of *Corynebacterium glutamicum* ATCC 13032 for gentisate uptake (5), and MhbT of *Klebsiella pneumoniae* M5a1 for 3-hydroxybenzoate (6).

On the other hand, only a limited number of studies characterized the substrate-binding protein (SBP)-dependent uptake systems such as the ATP-binding cassette (ABC) transporters and the tripartite ATP-independent periplasmic transporters (TRAP-T) involved in the uptake of aromatic acids. The ABC transporters, primary active transporters driven by direct ATP hydrolysis, consist of an SBP, an integral membrane protein, and an ABC protein (7). Recent studies genetically demonstrated that ABC transporters are involved in the uptake of o-phthalate (OPA) both in *Burkholderia* strains (8) and *Rhodococcus jostii* RHA1 (9). The involvement of ABC transport systems was also suggested in the uptake of homogentisate by *P. putida* U (10),
2-chlorobenzoate by *Pseudomonas huttiensis* D1 (11), 4-hydroxybenzoate by *Acinetobacter* sp. strain BEM2 (12), and 4-hydroxyphenylacetate by *K. pneumoniae* M5a1 (13).

The two known SBP-dependent secondary transporters are TRAP-T (14) and the tripartite tricarboxylate transporters (TTT) (15). These two families of transporters have a similar tripartite structure, which consists of an SBP and two transmembrane proteins of different sizes. However, both transporters are not related to each other at the amino acid sequence level. An example of the TRAP-T involved in the uptake of aromatic acids has only been reported on the *fcbT1T2T3* genes encoding the 4-chlorobenzoate transporter of *Comamonas* sp. strain DJ-12 (16). In contrast, there have been no reports on TTT-like aromatic acid transporters. The prototype of TTT is the TctCBA system, encoded by the *tctCBA* operon of *Salmonella enterica* serovar Typhimurium (*Salmonella Typhimurium*) (17-19). This prototype mediates the uptake of citrate, with a large transmembrane protein, TctA (504 aa) with twelve predicted TMSs, a small transmembrane protein, TctB (144 aa) with four putative TMSs, and a periplasmic citrate-binding protein TctC (325 aa). A decade ago, 78 genes predicted to encode periplasmic solute receptors (Bug receptors) were found in *Bordetella pertussis* (20). In this large number of Bug receptor genes, *bctC* (formerly *bug4*) in the *bctCBA* operon was characterized as a citrate-binding protein (20, 21). The X-ray crystal structure of one of the Bug receptors of unknown function, BugD (formerly Bug74) was determined. It was suggested that BugD is an aspartate receptor (22). Since the specific ligand-binding motif of BugD was highly conserved in the Bug receptors, these proteins were
considered as receptors of amino acids or other carboxylated solutes. In addition, large numbers of the Bug homologs were also found in the genomes of *Bordetella bronchiseptica* (181 bug homologs), *Bordetella parapertussis* (143 bug homologs), and *Cupriavidus metallidurans* (102 bug homologs) even though the genomes of these stains including *B. pertussis* have between only two to five membrane component gene homologs (*tctBA* homologs) each (20). These observations suggest that a number of SBPs play roles in the uptake of various solutes through their interaction with a limited number of membrane components.

In our previous studies, we characterized the two similar terephthalate (TPA) catabolic operons, *tphR*-*tphC*A2*A3*B1A1I and *tphR*II-*tphC*A2*A3*B1A1II (23), and the isophthalate (IPA) catabolic operon, *iphACBDR* (24) in a phthalate isomers-degrading bacterium, *Comamonas* sp. strain E6. Interestingly, the *tph* and *iph* operons contain *tphC* and *iphC*, respectively, which showed 35% identity at the amino acid sequence level to one of the bug receptors, *bugT* (*bugI*) of *B. pertussis* (25). An introduction of a plasmid carrying *tphR*II-*tphC*A2*A3*B1A1II conferred the TPA utilization phenotype on *Comamonas testosteroni* IAM 1152, which is able to grow on PCA but not on TPA (23). The presence of *tphC* was essential for this phenotype. Similarly, *iphC* was required for the growth of E6 on IPA (24). All these facts implied that *tphC* and *iphC*, respectively, encode a TPA-binding protein and an IPA-binding protein, and these SBPs interact with unidentified membrane components to uptake the substrates.

In this study, we identified and characterized the two gene sets, both of which encode a small transmembrane protein and a large transmembrane protein, involved in
the uptake of citrate and TPA.
MATERIALS AND METHODS

Bacterial strains, plasmids, and culture conditions. The bacterial strains and plasmids used in this study are listed in Table S1 in the supplemental material. *Comamonas* sp. strain E6 was grown in Lysogeny broth (LB; Bacto tryptone, 10 g, yeast extract, 5 g, and NaCl, 5 g/liter) or in Wx minimal salt medium (26) containing 10 mM TPA or 10 mM succinate at 30°C. *Pseudomonas putida* PpY1100 was grown in LB at 30°C. *Escherichia coli* strains were grown in LB at 37°C. For cultures of cells carrying antibiotic resistance markers, the media for *E. coli* transformants were supplemented with 100 mg of ampicillin (Ap)/liter, 25 mg of kanamycin (Km)/liter, and 12.5 mg of tetracycline (Tc)/liter. The media for PpY1100 transformants were supplemented with 25 mg of Tc/liter, and the media for E6 transformants and mutants were supplemented with 12.5 mg Tc/liter and 50 mg Km/liter, respectively.

