The Mouse Bcrp1/Mxr/Abcp Gene: Amplification and Overexpression in Cell Lines Selected for Resistance to Topotecan, Mitoxantrone, or Doxorubicin

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Abstract

Mouse fibroblast cell lines lacking functional Mdr1a, Mdr1b, and Mrp1 genes were selected for resistance to topotecan, mitoxantrone, or doxorubicin. Each of the resulting drug-resistant lines showed marked gene amplification of Bcrp1, the mouse homologue of the human ATP-binding cassette transporter gene BCRP/MXR/ABCP, and greatly elevated expression of Bcrp1 mRNA. All three of the resistant cell lines were highly cross-resistant to topotecan and mitoxantrone and, to a variable extent, doxorubicin. All showed greatly reduced cellular accumulation and greatly increased efflux of mitoxantrone that was dependent on cellular ATP and efficiently reversed by the compound GF120918. The mouse Bcrp1 cDNA encodes a 657-amino-acid protein with 81% identity (86% similarity) to the human breast cancer resistance protein (BCRP) and a virtually superimposable hydrophobicity profile. Our data argue strongly that mouse Bcrp1 is functionally comparable with human BCRP, conferring multidrug resistance to topotecan, mitoxantrone, doxorubicin, and related compounds. Mouse models and cell lines should, therefore, be highly informative in understanding the clinical, pharmacological, and physiological roles of BCRP.

Introduction

Several sources of MDR have been identified and well studied. They include elevated levels of P-gp or the MDR protein MRP1, both members of the ABC transmembrane protein family (1–4). The proteins are efflux pumps situated in the plasma membrane, with broad substrate specificities including several clinically important antineoplastic drugs. Despite extensive knowledge of their activity in vitro and evidence of their involvement in MDR in certain types of tumors, it is still unclear what mechanisms contribute most to MDR in many clinical tumors. It is very possible that as yet unidentified or poorly understood mechanisms will turn out to be as important in clinical practice as P-gp and MRP1. The recently identified ABC gene BCRP/ MXR/ABCP is a candidate for such a mechanism, inasmuch as its expression in transfected cell lines confers resistance to doxorubicin, mitoxantrone, and related drugs (5–7). Cross-resistance to mitoxantrone and doxorubicin that is associated with reduced drug accumulation but not elevated P-gp or MRP1 has been reported previously for a number of drug-selected cell lines (8–11). In some of these lines cross-resistance to topotecan was also noted (12, 13). Drug resistance in several of these lines has now been attributed to elevated expression of BCRP (5, 7, 14, 15).

Mouse cell lines lacking functional Mdr1a and Mdr1b (encoding mouse P-gps), and Mrp1 genes constitute a potentially fertile resource for identifying new mechanisms of drug resistance. Such lines are markedly more sensitive than equivalent wild-type lines to P-gp and MRPI substrate drugs, including doxorubicin, paclitaxel, topotecan, and vincristine. Selection of these lines for resistance to antineoplastic drugs may, therefore, invoke resistance mechanisms normally masked or overshadowed by the presence of P-gp or Mrp1. Indeed, we report here that selection with topotecan, mitoxantrone, or doxorubicin readily resulted in overexpression of the mouse Bcrp1 gene.

Materials and Methods

Cell Lines. Adherent, spontaneously immortalized embryo (MEF3.8) and ear (KOT52) fibroblast cell lines were derived by 3T3-like procedures (16) from Mdr1a−/− Mrp1−/− mice, obtained by crossing Mdr1a−/− Mdr1b−/− (17) and Mrp1−/− (18) knockout mice. Cells were grown in complete medium, i.e., DMEM supplemented with 10% FCS, and passaged by trypsinization. Drug-resistant sublines were selected by continuous exposure to topotecan, mitoxantrone, or doxorubicin, with repeated two-fold increments in drug concentration over a period of 4–8 months, corresponding to 20–40 passages.

Drug Resistance Assays. Growth inhibition (IC50) assays were performed by seeding 250 or 500 cells per well in 96-well plates in complete medium and applying drugs in a dilution series, each concentration in quadruplicate wells. After 4–4.5 days, when unselected wells were still subconfluent, cells were lysed in situ, nucleic acids were stained with a proprietary dye (Cyquant, Molecular Probes, Eugene, OR), and quantified by UV fluorescence (485 nm excitation, 530 nm emission). All such assays were performed three times.

Mitoxantrone Accumulation and Efflux Assays. Relative cellular accumulation of mitoxantrone was determined by flow cytometry using excitation at 633 nm and a 661 nm band-pass filter to detect emission. All of the assays were conducted at 37°C with 107 (subconfluent) cells per well in 12-well plates, seeded in complete medium without drug the night before. Mitoxantrone was added for timed intervals in fresh, prewarmed, complete medium containing 5% FCS. Accumulation or efflux was arrested by prompt cooling on ice, and the cells were maintained at 0°C during all of the subsequent steps, including trypsinizing. Where indicated (see “Results”), mitoxantrone accumulations were done in the presence of 2 μM GF120918; pilot experiments indicated that this concentration gave >95% maximal effect. Cells were preincubated with GF120918 for 30–60 min before adding mitoxantrone. Accumulation under ATP-depleting conditions was performed for 2 h in glucose-free, pyruvate-free DMEM containing 5% dialyzed FCS, plus 10 mM sodium azide to inhibit oxidative phosphorylation, as described previously (19). Mitoxantrone efflux was assayed after accumulation under ATP-depleting conditions: the medium and drug were removed by aspiration, wells were then incubated with prewarmed complete medium at 37°C for timed intervals prior to harvesting. Assays were performed at least twice, each time with triplicate wells.

