METCAM/MUC18 is a Novel Tumor and Metastasis Suppressor for the Progression of Human Ovarian Cancer Cells

ABSTRACT

METCAM/MUC18, an integral membrane cell adhesion molecule (CAM) in the Ig-like gene super-family, is capable of performing typical functions of CAMs, such as mediating cell-cell and cell-extracellular interactions, crosstalk with intracellular signaling pathways, and modulating social behaviors of cells. METCAM/MUC18 is expressed in about ten normal cells/tissues. Aberrant expression of METCAM/MUC18 has been associated with the progression of several epithelial tumors. Further in vitro and in vivo studies show that METCAM/MUC18 plays a dual role in the progression of different tumors. It can promote the malignant progression of breast cancer, melanoma, osteosarcoma, prostate tumors, and nasopharyngeal carcinoma type II. On the other hand, it can suppress the malignant progression of one mouse melanoma cell line and nasopharyngeal carcinoma type I. We suggest that the dual role of METCAM/MUC18 in the progression of different cancer types may be modulated by different intrinsic factors present...
in different cancer cells and also in different stromal microenvironment. The role of METCAM/MUC18 in the progression of ovarian cancer cells has not been well studied. Previous studies suggest that the expression of METCAM/MUC18 may serve as a biomarker for the malignant progression of clinical ovarian cancers and it has been implicated for playing a positive role in the progression of the cancer. Here we provided evidence from in vitro and in vivo studies to suggest that the above notion is a fortuitous correlation and that METCAM/MUC18 actually serves as a tumor and metastasis suppressor for the malignant progression of ovarian cancer cells. Many possible mechanisms mediated by this CAM during early tumor development and metastasis are suggested. We further suggest that METCAM/MUC18 may be used a therapeutic reagent to arrest the malignant progression of clinical ovarian cancer.

**Keywords:** Human METCAM/MUC18 expression; Ovarian cancer cells; SC & IP injections; Tumorigenesis and progression: Athymic nude mice

**Abbreviations:** CAM: Cell Adhesion Molecule; huMETCAM/MUC18: Human METCAM/MUC18; METCAM: Metastasis Cell Adhesion Molecule; IP: Intraperitoneal; SC: Subcutaneous

**INTRODUCTION-CURRENT STATUS OF OVARIAN CANCER**

Epithelial ovarian cancer (EOC) is the fifth leading cause of female cancers in USA with a high fatality rate of about 65% [1]. The high lethality of the cancer is because the early stage of the disease is mostly asymptomatic and therefore remains undiagnosed until the cancer has already disseminated throughout the peritoneal cavity (at clinical stages of III and IV) [2]. The early stage disease can be treated successfully with a five-year survival rate of more than 90%, however, effective therapy for the advanced-stage disease is lacking because of the strong chemoresistance of recurrent ovarian cancer [2]. The major challenges for combating ovarian cancer are: (a) the ovarian cancer is histologically and molecularly heterogeneous with at least four major subtypes, such as serous adenocarcinoma (75%), endometrioid adenocarcinoma (10%), mucinous adenocarcinoma (3%), and clear cell carcinomas (5-10%) [3,4], (b) there is a lack of reliable specific diagnostic markers for an effective early diagnosis of each subtype, though molecular signatures of the major subtypes are available [5], and (c) very little is known of how ovarian tumor emerges and how it progresses to malignancy [6].

