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Published in:
The Journal of Biological Chemistry

DOI:
10.1074/jbc.M500522200

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Document Version
Publisher's PDF, also known as Version of record

Publication date:
2005

Link to publication in University of Groningen/UMCG research database

Citation for published version (APA):

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Substrate Specificity and Ionic Regulation of GlnPQ from Lactococcus lactis

AN ATP-BINDING CASSETTE TRANSPORTER WITH FOUR EXTRACYTOPLASMIC SUBSTRATE-BINDING DOMAINS

Received for publication, January 14, 2005, and in revised form, March 23, 2005
Published, JBC Papers in Press, March 28, 2005, DOI 10.1074/jbc.M500522200

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We report on the functional characterization of GlnPQ, an ATP-binding cassette transporter with four extracytoplasmic substrate-binding domains. The first predicted transmembrane helix of GlnP was cleaved off in the mature protein and most likely serves as the signal sequence for the extracytoplasmic substrate-binding domains. Deletion analysis showed that the substrate-binding domain, in the primary sequence of GlnP nearest to the translocator domain, is used as the receptor that delivers the substrate to the translocator. Membrane reconstitution of the detergent-solubilized and purified GlnPQ complex yielded proteoliposomes that transported glutamine and glutamic acid at the expense of ATP. The transport activity of GlnPQ increased with luminal salt concentration and internal pH, but the mechanism of ionic activation of the transporter is distinct from that of other osmoregulatory ATP-binding cassette transporters and does not depend on the presence of anionic lipids. The regulation of GlnPQ conforms to an electrostatic switch in which protein domain(s) and low molecular weight electrolytes participate.

The basic unit of ATP-binding cassette (ABC) transporters consists of two translocator domains and two ATP-binding cassettes, together referred to as the translocator (1). The domains of the translocator can be present as separate subunits or fused to each other in any possible combination. In addition, prokaryotic ABC transport systems involved in solute uptake employ an accessory protein that captures the ligand and delivers it to the translocator. These so-called substrate-binding proteins (SBPs) are present in the periplasm of Gram-negative bacteria, or they can be tethered to the membrane via a lipid or protein anchor (Gram-positive bacteria, Archaea). Recently, we discovered that members within two families of the ABC superfamily, which are the OTCN and PAO families, can have the SBPs fused to the translocator domains (2). Within the OTCN family, one or two domains fused in tandem are present at the carboxyl terminus of the translocator subunit. Within the PAO family, one or two domains are linked to the amino-terminal end of the translocator subunit, and these are preceded by a predicted signal sequence. Two of these chimeric substrate-binding/translocator proteins along with two ATP-binding cassettes form the functional unit for transport, and these systems thus have two or four substrate-binding domains.

Previously, we have described the properties of the osmoregulatory glycine betaine transporter (OpuA) from Lactococcus lactis (3, 4), which has two substrate-binding domains in the functional complex. We now report the cloning and amplified expression of the glnPQ genes, encoding an ABC transporter with four substrate-binding domains. The domain structure and membrane topology of the GlnPQ system is schematically depicted in Fig. 1A. The GlnPQ complex has been purified and reconstituted in proteoliposomes, allowing us to determine the rather unique substrate specificity and salt and pH dependence of the system. We show that GlnPQ corresponds to the previously characterized glutamine-glutamate transport system from L. lactis, which has the unusual feature of transporting glutamic acid rather than glutamate anion, the dominant species at physiological pH values (5, 6). We also show that the first 26 amino acids of the GlnPQ open reading frame are cleaved off in the mature protein and, apparently, serve as signal sequence for the translocation of the two amino-terminal substrate-binding domains.