Uptake assays. E6 and its mutant cells were grown in Wx medium containing 10 mM succinate for 12 h. Cells were harvested by centrifugation at 5,000 × g for 10 min, and washed twice with Wx medium. The resultant cells were inoculated into Wx medium containing 10 mM succinate or 10 mM succinate plus 10 mM TPA to an optical density at 600 nm (OD600) of 0.2, and incubated for 4 h. After the incubation, cells were collected by centrifugation, washed twice with 50 mM Tris-MES buffer (pH 7.5; buffer A), and resuspended in the same buffer to an OD600 of 20. TPA uptake was measured at 30°C in a total volume of 650 μl mixture which contained the cells suspended in buffer A to an OD600 of 2.0, and 20 μM [carboxy-14C]TPA (60 mCi/mmol; American
Radiolabeled Chemicals Inc., MS). Uptake was started by adding the substrate to the cell suspension. The 100 μl of samples were collected from the reaction mixture at 10 s, 30 s, 1.0 min, 2.0 min, and 3.0 min, and filtrated through nitrocellulose membranes (0.45 μm pore size; Advantec, Tokyo, Japan). After washing the filtrates with 1 ml of buffer A three times, accumulated TPA inside the cells was determined by scintillation counting (AccuFLEX LSC-7400, Aloca Co. Ltd. Tokyo, Japan). The uptake rate was calculated from time points at 10 and 60 s, and expressed as the amount of substrates transported into the cells in 1 min per 1 mg of cellular proteins at 30°C. Each experiment was triplicated, and data were averaged with standard deviations. The protein concentration was determined using a DC protein assay kit (Bio-Rad, Hercules, CA).

Using 50 mM Tris-MES buffer, the optimal pH for TPA uptake was determined with pH ranging from 5.5 to 9.5. An inhibition experiment using carbonyl cyanide m-chlorophenylhydrazone (CCCP) was performed by incubation of the cell suspensions with 100 μM CCCP for 5 min at 30°C prior to adding the substrate. The effect of the presence of aromatic acids on TPA uptake was examined by adding 2 mM of TPA, IPA, OPA, benzoate, 3-hydroxybenzoate, 4-hydroxybenzoate, PCA, vanillate, or syringate to the reaction mixture containing 20 μM [14C]TPA and cells.

When the citrate uptake was measured, E6 and its mutant cells grown with succinate were inoculated into Wx medium containing 10 mM succinate or 10 mM succinate plus 10 mM citrate to an OD600 of 0.2, and incubated for 4 h. Utilizing these cells, citrate uptake was measured using 20 μM [1,5-14C]citrate (55 mCi/mmol; American Radiolabeled Chemicals Inc.).
Cloning of the genes. Degenerate primers for amplification of tctA homolog in E6, TCTF and TCTR were designed based on the sequences of tctA homologs in C. testosteroni KF-1 (CtesDRAFT_PD3800), Delftia acidovorans SPH-1 (Daci_2520), and Acidovorax sp. strain JS42 (Ajs_1644). A second primer set, 4157F and 4157R was used for the amplification of another tctA homolog found in KF-1 (CtesDRAFT_PD4157). Nucleotide sequences of these primers are shown in Table S2 in the supplemental material. A 405-bp fragment and a 452-bp fragment were PCR amplified using primer sets of TCTF-TCTR and 4157F-4157R, respectively. Their nucleotide sequences were then determined using a CEQ2000XL genetic analysis system (Beckman Coulter Inc., Fullerton, CA). The PCR-amplified fragments were used in colony hybridization as probes to isolate the EcoRI fragments carrying tctA homologs from the E6 gene library constructed in Charomid 9-36 containing EcoRI digests of the E6 total DNA. Colony and Southern hybridization analyzes were done using the digoxigenin (DIG) system (Roche, Mannheim, Germany). Deletion clones were constructed with the 6.1-kb EcoRV-EcoRI region carrying the 405-bp amplicon and the 4.6-kb EcoRV-EcoRI region carrying the 452-bp amplicon, and their nucleotide sequences were determined. Sequence analysis was performed using the MacVector program (MacVector, Inc., Cary, NC). Homology searches were carried out with the nonredundant (nr) protein sequence database using the BLAST program. A pairwise alignment was performed with the EMBOSS alignment tool at http://www.ebi.ac.uk/Tools/psa/emboss_needle/. Putative TMSs were predicted using the TMHMM (27), TopPred II (28), and SOSUI (29) programs.
Construction of mutants. Construction of p18TAK, pK19tAIIK, and pK18tBK for disruptions of tctA, tpiA, and tpiB, respectively, is described in the supplemental material. To obtain tctA, tpiA, and tpiB mutants, p18TAK, pK19tAIIK, and pK18tBK were independently introduced into E6 cells by electroporation, and candidate mutants were isolated as described previously (30). The disruption of each gene was examined by Southern hybridization analysis (Fig. S1 in the supplemental material).