**CELL ADHESION MOLECULES AND THE PROGRESSION OF OVARIAN CANCER**

In general, tumorigenesis is a complex process involving changes of several biological characteristics [7], including the aberrant expression of cell adhesion molecules (CAMs), such as cadherin’s, CD44, integrin’s, lectin-containing selectins, mucins, N-CAM and L1CAM, and Ig-like CAM superfamily [7]. CAMs play many important physiological functions, such as organ formation, tissue architecture, vascularization and angiogenesis, immune response, inflammation, wound healing, and cellular social behaviors [8]. Since CAMs govern the social behaviors of cells by affecting the adhesion status of cells and cross-talk and modulating intracellular signal
transduction pathways, they also play an important function in cancer cell metastasis. This is because tumor progression is induced by a complex cross-talk between tumor cells and stromal cells in the surrounding tissues [9]. These interactions are, at least in part, mediated by cell adhesion molecules (CAMs) [7-9]. Thus the altered expression of CAMs can change motility and invasiveness, affect survival and growth of tumor cells, and alter angiogenesis [7-9]. As such, CAMs may promote or suppress the metastatic potential of tumor cells [10]. Similar to other epithelial cancers, cell adhesion molecules must play a role in the progression of ovarian cancer, especially since aberrant expression of various CAMs, such as mucins [11], integrins [12], CD44 [13], L1CAM [14], cadherin [15], claudins [16], EpCAM [17], ALCAM [18] and METCAM/MUC18 [19,20], has been associated with the malignant progression of ovarian cancer. For examples, MUC4 [21], CD44 [22], L1CAM [23], ALCAM [18], and P-cadherin [24] promote the progression of ovarian cancer cells. In contrast, β3-integrin [25], E-cadherin [26], claudin-3, 4, 8 [27], EpCAM [28], and KAI1 [29] play a suppressor role in the progression of ovarian cancer. We have been focusing our studies on the possible role of METCAM/MUC18 in the progression of several epithelial tumors [30].

**THE ROLE OF METCAM/MUC18 IN THE PROGRESSION OF EPITHELIAL CANCERS**

Human METCAM/MUC18 (or MCAM, Mel-CAM, S-endo1, CD146, or A32), an integral membrane cell adhesion molecule (CAM) in the Ig-like gene superfamily, has an N-terminal extra-cellular domain of 558 amino acids, a transmembrane domain, and a short intra-cellular cytoplasmic domain (64 amino acids) at the C-terminus, as shown in the following [30,31].

![HuMETCAM protein structure](image)

**Figure 1:** HuMETCAM protein structure.

SP stands for signal peptide sequence, V1, V2, C2, C2’, C2” for five Ig-like domains (each held by a disulfide bond) and X for one domain (without any disulfide bond) in the extracellular region, and TM for transmembrane domain. P stands for five potential phosphorylation sites (one for PKA, three for PKC, and one for CK2) in the cytoplasmic tail. The six conserved N-glycosylation sites are shown as wiggled lines in the extracellular domains of V1, between C2’ and C2”, C2”, and X.
As shown in the above Figure 1, the extra-cellular domain of the protein comprises a signal peptide sequence and five immunoglobulin-like domains and one X domain [30,31]. The cytoplasmic domain contains five consensus sequences potentially to be phosphorylated by PKA, PKC, and CK2 [30,31]. Thus human METCAM/MUC18 is capable of performing typical functions of CAMs, such as governing the social behaviors by affecting the adhesion status of cells and modulating cell signaling. Therefore, an altered expression of METCAM/MUC18 may affect motility and invasiveness of many tumor cells in vitro and tumorigenesis and metastasis in vivo [30].

Human METCAM/MUC18 is only expressed in several normal tissues, such as hair follicular cells, smooth muscle cells, endothelial cells, cerebellum, basal cells of the lung, activated T cells, intermediate trophoblasts [32], normal breast epithelium [33], ovarian epithelium [20], and nasopharyngeal epithelium [34]. Human METCAM/MUC18 is also expressed in several epithelial tumors, such as melanoma, prostate cancer, osteosarcoma, breast carcinoma, and intermediate trophoblast tumors [30,32]. Over-expression of METCAM/MUC18 promotes the tumorigenesis of prostate cancer [35] and breast carcinoma [36,37], but it has a minimal effect on the tumorigenesis of melanoma [38]. Over-expression of METCAM/MUC18 also initiates the metastasis of prostate cancer [39] and promotes the metastasis of melanoma [30,38] and breast carcinoma [40].

On the contrary, the possibility that the over-expression of METCAM/MUC18 might play a tumor suppressor role was first suggested by Shih et al. [33], who found that METCAM/MUC18 expression suppressed tumorigenesis of a breast cancer cell line MCF-7 in SCID mice. However, this notion was contradicted by recently published evidence, which supported the positive role of METCAM/MUC18 in the progression of breast cancer cells [36,37,40], similar to its role in the progression of melanoma and prostate cancer cells. The role of METCAM/MUC18 in the progression of ovarian cancer has not been well studied. The following section describes the recent findings for the role of METCAM/MUC18 in this aspect.