EXPERIMENTAL PROCEDURES

Materials—M17 broth was obtained from Difco, MBS broth from Merck, nickel-nitritotriacetic acid resin from Qiagen Inc., N-dodecyl-β-D-maltoside from Anatrace Inc., Triton X-100 from Roche Applied Science, Biobeads SM-2 from Bio-Rad, total Escherichia coli lipid extracts, L-α-phosphatidylcholine from egg yolk, and synthetic lipids (dipalmitoyl phosphatidyl glycerol, DOPG, dipalmitoylphosphatidyl ethanolamine, DOPE, dipalmitoylphosphatidyl glycerol, DOPE, dipalmi
branched vesicles were prepared according to standard procedures (3).

Appropriate, a chemically defined medium was used to cultivate the cells, as described previously (18).

**Disruption of Chromosomal glnP—**The glnP gene of *L. lactis* JIM7049, a derivative of IL1403, was disrupted by plasmid integration via homologous recombination using an 886-bp EcoRI fragment of the glnP gene (bp 824–1710) ligated in the integration vector pORi28 (erythromycin-resistant), yielding pORi28disP. The integration of the vector was verified by PCR, and the disruption strain was designated JIM7049disglnP.

**Plasmid Construction—**For the overexpression of the GlnPQ complex from *L. lactis* IL1403 (GenBank™ accession numbers NP_267915 for *glnP* and NP_267916 for *glnQ*), the result of this strategy is the insertion of a glycine after the amino-terminal methionine of the GlnP protein and the addition of a His tag at the carboxy terminus of the GlnPQ protein.

For the construction of the deletion mutants ∆SBP1 and ∆SBP2, we took advantage of the homology between the two domains and the identity with GlnH from *E. coli*, for which crystal structures are available (8, 9); see also Fig. 1B. For ∆SBP1 (deletion of amino acids 33–265), two silent NruI sites were introduced into the glnP gene, one in the amino acid sequence 32–34(IAS) using glnPQfor as the forward primer and 5′-CTATGAGTCATGCTCAGATTTTACAAGCTC-3′ as the reverse primer and one at residues 264–266(IAS) using 5′-CCATTTAAAAGGTGTTTGAAATGTTGTTTGGG-3′ as the forward primer and glnPQrev as the reverse primer. The two PCR products were subjected to restriction with NruI, followed by ligation.

For purification, the ligation product was amplified with glnPQfor and glnPQrev and ligated into the NcoI and BamHI restriction sites of pNZglnPQhis, yielding pNZglnPQhisΔSBP1. The strategy for preparing ∆SBP2 was essentially the same, except that Scal sites were introduced 5′ and 3′ of the region specifying the second substrate-binding domain. The first Scal site was made by changing the sequence (residues 246–248) KYG into KLY, using glnPQfor as forward and 5′-GCTTTTTAGTGGCAGTAATTAAGTACTTTTTGAGGATTTTATCA-3′ as the reverse primer. The second Scal site, the sequence corresponding to amino acid 478 and 480 (KYL) was modified as the forward primer and glnPQrev as the reverse primer. The resulting plasmid was named pNZglnPQhisΔSBP2. ∆SBP2 corresponds to a deletion of residues 248–480.

**Whole Cell Uptake Experiments—** *L. lactis* strain JIM7049 was grown on MRS medium plus 2% w/v glucose to an OD600 of 0.6–1 and harvested by centrifugation (10 min, 4,000 × g). The cells were washed three times with ice-cold 50 mM potassium phosphate, pH 6.5, and suspended in this buffer to and an OD600 of 100. For the transport experiments, the cells were diluted to an OD600 of 5 into 50 mM potassium phosphate, pH 6.5, 5 mM MgCl2 plus 10 mM glucose and allowed to equilibrate at 30 °C. After 3 min of incubation, the uptake was started by adding substrate ([14]C)glutamine, [14]Cglutamate or substrate + inhibitor). The final protein concentration in the assays was 1 mg/ml. At given time intervals, 40-μl samples were taken and
diluted with 2 ml of ice-cold 50 mM potassium phosphate, pH 6.5. The samples were collected on 0.45-μm pore size cellulose nitrate filters (Schleicher and Schuell GmbH, Dassel, Germany) and washed twice with 2 ml of the same buffer. The radioactivity on the filters was determined by liquid scintillation spectrometry.

