Facilitated Drug Influx by an Energy-uncoupled Secondary Multidrug Transporter*  

Received for publication, June 20, 2003, and in revised form, August 25, 2003  
Published, JBC Papers in Press, October 14, 2003, DOI 10.1074/jbc.M306579200

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The majority of bacterial multidrug resistance transporters belong to the class of secondary transporters. LmrP is a proton/drug antiporter of Lactococcus lactis that extrudes positively charged lipophilic substrates from the inner leaflet of the membrane to the external medium. This study shows that LmrP is a true secondary transporter. In the absence of a proton motive force, LmrP facilitates downhill fluxes of ethidium in both directions. These fluxes are inhibited by other substrates of LmrP. The cysteine-reactive agent p-chloromercuri-benzene sulfonate inhibits these fluxes in wild type LmrP but not in the cysteine-less LmrP C270A mutant. Cysteine mutagenesis of LmrP resulted in three mutants, D68C/C270A, D128C/C270A, and E327C/C270A, with an energy-uncoupled phenotype. Asp128 is located in the periplasmic loop between transmembrane segments (TMS) II and III, is involved in the proton motive force (pmf)-driven influx of cationic drugs. The expression of such uncoupled secondary MDRs is disadvantageous and causes increased resistance to several clinically important antibiotics from different pharmacological classes (10), which indicates the frightening possibility that its homologues in pathogenic bacteria may reduce the efficacy of important antibiotics in clinical settings.

In this study we report that LmrP is a true secondary transporter and is able to mediate active efflux and, under non-energized conditions, downhill drug influx and efflux. We show that residue Asp128, located in the cytoplasmic loop between transmembrane segments (TMS) II and III, is involved in the energy-coupling mechanism but not in substrate binding, whereas Asp126 in the cytoplasmic loop between TMS IV and V is not participating in the binding of ethidium either, but it might be part of the structural framework responsible for retaining a correct folding of the transporter during the transport cycle. Glu327 appears not to be involved either in the binding of ethidium or the coupling of proton flux to ethidium transport. Energy-uncoupled mutants of LmrP were constructed, which showed increased rates of transmembrane electrical potential (Δψ)-driven influx of cationic drugs. The expression of such uncoupled secondary MDRs is disadvantageous and causes increased drug susceptibility to the host cells. This observation may be useful for developing alternative and more efficient strategies of antibiotic therapies.

EXPERIMENTAL PROCEDURES

Bacterial Strains, Plasmids, and Growth Conditions—L. lactis NZ9000 (ΔlmrA) (11), which lacks the gene encoding ATP-binding cassette-type MDR transporter LmrA (a kind gift from O. Gajic and J. Kok, Department of Genetics, University of Groningen), was used in combination with the NICE system (12, 13) for overexpression of wild type LmrP (WT LmrP) and the mutant proteins (14, 15). L. lactis cells were grown at 30 °C in M17 medium (Difco) supplemented with 0.5% (w/v) glucose and 5 μg/ml chloramphenicol. For the growth experiments, the M17 medium was prepared in 50 mM potassium phosphate (pH 7). Expression of LmrP variants from plasmid-derived plasmids was induced by adding −10 ng of nisin A per milliliter at an A660 of −0.6, and cells were harvested 60 min after induction.

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§ The abbreviations used are: MDR, multidrug resistance transporter; TMS, transmembrane segment; pCMBS, p-chloromercuri-benzene sulfonate; WT, wild type; pmf, proton motive force.

Multidrug resistance transporters (MDRs)1 play a crucial role in the resistance of prokaryotic and eukaryotic cells against cytotoxic compounds. In bacteria, including pathogens, the activities of MDRs contribute to the resistance against antibiotics (1–4). The control of spread and the prevention of selection of multidrug resistant strains has become a critical issue in the battle against contagious diseases (5). To fight antibiotic resistance efficiently, detailed knowledge of the molecular mechanisms underlying microbial drug resistance is required.

