Multidrug Resistance Proteins MRP3, MRP1, and MRP2 in Lung Cancer: Correlation of Protein Levels with Drug Response and Messenger RNA Levels

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ABSTRACT

Previously (L. C. Young et al., Clin. Cancer Res., 5: 673–680, 1999), we found, in a panel of 23 lung cancer cell lines that had not been selected for in vitro drug resistance, that the mRNA levels of MRP3 and MRP1, two members of the ATP-binding cassette superfamily of transport proteins, correlated with resistance to doxorubicin, vincristine, VP-16, and cis-diaminedichloroplatinum(II). To extend these studies, we measured multidrug resistance protein (MRP)1, MRP2, and MRP3 protein levels in a panel of 30 lung cancer cell lines that included the original 23 cell lines as well as an additional 7 unselected lung cancer cell lines. In the case of MRP3, a polyclonal antibody was developed that was found to be a sensitive reagent for the detection of MRP3 by Western blot analysis. We found good agreement in the original 23 cell lines between the cognate mRNA and protein levels for MRP1, MRP2, and, especially, MRP3 (r, 0.852), supporting the use of semiquantitative PCR to predict MRPI, MRP2, and MRP3 protein levels in patient samples. There were also strong correlations between the mRNA and protein levels of MRP3 and MRP1, which suggested that these genes might be expressed in a coordinate manner. MRP3, MRP1, and MRP2 protein levels were higher in the non-small cell lung cancer (NSCLC) than in the SCLC cell lines and, in addition, MRP3 and MRP2 were detected almost exclusively in the NSCLC cell lines. Finally, we found that both MRP3 and MRP1, but not MRP2, protein levels correlated with decreased sensitivity of these lung cancer cell lines to doxorubicin, VCR, VP-16, and cis-diaminedichloroplatinum(II). These findings are consistent with our hypothesis that both MRP3 and MRP1 are components of the multifactorial multidrug resistance phenotype of lung cancer and that MRP3 contributes to the intrinsic resistance of NSCLC cells.

INTRODUCTION

Chemotherapy plays a major role in the treatment of lung cancer, the primary cause of cancer-related death in North America. However, resistance to multiple chemotherapy agents remains a major obstacle to the cure of many forms of cancer, including SCLC and NSCLC. Most SCLCs acquire multidrug resistance, whereas NSCLCs tend to be intrinsically resistant to chemotherapy. Some members of the ABC superfamily of transport proteins have been shown to confer drug resistance in vitro, including members from subfamilies B, C, and G (1). Subfamily B includes P-glycoprotein (MDR1, gene symbol ABCB1), the first human ABC transporter shown to confer multidrug resistance. Although P-glycoprotein is implicated in drug resistance in several tumor types, it is infrequently expressed in lung cancer (2, 3), and in a panel of 23 lung cancer cell lines that had not been selected for drug resistance, we found that these low levels of expression did not correlate with drug response (4).

Like MRP1/ABCC1 as well as genes not associated with drug resistance, such as the cystic fibrosis transmembrane conductance regulator (CFTR) and the sulfonylurea receptors, SUR1/ABCC8 and SUR2/ABCC9 (recently reviewed in Ref. 1). MRP1, cloned from the doxorubicin-resistant H69AR SCLC cell line (5), is associated with drug resistance or poor patient outcomes in a variety of tumor types including lung carcinoma (6), breast carcinoma (7, 8), gastric carcinoma (9, 10), neuroblastoma (11, 12), retinoblastoma (13), endometrial carcinoma (14) and, possibly, acute myeloid leukemia (15). MRP3 (ABCC3) and MRP2 (ABCC2) are the ABC transporters that are most closely related to MRP1 with 58 and 49% amino acid identity, respectively (16).

Like MRP1, MRP2 and MRP3 mRNA (17–19) and protein levels (17) are increased in some drug-selected cell lines. However, the reported drug resistance profiles conferred by MRP3 and MRP2 are variable. The reasons for this are unclear.
but may be attributable to differences in cell culture conditions and to the choice of transfected host cell lines that affect both the expression level and the subcellular localization of these proteins (20–23). However, it seems clear that MRP3 and MRP2, like MRP1, can confer resistance to short-term methotrexate exposure (24, 25). Transfection of MRP2 cDNA into drug-sensitive cells has been reported to confer low levels of resistance to CDDP, DOX, etoposide, VCR, vinblastine, and, possibly, VP-16 (26–29). MRP3 may confer drug resistance (24, 30), but the resistance profile is different from those of MRP1 and MRP2. To date, the resistance conferred by MRP3-transfection has been difficult to evaluate because the protein expression and relative resistance levels have been low (24, 30).

