Purification and Reconstitution of the Glutamate Carrier GltT of the Thermophilic Bacterium Bacillus stearothermophilus†

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ABSTRACT: An affinity tag consisting of six adjacent histidine residues followed by an enterokinase cleavage site was genetically engineered at the N-terminus of the glutamate transport protein GltT of the thermophilic bacterium Bacillus stearothermophilus. The fusion protein was expressed in Escherichia coli and shown to transport glutamate. The highest levels of expression were observed in E. coli strain DH5α grown on rich medium. The protein could be purified in a single step by Ni2+-NTA affinity chromatography after solubilization of the cytoplasmic membranes with the detergent Triton X100. Purified GltT was reconstituted in an active state in liposomes prepared from E. coli phospholipids. The protein was reconstituted in detergent-treated preformed liposomes, followed by removal of the detergent with polystyrene beads. Active reconstitution was realized with a wide range of Triton X100 concentrations. Neither the presence of glycerol, phospholipids, nor substrates of the transporter was necessary during the purification and reconstitution procedure to keep the enzyme in an active state. In B. stearothermophilus, GltT translocates glutamate in symport with protons or sodium ions. In membrane vesicles derived from E. coli cells expressing GltT, the Na+ ion dependency seems to be lost [Tolner, B., Ubbink-Kok, T., Poolman, B., & Konings, W. N. (1995) Mol. Microbiol. 18, 123–133], suggesting a role for the lipid environment in the cation specificity. In agreement with the last observation, glutamate transport catalyzed by purified GltT reconstituted in E. coli phospholipid is driven by an electrochemical gradient of H+ but not of Na+. The gltT gene was expressed in a strain of E. coli deficient in glutamate transport. Studies with membrane vesicles derived from the recombinant strain revealed a surprising result. Expression of GltT in E. coli resulted in complete loss of the sodium ion dependency; glutamate transport was driven only by the proton motive force. Similar studies with membrane vesicles from B. stearothermophilus showed an increase in uptake activity in the presence of a sodium ion motive force, a feature that was most apparent at elevated temperatures (Tolner et al., 1995). The data suggest that, in addition to the primary sequence, the cation specificity of a carrier may depend also on conformation. Subtle conformational differences of GltT induced by the lipid environment and/or temperature may select for proton or sodium ion as the symported cation. Implicitly, it would mean that the difference between a proton and a sodium ion binding site on the carrier is extremely small.

Bacillus stearothermophilus is a thermophilic bacterium that grows optimally at 63 °C. Proteins of thermophiles are likely to be more stable than those of their mesophilic counterparts. This may be of particular importance in the study of membrane proteins when they are taken out of their natural phospholipid environment. Glutamate uptake in B. stearothermophilus is mediated via a secondary transporter termed GltT. Translocation of glutamate is coupled to translocation of two cations, a proton and a sodium ion, and, therefore, is driven by the proton and sodium ion motive forces (Heyne et al., 1991). The gene coding for the transporter GltT has been cloned and sequenced (Tolner et al., 1992a), and the deduced amino acid sequence showed significant homology with the members of a large family of carboxylic acid transporters in which carriers from related organisms like the glutamate transporter GltP from Escherichia coli are found (Tolner et al., 1992b) but also carriers from eukaryotic origin like the glutamate transporter from mammalian brain [e.g. Pines et al. (1992)]. The transporters in this family differ both in substrate specificity and cation specificity. Additional studies with membrane vesicles from B. stearothermophilus showed an increase in uptake activity in the presence of a sodium ion motive force, a feature that was most apparent at elevated temperatures (Tolner et al., 1995). The data suggest that, in addition to the primary sequence, the cation specificity of a carrier may depend also on conformation. Subtle conformational differences of GltT induced by the lipid environment and/or temperature may select for proton or sodium ion as the symported cation. Implicitly, it would mean that the difference between a proton and a sodium ion binding site on the carrier is extremely small.