Most bacterial MDRs known to date are secondary transporters. For example, LmrP is a proton motive force (pmf)-driven MDR of Lactococcus lactis (6). LmrP is a member of the major facilitator superfamily of membrane proteins and shows homology to Bmr and NorA, the MDRs of Bacillus subtilis (7) and Staphylococcus aureus (8), respectively, as well as to the transporters involved in tetracycline resistance and bicyclomycin resistance in Escherichia coli (9). Cells expressing LmrP have increased resistance to several clinically important antibiotics from different pharmacological classes (10), which indicates the frightening possibility that its homologues in pathogenic bacteria may reduce the efficacy of important antibiotics in clinical settings.

In this study we report that LmrP is a true secondary transporter and is able to mediate active efflux and, under non-energized conditions, downhill drug influx and efflux. We show that residue Asp128, located in the cytoplasmic loop between transmembrane segments (TMS) II and III, is involved in the energy-coupling mechanism but not in substrate binding, whereas Asp126 in the cytoplasmic loop between TMS IV and V is not participating in the binding of ethidium either, but it might be part of the structural framework responsible for retaining a correct folding of the transporter during the transport cycle. Glu327 appears not to be involved either in the binding of ethidium or the coupling of proton flux to ethidium transport.

Energy-uncoupled mutants of LmrP were constructed, which showed increased rates of transmembrane electrical potential (Δψ)-driven influx of cationic drugs. The expression of such uncoupled secondary MDRs is disadvantageous and causes increased drug susceptibility to the host cells. This observation may be useful for developing alternative and more efficient strategies of antibiotic therapies.

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FIG. 1. Secondary structure model of LmrP. Acidic residues and the native cysteine are indicated. The model is based on the hydropathy profile of the amino acid sequence, the distribution of the arginine and lysine residues according to the “positive inside rule” (6), and the accessibility of cysteine mutants for membrane-impermeant, cysteine-reactive agents (15). Circled letters are single-letter amino acid designations accompanied by their position numbers.

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Preparation of Membrane Vesicles—Membrane vesicles with an inside-out orientation were prepared from L. lactis NZ9000 (ΔlmrA) cells expressing LmrP variants by the French press procedure as described by Putman et al. (14). The vesicles were frozen in liquid nitrogen and stored at −80 °C at a protein concentration of 15–35 mg/ml in 50 mM potassium phosphate, pH 7, containing 10% (v/v) glycerol. Measurements of Active Transport—For ethidium transport experiments, whole cells expressing LmrP variants were washed with 50 mM potassium phosphate (pH 7) containing 5 mM MgSO4, and suspended in the same buffer to an A660 of 0.5. Cells (2 ml) were energized by the addition of 25 mM glucose. After 2 min, 10 μM ethidium was added to the cell suspension, and the accumulation of ethidium was measured indirectly by following the fluorescence of the ethidium-poly nucleotide complex in the cells. Fluorescence was monitored with a PerkinElmer LS 50B fluorometer using excitation and emission wavelengths of 500 and 580 nm, respectively. The ethidium concentration that inhibits the growth rate by 50% (IC50) of sterile silicon oil were pipetted on top of the sample to prevent evaporation. The cells were grown in microtiter plates with 0.5 mM freshly dissolved ethidium, the cell suspension was incubated for an additional 5 min and emission wavelengths of 355 and 457 nm, respectively, and slit width of 5 nm each.

