CD26 Overexpression Is Associated with Prolonged Survival and Enhanced Chemosensitivity in Malignant Pleural Mesothelioma

Keisuke Aoe1, Vishwa Jeet Amatya2, Nobukazu Fujimoto3, Kei Ohnuma4, Osamu Hosono4, Akio Hiraiki7, Masanori Fujii8, Taketo Yamada6, Nam H. Dang9, Yukio Takeshima2, Kouki Inai2, Takumi Kishimoto3, and Chikao Morimoto4,5

Abstract

Purpose: Malignant pleural mesothelioma (MPM) is an aggressive and therapy-resistant neoplasm arising from the pleural mesothelial cells, without established indicators to predict responsiveness to chemotherapy.

Experimental Design: Our study involving 79 MPM patients showed that 73.4% of MPM expressed CD26 on cell membrane.

Results: The majority of epithelioid and biphasic types of MPM expressed CD26 on the cell membrane, whereas the sarcomatoid type showed a lack of CD26 surface expression. Although the sarcomatoid type was associated with poor prognosis ($P < 0.0001$), no significant relationship between CD26 expression and survival was observed. On the contrary, there was a trend for an association between response rate to chemotherapy and CD26 expression ($P = 0.053$), with a higher level of CD26 expression more likely to be linked to better response to chemotherapy. Moreover, CD26 expression was a significant factor associated with improved survival in patients who received chemotherapy [median survival time (MST), 18.6 vs. 10.7 months, $P = 0.0083$]. Furthermore, CD26 expression was significantly associated with better prognosis in patients receiving non–pemetrexed-containing regimens (MST, 14.2 vs. 7.4 months, $P = 0.0042$), whereas there was no significant association between CD26 expression and survival time for patients receiving pemetrexed-containing regimens. Our in vitro and microarray studies showed that mesothelioma cells expressing high CD26 displayed high proliferative activity, and CD26 expression was closely linked to cell-cycle regulation, apoptosis, and chemotherapy resistance.

Conclusions: Our results strongly suggest that CD26 is a clinically significant biomarker for predicting response to chemotherapy for MPM. Clin Cancer Res; 18(5); 1447–56. ©2012 AACR.

Introduction

Malignant pleural mesothelioma (MPM) is an aggressive malignancy arising from the mesothelial cells lining the pleura (1). It is generally associated with a history of asbestos exposure and has a very poor prognosis (2). In fact, the median survival is less than 12 months, with most patients dying within 10 to 17 months of their first symptoms. Once rare, the incident of MPM has increased in industrialized nations as a result of past widespread exposure to asbestos (3). The incident is predicted to increase further in the next decades, especially in developing countries where asbestos has not yet been prohibited (1–3). Due to the lack of efficacy of conventional treatments, novel therapeutic strategies are urgently needed to improve outcomes.

The identification of potential biomarkers would be helpful in managing 3 clinical aspects of MPM: early diagnosis, prognosis, and response to therapy. However, there are at present no established indicators that have clinical significance for MPM. Given the fact that MPM remains a rare disease with several subtypes, the lack of accessibility to uniform tumor populations renders the search for biomarkers very difficult (4).

CD26 is a 110-kDa cell surface glycoprotein with known dipeptidyl peptidase IV (DPPIV; EC 3.4.14.5) activity in

Authors Affiliations:

1Department of Medical Oncology and Clinical Research, National Hospital Organization Yamaguchi-Ube Medical Center, Ube, Yamaguchi; 2Department of Pathology, Graduate School of Biomedical Sciences, Hiroshima University; 3Department of Respiratory Medicine, Okayama Rosai Hospital, Okayama; 4Department of Rheumatology and Allergy, Research Hospital; 5Division of Clinical Immunology, Advanced Clinical Research Center, Institute of Medical Science, University of Tokyo; 6Department of Pathology, Keio University school of Medicine, Tokyo; 7Department of Internal Medicine, Mizushima Daichi Hospital, Okayama; 8Department of Respiratory Medicine, Japanese Red Cross Kobe Hospital, Kobe, Japan; and 9Division of Hematology/Oncology, University of Florida, Gainesville, Florida

Note: Supplementary data for this article are available at Clinical Cancer Research Online (http://clincancerres.aacrjournals.org/).