Previously, we found that MRP3 and MRP1, but not MDR1, MRP2, MRP4, or MRP5, mRNA levels correlated with the resistance of a panel of 23 unselected lung cancer cell lines to four chemotherapeutic agents (3, 4). Additionally, MRP3 and MRP1 mRNA levels were higher in the NSCLC than the SCLC cell lines (4). In the present study, we measured the protein levels of MRP3, MRP1, and MRP2 in an expanded panel of 30 unselected lung cancer cell lines. We examined the relationships between: (a) the protein levels of these genes; (b) the protein levels and their cognate mRNA levels; and (c) the protein levels and the drug sensitivity of the cell lines. We also determined the distribution of these protein levels in the NSCLC and SCLC cell lines.

MATERIALS AND METHODS

Cell Lines. The cell lines examined in the present study consisted of 30 lung cancer cell lines that had not been selected for drug resistance in vitro. This panel included the 23 lung cancer cell lines (13 NSCLC and 10 SCLC) used previously by us (4) and 7 additional SCLC cell lines (AD-A, GL-E, JS-E, LG-T, OS-A, SM-E, WL-E, and TY-E; Refs. 3 and 31). The conditions for establishing and culturing these cell lines have been described previously (31).

Cytotoxicity Testing. The toxicity of a 48-h exposure of the lung cancer cell lines to DOX, VCR, VP-16, and CDDP was measured using a modified MTT assay and was expressed as the AUC, as calculated by the trapezoidal method (32, 33).

Anti-MRP3 Antiserum. An anti-MRP3 polyclonal antiserum, designated LY1, was generated by immunizing rabbits with a synthetic 15-amino-acid peptide (1163AYNRSRDEHIEH-DTK1177) in the form of a multiple antigen peptide (MAP). The sequence of the MRP3-specific MAP was based on regions of dissimilarity between the COOH terminus of MRP3 and the COOH termini of MRP1, MRP2, MRP4, and MRP5. The IgG fraction of the LY1 antiserum was purified on protein A-Sepharose CL-4B (Amersham Pharmacia Biotech, Baie d’Urfé, Québec, Canada) and was used at a dilution equivalent to 1:8000 of the original serum volume. Peptide synthesis and rabbit immunizations were performed by Research Genetics (Huntsville AL).

Preparation of Membrane-enriched Fractions. Membrane-enriched fractions were isolated from 60 × 10^6 cells as described previously (34). Protease inhibitors (Complete, Mini protease inhibitor cocktail tablets with 200 μg/ml benzamidine; Roche Diagnostics, Laval, Québec, Canada) were included to minimize protein degradation and protein concentrations were determined using the Bio-Rad Protein Assay Dye (Bio-Rad Laboratories Ltd., Mississauga, Ontario, Canada).

PNGase F Treatment. N-linked carbohydrates were removed from membrane proteins with PNGase F (New England Biolabs, Ltd., Mississauga, Ontario, Canada). Digestion was performed according to the manufacturer’s instructions except that samples were incubated for 30 min at 37°C in denaturing buffer instead of the recommended 10 min at 100°C. To minimize protein degradation, protease inhibitors were included in all of the steps, and digestion times were shortened to 45 min.