Measurements of Passive Fluxes—Cells were grown as described for measurements of active transport of ethidium. After the wash step, cells were resuspended to an A660 of 0.1. Cells present in 2 ml of this suspension were pelleted by centrifugation and loaded with 25 μM ethidium for 30 min at 30 °C in the final volume of 400 μl of 50 mM potassium phosphate (pH 7) containing 5 mM MgSO4. To determine the influence of p-chloromercuribenzenesulfonate (pCMBS) on passive fluxes of ethidium, the cell suspension was incubated for an additional 5 min with 0.5 mM freshly dissolved pCMBS prior to or after incubation with ethidium for influx and efflux experiments, respectively. After loading with ethidium, cells were pelleted by centrifugation in a table centrifuge (2 min at 14,000 rpm), and resuspended in 100 μl of 50 mM potassium phosphate (pH 7) containing 5 mM MgSO4. For fluxes, measurements 50 μl from this cell suspension were used. Determination of the Growth Rate—For the determination of growth rate in the presence of ethidium, cells were grown in microtiter plates as described (18). Overnight cultures of L. lactis NZ9000 (ΔlmrA), harboring pNZ2048, pHLP5, pHLP5::C270C, pHLP5::D128C/C270A, and pHLP5::E327C/C270A (14, 15) were diluted into fresh medium to an A660 of 0.05, and 150-μl aliquots of the cell suspension were transferred to sterile low protein binding 96-well microplates (Garneir, Germany) containing 50 μl of various concentrations of ethidium in fresh medium. For the induction of expression of LmrP, nisin (Sigma) was added to a final concentration of 100 pg/ml. Aliquots (50 μl) of sterile silicon oil were pipetted on top of the sample to prevent evaporation. The cells were grown at 30 °C, and the cell densities were monitored by measuring the absorbance at 690 nm every 10 min for 16 h in a multiscan photometer (Molecular Devices, Spectra Max 340). The ethidium concentration that inhibits the growth rate by 50% (IC50 value) was determined.

FIG. 2. Influence of pCMBS on transport of Hoechst 33342 in inside-out membrane vesicles prepared from cells expressing the WT and the cysteine-less variant (C270A) of LmrP. Membrane vesicles (20 mg of protein per milliliter) were incubated with or without 0.5 mM pCMBS for 5 min at 30 °C. Vesicles were subsequently washed once with 50 mM potassium phosphate, pH 7, and suspended to 0.5 mM Mg-ATP. Dotted lines, WT LmrP; dashed lines, mutant C270A; minus sign (−), not treated with pCMBS; and plus sign (+), treated with pCMBS.

RESULTS

Wild Type LmrP Is Sensitive to pCMBS—Wild type LmrP contains one native cysteine residue, Cys270, which is not accessible to the cysteine-reactive agent fluorescein maleimide and is most likely located in the putative TMS VIII (Fig. 1) (15). In a previous report (15), a cysteine-less mutant, C270A, was described that retained significant transport activity and was expressed to similar levels as wild type LmrP. To evaluate the role of Cys270, the effects of several cysteine-reactive agents were tested on LmrP-mediated transport of Hoechst 33342 and ethidium. These compounds are good substrates of LmrP and can be used for transport studies in whole cells and inside-out membrane vesicles (6, 14, 19).

Hoechst 33342 is highly fluorescent when present in the lipid environment of membranes but essentially non-fluorescent in the aqueous phase. Transport of Hoechst 33342 from the membrane into the aqueous phase can therefore be followed in membrane vesicles by monitoring the Hoechst 33342 fluorescence over time. The addition of ATP to inside-out membrane vesicles of L. lactis results in the generation of a pmf through proton pumping by the F1F0-ATPase. This pmf drives the transport of Hoechst 33342 by LmrP out of the membrane as indicated by the decrease in Hoechst 33342 fluorescence (Fig. 2). Wild type LmrP-mediated Hoechst 33342 transport was not affected by [2-(trimethylammonium)methyl]methanethiosulfon-
ate, 2-aminoethyl-methanethiosulfonate, or N-ethylmaleimide (data not shown), whereas pCMBS, a cysteine-reactive mercu-rial compound, inhibited Hoechst 33342 transport completely (Fig. 2). Inhibition of transport by pCMBS appears to be due to the reaction of Cys270 with pCMBS (Fig. 2), because pCMBS did not affect the generation of the pmf in inside-out membrane vesicles (data not shown) and did not inhibit Hoechst 33342 transport by the cysteine-less LmrP mutant C270A.