Corresponding Author: Chikao Morimoto, Division of Clinical Immunology, Institute of Medical Science, University of Tokyo, 4-6-1, Shirokanedai, Minato-ku, Tokyo 108-8639, Japan. Phone: 81-354-495-546; Fax: 81-354-495-448; E-mail: morimoto@ims.u-tokyo.ac.jp.


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Translational Relevance

Malignant pleural mesothelioma (MPM) is an aggressive cancer arising from the mesothelial cells lining the pleura. Due to the lack of efficacy of conventional treatments, novel therapeutic strategies are urgently needed to improve outcomes. In this study, we found that the CD26 molecule is expressed on the cell membrane of the epithelial and biphasic, but not the sarcomatoid, type of mesothelioma. Treatment outcome prediction study showed that CD26 membrane expression on MPM was closely correlated with disease responsiveness to chemotherapy. Mesothelioma cells expressing a high level of CD26 displayed high proliferative activity, and microarray analysis of CD26 knockdown and CD26-transfected mesothelioma cells showed that CD26 expression was closely linked to expression of genes contributing to cell proliferation, cell-cycle regulation, drug-induced apoptotic action, and chemotherapy resistance. Our results therefore suggest that CD26 is a clinically significant biomarker for the prediction of response to chemotherapy for MPM.

its extracellular domain (5) and is capable of cleaving N-terminal dipeptides with either L-proline or L-alanine at the penultimate position (5). CD26 activity is dependent on cell type and the microenvironment, factors that can influence its multiple biological roles (5–8). Although CD26 expression is enhanced following activation of resting T cells, CD4+ CD26high T cells respond maximally to recall antigens such as tetanus toxoid (5). Cross-linking of CD26 and CD3 with solid-phase immobilized monoclonal antibodies (mAb) can induce T-cell costimulation and IL-2 production by CD26+ T cells (5). In addition, anti-CD26 antibody treatment of T cells enhances tyrosine phosphorylation of signaling molecules such as CD3ζ and p56lick (7). Moreover, DPPIV activity is required for CD26–mediated T-cell costimulation (5). CD26 may therefore have an important role in T-cell biology and overall immune function. Association with various proteins, including fibroblast-activation protein-α, plasminogen, adenosine deaminase, CD45 and collagen, influences its activity (5). As a result, CD26 has an important, but complex, function in tumor behavior, with its biologic effect dependent on the tumor type and the microenvironment. Likely, as a result of this multifunctional characteristic, CD26 is associated with a high level of clinical aggressiveness in some tumors but a lower level in others (9, 10). For example, it is a marker of aggressive disease for certain subsets of T-cell non-Hodgkin lymphomas/leukemias, with expression of CD26 on T-lymphoblastic lymphomas/acute lymphoblastic leukemia cells being associated with a worse outcome compared with CD26-negative tumors (12). CD26 is also expressed at high levels on renal carcinoma cells (13–15). Two recent studies also correlated CD26 expression with tumorigenesis. In an immunohistochemical analysis of 152 patients with gastrointestinal stromal tumors (GIST), CD26 was found to be associated with a poorer overall survival (16). In addition, CD26 can serve as a prognostic marker in B-cell chronic lymphocytic leukemia (17). Furthermore, CD26 itself may be a novel therapeutic target. Anti-CD26 mAb treatment resulted in both in vitro and in vivo antitumor activity against several tumor types, including lymphoma and renal cell carcinoma (15, 18).

More recently, we showed that CD26 is preferentially expressed on malignant mesothelioma cells but not on normal mesothelial cells, and suggested that membranous expression of CD26 indicates an importance in treatment of patients with MPM (19). More importantly, humanized anti-CD26 antibody inhibited growth of malignant mesothelioma cells and induced long-term survival of tumor-transplanted severe combined immunodeficient mice (20). Although we recently showed that cells from certain CD26-positive mesothelioma cell lines seemed to include the cancer stem cell characteristics for malignant mesothelioma in addition to CD24- and CD9-positive cells (21), the role of CD26 for MPM in the clinical setting as a prognostic and therapeutic biomarker has not yet been clarified.

