Lactobacillus helveticus is a gram-positive, facultatively anaerobic thermotolerant lactic acid bacterium that is highly adapted to growth in milk. Although milk contains free amino acids, the amounts are too limited for growth to high cell adapted to growth in milk. Although milk contains free amino acids, the amounts are too limited for growth to high cell densities. In order to obtain the amino acids needed for growth, lactic acid bacteria, in general, use a proteolytic system that consists of an extracellular proteinase, peptide transport systems, and intracellular peptidases (11, 17).

The proteolytic system of L. helveticus has recently received a lot of attention (reviewed in reference 11), and the available data suggests that this system is very comparable to that of Lactococcus lactis. The proteinase and peptidases of L. helveticus are similar to those of Lactococcus lactis, but the overall proteolytic activity of L. helveticus is higher than that of Lactococcus lactis (18). L. helveticus also possesses several amino acid transport systems with properties similar to those of Lactococcus lactis (15). In our studies on peptide metabolism in L. helveticus, we found an open reading frame (ORF) downstream of the pepN gene whose deduced amino acid sequence is homologous to that of the di- and tripeptide transport protein of Lactococcus lactis (6). In this article, we report the cloning of this gene, the functional expression of the protein in Escherichia coli, and the characterization of this protein as a di- and tripeptide transporter.

Materials and Methods

Bacterial strains, plasmids, and growth conditions. The bacterial strains and plasmids used are listed in Table 1. L. helveticus was grown at 37°C in MRX broth plus 0.5% glucose (19). E. coli strains were grown aerobically at 37°C in Luria broth (17a). When needed, ampicillin (100 μg/ml) and kanamycin (40 μg/ml) were added to the indicated concentrations.

Chromosomal DNA preparation. Chromosomal DNAs of L. helveticus NCD02712 and SBT2171 were prepared essentially as described by Delley et al. (3). Exponentially growing cells (10 ml) were harvested by centrifugation and washed twice with 100 mM potassium phosphate (pH 7.0). The cells were re-suspended in 1 ml of 10 mM Tris-HCl (pH 7.8) containing 1 mM EDTA and treated with proteinase K (250 μg/ml) and proteinase E (500 μg/ml) for 30 min at 37°C. The cells were washed with TE (10 mM Tris-HCl plus 1 mM EDTA [pH 7.5]) and resuspended in 1 ml of TE. After a treatment of mutanolysin (160 U), the mixture was incubated at 37°C for 30 min. Subsequently, sodium dodecyl sulfate, EDTA, and proteinase K were added to final concentrations of 0.1%, 75 mM, and 200 μg/ml, respectively, and the incubation continued for 2 h at 65°C. After a wash with phenol-chloroform (50:50 [vol/vol]; three times), chromosomal DNA was precipitated and dissolved in TE with DNsase-free RNase (20 μg/ml) overnight at 4°C.

Southern hybridization. Chromosomal DNA, digested with the appropriate restriction enzymes, was separated by agarose gel electrophoresis and transferred to a Zeta-plus blotting membrane (Bio-Rad). DNA was labelled with digoxigenin by the Klenow reaction, hybridized at stringent conditions (65°C), and visualized with the CSPD luminescent detection kit (Boehringer Mannheim GmbH).

Other DNA manipulations. Plasmid DNA was isolated from E. coli strains by the alkaline lysis method (1). Other methods were performed according to standard procedures (17a). In vitro amplification of DNA was performed with PWO polymerase by using the recommended buffer plus 2 mM MgSO4 (Boehringer Mannheim GmbH). Amplified DNA was purified using a quick PCR purification kit (QIAIEN) and analyzed by agarose gel electrophoresis.