The effect of pCMBS on LmrP-mediated ethidium fluxes was also investigated. Ethidium crosses the membrane passively and intercalates subsequently into cellular polynucleotides, whereupon it becomes highly fluorescent. Ethidium transport in whole cells can be measured indirectly by monitoring the fluorescence of this intracellular ethidium-polynucleotide complex. Cationic compounds such as ethidium are electrophoretically imported into energized bacterial cells, and this process is driven by the Δψ (inside negative). Consequently, significant levels of accumulation of cationic compounds can occur even in the absence of an active uptake system (20, 21). Binding of ethidium to the cellular polynucleotides can further contribute to drug accumulation in cells relative to the environment. Ethidium accumulation by LmrA-deficient, glucose-energized cells expressing the WT LmrP and nonexpressing control cells demonstrated that WT LmrP can reduce the accumulation of ethidium in the cell by excreting this cationic compound (Fig. 3A) (6, 22). Also the C270A variant of LmrP is capable of reducing the cellular accumulation of ethidium, indicating that this mutant has retained significant transport activity (Fig. 3A) (15). The extrusion of ethidium is dependent on the presence of a pmf. In the absence of metabolic energy, ethidium is not actively extruded, and only the influx of ethidium across the membrane occurs. In control cells lacking LmrP, the influx of ethidium under non-energized conditions is very slow (Fig. 3B). On the other hand, non-energized cells expressing the WT or cysteine-less variant of LmrP have drastically higher rates of ethidium influx (Fig. 3B). Similar observations were made for the ethidium flux in the opposite direction. Under non-energized conditions, the rates of ethidium efflux were significantly lower from ethidium-preloaded, LmrP-nonexpressing
cells than from ethidium-preloaded WT LmrP and LmrP C270A mutant-expressing cells (Fig. 3C). The rates of the ethidium fluxes were proportional to the level of expression of LmrP (data not shown). These observations demonstrate that LmrP facilitates the flux of ethidium across the membrane in the absence of a pmf. Additional evidence that the ethidium flux is, to a large extent, LmrP-mediated was obtained by treatment of cells with pCMBS. pCMBS did not affect ethidium fluxes in control cells not expressing LmrP or in cells expressing C270A mutant LmrP, whereas it decreased drastically the fluxes of ethidium in cells expressing the WT LmrP (Figs. 2 and 3, D and E). These ethidium fluxes were inhibited by tetraphenylphosphonium, a well known substrate of LmrP (22), and the inhibitor verapamil (23), providing further support for the proposal that LmrP mediates facilitated fluxes of ethidium in non-energized cells (Fig. 3F and data not shown).

**Energy-uncoupled Mutants of LmrP Also Facilitate Drug Influx in Energized Cells**—Recently, the interesting observation was made that energized cells of *L. lactis* expressing variants of LmrP C270A with a single cysteine substitution (D68C/C270A, D128C/C270A, or E327C/C270A) accumulated ethidium rapidly (Fig. 4), whereas WT LmrP extrudes ethidium under these conditions. The ethidium influx rates into these cells were comparable with the influx rates observed in non-energized cells expressing WT LmrP (Fig. 3B).

These data indicate that the cysteine mutants D68C/C270A, D128C/C270A, and E327C/C270A are energy-uncoupled and capable of catalyzing only a facilitated diffusion of substrates. It is noteworthy that the influx rates into cells expressing these mutant proteins are slightly lower under non-energized conditions than under energized conditions (compare Figs. 4 and 5), which is consistent with the notion that the Δψ (inside negative) accelerates the facilitated diffusion process of this positively charged substrate.

