Functional reconstitution and osmoregulatory properties of the ProU ABC transporter from Escherichia coli

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Abstract
The ATP-binding cassette (ABC) transporter ProU from Escherichia coli translocates a wide range of compatible solutes and contributes to the regulation of cell volume, which is particularly important when the osmolality of the environment fluctuates. We have purified the components of ProU, i.e., the substrate-binding protein ProX, the nucleotide-binding protein ProV and the transmembrane protein ProW, and reconstituted the full transporter complex in liposomes. We engineered a lipid anchor to ProX for surface tethering of this protein to ProVW-containing proteoliposomes. We show that glycine betaine binds to ProX with high-affinity and is transported via ProXVW in an ATP-dependent manner. The activity ProU is salt and anionic lipid-dependent and mimics the ionic strength-gating of transport of the homologous OpuA system.

Keywords: Osmoregulation, ABC transporter, membrane reconstitution, lipid-anchoring of binding protein

Introduction
Osmotic stress is an important environmental parameter that influences the growth and adaptation of (micro)organisms in a given habitat. Microbial cells employ different strategies to overcome the 'osmotic challenges' in their environment. For instance, under hyperosmotic conditions, bacteria can accumulate osmoprotective compounds or compatible solutes, such as choline, proline, glycine betaine, carnitine and ectoine (Perroud and Rudulier 1985, Grothe et al. 1986, Wood et al. 2001). In addition to these zwitterionic compounds, organisms may transiently accumulate potassium ions together with glutamate or other anionic species as is best documented for Escherichia coli (Booth and Higgins 1990, Oghara et al. 1995). The accumulation of potassium ions is fast but also disturbs ionic homeostasis of the cell, and over time the potassium and counter ion(s) are replaced by neutral or zwitterionic solutes such as trehalose, proline, glycine betaine and others (Sutherland et al. 1986, Lucht and Bremer 1994). The accumulation of compatible solutes can be achieved via de novo biosynthesis or rapid uptake of solutes from the medium; the latter mechanism can be more effective in terms of costs of metabolic energy.

Osmoregulatory transport systems have been extensively studied in both Gram-positive and Gram-negative bacteria, e.g., OpuA from Lactococcus lactis and Bacillus subtilis, BetP from Corynebacterium glutamicum, OpuC from Pseudomonas syringae, and ProP and ProU from E. coli (Cairney et al. 1985, May et al. 1986, Kempf and Bremer 1995, Kempf et al. 1997, Horn et al. 2003, Mahmood et al. 2006, 2009, Karasawa et al. 2011, Perez et al. 2011, Culham et al. 2012). Other biochemically less well-studied systems include: Ota from Methanosarcina mazei, and ProP and ProU from Yersinia enterocolitica (Schmidt et al. 2007, Annamalai and Venkitanarayanan 2009). The OpuA, OpuC, Ota and ProU systems are all ATP-binding cassette transporters that have a cystathionine-β-synthase (CBS) module fused to the C-terminus of the nucleotide-binding domain. This CBS module has been shown to be critical for the osmoregulation of the OpuA transporter from L. lactis and OpuC from P. syringae (Biemans-Oldenhinkel et al. 2006, Chen and Beattie 2007, Mahmood et al. 2009). A particularly interesting system is ProU from E. coli as the osmotic regulation of
its expression is known in great detail (Perroutd and Rudulier 1985, Higgins 1992, Lucht and Bremer 1994). So far, little is known of the regulation of the activity of the protein itself but activation by osmotic stress has been observed (Faatz et al. 1988). The proU operon includes three open reading frames (ORFs) proV, proW and proX (Gowrishankar et al. 2009, Mimmack et al. 1989).

The proV gene encodes the NBD with the C-terminal tandem CBS domains. proW encodes the transmembrane domain (TMD) and has an N-terminal ~100 amino acid extension of unknown function (Haardt and Bremer 1996). ProX encodes the substrate-binding protein (SBD), which is localized in the periplasm. ProX has been purified to homogeneity and shown to bind glycine betaine with high affinity (Kd of ~1 μM); proline betaine is bound with a Kd of ~5 μM (May et al. 1986, Barron et al. 1987, Haardt et al. 1995).