Cloning of dtpT1H by inverse PCR. The 5′ region of an open reading frame downstream of pepN in L. helveticus (2) was found to be homologous to dtpT of Lactococcus lactis (dtpT1H). The PCR technique was used to clone a 2.4-kb DNA fragment that encompassed the 3′ end of pepN and part of the L. helveticus dtpT gene (dtpT1H). The oligonucleotides PF (5′-GGTCATCGAAAAGCAAGGT) and PR (5′-GTTTCTTACAGCCATC) were used to synthesize this fragment, which was subsequently used to identify a 2.4 kb HpaI fragment by Southern hybridization; the HpaI fragment contained the entire dtpT1H gene. HpaI fragments were extracted from an agarose gel and ligated with T4 DNA ligase (Boehringer Mannheim GmbH). By using oligonucleotides IF (5′-CCGCGGATTCCCTTCTGAGCAGCAAGGCC; EcoRV site introduced) and IR (5′-CCGCG GATCCATAATGCCATTGACACGTC; BamHI site introduced), the DNA was amplified by inverse PCR, following digestion with EcoRV and BamHI, and ligated into pTAQI (digested with EcoRV plus BamHI, removal of lac promoter region). The recombinant plasmids were used to transform the dipeptide transport-deficient and proline-auxotrophic E. coli E1772. The transformed bacteria were spread on M9 agar, supplemented with ampicillin (100 μg/ml) plus 100 μM Pro-Gly as sole source of proline.

DNA sequence. DNA was sequenced by the dideoxy method using 33P-ATP plus the T7 DNA polymerase kit (Pharmacia) or an automatic sequencing apparatus (Waters) using fluorescent oligonucleotides and cycle sequencing. Prior to the sequencing, fragments were subcloned or shortened by exonuclease III digestion using the Erase-Base system (Promega).

Membrane vesicles. E. coli E1772 harboring the appropriate plasmid vector was grown in M9 medium supplemented with 1.0 g of yeast extract and 10 g of sodium succinate per liter and 100 μg of ampicillin per ml. The cells were grown at 37°C in jar fermentors with a airflow of 15 liters/min until an A600 of 0.6. Membrane vesicles were prepared by the method of Kaback (9) and re-suspended...
TABLE 1. Bacterial strains and plasmids

<table>
<thead>
<tr>
<th>Bacterium or plasmid</th>
<th>Relevant characteristics</th>
<th>Source or reference</th>
</tr>
</thead>
<tbody>
<tr>
<td>E. coli E1772</td>
<td>W3110 dppC::Kan proC::Tn10ΔlacI169 RecA HsdR GyrA Deor lacZ∆M15</td>
<td>Institute of Food Research</td>
</tr>
<tr>
<td></td>
<td></td>
<td>DH5α</td>
</tr>
<tr>
<td>L. helveticus</td>
<td>Standard strain</td>
<td>Institute of Food Research</td>
</tr>
<tr>
<td>NCDO2712</td>
<td>Industrial strain</td>
<td>18</td>
</tr>
<tr>
<td>SBT2171</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Plasmids</td>
<td></td>
<td></td>
</tr>
<tr>
<td>pTAOI</td>
<td>pBR322, lacI behind penicillinase promoter</td>
<td>Gencorα</td>
</tr>
<tr>
<td>pTDH</td>
<td>pTAOI carrying dtpT&lt;sub&gt;1&lt;/sub&gt;</td>
<td>This study</td>
</tr>
<tr>
<td>pTD5</td>
<td>pTAOI carrying dtpT&lt;sub&gt;1&lt;/sub&gt;</td>
<td>6</td>
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<tr>
<td>pUC18</td>
<td>Amp&lt;sup&gt;r&lt;/sup&gt; cloning vector</td>
<td>Gibco BRL</td>
</tr>
<tr>
<td>pBluescript II SK&lt;sup&gt;+&lt;/sup&gt;</td>
<td>Amp&lt;sup&gt;r&lt;/sup&gt; cloning vector</td>
<td>Stratageneβ</td>
</tr>
</tbody>
</table>

α Reading, United Kingdom.
β South San Francisco, Calif.
γ Paisley, United Kingdom.
δ La Jolla, Calif.

in 50 mM 2-(N-morpholino)ethanesulfonic acid (MES)-KOH with 2 mM MgSO<sub>4</sub> (pH 6.5) and stored in liquid nitrogen until use.

Transport assay using nonradiolabelled peptides. Overnight cultures of L. helveticus NCDO2712 were diluted 20-fold into glucose-MRX medium and incubated for 5 h at 37°C. The cells were washed twice and resuspended in 50 mM potassium phosphate (KP<sub>i</sub>) (pH 6.5). Subsequently, the cells were de-energized with 10 mM 2-deoxyglucose for 20 min at 37°C. The de-energized cells were washed twice and resuspended in MES-KOH supplemented with 2 mM MgSO<sub>4</sub> (pH 6.5). The transport assays with alanine, dialanine, trialanine, and tetra-alanine as substrate were carried out as described by Kunji et al. (12), with glucose (0.5%, wt/vol) as energy source. The amino acid and peptides accumulated were separated by C<sub>18</sub> reverse-phase high-pressure liquid chromatography (HPLC) after labelling with dansyl chloride (12).