The importance of these findings requires that they are confirmed with the purified protein reconstituted in phospholipids. The isolated protein can be reconstituted in phospholipids from different origins and studied with respect to their cation selectivity at different temperatures. In addition, purification of the protein is essential to determine conformational changes by spectroscopic techniques. Here, we report on the first step in these studies, the purification and functional reconstitution of GltT in E. coli phospholipids. After optimization of the expression of the gltT gene in E. coli, the protein is purified in a single step by His tag affinity chromatography (Hochuli et al., 1987) and reconstituted by the detergent titration technique (Rigaud & Pitard, 1995). Specific precautions that have been reported for the suc-
cessful purification and reconstitution of several transporters from mesophiles were not necessary in the case of GltT (see Discussion). This may reflect the higher thermostability of this membrane protein from a thermophilic organism.

MATERIALS AND METHODS

Materials

Ni2+NTA resin was obtained from QIAGEN and L-[14C]-glutamate from Amersham, U.K.; synthetic oligonucleotides were obtained from Eurosequence, Groningen, The Netherlands. All other materials were obtained from commercial sources.

Bacterial Strains and Growth Conditions

The following E. coli strains were used: DH5α, JM101, and ECOMUT1. The latter strain lacks the genes coding for the glutamate transporters GltP and GltS (Tolner et al., 1995). Unless stated otherwise, the cells were grown at 37 °C in LB medium or minimal medium supplemented with 20 mM glycerol and 0.2% casamino acids. The antibiotics ampicillin and kanamycin were included when appropriate at concentrations of 100 and 50 µM, respectively.

Construction of the Expression Vector pGltThis

Construction of the Host Vector pKShis. All genetic engineering was done using the standard procedures described in Sambrook et al. (1989). A NcoI restriction site (CCATGG) was introduced around the start codon of the lacZ gene on phagemid pBlueScript II KS (Stratagene, La Jolla, CA) by site-directed mutagenesis using the Kunkel method, yielding vector pKSncol. The base sequence of the mutagenic primer and the other oligonucleotides used in this study are listed in Table 1. Transformants were screened by restriction analysis of the plasmids. Subsequently, the unique ClaI site in the multiple-cloning site of pKSncol was opened, and the ends were made blunt by filling in the overhangs with Klenow polymerase. Ligation yields vector pKSncolΔClaI. Deletion of the ClaI site results in a frame shift, making the downstream lacZ sequences out of frame and resulting in white colonies on XGal plates. The frame shift was restored by digesting pKSncolΔClaI with NcoI and BamHI, which removes the destroyed ClaI region, and inserting a DNA linker coding for a His tag of the appropriate length. Successful insertion of the linker was concluded from blue coloring on XGal plates. The 5′ end of the linker has an overhang compatible with a NcoI cleavage site but destroys the site after ligation, while the 3′ end of the linker is compatible with a BamHI cleavage site. The linker codes for a sequence of six histidines followed by an enterokinase proteolytic cleavage site. The coding regions are in frame with the lacZ gene. In front of the BamHI site, the linker contains a NcoI site (CCATGG) with the ATG bases in the same reading frame as the lacZ start codon. The linker was made by mixing 5 µg of two complementary synthetic oligonucleotides for 5 min at 37 °C (Table 1). The resulting vector is termed pKShis.

Cloning of gltT into pKShis. Plasmid pGBT102 containing the gltT gene has been described by Tolner et al. (1992a) and was used to amplify the gene by the polymerase chain reaction (PCR) technique. Two primers were used to amplify the 1.29 kb DNA fragment coding for GltT and to insert an NcoI cleavage site at the start codon of the gene and an XbaI site 25 nucleotides downstream of the stop codon (Table 1). The amplification results in a mutation in the second codon of gltT (Table 2). The purified PCR fragment was restricted with the NcoI and XbaI restriction enzymes and ligated into pKShis and pKSncol digested with the same enzymes. The resultant vectors are termed pGltThis and pGltTncol, respectively. Positive transformants were selected by blue/white screening and restriction analysis of the plasmids. The inserts were sequenced using an Amersham automated sequencer.