Here, we report on the in vitro reconstitution and biochemical characterization of the osmoregulatory ABC transporter ProU from E. coli. We engineered ProX with an N-terminal lipid anchor sequence for efficient tethering of the substrate-binding protein to the surface of proteoliposomes, in which ProVW was reconstituted first (Figure 1). We show that the ProU system is activated by osmotic stress and that, similar to OpuA, anionic lipids play an important role in the activity and regulation of transport.

Materials and methods

Bacterial strains and growth conditions

For expression and purification of ProX, L. lactis Opu401 was used as host and transformed with pAMP31proX. Opu401 is a derivative of L. lactis NZ9000 with the chromosomal oppA genes deleted (Biemans-Oldehinkel et al. 2006). L. lactis was cultivated semi-aerobically in M17 broth (Difco Laboratories, East Molesey, UK) at 30°C and temperature-controlled bioreactor. Cells were harvested, washed and resuspended in 50 mM potassium phosphate (KPi) pH 7.0 and stored at ~8°C after flash-freezing of 40 ml aliquots of cells in liquid nitrogen.

For expression and purification of ProVW, E. coli strain MC1061 (Casadaban and Cohen 1980) was used as host and transformed with pBADcLICproVW. The cells were cultivated under vigorous aeration in Luria broth supplemented with 100 μg/ml ampicillin at 37°C and 200 rpm. At A600 of 0.5–0.6 the temperature was decreased to 25°C, and, after equilibration for 15 min, membrane protein expression was induced by the addition of L-arabinose in growth medium at a final concentration of 0.001% (w/v). Cultivation was continued for 3 h and cells were harvested, washed and resuspended in 50 mM KPi pH 7.0.

Construction of pBADcLICproVW and pNZcLICproVW

The proVW genes were amplified using genomic DNA of E. coli K12 as template and the following oligonucleotides:

ProV fwd nLic: 5′ ATGGGTGAGTTTATATT
TTCAAGGTATGGCAAATGATTGAAAT
ProV rev nLic: 5′ TGGGAAGTGGGATTTT
TCA TTACTTAATGAATGGCGGGGTCA
ProV rev cLic: 5′ ATGGGTTGCTGAGTTGGC
ATGCAATTAAATTGAAAT
ProW rev nLic: 5′ TTGGAAGTATTAAATTTTC
CTTAATGATGGCGGGGT

Both genes were ligated in the pBADnLIC and pBAdLIC vector and modified at the 3′ end to specify a 10-histidine tag, using a ligation-independent cloning method as described in Geertsma and Poolman (2007).

Construction of pAMP31-proX and pAMP31-GGSGAGGGS-proX

The wild-type ProX is produced with a signal sequence for translocation of the protein into the E. coli periplasm. To provide ProX with a lipid anchor, the proX gene was cloned in pAMP31, downstream of the oppA signal sequence and upstream of a sequence specifying a C-terminal six-histidine tag (Picón et al. 2000). When expressed in L. lactis, the OppA signal sequence is cleaved at position 23 and the N-terminal Cys residue is lipid modified (Hutchings et al. 2009). For this purpose, a unique XhoI site was introduced at position 88 of the oppA gene in pAMP31OppA, which allowed replacing the oppA gene of pAMP31 for proX. The proX gene was amplified by PCR, using genomic DNA of E. coli K12 as template and the oligonucleotides ProX fwd (with XhoI site) and ProX rev (with BamHI) (Table I). The PCR product was digested with XhoI and BamHI and ligated into the vector pAMP31 (cut with XhoI and BamHI). The resulting plasmid was named pAMP31-proX and transformed into L. lactis Opu401 by electroporation.

To increase the space between the lipid anchor and the ProX protein, we introduced a flexible linker (sequence GGSGAGGGS) by inserting the corresponding synthetic DNA fragment into a unique BglII site that was created just after the proX signal sequence. Thus, pAMP31-proX-BglII was digested
Table I. Primers used for the construction pAMP31-GGGSAGGGS-proX. Restriction sites are indicated in bold and underlined. Nucleotides different from those in wild-type ProX are indicated in italics.