Transport assay using l-prolyl-[<sup>14</sup>C]alanine. E. coli strains were incubated with 10 mM Li<sup>+</sup>-l-tartrate in the presence of oxygen to generate a proton motive force, and transport of l-Pro-[<sup>14</sup>C]Ala was assayed as described by Hagting et al. (6). For transport in membrane vesicles, the electron donor system potassium ascorbate-phenazine methosulfate (PMS) plus oxygen was used to generate a proton motive force. Membrane vesicles were resuspended to a final concentration of 60 μg/ml in 50 mM MES-KOH–2 mM MgSO<sub>4</sub>–50 mM 2-(morpholino)ethanesulfonic acid (MES)–KOH with 2 mM MgSO<sub>4</sub> (pH 6.5) and stored in liquid nitrogen until use.

RESULTS

Characterization of peptide transport in L. helveticus. L. helveticus NCDO2712 takes up the presence of an energy source the l-alanine and the peptides dialanine, trialanine, and tetra-alanine. However, after dansylation and HPLC of the intracellular fraction only free alanine could be detected (Fig. 1). This suggests that the peptides are degraded immediately after uptake. A lag phase in the accumulation of alanine during uptake of alanine or peptides was found to be caused by the ATP synthesis and proton motive force generation during glucose metabolism, i.e., there is a lag in the energy generation of 2-deoxyglucose-treated cells. In order to eliminate the possibility that the peptides were degraded outside the cells, i.e., prior to uptake, the extracellular aminopeptidase activity was measured. Aminopeptidase activity (0.178 at A<sub>405</sub>) was detected in the cell extract (following sonication), but no such activity was found in the extracellular medium, not even after prolonged incubation of the cells in the buffer used for the transport assays. The same observations were made for the industrial strain SBT2171, which possesses very high proteolytic activity (18).

Cloning and functional expression of dtpT<sub>1</sub> in E. coli. Sequence comparisons showed that a gene encoding a putative di- and tripeptide transport protein was present downstream of pepN in L. helveticus (2). The N-terminal 55 amino acids of DtpT<sub>1</sub> are 55% identical with DtpT<sub>1</sub>. The entire gene encoding the peptide transport protein of L. helveticus was isolated by inverse PCR and ligated into pTAOI, yielding pTDH. Plasmid pTDH was used to transform the peptide transport-deficient and proline- auxotrophic E. coli E1772 (16). The recombinant strain was able to grow on a medium containing Pro-Gly as source of proline, suggesting that the peptide transport gene was expressed functionally.

Subsequent transport experiments confirmed this suggestion. E. coli E1772/pTDH takes up Pro-[<sup>14</sup>C]Ala at a higher rate than the parent strain (E1772/pTAOI) (Fig. 2). Figure 2 also shows the uptake of Pro-[<sup>14</sup>C]Ala by E1772/pDT5 (carrying dtpT<sub>1</sub>) for comparison. Since the tac promoter region of pTAOI is missing in pTDH, the cloned gene (dtpT<sub>1</sub>) is most likely expressed from its own promoter.

Southern hybridization experiments with the dtpT<sub>1</sub> gene as probe confirmed that dtpT<sub>1</sub> is present in both L. helveticus NCDO2712 and SBT2171.

The DNA sequence of dtpT<sub>1</sub> and the translated amino acid sequence are shown in Fig. 3. An open reading frame of 1,491 nucleotides, encoding a 497-amino-acid polypeptide, was found. The translation initiation site was selected on the basis of the alignment of the protein sequence to DtpT<sub>1</sub> (see below). A putative ribosome binding site (5′-GGGAG) is found 19 nucleotides upstream of the start codon. Putative −35 (5′-TGGACA) and −10 (5′-TATTATT) regions, separated by 18 nucleotides, are found in the noncoding region between pepN and dtpT<sub>1</sub>. Terminus-like structures are present downstream of pepN and dtpT<sub>1</sub>, suggesting that the two genes are
transcribed separately. The terminator downstream of dtpT<sub>LH</sub> consists of a stem of 12 nucleotides and has a $\Delta G$ of $-71$ kJ/mol at 25°C.