**Purification of GlnPQ**—Membrane vesicles were resuspended in 50 mM potassium phosphate, pH 8.0, 200 mM KCl, 20% glycerol (buffer A) to a concentration of 5 mg of protein/ml and solubilized with 0.5% DDM for 30 min on ice. After centrifugation, the supernatant was incubated with nickel-nitrilotriacetic acid resin (0.5 ml of resin/10 mg of membrane protein) for 1 h, rotating at 4 °C in the presence of 10 mM imidazole. Subsequently, the resin was washed with 20 column volumes of buffer A supplemented with 0.05% DDM and 10 mM imidazole. The His-tagged proteins were eluted from the column with 3 column volumes of buffer A supplemented with 0.5% DDM and 200 mM imidazole.

**Membrane Reconstitution of GlnPQ**—Liposomes composed of egg yolk PC and brain phosphatidylcholine, purified E. coli lipids in a 1:3 (w/w) ratio were prepared, and membrane reconstitution of the GlnPQ complex was performed essentially as described by Knol et al. (10), except that 20% (v/v) glycerol was added to the buffers. Briefly, preformed liposomes (4 mg/ml) were destabilized by titration with Triton X-100, and the turbidity of the suspension at 540 nm was used to monitor the physical state of the liposomes. Detergent-saturated liposomes were then mixed with purified GlnPQ complex in a GlnPQ:lipid (1:1, w/w) and incubated for 30 min at room temperature under gentle agitation. To keep the molar lipid-to-protein ratio the same as for the wild-type protein complex, purified GlnPQ/βS1 and GlnPQ/βS2 were reconstituted at 128:1 (w/w) lipid:protein. To remove the detergent, Biobeads SM-2 were added at a wet weight of 40 mg/ml, and the sample was incubated for another 15 min. Fresh Biobeads SM-2 (40 mg/ml) were added to the sample four times, and the incubations were continued at 4 °C for 15 min, 30 min, overnight, and 1 h, respectively. After 5× dilution into 50 mM potassium phosphate, pH 7.0, the proteoliposomes were collected by centrifugation (500,000 × g for 60 min) and washed twice with 10 mM potassium phosphate, pH 7.0. After sonication with a probe sonicator (15 s on/45 s off, 6 cycles at an intensity of 4 μm), the liposomes were frozen/thawed three times and stored in liquid nitrogen. The protocol used for incorporation of GlnPQ into these liposomes was essentially the same as described for the E. coli lipid/egg phosphatidylcholine mixture.

**ATP-Driven Uptake in Proteoliposomes**—An ATP regeneration system, consisting of creatine kinase (2.4 mg/ml), ATP (9 mM), MgSO4 (9 mM), and creatine phosphate (24 mM), together with 50 mM potassium phosphate, pH 7.0, was enclosed in the proteoliposomes by two freeze/thaw cycles. Following extrusion of the proteoliposomes through a polycarbonate filter (400-nm pore size), the proteoliposomes were thawed, washed with ethanol and dissolved in 50 mM potassium phosphate, pH 7.0. After sonication with a probe sonicator (15 s on/45 s off, 6 cycles at an intensity of 4 μm), the liposomes were frozen/thawed three times and stored in liquid nitrogen. The protocol used for incorporation of GlnPQ into these liposomes was essentially the same as described for the E. coli lipid/egg phosphatidylcholine mixture.