Bcrp Cloning and Sequencing. Mouse Bcrp1 cDNAs were amplified by PCR with primers based on mouse EST sequences homologous to the 5′ and 3′ ends of human BCRP, with XhoI linkers added: 5′-GAG TGA GAT CTA GAA GGC ATA AAT CCT AAA GAT GTC TTC C and 3′-GAG TGA GAT CTA GAA GGC ATA AAT CCT AAA GAT GTC TTC C and 3′-AAG GTA AGT

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3 The abbreviations used are: MDR, multidrug resistance; MRP, MDR-associated protein; ABC, ATP-binding cassette; BCRP, breast cancer resistance protein; P-gp, P-glycoprotein; EST, expressed sequence tag.

Results

Selection of Resistant Lines and Analysis of Cross-Resistance. Cell lines nullizygous for Mdr1a, Mdr1b and Mrpl were selected for resistance to topotecan, mitoxantrone or doxorubicin (see “Materials and Methods” for details). The embryo fibroblast line MEF3.8 yielded the topotecan-resistant subline T6400 and the mitoxantrone-resistant subline M32. The ear fibroblast line KOT52 yielded a doxorubicin-resistant subline, D320. Compared with their parental lines, the sublines were each more than 100-fold resistant to the selecting drug but remained sensitive to paclitaxel, vincristine and cisplatin (Table 1). The T6400, M32 and D320 lines were all highly cross-resistant to topotecan and mitoxantrone. The T6400 and M32 lines also showed some cross-resistance to anthracyclines and bisantrene (a compound structurally related to mitoxantrone) but at a much lower level than the doxorubicin-selected D320 line. The D320 line was also much more resistant to etoposide.

Reduced Drug Accumulation and Increased Efflux. Doxorubicin and mitoxantrone interfere with topoisomerase II activity, whereas topotecan acts on a different target, topoisomerase I. Cross-resistance to both types of drugs could be explained most easily by reduced cellular drug accumulation, which can be readily measured for mitoxantrone by flow cytometry. Indeed, as a function of either time (Fig. 1A) or drug concentration (Fig. 1B), mitoxantrone accumulation was greatly reduced in all three of the resistant sublines compared with the sensitive parental lines. The accumulation deficits could be largely reversed by performing the assays under conditions that deplete cellular ATP (Fig. 1C), which indicates that they are mediated by an ATP-dependent mechanism. The accumulation deficits were similarly reversed in the presence of GF120918, a known P-gp inhibitor (19) also reported to inhibit human BCRP (20). Confocal scanning microscopy revealed no qualitative differences in the subcellular localization of mitoxantrone in resistant versus sensitive cells (data not shown), implying that the mechanism responsible for reduced accumulation operates at the plasma membrane.

Comparisons of mitoxantrone efflux rates under normal cell culture conditions were forestalled by the large differences in drug accumulation; it was not feasible to load the drug-resistant sublines to intracellular mitoxantrone levels similar to those obtained in the drug-sensitive parental lines, even using 200-fold greater concentrations of applied mitoxantrone. Nevertheless, similar mitoxantrone loadings were possible under ATP-depleting conditions, and efflux could be monitored after returning the loaded cells to normal conditions. The results (Fig. 1D) show dramatically increased mitoxantrone efflux from the resistant sublines compared with the sensitive parental lines. Because recovery from ATP-depleted conditions is probably not immediate, the efflux curves likely underestimate the normal mitoxantrone efflux activity in these lines.

Cloning and Sequencing of Mouse Bcrp1. The cross-resistance patterns and the ATP-dependent changes in mitoxantrone accumulation and efflux and their inhibition by GF120918 suggested the possibility of up-regulation of a mouse homologue of BCRP in one or more of the resistant lines. We, therefore, cloned and analyzed a mouse cDNA, Bcrp1, closely homologous to human BCRP. cDNAs containing the full Bcrp1 coding sequence were obtained by high-fidelity PCR based on existing mouse EST sequences homologous to the 5’ and 3’ ends of human BCRP. The cDNA sequence contains an extended open reading frame starting four codons downstream of an in-frame stop codon. This encodes an ABC transporter “half molecule” of 657 amino acids corresponding closely in sequence and structure to human BCRP (Fig. 2). The mouse Bcrp1 and human BCRP amino acid sequences are 81% identical and 86% homologous. Conservation is, as expected, very high in the ATP-binding cassette. The level of conservation between the mouse and human polypeptides is comparable with that between human MDR1 and mouse Mdr1a (87% identity) or Mdr1b (81% identity). Hydrophobicity plots of mouse Bcrp1 and human BCRP are almost identical (Fig. 2), increasing confidence in the assignment of six putative transmembrane domains (5, 6). However, the locations of charged amino acids in the mouse sequence merit small shifts in the positions assigned to some of the transmembrane domains relative to those proposed for human BCRP. Four potential sites for N-linked glycosylation are apparent; the first two lie in what is likely to be the cytosolic part of the protein, whereas the latter two are closely spaced in the loop between the fifth and sixth putative transmembrane domains and are, thus, probably extracellular (only one is conserved in human BCRP).