**Sensitivity of Single Cysteine Mutants to pCMBS**—The effects of pCMBS on ethidium fluxes in *L. lactis* cells expressing the single cysteine mutants of LmrP were also investigated (Fig. 5). pCMBS (0.5 mM) strongly inhibited the influx and efflux of ethidium in cells expressing the D68C/C270A mutant or WT LmrP (Fig. 5, A and D). In contrast, pCMBS did not inhibit either influx or efflux of ethidium in cells expressing D128C/C270A (Fig. 5, B and E) or E327C/C270A (Fig. 5, C and F) mutants. Labeling of residues D128C/C270A and E327C/C270A by fluorescein maleimide could be prevented by preincubation of protein with pCMBS, demonstrating that both residues are accessible to this mercurial (data not shown).

**Phenotype of D68C, D128C, and E327C Mutants of LmrP**—To investigate whether the observed uncoupled phenotype of the D68C/C270A, D128C/C270A, and E327C/C270A mutants was caused by changing two residues in LmrP, the mutations giving an uncoupled phenotype in the cysteine-less background of the mutant C270A were also introduced into WT LmrP possessing Cys270. All three mutants were expressed to levels similar to that of WT LmrP (data not shown). The D68C mutant retained the uncoupled phenotype of the D68C/C270A mutant, whereas the D128C mutant catalyzed facilitated diffusion of ethidium into energized cells, but to a lower extent than the D128C/C270A mutant did. Unexpectedly, the E327C mutant exhibited a high transport activity of ethidium (Fig. 6), indicating that both mutations are responsible for the uncoupled phenotype of the E327C/C270A mutant.

**Cells Expressing the Energy-uncoupled Mutants of LmrP Are More Susceptible to Ethidium**—Because the LmrP mutants D68C/C270A, D128C/C270A, and E327C/C270A facilitate influx of ethidium, cells expressing these mutants should be more sensitive to drugs than nonexpressing control cells. To test this hypothesis, we followed the effects of ethidium on the growth of *L. lactis* NZ9000 (ΔlmrA) harboring the empty vector pNZ8048 or its derivatives encoding WT LmrP or mutants D270A, D68C/C270A, D128C/C270A, and E327C/C270A (Fig. 7). Concentrations of ethidium that resulted in a 50% reduction of the growth rates (IC_{50}) are given in Table I. For cells harboring the empty

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2 It should be noted that the annotation of the cysteine mutants used in this manuscript differs from the annotation used in Ref. 15 (D68C/C270A was D68C, D128C/C270A was D128C, and E327C/C270A was E327C).
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Fig. 6. Ethidium accumulation in energized L. lactis cells expressing WT and mutants of LmrP containing the endogenous Cys270. The cells were pre-energized for 2 min in the presence of 25 mM glucose, after which 10 µM ethidium was added. Solid line, cells harboring empty vector; dotted line, cells expressing WT LmrP; dash-dot line, cells expressing mutant D68C; long dashed line, cells expressing mutant D128C; dash-double dot line, cells expressing E327C mutant; and A.U., arbitrary units.

Fig. 7. Resistance of L. lactis NZ9000 (ΔlmrA) to ethidium. Cells carrying empty vector pNZ8048 (filled circle), plasmids coding for WT LmrP (inverted triangle), and the mutants C270A (square), D68C/C270A (diamond), D128C/C270A (triangle), and E327C/C270A (pentagon) were grown in M17 medium in the presence of different concentrations of ethidium. The relative growth rate is plotted as a function of the drug concentration. The data are from two independent experiments. The increase of viability of the cells expressing WT LmrP at low concentrations of ethidium was reproducible and observed in many experiments.

vector, the IC50 was 6.5 µM; the IC50 increased to 11 µM for cells expressing WT LmrP and to 7.8 µM for cells expressing C270A LmrP. In contrast, cells expressing LmrP mutants D68C/C270A, D128C/C270A, and E327C/C270A were significantly more sensitive to ethidium than the control cells not expressing LmrP and displayed IC50 values of ~1.9, 2, and 3.2 µM, respectively.