**Manipulation and Determination of the Internal pH**—Proteoliposomes were equilibrated with 100 mM potassium phosphate, pH 6.5, the ATP-regenerating system, and 0.5 mM of the pH indicator probe pyranine. After two freeze/thaw steps and extrusion through a 400-nm filter, the proteoliposomes were collected by centrifugation (300,000 × g for 15 min), washed four times in 50 mM potassium phosphate, 100 mM potassium acetate, pH 6.5, to remove external pyranine, and suspended to 40 mg/ml lipid. The internal pH was then measured by diluting the proteoliposomes in isotonic medium with varying ratios of potassium acetate and potassium-2(N-morpholino)ethanesulfonic acid (K-MES). The internal pH was followed by measuring the fluorescence of pyranine (excitation at 465 ± 2 nm and emission at 511 ± 5 nm) in a volume of 1 ml. At the end of each experiment, 0.5 μM nigericin was added to dissipate any pH gradient and the fluorescence signal was correlated to the pH by measuring the pH upon the addition of small amounts of KOH or HCl.

**RESULTS**

**Amino Acid Sequencing of GlnP**—To determine the amino-terminal amino acid sequence of GlnP, the purified complex was run on an SDS-PAGE gel, and the appropriate band was sliced out. Amino-terminal sequencing was carried out by Eurosequence B.V., Groningen, The Netherlands.

**Miscellaneous**—The protein concentration of membrane vesicles was determined by the method of Lowry et al. (19), using bovine serum albumin as a standard. The concentration of the purified GlnPQ complex was determined using calculated molar absorption coefficients of 83,200 mol−1·cm−1 for GlnP and 1,615 mol−1·cm−1 for GlnQ, respectively.

**Gene Disruption**—Integration of pOri28disP into the chromosome of L. lactis JIM7049 led to disruption of the glnP gene and abolished the uptake of glutamine and glutamate (Fig. 2). Although glutamine (or glutamate) is essential for growth of L. lactis, the disruption mutant was able to grow in complex MRS broth, probably because of the presence of glutamine- and/or glutamate-containing peptides. Using a chemically defined medium (18) supplemented with glutamine or glutamate as the sole source for glutamine or glutamate, growth was not observed for the disruption mutant, but growth in chemically defined medium could be rescued by the addition of the dipetide alanine-glutamine, which is taken up by a peptide transport system (11). These experiments strongly indicate that GlnPQ is the sole transport system for the uptake of glutamine and glutamate, which is consistent with previous observations that these amino acids compete for transport in L. lactis. In these experiments, it was also shown that glutamine and glutamic acid (and not the glutamate anion) are the actual substrates of, at that time, unknown transporter(s) (6).

**Amplification and Purification of GlnPQ**—The genes encoding the translocator subunit (GlnP) and the ATPase (GlnQ) were placed in tandem in the pNZOpuAA plasmid, using the NcoI and BamHI restriction sites. Hereby, an extra glycine residue is introduced into GlnP as the second amino acid, and a His6 tag is added to the carboxyl terminus of GlnQ. After nickel-nitrilotriacetic acid purification, the GlnPQ complex was separated on a 4%–15% polyacrylamide gel (Fig. 3), and the GlnP band was sliced out for amino-terminal amino acid sequencing. The amino-terminal sequence started with ETTVKI, demonstrating that GlnP is synthesized as pre-protein with an amino-terminal signal sequence corresponding to MKKLFAWMLATYV TAFLVAPSVK A (Fig. 1B).

**Substrate Specificity of GlnPQ and the Role of the Individual Substrate-binding Domains**—Glutamine uptake followed Michaelis-Menten kinetics (Fig. 4A), from which an apparent Km was determined for uptake of 6.3 ± 0.8 μM was estimated. Using 5 μM [14C]glutamine as the reporter ligand, we tested all natural L-amino acids (except Tyr), the dipeptide Ala-Gln and methyl-
ammonium as possible substrates at 1 and 10 mM concentration. Significant inhibition of glutamine transport was only observed in the presence of glutamate, arginine, and γ-glutamylhydrazide (data not shown). The inhibition by arginine and γ-glutamylhydrazide was competitive, with $K_i$ values of 2.2 ± 1.1 mM ($n = 4$; Fig. 4A) and 80 ± 50 μM ($n = 3$), respectively, where $n$ is the number of independent measurements. Competitive inhibition of glutamine transport by glutamate and uptake of [14C]glutamic acid was only observed at low pH (pH < 6), which most likely reflects the low fraction of glutamic acid at the ambient pH values; the $pK_a$ of the γ-carboxyl group is 4.25. Uptake of arginine could not be measured, possibly due to the low affinity of the transporter for arginine, but it could not be ruled out that arginine is only inhibiting and not transported. In summary, these measurements, together with the pH dependence of transport (see below), reveal the unusual substrate specificity of the transporter, which is that GlnPQ transports glutamine and glutamic acid and is competitively inhibited by arginine and γ-glutamylhydrazide.