Bcrp1 Overexpression and Amplification in Resistant Cell Lines. On Northern blots (Fig. 3A), the Bcrp1 coding sequence probe identified either one or two bands at about 2.6 kb in the resistant...
sublines and mouse liver, similar to observations for the human BCRP mRNA (5–7). Bcrp1 mRNA was expressed in each of the three resistant cell lines at roughly similar levels. The mRNA was not detectable in the parent cell lines at this sensitivity; this implies an increase in expression of more than 10-fold. The significance of the two transcripts is not known, but in humans, they may stem from alternate polyadenylation sites (7) or differences at the 5′ end of the mRNA (6). The elevated Bcrp1 expression was associated with heavy amplification of the gene locus, in each case greater than 20-fold compared with the drug-sensitive parent lines (Fig. 3B), as has been observed in several drug-resistant human cell lines overexpressing BCRP (7, 15).

Two mouse ESTs for a sequence related to human BCRP but distinct from Bcrp1 were also identified (AA277174 and AI463023). We tentatively denote this sequence Bcrp2. One might speculate that the molecule encoded by Bcrp2 represents a partner for Bcrp1 in heterodimers. However, its expression, already very low in the MEF3.8 and KOT52 parental lines as determined by RNase protection, was not elevated in the drug-resistant sublines (data not shown).

Discussion

Our data show that the mouse Bcrp1 gene is readily amplified and overexpressed in cell lines made resistant to three different drugs—topotecan, mitoxantrone, and doxorubicin. The resistant sublines display greatly reduced mitoxantrone accumulation via an ATP-dependent efflux mechanism. All of the lines are characterized by cross-resistance to topotecan and mitoxantrone, and also to...
doxorubicin, albeit to a lesser extent in the M32 and T6400 lines than in the doxorubicin-selected D320 line. The evidence at hand strongly favors the interpretation that Bcrp1 overexpression is responsible for much of this pattern of resistance. Cross-resistance to mitoxantrone and doxorubicin in drug-selected human cell lines has, in several cases, now been attributed to BCRP overexpression (5, 7, 15). Although concomitant cross-resistance to topotecan has been observed in a few cases (12, 13), we have now shown that Bcrp1 expression is also readily elevated by topotecan selection per se. The same could occur in human tumors, some of which are extensively treated with topotecan in the clinic.

Mouse Bcrp1, thus, appears functionally comparable with the human BCRP as a multidrug transporter. Functional homology is also suggested by the close structural similarities between the mouse and human polypeptides. Mouse models, therefore, will likely be appropriate and valuable for investigating the biochemistry and physiological functions of the BCRP/Bcrp1 protein, and its significance for drug pharmacokinetics and drug-resistance in tumors. We are currently developing such models.

The availability of effective inhibitors of Bcrp1 will be invaluable to such studies. It is of great interest that GF120918 turns out to be an effective inhibitor of both human BCRP (20) and mouse Bcrp1.

Fig. 2. The mouse Bcrp1 polypeptide sequence and superimposed hydrophobicity plots of the mouse Bcrp1 and human BCRP polypeptides. Amino acids that differ in the human BCRP sequence (taken from GenBank, accession AF098951) are shown below their mouse counterparts. Consols indicate conservative substitutions, and dashes are alignment gaps. Putative features are marked: overscore, transmembrane segments; double overscore, Walker A and B motifs; box, potential N-linked glycosylation sites, although the first two of these are presumed to lie within the cytosolic portion of the protein. The hydrophobicity plot was determined by the Kyte-Doolittle method using a window-length of 17 amino acids; bars, putative transmembrane regions.

Mouse Bcrp1 mRNA expression in the drug-resistant cell lines versus their sensitive parental lines. A 1.95-kb Bcrp1 coding sequence probe was used. A mouse liver sample was included for comparison of expression level, but its migration in the gel was slightly retarded by salt in the sample. Each lane on the blot contained 5 µg total RNA. Subsequent hybridization of the blot with an 18S-rRNA probe provided a loading control. B. Southern analysis of Bcrp1 copy number in the same panel of cell lines, using 5 µg of Kpn1-digested genomic DNA per lane. Hybridization of the blot with a glyceraldehyde phosphate dehydrogenase (gapdh) probe provided an independent loading control, indicating that the D320 lane was substantially underloaded. The quantitation of Bcrp1 amplification reported in the text included normalization for the gapdh signal.
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References


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