The overall G+C content of dtpT<sub>LH</sub> is 38.6%, which matches well with that of the genome of <i>L. helveticus</i> (from 38 to 40%). From the dtpT<sub>LH</sub> gene a primary amino acid sequence of the DtpT LH protein was deduced; the protein has 68% nonpolar amino acids, a value typical of a membrane protein. Hydropathy profiling suggested 12 hydrophobic stretches that are long enough to span the membrane in a zigzag fashion; the transmembrane segments are indicated in Fig. 3.

**Properties of DtpT<sub>LH</sub>.** Membrane vesicles prepared from <i>E. coli</i> E1772 do not transport Pro-[14C]Ala in the presence of the electron donor system ascorbate-PMS (data not shown). However, membrane vesicles of strain E1772/pTDH transport this peptide well under those conditions (Fig. 4). This shows that DtpT<sub>LH</sub> indeed codes for the di- and tripeptide transporter and that transport of Pro-[14C]Ala is driven by the proton motive force. The role of the proton motive force was further demonstrated by using ionophores. Valinomycin, which dissipates the membrane potential (K<sup>+</sup> ionophore), and nigericin, which dissipates the pH gradient (K<sup>+</sup>/H<sup>+</sup> ionophore), inhibited transport of Pro-[14C]Ala significantly (Fig. 4). The presence of both ionophores completely collapsed the proton motive force and reduced the uptake of Pro-[14C]Ala to equilibration.

---

**FIG. 2.** Functional expression of dtpT<sub>LH</sub> in <i>E. coli</i> E1772. Prolyl-[14C]alanine uptake was measured in <i>E. coli</i> E1772 harboring pTDH (●) or pTAQ1 (vector control) (○) and <i>E. coli</i> E1772 harboring pDT5 with dtpT<sub>LH</sub> (▲). Transport experiments were performed aerobically at 30°C in the presence of the electron donor Li-ß-lactate (10 mM); the concentration of Pro-[14C]Ala was 2.9 μM.

**FIG. 3.** Nucleotide sequence of dtpT<sub>LH</sub> and deduced amino acid sequence. The putative promoter regions (~35 and ~10), the ribosome binding site (RBS), and putative transmembrane-spanning segments (TMS) are underlined; putative terminator sequences are indicated by dotted lines.
levels. These observations indicate that transport of Pro-[\(^{14}\)C]Ala is most likely electrogenetic and occurs in symport with a proton(s).

Information about the substrate specificity of DtpT LH was obtained by following the transport of Pro-[\(^{14}\)C]Ala in the presence of an excess (50-fold) of amino acids or peptides (Table 2). Alanine, tetra-alanine, and Leu-enkephalin (pentapeptide) did not affect the transport of Pro-[\(^{14}\)C]Ala, while di- and trialanine, Pro-Gly, and Phe-Ala strongly inhibited the uptake. Also the branched-chain amino acid-containing peptides di-Leu and tri-Leu inhibited Pro-[\(^{14}\)C]Ala uptake to a great extent, whereas Phe-Val and Leu-Val had much smaller inhibitory effects. These results show that DtpT LH is a di- and tripeptide transporter just as DtpT LL.

**Sequence alignments.** The sequence alignment of DtpT LH and DtpT LL is shown in Fig. 5. Overall, DtpT LH has 34.0% amino acid identity to DtpT LL. Interestingly, the identity is confined largely to the N-terminal halves of the proteins (47.0% identity for the N-terminal 243 amino acids). Not only the sequences but also the hydropathy profiles of DtpT LH and DtpT LL were found to be significantly different at the extreme C-terminal ends of the proteins. Database searches showed that DtpT LH is a member of the peptide transport (PTR) family (19), which includes various peptide transporters of eukaryotic origin. The PTR consensus motif, \(\text{F-(Y/V/F)-(W/F/h)-X-I-N-(h/M)-G-(S/L)-(L/F)-(h/S)}\) (h indicates a hydrophobic residue) (19), is present in the fifth putative membrane-spanning region of DtpT LH as well as in eukaryotic members of the PTR family. Also in this family the similarity is confined mainly to the N-terminal halves of the proteins.