By aligning the sequences of the two substrate-binding domains (SBDs) of GlnPQ with the corresponding substrate-binding protein GlnH from *E. coli* and inspection of the crystal structures of GlnH (8, 9), we deduced a linker of ten residues that connects SBD1 with SBD2 (Fig. 1B, katpkdvdyt). To construct the transporter complex lacking the first substrate-binding domain (GlnPQΔSBD1), the sequence ettvk following the signal sequence was fused to the first conserved residue (Ile) in SBD2, resulting in a mature GlnPQΔSBD1 protein that started with the sequence ETTVKIASDNSF (which compares to ETTVKIASDSSY) in wild-type GlnPQ. For the construction of GlnPQΔSBD2, the sequence YDKILKKY (just before the end of SBD1) was fused to the sequence starting with LESDALT, leaving the last seven amino acids of SBD2 in place. The expression, purification, and membrane reconstitution of GlnPQΔSBD1 and GlnPQΔSBD2 was comparable with wild-type GlnPQ (Fig. 3). However, with GlnPQΔSBD2, uptake of glutamine or glutamate was no longer observed (data not shown).

### Salt and Lipid Dependence

After reconstitution in liposomes composed of *E. coli* phospholipid/egg phosphatidylcholine (3:1), the activity of the GlnPQ transporter was highest when the external medium was hyposmotic relative to the inside (Fig. 5A). Both salts (NaCl and KCl) and membrane-impermeant nonionic osmolytes (sucrose) stimulated the uptake to the same extent when added in equiosmolar concentrations (the membrane-permeant nonionic osmolyte glycerol had no effect), which is reminiscent of the activation of the osmoregulatory glycine betaine transporter OpuA from *L. lactis*. In the case of OpuA, the osmotic activation originates from the increase in luminal electrolyte concentration upon osmotic upshift, converting the osmotic signal into an ionic signal, which is sensed by the transporter through altered lipid-protein interactions (4, 12). Comparable increases in electrolyte concentration upon osmotic upshift take place in the proteoliposomes with GlnPQ. To determine whether possibly a similar osmoregulatory mechanism is operative in GlnPQ, we reconstituted the transporter complex in synthetic lipid mixtures (DOPC/DOPG/DOPG) with varying fractions of the anionic lipid DOPG and determined the osmotic activation profiles. Fig. 5B shows that the fraction of DOPG influenced the maximal activity of GlnPQ.
The glutamine-glutamic acid transporter from *L. lactis* IL1403 is a member of the PAO family of the ABC superfamily with a unique domain structure. The GlnP protein has two different SBDs fused in tandem at the amino-terminal side of the translocator domain. The first substrate-binding domain is preceded by a signal sequence, which thus far has only been shown for one other prokaryotic membrane protein, the ammonia transporter AmtB from *E. coli* (13). Whereas the function of the signal sequence in AmtB is unknown, in the case of GlnPQ, it serves a role in directing translocation across the membrane of the two SBDs.