DISCUSSION

In this study the sensitivity of WT LmrP to pCMBS was used to demonstrate that LmrP plays a major role in the high fluxes of ethidium across the membranes under non-energized conditions. Ethidium accumulation was followed by measuring fluorescence of the cellular ethidium-polynucleotide complex. The influx of ethidium into (Fig. 3D) and the efflux of ethidium out of non-energized cells (Fig. 3E) were blocked upon the incubation of cells with pCMBS in cells expressing WT LmrP but not in cells expressing the cysteine-less mutant C270A. The rate of facilitated diffusion of ethidium under non-energized conditions increased with the expression levels of LmrP, and the ethidium fluxes are inhibited by other substrates of LmrP. Furthermore, we have generated LmrP mutants that are energy-uncoupled. These mutants facilitate rapid entry and exit of drugs into and out of the cell but are unable to secrete the drugs against their concentration gradient. These mutants resemble previously described energy-uncoupled mutants of the lactose permease (24, 25) and demonstrate that LmrP behaves as a true secondary transporter capable of mediating facilitated diffusion of substrates in both directions, depending on the direction of the substrate gradient.

Cells expressing a single cysteine variant of C270A LmrP (D68C/C270A, D128C/C270A, or E327C/C270A) rapidly accumulate ethidium under both non-energized and energized conditions (Figs. 4 and 5, A–C) and clearly exhibit an energy-uncoupled phenotype. However, the influx of ethidium is slower under non-energized conditions than under energized conditions, suggesting that the Δψ (inside negative) pulls cationic drugs into the cells (20, 21). These data also demonstrate that the negatively charged residues Asp68, Asp128, and Glu327 are not essential for ethidium binding. pCMBS inhibited the facilitated diffusion of ethidium in the D68C/C270A mutant, but not in the D128C/C270A and E327C/C270A mutants (Fig. 5). Because these residues are all accessible to pCMBS (data not shown), it appears that Asp128 and Glu327 are not in close proximity to either the binding site for ethidium or the substrate translocation pathway. To determine whether the uncoupled behavior of the single cysteine variants D68C/C270A, D128C/C270A, and E327C/C270A of LmrP is due to introduction of two mutations, i.e. an acidic amino acid to cysteine and the native Cys270 to alanine, an additional set of mutants was constructed, namely D68C, D128C, and E327C using WT LmrP as the template. One of these mutants, D68C, catalyzed the facilitated diffusion of ethidium into energized cells (Fig. 6), confirming a role of the Asp68 in the energy-coupling mechanism. Asp68 is part of the conserved motif, GXXXD/E/R/KXGRK, located in the cytoplasmic loop between TMS II and TMS III of the major facilitator superfamily of secondary transporters that are involved in the transport of a variety of compounds (26). The function of this motif has been extensively studied in other transporters. It is of interest to note that, for the tetracycline transporter TetA(B), it has been demonstrated that Asp68 (homologous to Asp68 in LmrP) does not directly participate in substrate binding but is part of the gating mechanism of TetA(B) (27). Moreover, N-ethylmaleimide labeling of a cysteine residue introduced next to the Asp68 in TetA(B) inhibited tetracycline transport, further suggesting that this region is essential for coupling transport to the pmf. In the E. coli lactose permease (LacY), substitutions of the conserved Asp68 almost completely abolish transport activity of lactose permease (28, 29). However, these mutants have not been reported to be uncoupled and display very low rates of downhill transport of lactose (28, 29). Conservation of this motif among members of the major facilitator superfamily suggests that this region is not directly involved in substrate binding but, instead, may be critical in facilitating conformational changes following