SDS-PAGE and Western Blot Analysis. SDS-PAGE was performed by the Laemmli method with a 4% stacking gel and a 7.5% separating gel. Prior to loading, samples were diluted in solubilizing buffer [final concentration, 2.5% (w/v) SDS, 5% (v/v) 2-mercaptoethanol] and incubated for 30 min at 37°C. The separated proteins were electrotransferred onto Immobilon-P membranes (Millipore Ltd, Etobicoke, Ontario, Canada) in Tris-glycine-SDS transfer buffer, and blots were blocked in 4% (w/v) dry milk, Tris-buffered saline, and 0.05% Tween 20. Primary antibodies used were: LY1, a rabbit anti-MRP3 polyclonal antibody (IgG fraction, described above, 1:8,000); QCRL-1, a mouse anti-MRP1 mAb (1:10,000; Ref. 34, 35); MRP1, a rat anti-MRP1 mAb (1:2,000; Signet Laboratories, Inc., Dedham, MA; Ref. 36); EAG15, a rabbit anti-MRP2 polyclonal antibody (1:20,000; a generous gift of Dr. D. Keppler, Division of Tumor Biochemistry, Deutsches Krebsforschungszentrum, Heidelberg, Germany; Refs. 37 and 38); mouse monoclonal anti-MRP2 M3III-6 (1:250; Alexis Biochemicals Corp, San Diego, CA); and M3II-9, a mouse anti-MRP3 mAb (1:40; Kamiya Biomedical Company, Seattle, WA). Antibody binding was visualized using the appropriate horseradish peroxidase-conjugated secondary antibody and the Renaissance-enhanced luminol reagent (NEN Life Science, Mandel Scientific Co., Ltd. Guelph, Ontario, Canada) on X-Omat Blue film. X-ray films were scanned and analyzed using ImageQuantNT densitometry software v 4.2.a (Molecular Dynamics, Sunnyvale, CA).

Statistics. Statistical analyses were performed using the Systat software package, version 7 (SPSS Inc., Chicago, IL). Natural logarithmic (Ln) transformations of MRP1, MRP2, and MRP3 protein levels were performed so that these data would more closely approximate a normal distribution. The Pearson correlation coefficients (r) and associated probabilities (P) were calculated for the following combinations of data sets: MRP1–3 protein levels and cognate mRNA levels; MRP1, MRP2, and MRP3 protein levels; and MRP1–3 protein levels and AUC values. Values for mRNA levels (n = 23) are from our previous study (4). Descriptive terms for the strength of the correlations were defined as follows: strong, |r| ≥ 0.7; moderate, |r| ≥ 0.5; weak, |r| ≥ 0.3; and none (no appreciable correlation), |r| < 0.3.

RESULTS

Characterization of the LY1 Anti-MRP3 Polyclonal Antisera. We found that the LY1 antiserum (IgG fraction), raised against a 15-amino-acid MRP3-peptide, was a sensitive reagent for the detection of MRP3 by Western blot analysis. LY1 detected a Mr 200,000 integral membrane protein with properties consistent with those of MRP3 (Fig. 1). Digesting the...
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Fig. 1 LY1 polyclonal antiserum (IgG) is a sensitive reagent for the detection of MRP3. Immunoblots of A549 (10 μg) and LC-T (40 μg) NSCLC cell line membrane proteins as detected by LY1 polyclonal and MII-9 mAb. Before separation by 7.5% SDS-PAGE, membrane proteins were either incubated with PNGase F (+) or a glycerol control (−). LY1 detected a Mr 200,000 membrane protein that, on deglycosylation, migrated with an apparent molecular weight of Mr 170,000 (Lanes 2 and 3). Similar results were obtained with the MII-9 mAb (Lanes 1 and 2). However, in cell lines with low MRP3 levels (e.g., the LC-T NSCLC cell line), the LY1 polyclonal antiserum (1:8000) was at least as sensitive in detecting the Mr 200,000 band as the MII-9 mAb (1:40; Lanes 4, 5, and 8). Solubilization of the membrane proteins before deglycosylation was performed at 37°C because heating to 100°C greatly reduced the detection of MRP3 by LY1 (Lane 1) or MII-9 (data not shown).

MRP1, MRP2, and MRP3 Protein Levels. For each of the 30 lung cancer cell lines, 40 μg of PNGase F treated and 40 μg control membrane proteins were separated by SDS-PAGE and MRP3, MRP1, and MRP2 were detected by Western blot analysis with LY1, QCRL-1, and MII-3-6, respectively. We found that deglycosylation of the membrane proteins increased the ability to detect and quantitate low levels of glycoproteins (Fig. 2). MRP3 was detected in most of the NSCLC cell lines but was not detected in any of the SCLC cell lines (Fig. 3). Similarly, MRP2 was detected in most of the NSCLC cell lines but in only one SCLC cell line, SHP-77. However, relative MRP3 levels tended to be higher than MRP2 levels. MRP1 was detected in all of the 30 unselected lung cancer cell lines and, like MRP3 and MRP2, median levels were higher in the NSCLC than in the SCLC cell lines.