Measurement of Expression Levels

Cells from 10 mL cultures were harvested in the late log phase, washed once with 50 mM potassium phosphate (pH 8), and, subsequently, resuspended in the same buffer containing 600 mM NaCl. The suspension was supplemented with 1% Triton X100 and left at room temperature for 30 min. Undissolved material was removed by ultracentrifugation for 10 min at 100000g. The supernatant was mixed with 100 µL of Ni2+NTA resin and incubated for 30 min under continuous shaking. The resin was recovered by a short spin and washed once with 1 mL of buffer and eluted with 0.2 mL of buffer containing 250 mM imidazole. The eluate was loaded onto a 10% sodium dodecyl sulfate (SDS)–polyacrylamide gel that was stained with silver.

Purification of GltThis

Cells from a 6 L culture in LB medium harvested at a OD600 of about 0.7 were washed once with 250 mL of 50 mM potassium phosphate (pH 8) and resuspended in 40 mL of the same buffer containing 1 mM MgSO4 and a trace amount of deoxyribonuclease. Cells were broken by three passages through a French Press cell operated at 10 000 psi.

Table 1: DNA Sequences of the Oligonucleotides Used in This Study

<table>
<thead>
<tr>
<th>purpose</th>
<th>DNA sequence</th>
</tr>
</thead>
<tbody>
<tr>
<td>construction pKSncol</td>
<td>5′-AACTATGGCCATGGCTTGTTC-3′*</td>
</tr>
<tr>
<td>His tag linker (sense)</td>
<td>5′-CATGCTACCCATACCATACGATGACATGACAAAGCCATGGGG-3′*</td>
</tr>
<tr>
<td>His tag linker (antisense)</td>
<td>5′-GATCCCCTAGCTTTGTCATCGTCTAGTGATGTAGGTATG-3′*</td>
</tr>
<tr>
<td>PCR gltT (forward)</td>
<td>5′-GAAAGGGGCGAATCCATGGGGAAATTGGATTA-3′%</td>
</tr>
<tr>
<td>PCR gltT (backward)</td>
<td>5′-AAGGTCCTTTCTGAAAGGACAGCT-3′*</td>
</tr>
</tbody>
</table>

*Indicated in bold are the base (†) changes, the six histidine codons (§) the NcoI (*), and XbaI (†) restriction sites.

Table 2: Primary Sequences of the N-Terminal Part of the GltT Constructs

<table>
<thead>
<tr>
<th>protein</th>
<th>amino acid sequence*</th>
</tr>
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<tr>
<td>GltT</td>
<td>MRKIG...</td>
</tr>
<tr>
<td>GltTnco</td>
<td>MGKIG...</td>
</tr>
<tr>
<td>pGltThis</td>
<td>MHHHHHHDDDDDKAMGKL...</td>
</tr>
</tbody>
</table>

*The original GltT residues are indicated in bold, and the enterokinase site is underlined.
at 4 °C. Unbroken cells and debris were removed by centrifugation at 10000g for 10 min at 4 °C, and the membranes were collected from the supernatant by centrifugation at 100000g for 90 min at 4 °C. Membranes were washed once with 50 mM of potassium phosphate (pH 8) and 1 M NaCl and resuspended in 50 mM potassium phosphate (pH 8) at a protein concentration of 10 mg/mL. (Lowry et al., 1952). The membrane suspension was stored in liquid nitrogen. Membranes (4 mg/mL) were solubilized in 50 mM potassium phosphate (pH 8), 400 mM NaCl, 20% glycerol, and 0.1% Triton X100. The supernatant was mixed with Ni²⁺-saturated air in samples of 100 °X100, and 10 mM imidazole and incubated for 1 h at 4 °C, for 2 h, and the second and third were done at 4 °C for 20 min, after which the detergent was removed by three successive extractions with polystyrene beads (BioBeads, 80 µL). Liposomes treated with different amounts of the detergent were loaded with 50 mM potassium phosphate (pH 8), 300 mM NaCl, 10% glycerol, 0.1% Triton X100, and 10 mM imidazole and incubated for 1 h at 4 °C under continuous shaking and, subsequently, poured into a column. The column was washed with 1 mL of equilibration buffer containing 40 mM imidazole. The protein was eluted with 0.5 mL of the same buffer containing 150 mM imidazole and immediately used for reconstitution.