In this study, we showed that the CD26 molecule is expressed on the cell membrane of the epithelial and biphasic, but not the sarcomatoid, type of mesothelioma. Importantly, treatment outcome prediction study showed that CD26 membrane expression on MPM was closely correlated with disease responsiveness to chemotherapy. Meanwhile, our in vitro studies showed that mesothelioma cells expressing high level of CD26 displayed high proliferative activity, and microarray analysis of CD26 knockdown and CD26-transfected mesothelioma cells showed that CD26 expression was closely linked to expression of genes contributing to cell proliferation, cell-cycle regulation, drug-induced apoptotic action, and chemotherapy resistance. These data further argue for the potential clinical significance of CD26 in MPM. Our results therefore strongly suggest that the CD26 molecule is a clinically significant biomarker for the prediction of response to chemotherapy for MPM.

Materials and Methods

Patients and tissue samples

Seventy-nine MPM tissues were obtained from patients who had undergone biopsy or surgery at Okayama Rosai Hospital and National Hospital Organization (NHO) Yamaguchi-Ube Medical Center between 1998 and 2009. All patients were confirmed by histology. Histologic sections from the mesothelioma patients were previously examined and classified into epithelioid, sarcomatoid, and biphasic subtypes, according to the World Health Organization histologic classification by 3 independent pathologists (Y. Takeshima, V.J. Amatya, and K. Inai), who were blinded to the results of the studies discussed in this article. Sufficient specimen was collected from each patient to allow for evaluation by immunohistochemistry at Hosei University (22). The clinical stage and performance
status (PS) were determined according to the criteria of the International Mesothelioma Interest Group (IMIG) tumor-node-metastasis staging system for MPM (23), and Eastern Cooperative Oncology Group (ECOG) PS scale. Survival terms were calculated from the date of diagnosis of mesothelioma. Radiologic response rate was assessed by modified Response Evaluation Criteria in Solid Tumors, which have been validated in mesothelioma (24, 25).

**Immunohistochemical staining**

Immunohistochemical staining for CD26 was carried out in 3-μm tissue sections prepared from formalin-fixed, paraffin-embedded tissue blocks. Endogenous peroxidase inactivation by treatment with 0.3% H2O2 in PBS for 30 minutes of deparaaffinized sections was carried out, followed by incubation with anti-CD26/DPP IV antibody (NB100-59021; Novus BioSciences) at 4°C overnight in a humidified chamber. The reaction was visualized with the Histofine Simple Stain Kits (Nichirei Biosciences) and diaminobenzidine (Dojindo Laboratories) as the chromogen. The tissue sections were counterstained for nucleus with Mayer’s hematoxylin. A similar immunohistochemical procedure was carried out with the omission of the primary antibody as a negative control. CD26 reactivity on lymphocytes and/or endothelial cells in and around the tumor tissue was considered as internal positive control.

Membranous and cytoplasmic expression of CD26 was semiquantitatively analyzed. CD26 expression was evaluated and verified independently by 2 pathologists (V.J. Amatya and Y. Takeshima). Though cytoplasmic expression of CD26 was observed in many of the tumor cells in most of the cases, CD26 expression in mesothelioma was based on its membranous expression (19). In detail, it was scored as 0, absence of membranous expression on tumor cells; +1, membranous expression on up to 25% of tumor cells; +2, membranous expression on 26% to 50% of tumor cells; and +3, membranous expression on more than 50% of tumor cells. The representative figures of score 3, 2, and 0 are shown in Supplementary Fig. S1.

**Separation of mesothelioma cell line MESO-1 cells into CD26high and CD26negative cells and in vitro cell growth assay**

Naturally CD26-positive MESO-1 cells were sorted by flow cytometric cell sorter (BD FACS Aria; into CD26high and CD26negative cells following staining with anti–CD26-FITC (FITC, fluorescein isothiocyanate). These cells were subsequently grown in 10% FCS-RPMI medium (containing penicillin and streptomycin) for the indicated days, and living cells were then measured by MTT assay as described above.