Correlation Analyses. Pearson correlation coefficients (r) and associated probabilities (P) were calculated to determine whether (a) MRP1–3 protein levels correlated with the mRNA levels, (b) MRP1–3 protein levels were correlated with each other, and (c) MRP1–3 protein levels correlated with the resistance of the cell lines to DOX, VCR, VP-16, or CDDP.

Previously, we determined MRP1, MRP2, and MRP3 mRNA levels by semiquantitative PCR for 23 of the 30 cell lines (4). Using these values, we analyzed the correlations between the protein and mRNA levels of MRP3, MRP1, and MRP2 (Table 1). The high MRP2 values for the A549 NSCLC cell line were omitted from this calculation because they exerted undue influence on the correlation. The correlations between the protein levels and their cognate mRNAs were strong for both MRP3 and MRP2, and moderate for MRP1 (Table 1).

In our previous study, we found moderate-to-weak correlations between the mRNA levels of MRP3, MRP1, and MRP2 (r, 0.570–0.495) in the 23 cell lines (4). In comparing the protein levels in the expanded panel of 30 cell lines, we found an even stronger correlation between MRP3 and MRP1 levels (r, 0.716), whereas the correlation between MRP3 and MRP2 levels remained weak (r, 0.407), and there was no correlation between MRP1 and MRP2 levels (r, 0.131; Table 2).

Previously, when examining the correlations of MRP1 and MRP3 mRNA levels with the resistance of the 23 cell lines to DOX, VCR, VP-16, and CDDP, we found a strong correlation between MRP3 mRNA levels and DOX resistance and a weak correlation between MRP1 mRNA levels and CDDP resistance; all of the remaining correlations with these mRNAs were moderate (4). Also, we found no correlation between the MRP2, MRP4, or MRP5 mRNA levels and resistance to these drugs. The patterns of the correlation between the protein levels and chemosensitivity in this study (Table 3) were in agreement with those using mRNA levels (4) but generally were not as strong. One notable exception was the correlation between MRP1 and DOX resistance. The correlation coefficient of DOX resistance with MRP1 protein levels was 0.741 (Table 2) versus 0.519 with MRP1 mRNA levels (4). MRP3 protein levels also demonstrated a strong correlation with the resistance of the panel of cell lines to DOX (Table 3). The correlation between MRP1 protein levels and resistance of the cell lines to CDDP was moderate (Table 3). The correlations of the remaining MRP3 or MRP1 protein levels with the AUC data were weak (r, 0.423–0.477; Table 3). MRP2 protein levels did not correlate with resistance to any of the four drugs tested (Table 3).

DISCUSSION

MRP1 has been shown to confer multidrug resistance in vitro (39–42) and to be associated with poor patient outcomes for several types of cancer (7–13), including lung cancer (6). The response of lung cancer to chemotherapy treatment is characterized by multifactorial multidrug resistance that
may be either acquired (SCLC) or intrinsic (NSCLC) and results in treatment failure and death within 2 years of diagnosis in the majority of cases. Previously, we found that both MRP1 and MRP3 mRNA levels correlated with decreased chemosensitivity and that median mRNA levels were higher in NSCLC than in SCLC cell lines (3, 4). In the present investigation, we have analyzed the protein levels of MRP3, MRP1, and MRP2 in a panel of lung cancer cell lines comprised of 23 cell lines from our previous study plus an additional 7 cell lines that also had not been selected for drug resistance in vitro.

We found that the protein levels of MRP3, MRP1, and MRP2 were higher in the NSCLC cell lines than in the SCLC cell lines (Fig. 3). These results are in agreement with semi-quantitative PCR of MRP1 mRNA levels by us (4) and by Narasaki et al. (43), and with our immunohistochemical investigation of untreated NSCLC and SCLC tumors (44). Unlike MRP1, which was present in all 30 of the SCLC and NSCLC cell lines, we detected MRP3 and MRP2 only in the NSCLC cell lines with the exception of one cell line in which MRP2 was detected. Protein levels were normalized to those found in the A549 NSCLC cell line and then Ln-transformed for statistical analyses. Horizontal line, the median protein level for each data set.