**THE ROLE OF METCAM/MUC18 IN THE PROGRESSION OF OVARIAN CANCER**

Aldovini et al. [19] first showed that METCAM/MUC18 expression is significantly associated with advanced stage tumors, and serous and undifferentiated subtypes, and is a marker stronger than residual disease in predicting early tumor relapse and independent marker of poor prognosis for epithelial ovarian cancer. We recently reported that METCAM/MUC18 expression is correlated with the progression of ovarian cancer [20]. Wu et al. [41] reported that METCAM/MUC18 expression is high in metastatic ovarian cancers in comparison with other pathological types of ovarian epithelial tissues. From in vitro studies by using siRNAs to silence the endogenous METCAM/MUC18 expression in the SK-OV-3 cell line, they showed that decreasing endogenous METCAM/MUC18 expression in the cells increases apoptosis and cell spreading and invasion, suggesting that METCAM/MUC18 may play a positive role in the progression of ovarian cancer cells [41].
METCAM/MUC18 is Expressed at Lower Level in the Ovarian Cancer Cell Lines Established from Malignant Ascites than the Cell Lines from Adenocarcinomas.

The above notion that METCAM/MUC18 may play a positive role in the progression of ovarian cancer perhaps was based on a fortuitous correlation, as proven below. To directly test the role of METCAM/MUC18 in the progression of epithelial ovarian cancer, we re-evaluated the expression of METCAM/MUC18 in one immortalized normal ovarian epithelial cell line (IOSE) and five human ovarian cancer cell lines, BG-1, HEY, CAOV-3, SK-OV-3 and NIHOPCAR3 [42], as shown in the following Figure 2.

Figure 2: Expression of METCAM in various human ovarian cancer cell lines. The expression of METCAM/MUC18 in the lysates from various cells lines was determined by Western blot (WB) analysis. Cell lysate from a human melanoma cell line, SK-Mel-28, was used as a positive control (lane 1) and those from human ovarian cancer cell lines, BG-1 (lane 3) and SK-OV-3 (lane 6) as negative controls. METCAM/MUC18 expression in cell lysates from one immortalized human ovarian epithelial cells (IOSE) and in five human ovarian cancer cell lines is shown in lanes 2 to 7. The number under each lane indicates the relative level of METCAM/MUC18 of each cell line, assuming that in SK-Mel-28 as 100%. Only the house-keeping genes, actin and GAPDH, are shown here as the loading controls.

As shown in the above Figure 2, the expression level of METCAM/MUC18 in one immortalized normal ovarian epithelial cell line (IOSE) was about 10% and that in five ovarian cancer cell lines, BG-1, HEY, CAOV-3, SK-OV-3 and NIHOCAR3, ranged from zero to 50% (assuming that a positive control, human melanoma cell line SK-Mel-28, expressed 100% of METCAM/MUC18). Since METCAM/MUC18 was expressed at a level of 31-50% in two out of three cell lines established
from primary adenocarcinomas (HEY and CAOV3), but poorly expressed (1-11%) in two cell lines established from malignant ascites (SKOV3 and NIH0VCAR3), it appeared that METCAM/MUC18 was expressed poorer in malignant cell lines than in primary adenocarcinomas, suggesting that METCAM/MUC18 may play a negative role in the progression of ovarian cancer. The above result also provided an important information for us to possibly choose two ovarian cancer cell lines, BG-1 (established from a poorly differentiated adenocarcinoma) and SK-OV-3 (established from an adenocarcinoma metastasis as malignant ascites), which expressed very low levels of METCAM/MUC18 (zero and 1%, respectively), for in vitro and in vivo studies. However, BG-1 cell line in some laboratories has been reported to be contaminated with the breast cancer cell line [43], MCF7, we decided to choose the cell line, SK-OV-3 for the studies.