### TABLE 2. Substrate specificity of DtpT LH

<table>
<thead>
<tr>
<th>Addition (500 (\mu)M)</th>
<th>Relative uptake of Pro-[(^{14})C]Ala (%)</th>
</tr>
</thead>
<tbody>
<tr>
<td>None</td>
<td>100</td>
</tr>
<tr>
<td>Ala</td>
<td>115</td>
</tr>
<tr>
<td>Di-Ala</td>
<td>30</td>
</tr>
<tr>
<td>Tri-Ala</td>
<td>20</td>
</tr>
<tr>
<td>Tetra-Ala</td>
<td>98</td>
</tr>
<tr>
<td>Di-Leu</td>
<td>42</td>
</tr>
<tr>
<td>Tri-Leu</td>
<td>44</td>
</tr>
<tr>
<td>Leu-enkephalin(^a)</td>
<td>96</td>
</tr>
<tr>
<td>Pro-Gly</td>
<td>34</td>
</tr>
<tr>
<td>Phe-Val</td>
<td>86</td>
</tr>
<tr>
<td>Leu-Val</td>
<td>89</td>
</tr>
<tr>
<td>Phe-Val</td>
<td>38</td>
</tr>
</tbody>
</table>

\(^a\) Membrane vesicles were prepared from *E. coli* E1772 expressing DtpT LH. Transport of Pro-[\(^{14}\)C]Ala (10 \(\mu\)M) was measured for 30 s at pH 6.5 in the absence or presence of 500 \(\mu\)M compound. The electron donor system K-ascorbate-PMS was used to generate a proton motive force.

\(^b\) Tyr-Gly-Gly-Phe-Leu.
**DISCUSSION**

In this article, the cloning and characterization of the di- and tripeptide transport gene of *L. helveticus* (*dtpT* and *dtpLH*) are described. The *dtpT* gene is located downstream of the gene encoding the general aminopeptidase N (*pepN*). The *dtpLH* gene can be functionally expressed in *E. coli*, presumably from its own promoter.

Studies of peptide transport in *L. helveticus* suggested the presence of a di-, tri-, and also oligopeptide transport system(s). The cloning of the *dtpT* gene and the subsequent characterization of DtpT have established that this system is specific for transport of di- and tripeptides. Substrate specificity studies suggest that DtpT has a preference for more hydrophilic peptides just like DtpE (4). Dipeptides containing hydrophobic amino acids, such as Phe-Val and Leu-Val, inhibit Pro-[14C]Ala uptake only slightly, although the hydrophobic peptides Leu-Leu and Leu-Leu-Leu are quite effective inhibitors of Pro-Ala transport. Foucaud et al. (4) reported that the substrate specificities of DtpE and the ATP-dependent di- and tripeptide uptake system (DtpP) in *Lactococcus lactis* overlap but that hydrophobic branched-chain amino acid-containing peptides are transported preferentially by DtpP. Similar to what is suggested by this study, peptides like Leu-Leu and Leu-Leu-Leu are transported efficiently by DtpT of *Lactococcus lactis*, whereas other branched-chain-amino-acid-containing peptides are poor substrates.

Recently, Klein et al. (10) reported the cloning of a gene, *dppE*, encoding a protein involved in dipeptide transport in *Lactobacillus delbrueckii* subsp. *lactis*. Although the primary sequence has not been published, this transporter appears to be different from DtpT because DppE has been reported to be 30% identical to DciAE (14), which encodes the binding protein of the dipeptide transport system of *Bacillus subtilis*. DciAE is a member of the ATP-binding cassette (ABC) transporter superfamily (8). Possibly, DppE encodes a DtpP-like di- and tripeptide transporter.

The amino acid transport systems of *L. helveticus* were found to have properties similar to those of *Lactococcus lactis* (15). This study shows also that the di- and tripeptide transport system *dtpT* is very similar to that of *Lactococcus lactis* (6). On the other hand, the proteinase gene of *L. delbrueckii* subsp. *bulgaricus* (*prtB*) is quite different from the one of *Lactococcus lactis* (5). The proteins of *Lactococcus lactis* and *L. delbrueckii* subsp. *bulgaricus* belong to different serine proteinase subfamilies, i.e., subtilisin and cysteine-subtilisin, respectively. However, the peptides released from the β-casein by the two proteinases appear to be very similar (11). To what extent the proteolytic pathways of *Lactococcus lactis* and *L. helveticus* (or other lactobacilli) are similar or different remains to be determined.

**ACKNOWLEDGMENTS**

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**REFERENCES**