**In vitro cell proliferation assay of CD26 knockdown mesothelioma cell lines**

To further analyze the effect of CD26 expression on cell proliferation, in vitro cell proliferation assay was conducted with CD26 knockdown MM cells (CD26-KD). For this purpose, we generated CD26 knockdown MM cells (CD26-KD) with naturally CD26-expressing MESO-11, JMN, and H28 cells transfected with siRNA against human CD26 (sense strand, 5’-ACUCIUACUGAJUACUAAATT-3’ was selected and purchased from QIAGEN). Decreased expression of CD26-KD MM cells was confirmed through flow cytometry (Supplementary Fig. S2). These cells were subsequently grown in 10% FCS-RPMI medium (containing penicillin and streptomycin) for the indicated days, and living cells were then measured by MTT assay as described above.

**Microarray data generation**

To analyze potential mechanisms involved in the association between CD26 expression and anticancer drug sensitivity on MM cells, we conducted a comprehensive analysis of mRNA expression profiles of MM cells differing in the level of CD26 expression. For this purpose, we used CD26-KD cells as generated above. Moreover, we used CD26-overexpressed MM cells (CD26-Trf) generated with retroviral transfection of human CD26 into CD26-negative MSTO-211H (MSTO) cells (19). Total RNA was extracted from these cells using standardized protocols of conventional published methodology (RNeasy; QIAGEN). cRNA from these cells using standardized protocols of conventional published methodology (RNeasy; QIAGEN). cRNA was then hybridized on TORAY 3D-Gene Human 25k chip (TORAY). The amount of transcription product was measured, and a profile of mRNA in a sample was obtained by TORAY manufacturer’s protocol. Expression level was shown in log2 ratio with the heatmap.

**Statistical analysis**

The χ2 test or trend test was used to analyze the correlation between CD26 expression and clinicopathologic parameters. The probabilities of survival were estimated by the Kaplan–Meier method (26), and differences between patient groups were determined by the log-rank test. The multivariate analysis of prognostic factors in patients who received chemotherapy was conducted with the Cox proportional hazard model. All reported P values are 2-sided. A level of P < 0.05 was accepted as being statistically significant.

**Results**

**Patient characteristics**

Key patient characteristics in this study are summarized in Supplementary Table S1. The mean age of the MPM patients was 65.4 years. Most patients were men (89.9%) and had good PS (PS 0, 1; 84.8%). Forty-nine patients (62.0%) had epithelioid histology. Fifty-three patients (67.1%) had stage I/II disease. Thirty-two patients (40.5%) underwent extrapleural pneumonectomy (EPP). Of the 56 patients who received chemotherapy, 31 patients were treated with pemetrexed (PEM) +...
cisplatin (CDDP), 4 with PEM + carboplatin (CBDDA),
2 with PEM only, 11 with gemcitabine (GEM) + vinorelbine,
4 with GEM + CDDP, 2 with GEM only, 1 with
doxorubicin + CDDP, and 1 with mitomycin C + CDDP.
Fifteen patients were treated with adjuvant chemotherapy.
Thirty-seven patients (66.1%) received PEM-containing
regimen. Seventeen patients (21.5%) received best
supportive care (BSC) only.

**CD26 expression in mesothelioma tissues**

As shown in Supplementary Table S1, 58 patients with
mesothelioma (73.4%) expressed CD26 on the mesotheli-
om cell membrane. The majority of patients with epithe-
lioid and biphasic types of mesothelioma expressed CD26
on the mesothelioma cell membrane, whereas none of the
patients with the sarcomatoid type did. It should be noted
that diffuse staining for CD26 in the cytoplasm of the
mesothelioma cells was observed in all patient samples,
even in patients with the sarcomatoid type (Supplementary
Fig. S1C).