**Table 1** Pearson correlation coefficients ($r$) and associated probabilities ($P$) for the correlation of mRNA and protein levels for MRP3, MRP1, and MRP2 in a panel of 23 unselected lung cancer cell lines.

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<th>MRP3</th>
<th>MRP1</th>
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<tr>
<td>$r$</td>
<td>0.852</td>
<td>0.519</td>
<td>0.787</td>
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<td>$P$</td>
<td>$&lt;0.001$</td>
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$n = 23$.

**Table 2** Pearson correlation coefficients ($r$) and associated probabilities ($P$) for the correlation of MRP3, MRP1, and MRP2 protein levels in a panel of 30 unselected lung cancer cell lines ($n = 30$).

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<th>MRP3</th>
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<tr>
<td>$r$</td>
<td>0.716</td>
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<td>$r$</td>
<td>0.407</td>
<td>0.131</td>
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<td>$P$</td>
<td>0.028</td>
<td>0.439</td>
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$n = 22$.

Fig. 2 An example of MRP3 detection in NSCLC cell lines. For each cell line, 40 μg of both PNGase F treated (+) and glycerol control (−) membrane proteins were separated by 7.5% SDS-PAGE and analyzed by Western blotting. PNGase F digestion of the membrane proteins concentrated the MRP3 band, which allowed for more sensitive detection and more accurate quantitation of low levels of MRP3. Also, 10 μg of A549 NSCLC cell line membrane protein were included on each blot to serve as a positive control and to allow for comparison between blots.

Fig. 3 A columnar scatter plot of MRP1–3 protein levels in 30 lung cancer cell lines. MRP1, MRP2, and MRP3 protein levels were measured by immunoblot analysis. MRP1 was detected in all of the 30 lung cancer cell lines. The levels of MRP2 and MRP3 proteins were below detection in the SCLC cell lines with the exception of one cell line in which MRP2 was detected. Protein levels were normalized to those found in the A549 NSCLC cell line and then Ln-transformed for statistical analyses. Horizontal line, the median protein level for each data set.
found previously that MRP3 mRNA levels were significantly higher in samples from NSCLC patients than in samples from SCLC (4). These data indicate that MRP3 protein, like MRP1, may have a role in the drug resistance of lung cancer and that the role of MRP3 may be specific to the intrinsic resistance of NSCLC cells.

In our panel of lung cancer cell lines, we found that there was a strong correlation between MRP3 and MRP1 protein levels, a weak correlation between MRP3 and MRP2 protein levels, and no significant correlation between MRP1 and MRP2 protein levels (Table 2). These data confirm our previous observation that MRP1 and MRP3 mRNA are positively correlated (4) and, together, suggest that there is a relationship between the expression of MRP1 and MRP3.

We found that MRP3 and MRP1, but not MRP2, levels correlated with the resistance of the lung cancer cell lines to DOX, VCR, VP-16, and CDDP (Table 3). The multidrug resistance of lung cancer is considered to be multifactorial, and these correlation analyses do not presume to separate this resistance into its components or establish “cause and effect” relationships. These analyses show that cell lines with higher levels of MRP3 and MRP1 also tend to exhibit higher levels of drug resistance. For example, the correlation of MRP1 levels with CDDP-resistance is surprising because MRP2 is expressed, it does not contribute to the multidrug resistance of these cell lines.

In conclusion, we measured MRP3, MRP1, and MRP2 in a panel of 30 lung cancer cell lines that had not been selected for in vitro drug resistance, and we found that there was good agreement between the protein levels of MRP1–3 and their cognate mRNAs, particularly for MRP3 (r, 0.852). Our data support the use of semiquantitative PCR to estimate the levels of MRP1, MRP2, and MRP3 proteins in samples in which material is limited. Also, the MRP3-specific LY1 polyclonal antibody that we developed was a sensitive reagent for the measurement of MRP3 by Western blot analysis. Correlation analyses indicated a relationship between the expression of MRP3 and MRP1 and, in agreement with our mRNA studies (3, 4), both the MRP3 and the MRP1 protein levels correlated with the drug response of these lung cancer cell lines. Our data are consistent with the idea that MRP3, like MRP1, is a component of the multifactorial multidrug resistance phenotype of lung cancer cells and that MRP3 contributes in particular to the intrinsic multidrug resistance of NSCLC.

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