Reconstitution of GltThis in Proteoliposomes

Reconstitution was performed essentially as described by Knol et al. (1996). A 3:1 (w:w) mixture of E. coli total lipid extract and egg yolk phosphatidylcholine was resuspended in 50 mM potassium phosphate (pH 7) at a final concentration of 20 mg of lipid per milliliter. The suspension was frozen in liquid nitrogen, thawed slowly, and extruded through 400 nm polycarbonate membranes (Avestin). The liposomes thus obtained were diluted 6-fold in the same buffer and stored with increasing amounts of Triton X100. The solubilization of the liposomes was followed by measuring the optical density at 540 nm (Rigaud & Pitard, 1995). Liposomes treated with different amounts of the detergent were mixed with purified GltT at a ratio of 10 µg of protein per 5 mg of lipid. The mixture was left at room temperature for 30 min, after which the detergent was removed by three successive extractions with polystyrene beads (BioBeads, 80 mg/mL). The first extraction was done at room temperature for 2 h, and the second and third were done at 4 °C for 2 and 16 h, respectively. The beads were removed by filtration over glass wool, and the proteoliposomes were recovered by centrifugation at 250000g for 20 min. The proteoliposomes were resuspended in the appropriate buffer and stored in liquid nitrogen.

Transport Assays

Right-Side-Out (RSO) Membrane Vesicles. Membrane vesicles of E. coli strains DH5α and ECOMUT1 were prepared by the osmotic lysis procedure as described by Kaback (1971). The membranes were resuspended in 50 mM potassium phosphate (pH 6) at a protein concentration of 15 mg/mL and stored in aliquots in liquid nitrogen. The membrane vesicles were energized by the potassium ascorbate/phenazine methosulfate (PMS) electron donor system. The membranes were diluted to a concentration of 0.6 mg/mL in 50 mM potassium phosphate (pH 6), 2 mM MgSO₄, and 10 mM potassium ascorbate. The experiments were performed in 100 µL at 30 °C under a constant flow of water-saturated air in samples of 100 µL. PMS was added at a concentration of 100 µM, and the proton motive force was allowed to develop for 1 min, after which L-[^14]C]glutamate was added to a final concentration of 1.9 µM. The uptake was stopped by adding a 20-fold volume of ice cold 0.1 M LiCl solution, followed by immediate filtration over cellulose nitrate filters (0.45 µm pore size). The filters were washed once with 2 mL of 0.1 M LiCl and assayed for radioactivity.

Proteoliposomes. For counterflow experiments, proteoliposomes were loaded with 50 mM potassium phosphate (pH 7), 5 mM potassium glutamate, and 2 mM MgSO₄ by freezing, thawing, and extrusion through polycarbonate filters (400 nm pore size). The proteoliposomes were collected by centrifugation and resuspended in the same buffer at a concentration of approximately 100 mg of lipid per milliliter. Counterflow was initiated by diluting the proteoliposomes 75-fold in the same buffer without unlabeled glutamate but with 1.3 µM L-[^14]C]glutamate. The uptake was stopped as described above.

For assays of L-glutamate uptake driven by artificial gradients, the proteoliposomes were washed twice with 20 mM morpholineethanesulfonic acid (Mes) (pH 6) and 100 mM potassium acetate and concentrated as described above. Proton motive force-driven uptake was initiated by diluting the proteoliposomes 75-fold in 120 mM Mes, 100 mM methylglucamine, 0.7 µM valinomycin, and 1.3 µM L-[^14]C]glutamate prewarmed at 30 °C. Both a proton motive force and a sodium ion motive force were created by dilution into the same buffer containing 100 mM NaOH instead of methylglucamine. Control experiments were performed by diluting the proteoliposomes into the buffer with which they were loaded.