The association between CD26 expression and key
clinicopathologic factors is summarized in Supplementary
Table S1. A statistically significant correlation was observed
between membranous CD26 expression on the malignant
mesotheliomas and histologic type ($P < 0.0001$). However
no statistically significant correlation between CD26 expres-
sion and gender ($P = 0.901$), age ($P = 0.552$), or clinical
stage ($P = 0.555$), PS ($P = 0.565$), EPP ($P = 0.069$), chemother-
apy ($P = 0.236$), or BSC ($P = 0.748$) was observed.

**CD26 expression and survival of mesothelioma
patients**

The prognostic significance of CD26 membrane expres-
sion and other clinicopathologic factors in patients with

<table>
<thead>
<tr>
<th>Table 1. Univariate analysis of survival for MPM cases</th>
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<tr>
<td>Clinicopathologic parameters</td>
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<td>-------------------------------</td>
</tr>
<tr>
<td>Membranous CD26 expression</td>
</tr>
<tr>
<td>Positive</td>
</tr>
<tr>
<td>Negative</td>
</tr>
<tr>
<td>Sex</td>
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<tr>
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<td>BSC</td>
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MPM was evaluated by univariate analysis. As shown in Table 1, the median survival time (MST) for all mesothelioma patients in this study was 13.9 months, with the 1-year survival rate being 58.9%. Older age, sarcomatoid histology, advanced stage, absence of EPP, absence of chemotherapy, and BSC were factors associated with poor prognosis. However, as shown in Fig. 1A, no significant relationship between membranous CD26 expression in malignant mesothelioma and survival was observed (MST, 15.0 vs. 10.8 months, \( P = 0.1384 \)).

CD26 expression and chemotherapy response and survival

Of the 56 patients treated with chemotherapy, 15 patients had adjuvant chemotherapy, and 1 patient died before evaluation of response to chemotherapy. Therefore, we evaluated the relationship between membranous CD26 expression and response to chemotherapy for 40 patients. As shown in Table 2, the response rate to chemotherapy was marginally associated with membranous CD26 expression (\( P = 0.053 \)). There was a trend toward an association between higher level of CD26 membrane expression and better response to chemotherapy. Univariate analysis of survival time for patients who received chemotherapy is shown in Table 2 and Fig. 1A. As shown in Table 2 and Fig. 1A, membranous CD26 expression was a significant factor associated with better survival in patients who received chemotherapy and PEM (\( P = 0.0083 \)) (Fig. 1B).

**Table 2. Membrane CD26 expression and chemotherapy response**

<table>
<thead>
<tr>
<th>Membrane</th>
<th>PR</th>
<th>SD</th>
<th>PD</th>
<th>Total</th>
</tr>
</thead>
<tbody>
<tr>
<td>CD26 expression</td>
<td>0</td>
<td>1</td>
<td>6</td>
<td>6</td>
</tr>
<tr>
<td></td>
<td>1</td>
<td>1</td>
<td>6</td>
<td>9</td>
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<tr>
<td></td>
<td>2</td>
<td>4</td>
<td>2</td>
<td>10</td>
</tr>
<tr>
<td></td>
<td>3</td>
<td>1</td>
<td>0</td>
<td>8</td>
</tr>
<tr>
<td>Total</td>
<td>8</td>
<td>22</td>
<td>10</td>
<td>40</td>
</tr>
</tbody>
</table>

**Note:** \( P = 0.053 \).

Abbreviations: PR, partial remission; SD, stable disease; PD, progressive disease.
chemotherapy (MST, 18.6 vs. 10.7 months, \( P = 0.0083 \)). Other clinicopathologic factors, histology type, stage, EPP, or PEM were also observed to be associated with overall survival (Table 2). Multivariate analysis for the chemotherapy response showed histology (\( P = 0.016 \)) and EPP (\( P = 0.005 \)) had independent prognostic significance (Supplementary Table S2). Membranous CD26 expression showed an HR of 1.947, but without statistically significant value (\( P = 0.067 \); Supplementary Table S2).