E6 mutant cells were pregrown in 10 ml of LB containing Km. The cells were harvested by centrifugation at 5,000 $\times$ g for 10 min, washed twice with Wx medium, and resuspended with 3 ml of the same medium. The cells were inoculated into Wx medium containing 10 mM of TPA, IPA, OPA, PCA, or citrate to an OD$_{600}$ of 0.1. Cell growth was periodically monitored by measuring OD$_{600}$. Complementary plasmids pJBtpiA carrying tpiA and pJBtpiB carrying tpiB constructed using pJB866 were independently introduced into cells of EME019 by electroporation, and the growth of the resulting transformant cells was examined.

Reverse transcription (RT)-PCR and quantitative RT-PCR (qRT-PCR). Cells of E6 grown in LB were washed twice with Wx medium and resuspended in the same medium containing 10 mM succinate with or without 10 mM TPA to an OD$_{600}$ of 0.2. The cells were then incubated for 4 h at 30°C. Total RNA was isolated using ISOGEN II (Nippon Gene, Tokyo, Japan), followed by treatment with RNase-free DNase I (Roche). Single-strand cDNA was synthesized from 2 $\mu$g of total RNA utilizing PrimeScript reverse transcriptase (Takara Bio Inc., Otsu, Japan) with random hexamer primers. PCR
was performed with the cDNA mixture, specific primers (Table S2), and PrimeStar GXL DNA polymerase (Takara Bio Inc.).

A qRT-PCR analysis was carried out using a Fast SYBR green master mix (Applied Biosystems, Foster City, CA) with a StepOne real-time PCR system (Applied Biosystems) according to previously reported methods (31). Primers used for real-time PCR are listed on Table S2. To normalize the amount of RNA in each sample, 16S rRNA was used as an internal standard.

Expression of *tpiBA* and *tphC* with *tphA2A3B1A1* in *P. putida*. The pJB866-based plasmids, pJBA, pJC, and pJCBA, which carry *tpiBA*, *tphC*, and *tphC*-tpiBA, respectively, under the control of *Pm* promoter, were constructed. To obtain pJB866-based plasmids expressing *tpiBA*, *tphC*, or *tphC*-tpiBA with the *Pm* promoter and *xylS* encoding a transcriptional regulator for the expression from the *Pm* promoter, the DNA fragments, which contain *tpiBA*, *tphC*, or *tphC*-tpiBA with the *Pm* promoter, were ligated into pJSK63 carrying *tphA2A3B1A1* under the control of *Pm* promoter. The plasmids, pJBA*tG, pJCtG, and pJCBA*tG carrying *tpiBA*, *tphC*, and *tphC*-tpiBA, respectively, with *tphA2A3B1A1* were constructed. The details of the plasmid constructions are described in the supplemental material.

The plasmids, pJCA, pJBA*tG, pJC*tG, and pJCA*tG were introduced into the cells of *P. putida* PpY1100 by electroporation, and then the resulting transformant cells were pregrown in LB containing Tc. The cells were grown in fresh LB containing Tc and 1 mM *m*-toluate, which is an inducer for the expression from the *Pm* promoter, for 10 h at 30°C. The cells were harvested by centrifugation at 5,000 × *g* for 5 min, washed three
times with 50 mM Tris-HCl buffer (pH 7.5), and resuspended in the same buffer. Cells suspended in the buffer were sonicated, and the cell lysate was centrifuged at 19,000 × g for 15 min to obtain cell extracts. Conversions of TPA by the cell extracts of transformants were examined in a 1-ml reaction mixture containing 150 μM TPA, 200 μM NADPH, cell extract (500 μg of protein), and 50 mM Tris-HCl buffer (pH 7.5). Portions of the reaction mixtures were periodically removed, and the reaction was stopped by the addition of HCl. The remaining TPA was extracted with ethyl acetate, dissolved in 25% acetonitrile in water, filtrated, and analyzed by high-performance liquid chromatography (HPLC; ACQUITY UPLC system; Waters, Milford, CT) coupled to electrospray ionization-mass spectrometry (ESI-MS; ACQUITY TQ detector; Waters). HPLC separation was achieved using a TSKgel ODS-140HTP column (2.0 by 100 mm; Tosoh, Tokyo, Japan). The mobile phase of HPLC system was a mixture of water (75%) and acetonitrile (25%) containing 0.1% formic acid at a flow rate of 0.3 ml/min. TPA and its metabolite PCA were detected at 242 nm. In the ESI-MS analysis, mass spectra were obtained using the negative ion mode with the settings specified in a previous study (31). Conversions of TPA by the resting cells of transformants were examined in a 0.5-ml reaction mixture containing 1 mM TPA, the cells with an OD<sub>600</sub> of 20, and 50 mM Tris-HCl buffer (pH 7.5). The reaction mixtures were incubated with shaking for 60 min at 30°C. Portions of the mixtures (20 μl) were periodically collected, and the cells were removed by centrifugation. The supernatants were then diluted 5-fold in water, filtrated, and analyzed by HPLC as described above.
Nucleotide sequence accession numbers. The nucleotide sequences reported in this paper were deposited in the DDBJ, EMBL, and GenBank nucleotide sequence databases under accession numbers AB822590 and AB822591.
RESULTS