**Two Complementary Methods are Commonly Used to Biochemically Alter the Expression of METCAM/MUC18 in the Cell Lines**

To determine the effect of a specific gene on cellular behaviors, two complementary methods are commonly used to alter the expression of a gene in cells: (a) enforced expression of a gene in cell lines that did not or weakly express the protein and (b) siRNA (small interference RNA)-knockdown expression of the gene in cell lines that endogenously express the protein. To facilitate isolation of the cells/clones that express gene-specific siRNAs or a cDNA gene, a DNA fragment that encodes a gene-specific shRNA, or a cDNA gene that encodes a specific protein, is inserted into a plasmid expression vector that also contains on the same DNA vector an antibiotic-resistant gene. The antibiotic resistant gene allows only those bacteria, which were successfully transfected with the expression vector (either being inserted into the bacterial genome or existing in a plasmid state), to live (perhaps only less than 1%) and grow into colonies. In this way the plasmid DNA is amplified to obtain enough DNA for later transfection into mammalian cells. The plasmid expression vector also contains another antibiotic-resistant gene to allow only the mammalian cells, which were successfully transfected with the gene, to live (perhaps only less than 0.1%) and grow into colonies.

For an example of the siRNA-knockdown expression of a gene in a cancer cell line, a DNA fragment, which encodes a gene-specific shRNA, is inserted behind and driven by a strong CMV promoter in a plasmid lentivirus vector (pGIPZ, Thermo Scientific) [44]. The plasmid lentivirus vector also contains on the same DNA vector the ampicillin-resistant gene that allows only those bacteria, which had been successfully transfected with the DNA, to survive the killing of ampicillin. In this way, the plasmid DNA, which now contains the lentivirus vector and the shRNA-encoding DNA, is amplified in bacteria to obtain enough quantity for being used for later transfection into mammalian cells. Since this plasmid also contains a puromycin-resistant gene, only those mammalian cells, which are successfully transfected with the plasmid, are resistant to the killing by puromycin. As such, only the cells that contain the hybrid lentivirus plasmid can be enriched and grown into colonies, which express the shRNA. The efficiency of the knockdown-expression of the gene in each clone can be assessed by using the standard Western blot method.
Likewise, for an example of the enforced expression of a gene in a cancer cell line, the cDNA gene is inserted behind a CMV promoter in a mammalian expressible plasmid vector, pcDNA3.1, which also contains the ampicillin-resistant gene. The hybrid plasmid DNA is then transfected into bacteria and only amplified in bacteria that survive the killing of ampicillin. The bacteria-enriched hybrid plasmid DNA containing the cDNA is then used for transfection into mammalian cells [35]. Since the plasmid also contains a neomycin (or G418)-resistant (G418R) gene, which is driven by the SV40 promoter, only the mammalian cells, which have been successfully transfected with the plasmid DNA, can survive the killing of G418 and grow into colonies. The expression level of the gene in each mammalian clone can also be assessed by using the Western blot method.

**METCAM/MUC18 Expression in G418R-Clones Derived from the SK-OV-3 Cell Line**

Since SK-OV-3 cell line did not or weakly express METCAM/MUC18, to determine if METCAM/MUC18 expression affects the *in vitro* and *in vivo* cellular behaviors of the cells, only the enforced expression method was used to increase the expression of the gene in this cell line. All the G418R-clones should express METCAM/MUC18, albeit at different levels in different clones. The control cells, which were transfected with the empty vector that did not contain the human METCAM/MUC18 cDNA, were also G418R and should not express METCAM/MUC18, similar to the parental SK-OV-3 cells. Figure 3 shows the expression of METCAM/MUC18 in three typical G418R clones derived from SK-OV-3 cell line [42].
Figure 3: Human METCAM/MUC18 expression in lysates prepared from various clones/cells. METCAM/MUC18 expression in the cell lysate from a human melanoma cell line, SK-Mel-28, was used as a positive control (lane 1) and that from the parental human ovarian cancer cell line, SK-OV-3, as a negative control (lane 2). METCAM/MUC18 expression in cell lysates from one single SK-OV-3 clone (METCAM Clone 2D-9) and two pooled SK-OV-3 clones (METCAM Clone 2D and Control (Vector) Clone 3D) are shown in lanes 3-5. Both the METCAM Clone 2D-9 and the METCAM Clone 2D were derived from SK-OV-3 cells transfected with the human METCAM/MUC18 cDNA gene. The Control (Vector) Clone 3D was from SK-OV-3 cells which were transfected with the empty vector. The number under each lane indicates the relative level of METCAM/MUC18 of each cell line, assuming that in SK-Mel-28 as 100%. β-tubulin is shown as the loading control.