Because membranous CD26 expression seems to predict for treatment outcome in patients undergoing chemotherapy, patients who received chemotherapy were subdivided into 2 groups, patients with PEM-containing regimen and patients without PEM-containing regimen. As shown in Fig. 1B, for patients treated with non–PEM-containing regimen, membranous CD26 expression was significantly associated with better survival (MST, 14.2 vs. 7.4 months, \( P = 0.0042 \)). On the contrary, for those treated with PEM-containing regimen, CD26 expression was not significantly associated with survival (\( P = 0.1225 \)). However, in the PEM-treated cohort, there was a trend toward better cumulative survival for patients with CD26-positive disease as compared with those with CD26-negative disease in 30+ months of follow-up (MST, 19.5 vs. 12.8 months, 2-year survival rate 37.9% vs. 20.0%). These results therefore suggest that membranous CD26 expression can potentially be a marker of response to chemotherapy in malignant mesothelioma.

**CD26 expression and proliferative activity of mesothelioma cells**

Because CD26 membrane expression on mesothelioma cells seems to be a predictive marker of response to chemotherapy, we next attempted to characterize in details the CD26-positive cells of mesothelioma cell lines. For this purpose, we sorted naturally occurring CD26-positive MESO-1 mesothelioma cells and subdivided them into CD26-positive and CD26-negative cells. Such cells were subsequently cultured for the indicated days. As shown in Fig. 2A and B, CD26\textsuperscript{high} cells always exhibited a higher level of proliferative activity than CD26\textsuperscript{negative} cells. Similarly, CD26\textsuperscript{high} cells from other naturally occurring CD26-positive mesothelioma cell lines such as H226 and H28 cell lines consistently had a higher level of proliferation than CD26\textsuperscript{negative} cells from the same cell lines (data not shown). Moreover, CD26 knockdown of MESO-1, JMN, and H28 cells resulted in reduced proliferation as compared with wild-type CD26-positive MESO-1, JMN, and H28 cells, respectively (Figs. 2C (a)–(c)). These results hence suggest that CD26-positive mesothelioma cells have generally robust growth activity. Because highly proliferative cells are typically...
sensitive to chemotherapeutic agents, our data support the notion that mesothelioma patients with tumors expressing a high level of CD26 generally have chemosensitive disease.

**Microarray analysis for gene profiles in CD26-transfected or CD26 knockdown mesothelioma cells**

To understand the mechanism involved with the relatively greater level of chemosensitivity of CD26\textsuperscript{high} mesothelioma cells, we analyzed the gene expression profiles of mesothelioma cells differing in CD26 expression level. For this purpose, we used the naturally CD26-positive mesothelioma cell line MESO-1, and the naturally CD26-negative mesothelioma cell line MSTO. As described in Materials and Methods, expression of CD26 protein in MESO-1 was reduced by siRNA against human CD26 (CD26-KD cells), and overexpression of CD26 was achieved in MSTO by human CD26 transfection (CD26-Trf cells). The expression profiles of genes in CD26-KD or CD26-Trf cells were analyzed by cDNA chips mounted with approximately 25,000 human oligogenes. Table 3 lists the 5 genes that differ in expression levels and that play a role in tumor proliferation, cell cycle, or anticancer drug sensitivity. Expression of the CD26 gene was found to validate CD26 knockdown or CD26 overexpression in CD26-KD MESO-1 or CD26-Trf MSTO, respectively (top of list in Table 3). IHPK2, inositol hexakiphosphate kinase 2, is a member of a family of enzymes generating inositol pyrophosphate and mediates cell apoptosis (27). It had been shown that increased IHPK2 activity sensitizes cancer cells to anticancer drugs, whereas its depletion blocks cell death (28). The IHPK2 mRNA level was decreased in CD26-KD cells and was increased in CD26-Trf cells [Table 3], which may partly explain the enhanced chemosensitivity of CD26\textsuperscript{high} mesothelioma cells. Cyclin-dependent kinase inhibitor p21\textsuperscript{Cip1} mRNA was increased in CD26-KD cells and was reduced in CD26-Trf cells. The p21\textsuperscript{Cip1} protein binds to and inhibits the activity of cyclin–CDK2 or cyclin–CDK4 complexes, and thus functions as a cell-cycle stopper at the G\textsubscript{1} phase (29). The reduced level of p21\textsuperscript{Cip1} expression in CD26\textsuperscript{high} mesothelioma cells would allow the cells to progress through the cell cycle, resulting in greater chemosensitivity. DUSP1 (dual specificity protein phosphatase 1) is a mitogen-activated protein kinase phosphatase-1 and is a mediator of cancer chemoresistance (30). As shown in Table 3, DUSP1 level in CD26-Trf cells is lower than that in CD26-KD cells, data which support our findings of greater chemoresistance of CD26\textsuperscript{negative} mesothelioma cells. PTTG1 (pituitary tumor-transforming 1), or securin, is a protein involved in regulating the metaphase–anaphase transition and anaphase onset. Increased securin level is associated with favorable outcomes in invasive breast cancer (31). Securin (PTTG1) level was increased in CD26-Trf mesothelioma cells and decreased in CD26-KD mesothelioma cells (Table 3), hence suggesting that this protein may be a marker of favorable outcome for malignant mesothelioma. Our data also indicated a difference in the expression of TRIM7 (tripartite motif-containing protein 7). Although the role of TRIM7 in cancer has not yet been elucidated, this ubiquitin E3 ligase protein might function as a regulator of cell cycle and proliferation, as had been shown with other E3 ligases (32).