RESULTS

Construction of the Expression Vector pGltThis. A derivative of pBlueScript pKS II was constructed that facilitates the construction of genes fused downstream of a sequence coding for six histidines (His tag) and an enterokinase cleavage site. The vector, pKShis, was constructed in two steps as described in detail in Materials and Methods. In pKShis, downstream of the lac promoter are the ribosomal binding site and the start codon of the lacZ gene followed by in frame sequences coding for the His tag and the enterokinase cleavage site and a NcoI restriction site (CCATGG) with the ATG bases in frame with the lacZ binding site and the start codon of the lacZ gene followed by in frame sequences coding for the His tag and the enterokinase cleavage site (CCATGG) with the ATG bases in frame with the lacZ start codon. Downstream of the NcoI site are the BamHI to SacI restriction sites of the original pBlueScript multiple-cloning site. The downstream lacZα sequences are in frame with the lacZ start codon and allow blue/white screening of inserts on XGal indicator plates.

The 1.3 kb gene coding for the glutamate carrier of B. steaetherophilus, GltT, was amplified by the PCR technique from plasmid pGBT102 (Tolner et al., 1992a) using a forward primer that introduces an XbaI site, a backward primer that introduces an NcoI site, and the start codon and a backward primer that introduces an NcoI site. In pKShis, downstream of the lac promoter, pGltThis codes for GltT with a N-terminal His tag and an enterokinase cleavage site. In addition, the PCR product was cloned into vector pKSancoI which results in the same construct except that the sequences coding for the His tag and the enterokinase site are missing (construct
pGltTncoI. The N-terminal amino acid sequences of the different constructs are indicated in Table 2. The inserts in the two plasmids were sequenced and found to be the same as the published base sequence of the gltT gene (Tolner et al., 1992a) except for the changes indicated in Table 2.

Activity of GltThis. Plasmid pGltThis and pGltTncoI, coding for the GltT transporter with and without the His tag, respectively, were transformed to E. coli DH5α. Membrane vesicles of the recombinant strains were prepared and assayed for glutamate uptake activity. Since E. coli for glutamate uptake activity, vesicles of the recombinant strains were prepared and assayed for glutamate uptake as described in Materials and Methods.

Figure 1: Glutamate uptake catalyzed by GltThis. Right-side-out membrane vesicles were prepared from E. coli DH5α cells harboring plasmids pGltThis (■) and pKShis (□) and assayed for glutamate uptake as described in Materials and Methods.

Optimization of Expression. The level of expression of GltThis in E. coli was measured after a rapid partial purification procedure over a Ni2+-NTA affinity resin, followed by SDS–polyacrylamide gel electrophoresis and visualizing the proteins by silver staining (see Materials and Methods). E. coli strains DH5α, JM101, and ECOMUT1 were tested for their ability to overexpress GltThis. Expression of GltThis in DH5α cells results in an additional protein band at an apparent molecular mass of 33 kDa that is not observed in the control cells (Figure 2A). An apparent molecular mass of about 33 kDa is typical for an integral membrane protein of about 45 kDa and is in agreement with a similar molecular mass observed after [35S]methionine labeling (Tolner et al., 1992a). A second but much less intense band is visible at about twice the apparent molecular mass and corresponds most likely to the dimeric form of GltT. These results show that the His-tagged GltT molecule binds to the Ni2+-NTA resin. The levels of expression are remarkably different in the different strains. The highest expression is observed in DH5α which is in line with the uptake activity observed in membrane vesicles (Figure 1). Expression in strains JM101 and ECOMUT1 is significantly lower. Induction with IPTG results in higher levels of expression in strain JM101 which overproduces the repressor LacI. In ECOMUT1 and DH5α, the level of expression is not significantly affected in the presence of IPTG. In these strains, the number of repressors relative to the high copy number of the plasmid is likely to be too low to cause a significant inhibition of transcription. The effect of the medium composition on the expression of GltThis in DH5α is analyzed in Figure 2B. The highest expression is observed in the rich LB medium. Addition of glucose represses expression significantly as expected, and hardly any expres-
Essentially all the GltT protein bound to the column and eluted with 150 mM imidazole, indicating that the His tag was not removed by the proteolytic enzyme. Apparently, the enterokinase cleavage site is not accessible to enterokinase in the GltT fusion protein.

Reconstitution in Proteoliposomes. Glutamate counterflow activity was measured in proteoliposomes prepared by mixing purified GltT with liposomes that were saturated with detergent (●), partially solubilized (▲), and completely solubilized (▼). The three states of solubilization are indicated by the arrows from left to right in the inset. (Inset) Light scattering was measured in a suspension of proteoliposomes containing 20 mg of lipid in a total volume of 2.4 mL in the presence of different amounts of Triton X100.