As shown in Figure 3, in comparison to the positive control cell line human melanoma SK-Mel-28 cells (assuming as100% of METCAM/MUC18) (lane 1), the METCAM clone 2D-9 (lane 3) and the METCAM clone 2D (lane 4) of SKOV3 cells showed much higher expression of METCAM/MUC18 (137% and 51%, respectively) than that of the control (vector) clone 3D (lane 5) and the parental SK-OV-3 cells (lane 2), which expressed 0% and 0.8% of METCAM/MUC18, respectively.
The above G418R clones from the SK-OV-3 cell line are then used to study effects of over-expression of the METCAM/MUC18 gene on their in vitro cellular behaviors, such as cellular motility and invasiveness, and on in vivo tumorigenesis or metastasis in animal models.

**Over-expression of METCAM/MUC18 Inhibited Epithelial-To-Mesenchymal Transition (EMT) of SK-OV-3 Cells.**

Epithelial-to-mesenchymal transition (EMT) is a biological process by which carcinoma cells (cancer cells derived from epithelial cells) detach from the surrounding tissue and acquire characteristics of mesenchymal cells, which are unique motile and spindle-shaped cells with end-to-end polarity [45]. Cells that have undergone EMT can migrate out of their epithelial layers to distant organs, at where they may remain mesenchymal or re-differentiate into epithelial cells by a process known as mesenchymal-to-epithelial transition (MET). Thus EMT may be a process pre-required for tumor progression. In addition to increased motility, carcinoma cells via EMT may become stem cell-like, protected from senescence, apoptosis and immune surveillance, and resistant to conventional and targeted therapies [45]. The degree of EMT in cells usually can be determined by the extent of motility and invasiveness of the cells in vitro.

Since the SK-OV-3 cell line nearly does not endogenously express any METCAM/MUC18 (as shown in Figure 2), to determine if METCAM/MUC18 plays a role in mediating EMT in this cell line, we ectopically increase the METCAM/MUC18 expression in this cell line, as shown above, and use the G418R clones to determine the effects of enforced expression of METCAM/MUC18 on their in vitro motility and invasiveness.

If METCAM/MUC18 plays a positive role in mediating EMT in this cell line, we should observe an increased motility and invasiveness of these stable clones that overly express METCAM/MUC18. On the contrary, if it plays a negative role in EMT, we should observe a decreased motility and invasiveness of these stable clones that overly express METCAM/MUC18.

As shown in Figure 4 (left panel), the motility of the METCAM clone 2D, which expressed a high level of METCAM/MUC18, was 1.65-fold lower than that of the control (vector) clone 3D, which expressed 0% of METCAM/MUC18. As shown in Figure 4 (right panel), the invasiveness of the METCAM clone 2D was 1.57-fold lower than that of the control (vector) clone 3D. Thus over-expression of huMETCAM/MUC18 in SK-OV-3 cell line decreased its in vitro motility (Figure 4, left panel) and invasiveness (Figure 4, right panel).
Figure 4: Effects of METCAM/MUC18 expression on the motility (left panel) and invasiveness (right panel) of SK-OV-3 cell line. (Left panel) For the motility test, the METCAM clone 2D and the Control (Vector) clone 3D of SK-OV-3 cells were used. Six hours after seeding to the top wells, cells migrating to the bottom wells were determined. Means and standard deviations of triplicate values of the motility tests are indicated. P value, which was determined by analyzing two sets of data with the Student’s t test by using the one-tailed distribution-type 2 method, was 0.014, indicating that the result is statistically different. (Right panel) For invasiveness test, the METCAM clone 2D and the Control (Vector) clone 3D of SK-OV-3 cells were used. Six hours after seeding cells to the top wells, cells migrating to the bottom wells were determined. Means and standard deviations of triplicate values of the invasiveness tests are indicated. P value, which was determined by analyzing two sets of data with the Student’s t test by using the one-tailed distribution-type 2 method, was 0.0015, indicating that the result is statistically different.