Taken together, our results described above suggest that CD26 expression on mesothelioma cell membrane is a reliable biomarker for predicting potential chemosensitivity and clinical outcome for malignant mesothelioma.

**Discussion**

In this study, we showed that the majority of the epithelioid and biphasic types of mesothelioma expressed CD26 on the cell membrane while there was no CD26 surface expression for the sarcomatoid type. We also showed that CD26 membrane expression was associated with improved survival in MPM patients who had received chemotherapy. Moreover, our in vitro studies of CD26-positive mesothelioma cell lines and microarray analysis of CD26 knockdown and CD26-transfected

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**Table 3.** Heatmap view showing the results of gene expression analysis of CD26 knockdown (CD26-KD) MESO1 or CD26-transfected (CD26-Trf) MSTO cells

<table>
<thead>
<tr>
<th>Symbol</th>
<th>Name</th>
<th>CD26-KD</th>
<th>CD26-Trf</th>
</tr>
</thead>
<tbody>
<tr>
<td>DPP4</td>
<td></td>
<td>–3.9</td>
<td>+5.5</td>
</tr>
<tr>
<td>IHPK2</td>
<td></td>
<td>–1.5</td>
<td>+0.5</td>
</tr>
<tr>
<td>CDKN1A</td>
<td></td>
<td>+1.3</td>
<td>–0.4</td>
</tr>
<tr>
<td>DUSP1</td>
<td></td>
<td>+1.4</td>
<td>–0.7</td>
</tr>
<tr>
<td>PTTG1</td>
<td></td>
<td>–1.1</td>
<td>+0.4</td>
</tr>
<tr>
<td>TRIM7</td>
<td></td>
<td>–1.0</td>
<td>+1.2</td>
</tr>
</tbody>
</table>

Color key

| Expression value | -3.0 | -2.0 | -1.0 | 0 | 1.0 | 2.0 | 3.0 |

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mesothelioma cells support the conclusion that CD26 surface expression is associated with and potentially contributes to mesothelioma chemosensitivity. Therefore, our work strongly suggests that the CD26 molecule is a reliable biomarker for predicting potential therapeutic outcome following chemotherapy.

MPM is a fatal malignancy (1, 2). The overall survival of patients with MPM varies among different treatments and is also dependent on patients’ overall condition. Various patients’ characteristics have been studied for their potential effects on the survival of patients with MPM. Patients’ age, histology, stage, PS, and therapeutic modality (e.g., EPP and/or chemotherapy) were identified as important predictors of prognosis in our study, consistent with previous reports by other investigators (33, 34).