Characterization of TPA uptake by *Comamonas* sp. E6 cells. Uptake of TPA by *Comamonas* sp. strain E6 cells grown in Wx medium containing 10 mM succinate or 10 mM succinate plus 10 mM TPA was examined using [14C]TPA. Cells suspended to an OD$_{600}$ of 2.0 in 50 mM Tris-MES buffer (pH 7.5) were incubated with 20 μM [14C]TPA, and the amount of [14C]TPA incorporated into the cells was periodically measured. As shown in Fig. 1A, only the cells grown on TPA showed the uptake of TPA. This result indicated that the transcription of at least a part of the component genes for the TPA transporter was induced during the growth on TPA. When the TPA uptake rate was determined at pH ranges between 5.5 and 9.5, the maximum uptake rate was observed at pH 7.5 (2.55 ± 0.88 nmol/mg of protein-min). At pH 5.5, the uptake rate was approx. 10% of that at pH 7.5, and TPA uptake was not seen at pH 9.0 and 9.5.

In order to determine the energy dependence of TPA transport, inhibition of TPA uptake was assessed using E6 cells treated with a protonophore, CCCP. CCCP completely inhibited TPA uptake (Fig. 1A); therefore, the transport of TPA into E6 cells was found to be dependent on a proton motive force.

TPA uptake rates were examined in the presence of other aromatic acids (OPA, IPA, benzoate, 3-hydroxybenzoate, 4-hydroxybenzoate, PCA, vanillate, or syringate) or citrate as competitors (Fig. 1B). When using 2 mM unlabeled-TPA as a competitor, the uptake rate of 20 μM [14C]TPA by E6 cells was reduced to 6.7% of the rate in the absence of a competitor. Among other compounds, the addition of PCA resulted in a
significant decrease in the TPA uptake rate (approx. 50% of the rate in the absence of PCA).

Isolation of the genes encoding TTT-like transmembrane proteins. In order to isolate the *Comamonas* sp. strain E6 genes that encode predicted transmembrane proteins of the TPA transporter, we searched the *Comamonas testosteroni* KF-1 genome for *tctA* homologs, which are similar to the gene encoding large transmembrane protein of the citrate transporter of *S. Typhimurium*. Since *C. testosteroni* KF-1 carries almost the same gene set of *tphCA2A3BA1* of E6, KF-1 was expected to have the genes encoding TTT-like transmembrane proteins involved in TPA uptake. A database search revealed the presence of two open reading frames (ORFs), CtesDRAFT_PD3800 and CtesDRAFT_PD4157 of unknown functions, both of which showed 39% identity with the deduced amino acid sequence of *tctA* of *S. Typhimurium*. CtesDRAFT_PD3802 and CtesDRAFT_PD3801 upstream of CtesDRAFT_PD3800 showed similarities with *tctC* and *tctB* encoding the citrate-binding protein and the small transmembrane protein of *S. Typhimurium*, respectively. In the case of CtesDRAFT_PD4157, only *tctB* ortholog (CtesDRAFT_PD4158), which showed 18% identity with *S. Typhimurium* TctB, was found just upstream of CtesDRAFT_PD4157. Since the similar gene set of CtesDRAFT_PD3800-3802 was also found in the genomes of *Delftia acidovorans* SPH-1 and *Acidovorax* sp. strain JS42, we designed a primer pair to amplify a partial sequence of a CtesDRAFT_PD3800 ortholog of E6 on the basis of the highly conserved sequences between KF-1, SPH-1, and JS42. Primers used for the amplification of a CtesDRAFT_PD4157 ortholog were designed using the KF-1 sequences. With these
primer pairs, 405-bp and 452-bp fragments (fragments A and B) were amplified from E6 total DNA by PCR. Nucleotide sequences of the fragments A and B showed 92.6% and 93.4% identities with the same regions of CtesDRAFT_PD3800 and CtesDRAFT_PD4157, respectively. This suggested that E6 has similar gene sets to CtesDRAFT_PD3800 and CtesDRAFT_PD4157. In order to isolate these presumed gene sets, the E6 Charomid libraries were screened by colony hybridization using the fragments A and B as probes. Then 8.9-kb and 7.6-kb EcoRI fragments containing the fragments A and B were isolated. Nucleotide sequence of the 6,106-bp EcoRV-EcoRI region in the 8.9-kb EcoRI fragment revealed the presence of six ORFs highly homologous to CtesDRAFT_PD3804-PD3799 (89.3-99.1% identities; Fig. 2A). Based on the similarities to the citrate transporter of S. Typhimurium, we designated the ORFs homologous to CtesDRAFT_PD3802, CtesDRAFT_PD3801, and CtesDRAFT_PD3800 as tctC, tctB, and tctA, respectively. Upstream of E6 tctC, there are two divergently transcribed ORFs that encode a putative histidine kinase (tctE) and a response regulator (tctD), which are similar to CtesDRAFT_PD3804 and CtesDRAFT_PD3803, respectively. On the other hand, nucleotide sequence of the 4,567-bp EcoRV-EcoRI region in the 7.6-kb EcoRI fragment showed the presence of four ORFs highly similar to CtesDRAFT_PD4159-PD4156 (94.4-98.7% identities; Fig. 2B). The ORFs similar to CtesDRAFT_PD4158 and CtesDRAFT_PD4157, which appeared to encode small and large transmembrane proteins, respectively, were designated tpiB and tpiA. In the vicinity of tpiBA, SBP-like genes were not found.