### Table I

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<th>Drug Influx via a Multidrug Transporter</th>
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<td>Data are ± S.E. and represent the average of two independent experiments.</td>
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substrate binding (30). The motif is connected with TMS II, which undergoes a conformational change upon interaction of lactose permease with ligands (25, 31) and faces the substrate binding cavity (32). We hypothesize that mutation D68C alters the structure of the loop connecting TMS II and TMS III and further disturbs the orientation of these two TMSs, thereby interfering with the coupling between the H⁺ flux and substrate translocation. The D128C mutant appeared to be less efficient in facilitating influx of ethidium into energized cells than the D12SC/C270A mutant (compare Figs. 4 and 6). At this stage, the function of Asp128 remains obscure. For the TetA(B) transporter, it has been proposed that Asp128 (corresponding to Asp128 in LmrP) forms an ion pair with an arginine residue present in a loop region between TMS II and TMS III, thereby ensuring a correct structure of the protein (33, 34). The third mutant, E327C, extrudes ethidium efficiently (Fig. 6), ruling out a role of Glu327 in proton translocation or ethidium binding. However, the presence of a negative charge at this location is critical for the interaction of LmrP with the divalent cation Hoescht 33342 (15), suggesting that Glu327 is part of the substrate binding pocket of LmrP. The two mutations in the E327C/C270A mutant thus seem to affect the conformation in this binding region in such a way that pmf-driven transport of ethidium and Hoescht 33342 is no longer possible. In summary, the uncoupled phenotype of mutants D68C and D128C is most likely the result of structural perturbations within LmrP, and these residues most likely do not play a direct role in H⁺ translocation.

The observations described above demonstrate that mutations of the native cysteine in LmrP, Cys270, somehow affect the activity of the transporter. In a previous study (15), we have shown that Cys270 is not accessible to fluorescein maleimide labeling and, therefore, is most likely membrane-embedded. In this report we tested several other cysteine-reactive compounds to probe the role of Cys270, but only pCMBS was found to inhibit the transport activity of WT LmrP. Because pCMBS had no effect on the activity of the cysteine-less mutant C270A, we conclude that this mercuリアル targets Cys270. This residue is likely located in a transmembrane region of the protein that is poorly accessible to the water phase, because the maleimide probe was not reactive with the Cys270. Nevertheless, Cys270 is not essential for transport, as the C270A mutant showed substantial activity. Inhibition of transport by pCMBS could be due to the location of Cys270 close to a substrate binding site or to the translocation pathways of substrates and/or protons. A location in the substrate binding site seems unlikely, because the affinity of the C270A mutant for Hoescht 33342 is unchanged upon reaction with pCMBS. Alternatively, pCMBS-labeling of Cys270 may interfere with conformational changes of LmrP during the transport cycle. It is noteworthy that the significant Hoescht 33342 and ethidium transport activity of the C270A mutant excludes a direct role of Cys270 in proton translocation.

One conclusion of our work is that the presence of a secondary WT MDR, such as LmrP, causes the rapid influx of drugs under non-energized conditions. This observation demonstrates that LmrP is a proper secondary transporter and mediates active transport and, in the absence of pmf, downhill fluxes of substrates. These modes of transport are typical for secondary transporters and have been described previously (37, 38). Notably, we report here a new important finding that expression of an uncoupled MDR increases the sensitivity of cells to ethidium even under energized conditions. Clearly, expression of such an energy-uncoupled secondary MDR allows a membrane potential-driven accumulation of a toxic cationic substrate in cells. Consequently these cells are more susceptible to drugs than cells that do not express the transporter at all. On the contrary for neutral substrates, as reported for uncoupled mutants of lactose permease, only fluxes down a chemical substrate gradient or exchange reaction are possible (39). For a neutral substrate, such concentration-driven fluxes do not lead to accumulation in cells. This knowledge may be used to develop new strategies in the battle against multidrug-resistant pathogens. Modulators of secondary MDRs, which do not compete with the antibiotic for the same binding site but uncouple drug efflux from proton influx, will allow ΔpH-driven accumulation of cationic antibiotic substrates, resulting in an increased drug sensitivity of the pathogens.

REFERENCES