<table>
<thead>
<tr>
<th>Primer</th>
<th>Sequence</th>
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<tbody>
<tr>
<td>ProX fwd</td>
<td>ATGCCCTCGAGTATGGCATAGCTACTTTTTGCG</td>
</tr>
<tr>
<td>ProX rev</td>
<td>GCATGGATCCCTCTGCGTGCAGCTGGCCTGC</td>
</tr>
<tr>
<td>ProX BglII fwd</td>
<td>CATGGCGGAGGCAGCGCCTGTTAATCCAG</td>
</tr>
<tr>
<td>ProX BglII rev</td>
<td>CATGCGGAGACAAACGTAGTGGGATCAGCA</td>
</tr>
<tr>
<td>ProX(GGGSAGGGS)fwd</td>
<td>TCGAGTGGTGGAGGTTCAGCTGGAGGTGGATCAGCA</td>
</tr>
<tr>
<td>ProX(GGGSAGGGS)rev</td>
<td>GCATGGATCCCTCTGCGTGCAGCTGGCCTGC</td>
</tr>
</tbody>
</table>

with XhoI and BglII, and the synthetic DNA with complementary ends was introduced. The synthetic DNA was prepared from complementary oligonucleotides ProX (GGGSAGGGS) fwd and rev; Table I; the oligonucleotides were annealed by slowly decreasing the temperature from 94–40°C (over 3 min). The resulting plasmid, pAMP31-GGGSAGGGS-proX, was transformed into L. lactis Opu401 by electroporation. Initial experiments showed that the GGGSAGGGS linker is required for substrate transfer from ProX to ProVW, and in the experiments described below pAMP31-GGGSAGGGS-proX was used to produce lipid-anchored ProX (Figure 1).

Co-transformation with pNZcLICproVW and pAMP31-GGGSAGGGS-proX

L. lactis Opu401 was transformed with pNZcLIC-proVW and pAMP31-GGGSAGGGS-proX for the simultaneous expression of ProVW and ProX. The mechanism of replication (rolling circle versus theta replication) and antibiotic resistance markers (chloramphenicol versus erythromycin) of these plasmids differ, which makes them suitable for co-expression studies. 100 ng of each of the plasmid was plated for electroporation, after which the cells were plated on GM17 or GCDM supplemented with 2.5 μg/ml of chloramphenicol and 25 μg/ml erythromycin plus 25 μg/ml chloroamphenicol plus 25 μg/ml erythromycin was present during the assay. At given time intervals, 80 μl samples were withdrawn and diluted with 2 ml ice-cold assay buffer of equal osmolarity and immediately filtered through 0.45 μm cellulose nitrate filters under high vacuum. After washing with 50 mM HEPES-methylglucamine pH 7.3 with the appropriate sucrose concentration, the filters were dried and dissolved in 2 ml scintillation liquid and radioactivity was determined in a scintillation counter.

Membrane vesicle preparation

Membrane vesicles were prepared by lysing the cells in a cell disruption system (high pressure Constant Systems cell disrupters, UK) at a pressure of 39,000 psi for L. lactis and 25,000 psi for E. coli at 4°C in 50 mM potassium phosphate (KPi) with 1 mM MgSO4, 1 mM PMSF, 100 μg/ml DNase plus 100 μg/ml RNase. Subsequently, differential (ultra) centrifugation steps were carried out to separate membrane vesicles from cell debris and cytosolic fractions.

In vivo uptake experiments

For in vivo glycine betaine uptake, L. lactis Opu401, containing pNZcLICproVW and pAMP31-GGGSAGGGS-proX, was grown in GM17 or GCDM supplemented with 2.5 μg/ml chloramphenicol plus 2.5 μg/ml erythromycin. At OD600~0.5, nisin A was added at a final concentration of 0.01% (v/v) to induce the expression of proVW. The expression of proX was driven from the constitutive lactococcal promoter P32 (van der Vossen et al. 1987). After 2 h of nisin A induction, the cells were washed twice and resuspended to OD600 of ~12.5 (which corresponds to ~2.5 mg/ml protein) in 50 mM HEPES-methylglucamine pH 7.3. For the uptake assays, the cells were diluted to 0.2 mg/ml of total cell protein and pre-energized with 10 mM glucose for 5 min at 30°C. At t = 5 min, 50 mM HEPES-methylglucamine pH 7.3 supplemented with varying amounts of sucrose (0–600 mM) plus 14C glycine betaine (final concentration of 1 mM; the total reaction mixture was 500 μl) was added, and uptake was monitored over time. To prevent protein synthesis, 25 μg/ml chloroamphenicol plus 25 μg/ml erythromycin was present during the assay. At given time intervals, 80 μl samples were withdrawn and diluted with 2 ml ice-cold assay buffer of equal osmolarity and immediately filtered through 0.45 μm cellulose nitrate filters under high vacuum. After washing with 50 mM HEPES-methylglucamine pH 7.3 with the appropriate sucrose concentration, the filters were dried and dissolved in 2 ml scintillation liquid and radioactivity was determined in a scintillation counter.