**Characterization of tctA mutant.** To examine the function of tctA, tctA in
Comamonas sp. strain E6 was disrupted by the insertion of the Km resistance gene (Fig. S1 in the supplemental material). The resulting mutant, EME018 grew on TPA similar to that of the wild type (Fig. S2). The uptake rate of [\(^{14}\)C]TPA by EME018 cells grown on TPA was almost the same as that of the wild type (Fig. 3A). On the other hand, EME018 cells were unable to grow on citrate (Fig. 3B). In order to evaluate the ability of EME018 cells to uptake citrate, uptake of [\(^{14}\)C]citrate by E6 cells was verified using the cells grown on 10 mM succinate or 10 mM succinate plus 10 mM citrate. Since only the cells grown in the presence of citrate showed a significant uptake of citrate (Fig. 3C), the citrate uptake genes appeared to be expressed during the incubation of E6 cells on citrate. In contrast, the cells of EME018 grown in the presence of citrate had no citrate uptake activity (Fig. 3C). All these results strongly suggested that tctA is involved in the transport of citrate.

Characterization of tpiA and tpiB mutants. In order to examine the involvement of tpiA and tpiB in TPA uptake by Comamonas sp. strain E6, tpiA mutant (EME019) and tpiB mutant (EME020) were created by the insertion of the Km resistance gene in each gene (Fig. S1). EME019 completely lost the ability to grow on TPA and IPA (Fig. 4A and B), suggesting that tpiA is involved in the uptake of these substrates. Introduction of pJBtpiA carrying tpiA into the cells of EME019 partially restored the growth of the mutant on TPA and IPA (Fig. S3). These results indicated that tpiA is indispensable for the growth of E6 on TPA and IPA. Similarly, EME020 lost the ability to grow on TPA and IPA, and the introduction of pJBtpiB carrying tpiB into the cells of EME020 restored the growth of the mutant on TPA (Fig. S4). These results indicate that tpiB is also
involved in the growth of E6 on these substrates. Interestingly, the growth of EME019 on OPA, PCA, and citrate were significantly retarded (Fig. 4C-E). Similar growth defects on OPA and PCA were also observed for EME020 (Fig. S4). These observations suggested that *tpiA* and *tpiB* contribute in part to the uptake of OPA, PCA, and citrate.

To confirm whether the growth deficiency of EME019 on TPA was caused by the incapability of the mutant cells to uptake TPA, [14C]TPA uptake by EME019 cells grown on TPA was evaluated. As a result, EME019 cells showed no TPA uptake activity, while the introduction of pJBtpiA into EME019 cells restored the activity (Fig. 5A). In addition, the cells of EME020 grown on TPA also exhibited no TPA uptake activity (Fig. 5B). These results indicated that *tpiA* and *tpiB* are essential for the uptake of TPA, and probably also IPA uptake. Since the growth of EME019 on citrate was considerably retarded, citrate uptake by EME019 cells grown in the presence of citrate was also assessed (Fig. 5C). Consequently, the uptake rate of [14C]citrate by EME019 cells decreased to approx. 54% of the rate of the wild type.

**Transcription of *tpiBA* and *tphC* in *Comamonas* sp. strain E6.** RT-PCR analysis was performed to define the transcriptional unit of *tpiBA* using the total RNA isolated from E6 cells grown on TPA, and primers amplifying the intergenic regions of neighboring ORFs. Amplifications of the internal regions of *tpiB* and *tpiA*, and the intergenic region of *tpiB*-tpiA were observed whereas the regions *orf2*-tpiB and *tpiA*-orf3 showed no amplification (Fig. S5). Therefore, it is concluded that *tpiBA* is transcribed in a single transcriptional unit. In a previous study, we reported that the transcription of *tphCA2A3BA1* is positively regulated by an IclR-type transcriptional
regulator, TphR, in the presence of TPA. To examine whether tpiBA is inducibly expressed in E6, qRT-PCR analysis was performed using total RNA isolated from E6 cells grown in the presence or absence of TPA. This analysis showed that the transcription of tphC was induced approx. 21-fold in the cells grown in the presence of TPA (Fig. 6). On the other hand, the transcriptions of tpiB and tpiA in the cells grown with TPA were almost equal to those of the cells grown without TPA (Fig. 6). These results indicate that tpiBA is constitutively expressed in E6 cells.