The two SBDs of GlnPQ are 50% identical, and SBD1 and SBD2 are 32 and 34% identical to the periplasmic substrate-binding protein GlnH from *E. coli*. The structures of GlnH in the open and liganded form have been determined (8, 9), and most of the residues in the substrate-binding pocket of GlnH are conserved in SBD1 and SBD2 of GlnPQ. Our experiments indicate that, surprisingly, deletion of the first SBD has little or no effect on the kinetics of glutamine uptake, whereas the deletion of the second SBD is detrimental for transport. Because SBD1 has been preserved through evolution, it may have a regulatory role, although not directly participating in the transport cycle. However, functional analysis of wild-type GlnPQ and GlnPQΔSBD1 did not reveal noticeable differences in the specificity of transport; only the turnover number was somewhat reduced. In contrast to the glycine betaine transporter OpuA with two identical SBDs in the functional complex (14), we did not observe any cooperativity in the substrate dependence of uptake mediated by GlnPQ or GlnPQΔSBD1. The fact that wild-type GlnPQ and both deletion mutants were produced in similar amounts, behaved protein chemically very similarly (each complex was expressed in the membrane and had no tendency to aggregate after solubilization and/or purification), and were highly similar in sequence makes us believe that not only SBD2 in GlnPQΔSBD1 but also SBD1 in GlnPQΔSBD1 are correctly folded. The fact that wild-type GlnPQ and both deletion mutants were produced in similar amounts, behaved protein chemically very similarly (each complex was expressed in the membrane and had no tendency to aggregate after solubilization and/or purification), and were highly similar in sequence makes us believe that not only SBD2 in GlnPQΔSBD1 but also SBD1 in GlnPQΔSBD1 are correctly folded. In respect to the failure to detect any transport activity of the GlnPQΔSBD2 mutant, we note that it may be more tedious to engineer an internal (ΔSBD2) than amino-terminal deletion (ΔSBD1) and allow the remaining domain to functionally interact with the translocator. However, as detailed under “Results” and Fig. 1B, both deletion mutants were carefully designed, and it is unlikely that the linker region in GlnPQΔSBD1 is too short to allow SBD1 to donate the substrate to the translocator. Future studies are aimed at the further elucidation of the roles of the different SBDs in the transport process and/or physiology of the cell by structure-guided site-directed mutagenesis of SBD1 and SBD2.

Recently, it has been observed that the glnPQ genes of group B streptococci are playing a role in virulence (15). This GlnPQ transporter is homologous to the *L. lactis* system studied here. For GlnPQ from group B streptococci, it has been proposed that the transporter plays a role in the regulation of expression of fibronectin adhesins and virulence of this pathogen. Whether GlnPQ from *L. lactis* has analogous regulatory roles remains to be determined.

Disruption of the glnPQ gene resulted in the loss of glutamine and glutamic acid uptake, and the cells were no longer able to grow on chemically defined medium with glutamine or glutamate as the sole source of glutamine or glutamate. The disruption mutant grew normally when glutamine was added.
to the medium in the form of a dipeptide (Ala-Gln). Here, one of the dipeptide transport systems of *L. lactis* is used to compensate for the loss of Gln/Glu transport function. The GlnPQ transporter is therefore the only transporter for glutamine (and glutamic acid) uptake in *L. lactis*.

The GlnPQ complex is responsible for glutamine and glutamate transport, but the latter is only transported in the protonated form, which is glutamic acid. Previously (6), the surprising observation was made that arginine inhibited the uptake of glutamine in whole cells with an apparent *K* of 2 mM in the submillimolar range. Using purified and membrane-reconstituted GlnPQ, we now confirm that competitively inhibits Gln uptake with a *K* of ~2 mM. Except for glutamic acid, arginine, and γ-glutamylhydrazide, there was no clear inhibition of glutamine uptake by any of the other amino acids tested. The substrate specificity of GlnPQ and GlnPQΔSBD1 were very similar and seems to be determined by SBD2. The amino acid-binding site of SBD2 seems to tolerate fairly large neutral and basic side chains. Asparagine and aspartic acid, on the other hand, residues that are only one methylene shorter than glutamine and glutamic acid, did not inhibit the transport. Thus, the positioning of the amide and carboxylic acid moiety is crucial for high affinity transport. In contrast to lysine, arginine is competing with glutamine, although with a low affinity. It is possible that the guanidinyl moiety in arginine makes critical contacts with the protein, which are not possible with lysine. In respect to the region in the binding pocket of SBD2 that accommodates the side-chain amine moiety of glutamine or the hydroxyl of the glutamic acid, larger functionalities are also tolerated, which are the hydradize of γ-glutamylhydrazide and even (part of) the bulky guanidinyl of arginine. However, for binding (and transport) of substrate, it is prerequisite that the overall charge is neutral (high affinity transport) or positive (low affinity competition by arginine).