Purification of ProVW

For purification of ProVW, membrane vesicles (10 mg of total protein) of E. coli MC1061/pBAdaLICproVW were solubilized with 1% (w/v) dodecyl-β-D-maltoside (DDM) for 45 min at 4°C; the membranes at 5 mg/ml of protein were present in buffer A (50 mM KPi, 200 mM KCl plus 20% glycerol [pH 7.0]) plus 1 mM dithiothreitol (DTT). Following ultracentrifugation at 347,000 g for 15 min, the solubilized material was incubated with Ni-Sepharose (GE Healthcare) (20 mg of protein/ml resin) for 1 h at 4°C, i.e., after the addition of 15 mM imidazole plus 1 mM DTT.
Next, the resin was washed with 20 column volumes of buffer A with 0.05% DDM plus 50 mM imidazole. ProVW was eluted in buffer A with 0.05% DDM plus 200 mM imidazole.

Purification of ProX

For purification of lipid-anchored ProX, membrane vesicles of L. lactis Opu401/pAMP31-proX were solubilized with 1% DDM for 45 min in buffer B (25 mM KPi, 100 mM KCl plus 10% glycerol [pH 7.0]) at a final concentration of 5 mg/ml of protein. Following ultracentrifugation at 347,000 g for 15 min, the solubilized material was incubated with Ni-Sepharose (20 mg of protein/ml resin) for 1 h at 4°C in the presence of 15 mM imidazole. Next, the resin was washed with 20 column volumes of buffer A with 0.05% DDM plus 50 mM imidazole. The protein was eluted in buffer B with 0.05% DDM plus 200 mM imidazole. Next, the buffer was exchanged to buffer B with 0.05% DDM plus 15 mM imidazole. The protein was eluted in buffer B with 0.05% DDM plus 50 mM imidazole. The protein was eluted in buffer B with 0.05% DDM plus 100 mM KPi plus 0.05% DDM for membrane reconstitution or 100 mM KPi plus 0.05% DDM for fluorescence measurements, using a NAP10 column (GE Healthcare).

Membrane reconstitution of ProVW and surface tethering of lipid-anchored ProX

For membrane reconstitution of ProVW, preformed liposomes composed of E. coli polar lipids and L-α-phosphatidylcholine from egg yolk in a ratio of 3:1 (w/w) or synthetic lipid mixtures composed of dioleoyl-phosphatidylethanolamine (DOPE), dioleoyl-phosphatidylglycerol (DOPG) and dioleoylphosphatidyldcholine (DOPC), at mole ratios specified in the Figure legends, were used. Liposomes were extruded through a 400 nm pore diameter (400nm pore diameter) polycarbonate filter, and, subsequently, detergent-destabilized by adding increasing amounts of Triton X-100; typically, 70–100 μl of 10% (v/v) of Triton X-100 was used for 2.5 ml of liposomes at a lipid concentration 4 mg/ml (Geertsma et al. 2008a). Purified ProVW was incorporated in the Triton X-100-destabilized liposomes at a protein-to-lipid ratio (w/w) of 1:100. Subsequently, Biobeads™ were added in steps to remove the detergent (Geertsma et al. 2008a); 1 mM DTT was present in all steps of the purification and membrane reconstitution. For membrane tethering of lipid-anchored ProX, proteoliposomes containing ProVW were extruded through a 400 nm polycarbonate filter, diluted to 4 mg/ml in 50 mM KPi pH 7.0 and mixed with purified ProX at a protein-to-lipid ratio of 1:50 (w/w). Residual detergent was removed by incubation of the (proteo) liposomes with Biobeads. The ATP regenerating system (ARS), composed of 10 mM Mg-ATP, 24 mM phosphocreatine plus 2.4 mg/ml creatine kinase in 50 mM KPi, pH 7.0, was included in the proteoliposomes by two cycles of freezing in liquid nitrogen and thawing at room temperature (Doeven et al. 2004, Geertsma et al. 2008a) (Figure 1B).