From the results of Figure 4, we strongly suggested that huMETCAM/MUC18 plays a negative role in the EMT of SK-OV-3 cells and METCAM/MUC18 directly causes the decreased EMT of SK-OV-3 cells.

Taken together, we conclude that increased METCAM/MUC18 expression decreased EMT of human ovarian cancer cells.

**Over-expression of METCAM/MUC18 Suppressed in vivo Tumorigenesis And The Malignant Progression of the Human Ovarian Cancer Cell Line SK-OV-3.**

Previously published research findings show that METCAM/MUC18 expression appears to be increased in human ovarian cancer specimens and may be used as a marker for the poor prognosis of ovarian cancer patients [19]. Further *in vitro* studies show that siRNA-reduced expression of METCAM/MUC18 in SK-OV-3 cells increased apoptosis and reduced cell spreading and invasion, suggesting that METCAM/MUC18 may play a positive role in the development of ovarian cancer [41]. However definitive proof of this notion requires studies in model animals.
For this purpose we determined effects of METCAM/MUC18 over-expression on *in vivo* tumorigenicity of SKOV3 cells in female nude mice after SC injection at either dorsal (DSC) or ventral (VSC) side. As shown in Figure 5 (left panel) that tumor proliferation of the METCAM clone 2D was much lower than that of the control (vector) clone at both sites, indicating that over-expression of METCAM/MUC18 decreased tumorigenicity of SK-OV-3 cells in nude mice. Consistent with the results in Figure 5 (left panel), Figure 5 (right panel) shows that final tumor weights of the METCAM clone 2D were also lower than those of the control (vector) clone 3D at both sites, indicating that over-expression of METCAM/MUC18 decreased the final tumor weights of SK-OV-3 cells in nude mice. Interestingly, as also shown in Figure 5, tumorigenicity of the control clone 3D on the dorsal side was significantly better than that on the ventral side, but tumorigenicity of the METCAM clone 2D on the ventral side was significantly better than that on the dorsal site [42]. We don’t know the reason (s) why different SC sites have different effects on tumorigenicity.

**Figure 5:** Effect of over-expression of huMETCAM/MUC18 on the tumor proliferation (left panel) and final tumor weight (right panel) at S.C. sites of human ovarian cancer SK-OV-3 clones. The pooled 2D clone expressed 51% of METCAM, whereas the pooled 3D clone (Vector) expressed 0% of METCAM.

Taken together, we conclude that over-expression of METCAM/MUC18 suppressed *in vivo* tumorigenesis of SK-OV-3 cells at non-orthotopic (ventral and dorsal) subcutaneous sites in nude mice. One point worth noting is that the tumors induced by the METCAM clone 2D were confined to small regions, as shown in the results of H&E and IHC [42], whereas the tumors induced by the control (vector) clone 3D developed serious tumors, suggesting that tumors from the 2D clone appeared to be dormant; thus METCAM/MUC18 may function similarly to other tumor/metastasis suppressors in other tumor cells [46].

To further determine the effect of METCAM/MUC18 over-expression on *in vivo* tumorigenicity of SK-OV-3 cells in the orthotopic site (intraperitoneal (IP) cavity), SK-OV-3 cells from the pooled METCAM clone 2D and the control (vector) clone 3D were *IP* injected into female nude mice. The mice in the control group, which were injected with the control vector clone 3D, developed swollen...
abdominal cavity, but not the mice in the test group, which were injected with the METCAM clone 2D. After dissection of the abdominal cavities, we found that tumors and ascites were formed in four of five mice in the control group, whereas no tumors and ascites were found in the test group. Consistent with the observation, the final weights of abdominal tumors, as shown in Fig. 6 (left panel), and volumes of ascites were measured, as shown in Figs. 6 (right panel), were significantly larger in the group injected with the control vector clone 3D than those injected with the METCAM/MUC18-expressing clone 2D. We concluded that over-expression of METCAM/MUC18 suppressed the tumorigenicity and ascites formation of SK-OV-3 cells in IP cavities in nude mice [42].