The uptake of glutamine in proteoliposomes was highly stimulated when the concentrations of ionic osmolytes on the luminal side of the membrane were increased, *i.e.* by osmotic upshift. These observations mimic the activation of the osmoregulatory OpuA from *L. lactis*, ProP from *E. coli*, and BetP from *Corynebacterium glutamicum* (4, 12, 16, 17) and contrast with that of other, non-osmoregulatory (ABC) transporters, such as Opp. Because osmosensing by the OpuA system is mediated by anionic lipid-protein interactions (4), it was important to investigate the osmotic activation of the GlnPQ complex and to determine the (anionic) lipid dependence of the system. Although there was an optimal DOPG concentration for maximal activity of GlnPQ, the activation profiles were very similar at every DOPG concentration, which contrasts the situation for OpuA, where the activation profiles shift to higher osmolalities with increasing fractions of anionic lipids in the membrane. Thus, the osmotic activation of GlnPQ seems to be a direct consequence of the concentrated (ionic) osmolytes at the luminal (“cytoplasmic”) side of the membrane on the protein, rather than a modulation of (anionic) lipid-protein interactions. Even though this mode of activation is different from that described for OpuA (3, 4), it would allow the cell to accumulate faster (and more) glutamine and glutamate when it is confronted with hyperosmotic stress, wherein the cytoplasmic volume decreases and the ion concentration (ionic strength) increases as a consequence of water efflux.

Recently, we proposed a common physicochemical mechanism of osmosensing (12), which for OpuA has been modeled as an on/off electrostatic lever that assumes “electrostatically locked” or “thermally relaxed” conformations. The on/off activation was found to correlate with the theoretical prediction of transitions in ionic clouds according to the Maxwellian version of the Poisson-Boltzmann equation. A similar electrostatic mechanism may be operative in GlnPQ, except that screened electrostatic forces playing a role in the different conformational states of the transporter are not mediated by lipid-protein interactions but only involve protein domains and low molecular weight electrolytes. Because the pH inside the proteoliposomes influences the ionization state of GlnPQ and low molecular weight electrolytes (phosphate, creatine-phosphate, ATP, and ADP in our experimental setup), it is well possible that the internal pH and salt dependence of GlnPQ activity have a common electrostatic basis.

How relevant is the observed regulation of GlnPQ for *L. lactis*? Molenaar et al. (18) measured an increase in the pool of glutamate after growing *L. lactis* ML3 under hyperosmotic conditions, implying that glutamate could serve as an osmoprotectant in this organism. Similar to OpuA, a decrease in cell volume and the accompanying increase in ion concentration upon osmotic upshift could activate GlnPQ *in vivo*, and the further accumulation of glutamate (up to ~50 mM) would offset the deleterious effects of the stress. However, we emphasize that the role of OpuA in osmoprotection is far greater than that of GlnPQ (glycine betaine is accumulated to >0.5 mM, whereas glutamate plus glutamine reach levels of at most (50 mM), which may also be reflected in the more advanced electrostatic switching mechanism of OpuA. The activity of OpuA is modulated over 2–3 orders of magnitude, whereas regulation of GlnPQ is <10-fold.

Acknowledgments—We thank Esther Biemans-Olethinkel, Sytsje Henstra, and Mark Doeven for stimulating discussions.

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2 M. K. Doeven, unpublished observations.