**Expression of tphCII and tpiBA with tphA2IIA3IIBIIA1II in P. putida.** In a previous study, we observed that the introduction of pEJ89 carrying tphRII-tphCIIA2IIA3IIA1II, conferred the TPA utilization phenotype on C. testosteroni IAM 1152, which is able to grow on PCA but not on TPA (23). In contrast, introduction of the same plasmid was not able to confer the ability to convert TPA on P. putida PpY1100, which is unable to grow on neither PCA nor TPA. These observations implied that PpY1100 was not able to uptake TPA due to the lack of the tpiBA ortholog. Therefore, we examined whether the introduction of tpiBA could provide an ability to convert TPA for PpY1100 cells. In these experiments, we first observed that the resting cells of PpY1100 harboring pJCtG, which carries tphCII and tphA2IIA3IIA1II, were scarcely able to convert TPA (Fig. 7). Because the extract of the same cells converted TPA into PCA (Fig. S6), this deficiency of TPA conversion appeared to be the lack of the ability to uptake TPA by PpY1100 cells. On the other hand, no conversion was achieved by the cell extract of PpY1100 harboring pJCBA, which carries tphCII and tpiBA (Fig. S6). The resting cells of PpY1100 harboring pJBAtG, which carries tpiBA and
tphA2IIA3IIBIIA1II, showed no TPA-converting activity as well. However, the resting cells of PpY1100 harboring pJCBAgt, which contains tphCII, tpiBA, and tphA2IIA3IIBIIA1II, showed the ability to transform TPA (Fig. 7). All the above results strongly support the conclusion that the TPA transporter of E6 consists of the TPA-binding TphC and the TpiA-TpiB transmembrane proteins.
We identified tctBA and tpiBA in *Comamonas* sp. strain E6, both of which encode TTT-like small and large transmembrane proteins (Fig. 2). The deduced amino acid sequences of *tpiA* and *tpiB* showed 42.0% and 16.6% identities with those of *tctA* and *tctB*, respectively. The similarity of these trends corresponded to the observation that many residues are fully conserved in TctA homologs, and no residues are fully conserved in TctB homolog (15). It was predicted that TctA homologs have 11 or 12 TMSs while TctB homologs have four or infrequently five TMSs (15). Hydropathy analysis by the TMHMM, TopPred II, and SOSUI programs suggested that TctA and TpiA of E6 have 10-11 and 11-12 TMSs, and TctB and TpiB have four and five TMSs. The 15-residue motif, G-Hy3-G-Hy3-G-Hy2-P-G-Hy-G (Hy, an aliphatic hydrophobic amino acid; underlined, a fully conserved residue), well conserved in putative TMS 1 of TctA homologs (15) was also conserved in both TctA and TpiA (amino acids from positions 26 to 40).

Disruption of *tctA* did not affect TPA uptake but resulted in complete losses of citrate uptake and growth on citrate (Fig. 3). These results indicate that *tctA* is essential for citrate uptake, and suggest that *tctA* and *tctB* encode transmembrane proteins for the citrate transporter in E6. Similar to the TTT of citrate in *S. Typhimurium*, a putative citrate-binding protein gene, *tctC* is located just upstream of *tctB* in E6. Moreover, the divergently transcribed *tctDE* genes that encode a two-component regulatory system were found immediately upstream of *tctC* (Fig. 2A). It is known that the TTT operon of
S. Typhimurium is flanked by the genes encoding a putative two-component regulatory system (32). Recently, expression of the TTT genes involved in citrate uptake, bctCBA, in *Bordetella pertussis* was reported to be positively regulated in response to citrate by a two-component regulatory system, which consists of BctE histidine kinase and BctD response regulator (21). bctE and bctD are located just upstream of bctC. Based on the fact that citrate uptake by E6 cells was observed only in the cells grown on citrate, and the tctDE genes are present in the vicinity of tctC, expression of E6 tctCBA seems to be regulated by TctD and TctE. A homologous gene set of tctDE and tctCBA is conserved among the genomes of β-proteobacteria including *C. testosteroni* CNB-2 (33), *C. testosteroni* S44 (34), *C. testosteroni* ATCC 11996 (35), *Delftia* sp. Cs1-4 (NC_015563), *C. testosteroni* KF-1 (NZ_AAUJ02000001), *Delftia acidovorans* SPH-1 (NC_010002), *Acidoborax* sp. KKS102 (36), *Acidoborax* sp. JS42 (NC_008782), *Acidovorax avenae* subsp. *avenae* ATCC 19860 (NC_015138), *Alicyclobacillus* denitrificans BC (37), *Polaromonas naphthalenivorans* CJ2 (38), *Polaromonas* sp. JS666 (39), *Leptothrix cholodnii* SP-6 (NC_010524), *Rambliibacter tataouinensis* TTB310 (40), and *Variovorax paradoxus* S110 (41). The tctDE and tctCBA genes appear to play a major role in citrate uptake in this group of β-proteobacteria.