Mesothelioma tumor growth is generally insidious but the usual clinical signs/symptoms of mesothelioma (dyspnea, cough, and chest pain) are nonspecific, leading to late diagnosis for curative treatment. It is therefore important to search for disease markers that can help with early diagnosis and potentially improve prognosis. In this regard, serum osteopontin and mesothelin levels have been proposed to be early diagnostic markers for MPM (35, 36), although there have been doubts relating to their specificity and sensitivity. Mesothelin is directly produced by the tumor itself, and its level could mirror tumor burden, as suggested by Robinson and colleagues (37), who found higher serum mesothelin levels in patients having larger tumors. Furthermore, elevated osteopontin level could stimulate tumor growth and spread, and thus high level of osteopontin may be associated with shorter survival (38). A similar correlation between high osteopontin expression and a shorter survival have been described in other tumors (39, 40). However, mesothelin and osteopontin have not been found to be predictors of treatment outcome, and more work is therefore needed to identify indicators of responsiveness to therapy that can be used to optimize treatment in MPM.

Few studies have identified potential predictors of responsiveness to chemotherapeutic agents as PEM and/or CDDP/CBDCA in patients with MPM (4). It is hypothesized that low expression of excision repair cross-complementation group 1 (ERCC1) might predict for increased sensitivity to platinum-based chemotherapy, possibly due to the saturation of the enzyme complex; conversely, high levels of ERCC1 may predict for resistance to platinum-based chemotherapy (4). Regarding PEM treatment, thymidylate synthase expression level has been used to predict PEM effectiveness (41, 42). Righti and colleagues investigated the correlation between baseline expression levels of thymidylate synthase and ERCC1 genes evaluated by real-time PCR and immunohistochemistry and clinical outcomes in MPM patients treated with PEM-based chemotherapy (42). They observed that low thymidylate synthase protein and mRNA levels are predictive of improved time to progression and overall survival.

Our work showed that the response rate to chemotherapy was marginally associated with CD26 membrane expression, with higher expression level tending to be associated with better response to chemotherapy. This is the first report showing that CD26 membrane expression level in mesothelioma is a marker for predicting treatment outcome for MPM patients receiving chemotherapy.

Previous studies on CD26 have yielded various results in different cancers. Preclinical studies showed that increased CD26 expression inhibited metastasis in ovarian cancer (10), whereas suppression of CD26 promoted metastasis in prostate cancer (43). On the contrary, inhibition of CD26 in renal cell carcinoma decreased tumor growth and reduced binding of the cancer cells to fibronectin and collagen (15). Moreover, clinical studies in thyroid cancer, GIST, and T-cell non-Hodgkin lymphoma/leukemias suggested that CD26 expression was associated with distant metastasis, recurrence after resection, or poor survival (16, 18, 44). The multifunctional roles of CD26 may account for its varied roles in different cancers (11). Our recent studies also showed that humanized anti-CD26 mAb treatment of mouse xenograft models of human malignant mesothelioma cells drastically inhibited tumor growth in tumor-bearing mice, resulting in enhanced survival (20).

Our current in vitro studies showed that CD26 expression on mesothelioma cells was associated with enhanced proliferative activity. More importantly, microarray analyses of gene expression profiles in CD26-overexpressed or CD26 knockdown mesothelioma cells showed that CD26–expressing mesothelioma cells exhibited the upregulation of several genes which play a role in sensitizing cancer cells to anticancer drugs and which are associated with favorable outcome in invasive cancers. On the contrary, expression of CD26 in these mesothelioma cells was linked with the downregulation of genes that have a role in cell-cycle progression and tumor sensitivity to chemotherapy.

In conclusion, our work suggests that CD26 is an important biomarker for predicting sensitivity to chemotherapy, supported by our in vitro studies and microarray analyses. Moreover, since membranous CD26 expression can potentially predict tumor sensitivity to chemotherapy, knowledge of membranous CD26 expression in MPM may affect clinical care of patients and treatment decision.

Disclosure of Potential Conflicts of Interest
No potential conflicts of interest were disclosed.

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