### Table 3: Effect of Additions during Solubilization, Purification, and Reconstitution on the Yield and Activity of GltT

<table>
<thead>
<tr>
<th>additiona</th>
<th>yield (µg/mg of membrane protein)</th>
<th>initial uptake rateb (pmol µg⁻¹ min⁻¹)</th>
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</thead>
<tbody>
<tr>
<td>none</td>
<td>8.5</td>
<td>55.9</td>
</tr>
<tr>
<td>glycerol</td>
<td>6.5</td>
<td>109.7</td>
</tr>
<tr>
<td>glutamate</td>
<td>6.7</td>
<td>92.6</td>
</tr>
<tr>
<td>lipids</td>
<td>7.0</td>
<td>71.8</td>
</tr>
<tr>
<td>all</td>
<td>7.2</td>
<td>84.5</td>
</tr>
</tbody>
</table>

aConcentrations during solubilization/purification were as follows: glycerol, 10%; lipids, 0.2 mg/mL; and glutamate, 1 mM. Concentrations during reconstitution were as follows: glycerol, 2%; and glutamate, 0.2 mM. bThe uptake of glutamate was driven by an artificially imposed proton motive and ion motive force as described in the legend to Figure 5.

A SDS–PAGE of purified GltT was loaded with molecular mass markers (lane 1), 50 µg of French Press-derived membrane vesicles derived from DH5α/ pGltT cells (lane 2, and 3 µg of purified GltT (lane 3). The gel was stained with Coomassie Brilliant Blue.

Figure 3: SDS–PAGE of purified GltT. A 12% SDS–PAGE gel was loaded with molecular mass markers (lane 1), 50 µg of French Press-derived membrane vesicles derived from DH5α/ pGltT cells (lane 2, and 3 µg of purified GltT (lane 3). The gel was stained with Coomassie Brilliant Blue.

Figure 4: Reconstitution of GltT in proteoliposomes. Glutamate counterflow activity was measured in proteoliposomes prepared by mixing purified GltT with liposomes that were saturated with detergent (●), partially solubilized (▲), and completely solubilized (▼). The three states of solubilization are indicated by the arrows from left to right in the inset. (Inset) Light scattering was measured in a suspension of proteoliposomes containing 20 mg of lipid in a total volume of 2.4 mL in the presence of different amounts of Triton X100.
active, and the activity is, considering the complexity of the procedure, most likely not significantly different after the different reconstitution procedures.

Purification and reconstitution of other secondary transporters have been reported to require special precautions to preserve the activity of the protein (see Discussion). These include the presence of glycerol, phospholipids, and substrates or combinations thereof during some or all steps of the solubilization, purification, and reconstitution procedure. The procedure for GltT This purification and reconstitution was repeated in the presence of the additions indicated in Table 3, and the resulting proteoliposomes were assayed for activity. The additions did not affect the purity of the preparation (not shown), and the differences in the yields were within experimental error. The specific initial uptake rates catalyzed by the reconstituted transporters differed maximally by a factor of 2 with no additions and the presence of glycerol giving the lowest and highest activity, respectively. On the other hand, the presence of all additions resulted in an average specific activity, suggesting that the observed differences are not significant.

Cation Specificity. Proteoliposomes of E. coli phospholipids containing purified GltT were prepared in the absence of Na⁺ ions. The proteoliposomes were loaded with 100 mM potassium acetate and diluted to 100 mM methylglucamine in the presence of valinomycin. Passive diffusion of protonated acetic acid and valinomycin-mediated potassium efflux down their concentration gradients result in the formation of a pH gradient, inside alkaline, and a membrane potential, inside negative. The resulting proton motive force drives the uptake of glutamate into the proteoliposomes (Figure 5, O), showing that GltT does not require Na⁺ to translocate glutamate across the membrane. Dilution of the same proteoliposomes into 100 mM NaCl instead of methylglucamine results, in addition to the generated proton motive force, in an inward-directed Na⁺ ion gradient. The additional sodium ion motive force has no effect on the initial rate of glutamate uptake or on the level of accumulation (Figure 5, □). This data indicate that purified GltT reconstituted in E. coli phospholipid does not translocate Na⁺ ions which is consistent with the cation specificity of GltT in membrane vesicles derived from E. coli cells expressing GltT (Tolner et al., 1995).