RT-PCR and qRT-PCR analyses indicated that tpiB and tpiA are constitutively transcribed as a single operon (Fig. 6 and Fig. S5). Disruption of tpiA or tpiB resulted in complete losses of both the growth on TPA (Fig. 4 and Fig. S4) and TPA uptake (Fig. 5). These results suggest that the gene products of tpiA and tpiB encode transmembrane proteins of the TPA transporter. In order to obtain clearer evidence, we carried out
coexpression of tpiBA and tphCII with tphA2IIA3IIA1II in P. putida PpY1100. Only when both tphCII and tpiBA are present in the cells of PpY1100 together with tphA2IIA3IIA1II, the resting cells of the transformant were able to convert TPA (Fig. 7). These results strongly support the conclusion that the TPA transporter of E6 consists of the three components: the TPA-binding TphC, the large transmembrane protein, TpiA, and the small transmembrane protein, TpiB. It should be noteworthy that successful expressions of the TPA transporter genes with the tphA2A3BA1 in a heterologous host will support the establishment of bioprocesses for the conversion of TPA into industrially valuable intermediate metabolites, such as 2-pyrene-4,6-dicarboxylate, which is a building block for highly functional polymers (42-44).

In the genomes of the above-mentioned β-proteobacteria, which have tctDE and tctCBA, a highly similar gene set of tpiBA is completely conserved even though only C. testosteroni CNB-2, C. testosteroni KF-1, and R. tataouinensis TTB310 have the tph gene cluster. This fact implies that tpiBA orthologs are involved in the uptake of any other solutes except TPA in these bacteria. Disruption of tpiA or tpiB indeed caused not only the growth deficiency of E6 on TPA but also on IPA (Fig. 4 and Fig. S4). This fact strongly suggests that the TpiA-TpiB membrane components interact with at least TphC and the IPA-binding IphC. Furthermore, the growth of both tpiA and tpiB mutants on OPA and PCA was significantly retarded (Fig. 4 and Fig. S4). These results suggest that the TpiA-TpiB membrane components also interact with an unidentified OPA-binding protein and PCA-binding protein. Because the involvement of both an MFS transporter (OphD) and an ABC transporter (OphFGH) in OPA uptake by Burkholderia strains was
demonstrated (8, 45), we searched the genome of *C. testosteroni* KF-1 for *ophD* and the putative SBP gene (*ophF*) orthologs. CtesDRAFT_PD0442 revealed 44% identity with OphD, however, similar ORF showing >30% identity with OphF was not found. E6 and KF-1 may employ both the TpiA-TpiB system and an MFS transporter to uptake OPA.

In regard to PCA uptake, we found an MFS transporter gene, *pmdK*, in the PCA 4,5-cleavage pathway operon, *pmdUKEFDABC* of E6 (31). The deduced amino acid sequence of E6 PmdK shows 47% identity with the PcaK transporter of 4-hydroxybenzoate/PCA in *P. putida* (2). Because the growth of *pmdK* mutant of E6 on PCA was considerably delayed at neutral pH, both PmdK and the TpiA-TpiB system appear to be involved in PCA uptake. In addition, the uptake rate of citrate by *tpiA* mutant decreased to approx. 54% of the rate of the wild type, suggesting the involvement of the TpiA-TpiB system in citrate uptake. However, the reason why *tctA* mutant lost the ability to uptake citrate in spite of the existence of *tpiBA* remains unexplained at present.

It was documented that uptake by the TctCBA system is dependent on Na⁺ and the membrane potential, and is completely blocked by the addition of protonophores (15). Uptake of TPA by the cells of E6 was observed in the absence of Na⁺, and the addition of Na⁺ did not enhance the uptake activity (data not shown). However, a protonophore, CCCP, completely inhibited TPA uptake, indicating that the TpiA-TpiB system is dependent on the proton motive force.

Uptake of [¹⁴C]TPA by E6 cells was not inhibited by the presence of the excess amount of IPA, OPA, benzoate, 3-hydroxybenzoate, 4-hydroxybenzoate, vanillate,
syringate, and citrate, suggesting that TphC strictly recognizes its proper substrate. On the other hand, uptake of [14C]TPA by E6 cells was considerably inhibited in the presence of PCA. Because TPA is catabolized through PCA, expression of the genes involved in the PCA catabolism, including the pmd operon, are induced in E6 cells when grown on TPA. One possible explanation for the inhibition of TPA uptake by PCA is that an unidentified gene encoding a PCA-binding protein was inducibly expressed in E6 cells grown on TPA, and then the PCA-binding protein and TphC competed with each other for the interactions with the TpiA-TpiB membrane components.