Glycine betaine uptake in proteoliposomes

For ATP-driven uptake of glycine betaine into proteoliposomes, the membranes with ARS inside were extruded and resuspended in 100 mM KPi pH 7.0, and, prior to the start of the assay, they were diluted to a final lipid concentration of 5 mg/ml. The assay buffer was composed of 100 mM KPi pH 7.0 plus 0–300 mM KCl. Following 2 min of equilibration at 30°C, the transport reaction was started by the addition of 40 μM [14C]glycine betaine. At given time intervals, 25 μl samples were withdrawn and diluted with 2 ml ice-cold assay buffer (isotonic with the reaction conditions) and immediately filtered through 0.45 μm cellulose nitrate filter. Following washing of the filter with another 2 ml of ice-cold assay buffer, the radioactivity was determined in a scintillation counter.

Glycine betaine binding

Binding of radiolabeled glycine betaine was measured by the precipitation method (Richarme and Kepes 1983), which is based on the principle that, upon salting-out of the protein by ammonium-sulfate, the substrate remains trapped in the ligand-binding site. Binding assays were carried out in a volume of 100 μl with 100 μg/ml of purified ProX in 100 mM KPi, pH 7.0, plus 0.05% (w/v) DDM. Following equilibration for 2 min at 30°C, tracer amounts of [3H]-glycine betaine plus varying amounts of non-labeled glycine betaine were added to the assay mixture, yielding final concentrations of glycine betaine ranging from 0.1–20 μM. The binding reaction was quenched after 2 min by dilution of the sample into 2 ml ice-cold 50% (w/v) ammonium sulfate solution. The mixture was filtered rapidly through 0.45 μm pore-size cellulose nitrate filters. The filters were washed once with 2 ml ammonium sulfate solution. Subsequently, the filters were placed in an open plastic vial and dried overnight at room temperature. The radioactivity on the filters was measured via liquid-scintillation counting, using emulsifier plus scintillation liquid (Perkin Elmer).

Immunodetection

Protein samples were analyzed by 12.5% SDS-PAGE electrophoresis, semi-dry electroblotting and immunodetection with a primary antibody directed against a hexa-His tag (Amersham Pharmacia Biotech).
Subsequently, the gels were submitted to Chemiluminescence detection, using the Western-Light kit (Tropix Inc).

Miscellaneous

Radiolabeled [N-methyl-14C] choline chloride (55 mCi/mmol) was obtained from Amersham Biosciences, NJ, USA. The [N-methyl-14C] choline chloride was used as precursor for the synthesis of [N-methyl-14C] glycine betaine as described (Landfald and Strom 1986). Radiolabeled [3H]-glycine betaine was prepared via a conversion of [3H]-choline chloride (Amersham, specific activity: 2.01x10^6 MBq/mmol) to glycine betaine. Creatine kinase and creatine phosphate were obtained from Sigma Chemical Co. All other chemicals were of reagent grade and purchased from commercial sources, unless specified otherwise.

Results and discussion

Cloning and functional expression of proVW and proX

The osmoregulatory ABC transporter ProU is composed of an ATPase subunit ProV, a TMD subunit ProW and the substrate-binding protein ProX (Gowrishankar 1989). ProX is located in the periplasm of E. coli, unlike homologues in Gram-positive bacteria or Archaea where the protein is either fused to a TMD or tethered to the membrane via lipid anchor (Amersham, specific activity: 2.01x10^6 MBq/mmol) to glycine betaine. Creatine kinase and creatine phosphate were obtained from Sigma Chemical Co. All other chemicals were of reagent grade and purchased from commercial sources, unless specified otherwise.