DISCUSSION

The purification of membrane proteins requires that the proteins are taken out of their natural environment. At least for a while, the phospholipid bilayer is replaced with the unnatural environment of the detergent micelle which may destabilize the protein and result in unfolding. In many purification and reconstitution procedures of transport proteins, special precautions have been described that were essential to keep the protein in the active state [see Poolman and Konings (1993)]. For example, the lactose transporter of E. coli, LacY, could only be purified in a functional state when additional phospholipids were added in the detergent-solubilized state (Newman et al., 1981). A high concentration of the osmolyte glycerol was essential in the purification of, for instance, the oxalate transporter of Oxalobacter formigenes (Ruan et al., 1992). The presence of substrates of the transporter usually has a stabilizing effect as was claimed for the same carrier and also for the citrate carrier of Klebsiella pneumoniae (Pos et al., 1994). In this paper, the purification of the glutamate transporter of the thermophilic bacterium B. stearothermophilus is described. Proteins from thermophiles are likely to be more stable at ambient temperatures than proteins from mesophiles, a property that may prove to be of special importance in crystallization studies of membrane proteins. The properties of the GltT protein during the purification and reconstitution procedure support the claim of higher stability in that none of the above precautions seemed to be necessary to keep the protein in the functional state. In this respect, it may be of interest that the alanine carrier of the thermophilic bacterium PS3 also could be purified and reconstituted in the absence of any special additions (Hirata et al., 1984). It is not clear whether the presumed higher stability also relates to the ease by which the protein reconstitutes into liposomes. The stage of solubilization of the preformed liposomes by detergent is much less critical than has been observed for other transport proteins (Rigaud & Pitard, 1995).

Studies in membrane vesicles of B. stearothermophilus have demonstrated that GltT catalyzes proton motive force-driven glutamate uptake in the absence of Na⁺ ions. In the presence of a Na⁺ ion gradient, the uptake activity was significantly higher, especially at elevated temperatures (Tolner et al., 1995). Apparently, GltT translocates glutamate in symport with a proton or a Na⁺ ion which places GltT in the same category as, for instance, the melibiose carrier MelB of E. coli (Bassilana et al., 1985). In contrast, a glutamate carrier of E. coli, GltS, a citrate carrier of K. pneumoniae, CitS, and all other amino acid transporters that have been studied in B. stearothermophilus translocate their substrates obligatorily coupled to Na⁺ ions (Heyne et al., 1991; Tolner et al., 1995; Lolkema et al., 1994a). The differences between these two categories must reflect differences in the structure of the cation binding sites of the proteins. The cation binding pockets of the GltS and CitS type of carriers appear to be more stringent than those of the GltT and MelB types (Lolkema et al., 1994b). The structural difference between binding pockets that accept H⁺ or Na⁺ may be very small [see for instance Zhang and Fillingame (1995)], and in the case of a pocket that accepts both H⁺ and Na⁺, a small

FIGURE 5: Na⁺ dependency of reconstituted GltT in proteoliposomes. Glutamate uptake was driven by an electrochemical proton gradient in the absence of Na⁺ ions (O) and by both a proton and sodium ion electrochemical gradient (D).
change in conformation may result in a significant shift in the relative affinities for the two cations. This may be the explanation for the apparent loss of Na\(^+\) dependency after expression of GltT in *E. coli* when the different lipid environment would cause a change in conformation of the cation binding pocket. The results presented here with the purified protein reconstituted in liposomes prepared from *E. coli* lipid are consistent with the observation made in membrane vesicles derived from *E. coli* cells expressing GltT, i.e. loss of Na\(^+\) ion dependency. At the present, experiments are in progress to reconstitute purified GltT in liposomes prepared from lipids isolated from *B. stearothermophilus*.

REFERENCES


BI953005V