In this study, we identified and characterized a novel TTT-like system for TPA uptake in *Comamonas* sp. strain E6. This is the first report on the characterization of a TTT-like system involved in the uptake of aromatic acids. In addition, our results suggest for the first time that specific membrane components indeed interact with multiple SBPs of various substrates. While the *tctCBA* operon is specialized for citrate uptake in respect to the substrate recognition and the gene expression, the constitutive expression of *tpiBA* appears to be essential for multiple interactions of the TpiA-TpiB membrane components with various SBPs. However, further study will be necessary to uncover the actual involvement of the TpiA-TpiB system in the uptake of OPA, PCA, and citrate.
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REFERENCES


41. Han JI, Choi HK, Lee SW, Orwin PM, Kim J, Laroe SL, Kim TG, O’Neil J,


**Figure legends**

**FIG 1** Uptake of [14C]TPA by cells of *Comamonas* sp. strain E6. (A) [14C]TPA uptake by E6 cells grown in the presence and absence of TPA are indicated by closed circles and open circles, respectively. [14C]TPA uptake by TPA-induced E6 cells treated with 100 μM CCCP is indicated by diamonds. Each value is the average ± standard deviation of three independent experiments. (B) Substrate inhibition of TPA uptake. The uptake rates of TPA were examined by adding 2 mM of aromatic acids or citrate as competitors to the reaction mixture containing 20 μM [14C]TPA. The TPA uptake rate in the absence of competitors was 2.62 ± 0.38 nmol/mg of protein-min. Inhibition was evaluated by comparing the TPA uptake rates in the presence and absence of competitors. Each value is the average ± standard deviation of three independent experiments. Abbreviations: BA, benzoate; 3HB, 3-hydroxybenzoate; 4HB, 4-hydroxybenzoate.

**FIG 2** Restriction maps of the 6.1-kb EcoRV-EcoRI fragment carrying *tctCBA* (A) and the 4.6-kb EcoRV-EcoRI fragment carrying *tpiBA* (B). *tctE*, *tctD*, *tctC*, *tctB*, *tctA*, *orf1*, *orf2*, *tpiB*, *tpiA*, and *orf3* are indicated by the filled arrows. Vertical bars indicate the positions of the *kan* gene insertion of *tctA* mutant (EME018), *tpiB* mutant (EME020), and *tpiA* mutant (EME019). Abbreviations for restriction enzymes: A, Apal; B, BamHI; Bg, BglII; E, EcoRI; Ev, EcoRV; H, HindIII; K, KpnI; P, PstI; Sa, Sall; Sc, Scal; Sm, SmaI; Sp, SphI.
FIG 3 Characterization of tctA mutant. (A) $[^{14}\text{C}]$TPA uptake assays were performed with E6 cells (circles) and tctA mutant cells (EME018; triangles) grown in the presence (closed symbols) or absence (open symbols) of TPA. (B) Growth of E6 cells (circles) and EME018 cells (triangles) on Wx medium containing 10 mM citrate. (C) $[^{14}\text{C}]$citrate uptake assays were performed with E6 cells (circles) and EME018 (triangles) cells grown in the presence (closed symbols) or absence (open symbols) of citrate. Each value is the average ± standard deviation of three independent experiments.

FIG 4 Growth of tpiA mutant on various aromatic acids and citrate. E6 cells (circles) and tpiA mutant cells (EME019; diamonds) were incubated in Wx medium containing 10 mM of TPA (A), IPA (B), OPA (C), PCA (D), and citrate (E). Each value is the average ± standard deviation of three independent experiments.

FIG 5 Characterization of tpiA and tpiB mutants. (A) $[^{14}\text{C}]$TPA uptake assays were performed with E6 cells (circles), tpiA mutant cells (EME019; diamonds), and EME019 harboring pJBTpiA (squares) grown in the presence of TPA. (B) $[^{14}\text{C}]$TPA uptake assays were performed with E6 cells (circles) and tpiB mutant cells (EME020; squares) grown in the presence of TPA. (C) $[^{14}\text{C}]$citrate uptake assays were performed with E6 cells (circles) and EME019 cells (diamonds). Each value is the average ± standard deviation of three independent experiments.

FIG 6 qRT-PCR analysis of the expression of tpiA, tpiB, and tphC in Comamonas sp.
strain E6. Relative mRNA abundance was determined for \textit{tpiA}, \textit{tpiB}, and \textit{tphC} (\textit{tphC}_{1} + \textit{tphC}_{II}). Total RNA was isolated from E6 cells grown in the presence (white bars) or absence (black bars) of 10 mM TPA. The data represent mRNA abundance normalized to 16S rRNA. Each value is the average ± standard deviation of three independent experiments.

\textbf{FIG 7} Conversion of TPA by the resting cells of \textit{P. putida} PpY1100 carrying \textit{tpiBA}, \textit{tphC}_{II}, and \textit{tphA}_{2II}A_{3II}B_{II}A_{1II}. TPA (1 mM) was incubated with the resting cells of PpY1100 cells harboring pJCBA (\textit{tphC}_{II} + \textit{tpiBA}; triangles), pJCtG (\textit{tpiBA} + \textit{tpiBA}; squares), pJBAtG (\textit{tphA}_{2II}A_{3II}B_{II}A_{1II}; diamonds), or pJCBAtG (\textit{tpiBA} + \textit{tphA}_{2II}A_{3II}B_{II}A_{1II}; circles). The remaining TPA in the reaction mixture was periodically monitored by HPLC. Each value is the average ± standard deviation of three independent experiments.