Glycine betaine binding to ProX

Previous studies showed that genuine ProX binds glycine betaine with a KD of \( \sim 1 \) μM (Barron et al. 1987, Haardt et al. 1995). To test whether or not the lipid anchor has an effect on the binding of glycine betaine by ProX, we used the protein precipitation method of Richarme and Kepes (1983). Figure 4 shows the binding isotherm from which we estimate a KD of 1–2 μM. Thus, we conclude that the lipid anchor and His-tag do not affect the functionality of ProX.

Purification and membrane reconstitution of ProVW-ProX system

For further characterization of the ProU system, large scale fermentations were performed and ProVW and
ProX were purified (Figure 3A). As ProV contains 1 cysteine residue in the CBS2 domain and ProW contains 1 cysteine residue in transmembrane helix III, 1 mM of freshly prepared 1 mM DTT was present in each step of membrane vesicle solubilization, protein purification and membrane reconstitution. In fact, ProU lost activity when DTT was omitted in these steps (data not shown). The reconstitution of ProVW and ProX was carried out in three steps: (i) Incorporation of ProVW into liposomes; (ii) membrane-tethering of ProX; and (iii) enclosing in the proteoliposome lumen of an ATP-regenerating system consisting of creatine-phosphate, creatine kinase and Mg-ATP. The procedure is in essence the same as previously described for the OppBCDF-OppA system (Doeven et al. 2004) and further specified in (Geertsma et al. 2008a), except that in the course of the project, the order of step (ii) and (iii) was reversed. We noted that a higher transport activity, presumably corresponding to a higher reconstruction efficiency, was observed when ProX was tethered to the membrane after the incorporation of the ATP-regenerating system.

Osmotic activation of membrane-reconstituted ProU

Previous studies have shown that the expression of proU is regulated by the osmotic conditions of the medium (Perroudt and Rudulier 1985, May et al. 1986, Lucht and Bremer 1994). Furthermore, there are indications that the activity of ProU is also affected by osmotic stress (e.g., Figure 4 in Faatz et al. 1988). To circumstantiate these findings, we determined the regulation of activity of ProU reconstituted in proteoliposomes. To discriminate binding of glycine betaine to surface-tethered ProX from uptake via ProU, we performed a chase experiment with unlabeled glycine betaine. ProX-bound [14C]glycine betaine will be chased upon the addition of an excess of unlabeled glycine betaine, whereas accumulated [14C]glycine betaine will not be chased when the transport reaction is unidirectional. Indeed, a more than 100-fold excess of unlabeled glycine betaine to proteoliposomes that had taken up [14C]glycine betaine for 3 min (Figure 5A) did not result in efflux. Also, the presence of external Mg-ATP did not elicit [14C]-glycine betaine efflux, demonstrating that inside-out-oriented ProVW (without luminal ProX) does not facilitate transport.

Figure 5B shows that the rate of glycine betaine is stimulated significantly when the external salt concentration is raised by 300 mM KCl; the basal assay medium is composed of 100 mM KPi, pH 7.0. In this experiment, we monitored the uptake reaction in the absence and presence of 5 mM glycine betaine in the stop buffer. In the absence of glycine betaine in the stop buffer, the offset at the y-axis represents the amount of [14C]glycine

Figure 1. Panel A: Schematic representation of the organization of the subunits in ProU (Panel A); the engineered lipid-anchored ProX, the membrane-embedded TMD ProW, and the NBD ProV are shown. Panel B: Schematic of proteoliposomes with ProVW in two orientations, ProX tethered to the external surface, and the ATP-regenerating system (ARS) in the vesicle lumen. Only right-side-out ProVW plus ProX will facilitate the uptake of glycine betaine. This Figure is reproduced in colour in Molecular Membrane Biology online.
The actual uptake (rate) is obtained by subtracting the bound glycine betaine or by including 5 mM glycine betaine in the stop buffer. Figure 5B shows that rapid binding is followed by true transport (accumulation) of [14C]glycine betaine. The rate of uptake increases with the salt concentration and a sigmoidal dependence was observed (Figure 5C), similar to the activation of OpuA (Van der Heide et al. 2001).