Figure 6: Effect of over-expression of huMETCAM/MUC18 on the final weight of solid tumors (left panel) and final ascites volumes of ascites formed in the intraperitoneal cavity (right panel) at orthotopic sites (the intraperitoneal cavity) from human ovarian cancer SK-OV-3 clones. The pooled 2D clone expressed 51% of METCAM, whereas the pooled 3D clone (Vector) expressed 0% of METCAM.

Taken together, METCAM/MUC18 expression in SK-OV-3 cells decreased the tumor proliferation and tumorigenesis at SC sites as well as at the orthotopic IP site. We conclude that expression of METCAM/MUC18 suppressed tumorigenesis and the malignant progression of human ovarian cancer cells, suggesting that METCAM/MUC18 is a novel tumor and metastasis suppressor for the progression of human ovarian cancer cells.

Preliminary Mechanisms of METCAM/MUC18-Mediated Suppression of the Progression of SK-OV-3 Cells

Mechanisms of METCAM/MUC18-mediated suppression of the progression of human ovarian cancer cells have not been studied. By deducing knowledge learned from METCAM/MUC18-induced tumorigenesis of other tumor cell lines, such as, melanoma, cancers in breast and prostate and nasopharyngeal carcinoma, METCAM/MUC18 may affect tumorigenesis by cross-talk with many downstream signaling pathways that regulate proliferation, survival pathway,
apoptosis, metabolism, and angiogenesis of tumor cells [7,30]. To investigate if METCAM/MUC18-mediated tumor suppression also affected expression of its downstream effectors, such as indexes of apoptosis/anti-apoptosis, proliferation, survival, aerobic glycolysis, and angiogenesis, we determined the expression of levels of Bcl2, Bax, PCNA, LDH-A, pan-AKT, phospho-AKT(Ser 473), and the ratio of phospho-AKT/AKT in tumor lysates by using Western blot analyses [42]. The ratios of Bax/Bcl2 were not statistically different between tumors derived from the METCAM clone 2D and those from the control (vector) clone 3D, indicating that over-expression of METCAM/MUC18 did not affect apoptosis or anti-apoptosis of SK-OV-3 cancer cells during in vivo tumorigenesis. The levels of PCNA, LDH-A, pan-AKT, and phospho-AKT (Ser473) in the tumor lysates from the METCAM clone 2D were lower than in those from the control (vector) clone 3D, indicating that over-expression of METCAM/MUC18 decreased aerobic glycolysis, proliferation, and angiogenesis perhaps via down-regulating the PI3K-AKT signaling pathway of SK-OV-3 cancer cells during in vivo tumorigenesis. However, the ratios of phospho-AKT (Ser 473)/AKT in tumors of the METCAM clone 2D were not statistically significantly different from those in tumors of the control (vector) clone 3D, indicating that METCAM over-expression did not affect the survival pathway of SK-OV-3 cancer cells during in vivo tumorigenesis. Taken together, we suggest that over expression of METCAM/MUC18 may suppress tumorigenesis and malignant progression of ovarian cancer cells in nude mice by decreasing their abilities in proliferation, aerobic glycolysis, and angiogenesis via decreasing the absolute levels of pan-AKT and phospho-AKT, but not altering the apoptosis/anti-apoptosis and survival pathways [42]. This is consistent with the results from clinical specimens [20].

CONCLUSION

In summary, we provided evidence to show that METCAM/MUC18 is a novel suppressor for the tumorigenesis and malignant progression of the human ovarian cancer SK-OV-3 cells: (a) METCAM/MUC18 was expressed at lower levels in malignant cell lines than in primary adenocarcinomas, suggesting that METCAM/MUC18 may play a negative role in the progression of ovarian cancer. (b) A high expression level of METCAM/MUC18 inhibits the EMT of SKOV3 cancer cells. (c) METCAM/MUC18 expression inhibited the tumorigenicity at the subcutaneous sites as well as the tumorigenicity and ascites formation in the intra-peritoneal cavity of an athymic nude mouse model. Since the METCAM/MUC18 expressed in the tumors and ascites cells were similar to that in the injected clones/cells, the protein was not modified to manifest these processes. Taken together, we conclude that METCAM/MUC18 serves as a tumor suppressor as well as a metastasis suppressor for the human ovarian cancer SK-OV-3 cells. METCAM/MUC18 may suppress tumorigenesis and malignant progression of ovarian cancer cells in nude mice by decreasing their abilities in proliferation, aerobic glycolysis (metabolism), and angiogenesis via down-regulating the PI3K-AKT signaling pathway.

This conclusion contradicts the results of a positive correlation of clinical prognosis with the increased expression of METCAM/MUC18 in malignant ovarian cancer specimens [19,20,41].
suggests that the positive correlation in this case is fortuitous and that we should not assume a positive role of METCAM/MUC18 in the progression of ovarian cancer without the support of tests in an animal model. Our results also contradict the previously established notion that METCAM/MUC18 serves as a tumor promoter in both prostate cancer cells and breast cancer cells, and as a metastasis promoter in human melanoma cells, prostate cancer, and breast cancer [30,35-40]. The role of METCAM/MUC18 as a tumor suppressor was not only conclusively demonstrated in the human ovarian cancer cell line, SK-OV-3 [42], as well as in a mouse melanoma cell line, K1735-9 [47], one NPC cell line, NPC-TW01 [34,48,49]. METCAM/MUC18 has also been demonstrated as a metastasis suppressor in the two human ovarian cancer cell lines, SK-OV-3 cells and BG-1 cells [42,49], and one mouse melanoma cell line [47]. Thus sufficient evidence is provided to support the novel suppressor role of METCAM/MUC18 in the progression of these human cancers.

The most intriguing, unique biological function of METCAM/MUC18 in tumorigenesis and metastasis is that it seems to play a dual role in the progression of some tumor cell lines [49]. It is not clear why METCAM/MUC18 plays a dual role in tumorigenicity and metastasis. One point is clear, which is that METCAM/MUC18 plays an opposite role in different cancer types or in different clones/sublines of the same cancer type [49]. Thus it is logical to propose that the effect of METCAM/MUC18 on the progression of epithelial cancers is modulated by different intrinsic factors in different tumor cells/types. The dual role of METCAM/MUC18 is very likely due to the presence of different interacting partners intrinsic to each cancer cell type and different clone, or perhaps due to different heterophilic ligands, which unfortunately have not been identified [30,49]. Interactions of METCAM/MUC18 with different sets of intrinsic partners may result in the promotion or suppression of tumorigenicity and metastasis via increasing or decreasing aerobic glycolysis, proliferation, angiogenesis, other growth-promoting pathways, as well as altering tumor cell motility, invasiveness, and vascular metastasis.

The tumor/metastasis suppressor role of human METCAM/MUC18 in the progression of human ovarian cancer cells may point to the possibility that METCAM/MUC18 may induce tumor dormancy. How METCAM/MUC18 affects tumor dormancy should be an interesting aspect for future investigation, since tumor dormancy may be due to intrinsic growth inhibition, immunological suppression, and/or angiogenic suppression [50].

Perspectives and Clinical Applications

The tumor suppressor function of METCAM/MUC18 may be useful for clinical application. Indeed many tumor and metastatic suppressors, such as KISS1, KAI1, nm23, MAP2K4, and some microRNA have been used for clinical applications [51]. Three strategies have been developed, such as (a) reconstitution of suppressor genes by induction of the endogenous locus or by gene therapy, (b) direct administration of the suppressor proteins, (c) targeting essential downstream pathways that are activated by loss of suppressor function. In light of these, METCAM/MUC18 cDNA gene may be used for gene therapy by using the adeno-virus-associated virus vector or a
replication-defective adenovirus. The recombinant METCAM/MUC18 protein, or METCAM-derived peptides, or small molecule mimetics of METCAM may also be used directly. The recombinant cognate ligand of METCAM/MUC18 may potentially be used also. However, many downstream pathways of METCAM/MUC18 may not be useful because METCAM/MUC18 appeared to involve many of them. The above strategies may be used for clinical trials by keeping ovarian cancer cells in a dormant state or arresting the cancer cells at the stage of micro-metastases.

**AUTHORS’ CONTRIBUTIONS**

GJW conceived of the idea and study, participated in its design and coordination, carried out in vivo animal studies, performed the statistical analysis, and revised the manuscript many times suitable for publication.

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