**Effect of anionic lipids on ProU activity**

The experiments described heretofore were carried out with ProU reconstituted in liposomes composed of *E. coli* polar lipids plus L-α-phosphatidyl choline from egg yolk in a ratio of 3:1 (w/w). The fraction of phosphatidylethanolamine in *E. coli* can be up to 75%; the remaining lipids are mostly anionic, i.e., phosphatidylglycerol (PG) and cardiolipin, typically at 20 and 5 mole% (Cronan 2003). The relative amounts of PE, PG and cardiolipin vary with osmotic.

**Figure 2.** In vivo glycine betaine uptake. Panel A: Expression levels of ProX and ProW in *L. lactis* Opu401 co-transformed with pNZcLICproVW and pAMP31-GGGSAGGGS-proX and grown in GM17 and GCDM. Panel B: Rate of glycine betaine uptake as a function of sucrose concentration for GCDM- (○) and GM17-grown (□) cells of *L. lactis* expressing ProVW and ProX. *L. lactis* Opu401 cells, co-transformed with pNZcLICproVW and pAMP31-GGGSAGGGS-proX, were grown semi-aerobically at 30°C in GM17 and GCDM with 2.5 µg/ml chloroamphenicol plus 2.5 µg/ml erythromycin. Induction with 0.01% (v/v) nisinA was performed for 2 h, prior to harvesting of the cells for the transport assays. Uptake of [14C]glycine betaine (1 mM, final concentration) was assayed in 50 mM HEPES-methylglucamine pH 7.0 in the presence of 10 mM glucose plus 25 µg/ml chloroamphenicol and erythromycin; the final cell concentration in the assay buffer was 0.5 mg/ml. The initial rates of uptake were determined from the linear parts of the progress curves; measurements were done in duplicate. This Figure is reproduced in colour in Molecular Membrane Biology online.

**Figure 3.** Expression of ProVW and ProX. SDS-PAGE (12% gel) stained with Coomassie brilliant blue. Lane 1: Membrane vesicles of *E. coli* harboring pBADcLICproVW; lane 2: Purified ProVW; lane 3: Membrane vesicles of *L. lactis* harboring pAMP31 + GGGSAGGGS + proX; lane 4: Purified ProX; lane 5: proteoliposomes with ProVW; and lane 6: proteoliposomes with ProVW and ProX. This Figure is reproduced in colour in Molecular Membrane Biology online.

**Figure 4.** Glycine betaine binding to ProX. Glycine betaine binding to purified ProX with lipid anchor and flexible linker. The lipid-anchored ProX was kept soluble by including of 0.05% (w/v) DDM in the assay buffer (100 mM KPI, pH 7.0). See Materials and methods for further details. This Figure is reproduced in colour in Molecular Membrane Biology online.
stress as shown by Romantsov et al. (2009). As osmotic (ionic) regulation of OpuA has been shown to be critically dependent on the fraction of anionic lipids (Biemans-Oldehinkel et al. 2006), we reconstituted ProU in 50 mole% of DOPE (zwitterionic, non-bilayer-forming lipid) plus varying ratios of DOPG (anionic, bilayer-forming lipid) and DOPC (zwitter-ionic, bilayer-forming lipid). Figure 6 shows that ProU activity was not affected by the osmotic stress, i.e., KCl concentration in the range of 0–300 mM in assay buffer composed of 100 mM KPi, pH7.0 (above 300 mM KCl the activity decreased) when DOPG was absent or
present at 12 mole%. Importantly, osmotic stress-activated activity was observed at 25 mole% of DOPG and even more so at 38 mole%. The activation was instantaneous, that is, within seconds following the addition of threshold levels of KCl. Although the fraction of anionic lipids in the corresponding parent cells, E. coli and L. lactis, respectively. We speculate that the mechanism of osmotic regulation of ProU in E. coli is in essence similar to what has been observed for OpuA in L. lactis. The two transporters have likely evolved to match the physicochemical conditions (internal ionic strength, K⁺ concentration, water activity, lipid composition) that E. coli and L. lactis face. We are currently exploring the possibility to crystallize the OpuA and ProU proteins to gain further insight in the mechanism of transport and regulation of these ABC transporters.

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References


