Abstract

The acquisition of the metastatic melanoma phenotype is associated with increased expression of the melanoma cell adhesion molecule MCAM/MUC18 (CD146). However, the mechanism by which MUC18 contributes to melanoma metastasis remains unclear. Herein, we stably silenced MUC18 expression in two metastatic melanoma cell lines, A375SM and C8161, and conducted cDNA microarray analysis. We identified and validated that the transcriptional regulator, inhibitor of DNA binding-1 (Id-1), previously shown to function as an oncogene in several malignancies, including melanoma, was downregulated by 5.6-fold following MUC18 silencing. Additionally, we found that MUC18 regulated Id-1 expression at the transcriptional level via ATF-3, which itself was upregulated by 6.9-fold in our cDNA microarray analysis. ChIP analysis showed increased binding of ATF-3 to the Id-1 promoter after MUC18 silencing. To complement these studies, we rescued the expression of MUC18, which reversed the expression patterns of Id-1 and ATF-3. Moreover, we showed that MUC18 promotes melanoma invasion through Id-1, as overexpression of Id-1 in MUC18-silenced cells resulted in increased MMP-2 expression and activity. To our knowledge, this is the first demonstration that MUC18 is involved in cell signaling regulating the expression of Id-1 and ATF-3, thus contributing to melanoma metastasis.

Introduction

Melanoma develops in a multistep, sequential process by which normal melanocytes are transformed to nevi, continuing to the radial growth phase (RGP) and subsequently to the vertical growth phase (VGP) and the metastatic phenotype (1). During the transition from the nonmetastatic to the metastatic phenotype, the interactions between the transformed melanoma cells, the microenvironment, and the extracellular matrix (ECM) are altered (2, 3).

One adhesion molecule that has been shown to play an important role during melanoma progression from the RGP to the VGP is MCAM/MUC18 (4, 5). MUC18, also known as CD146, is a 113-kDa transmembrane glycoprotein (5). MUC18 contains an extracellular domain composed of 5 immunoglobulin-like domains, a single transmembrane domain, and a short cytoplasmic domain consisting of several protein kinase–like recognition motifs, suggesting its potential involvement in cell signaling (6). MUC18 was first identified as a human melanoma antigen, rarely expressed on normal epidermal melanocytes, but abundantly expressed in advanced primary and metastatic melanoma (5). Furthermore, MUC18 expression correlates with poor patient prognosis (7).

We have previously shown that ectopic expression of MUC18 in the nonmetastatic melanoma cell line, SB-2 (MUC18 negative), increased the cells’ tumorigenic and metastatic potential in vivo (8, 9). The role of MUC18 in melanoma tumor growth and metastasis was further studied with the use of a fully human anti-MCAM/MUC18 monoclonal antibody (ABX-MA1; produced by Abgenix). Treatment with ABX-MA1 decreased tumor growth and experimental lung metastases both in vitro and in vivo via regulation of matrix metalloproteinase (MMP)-2 (10).

Nevertheless, the role of MUC18 in melanoma intracellular signaling has not yet been fully elucidated. To further define the mechanism of MUC18 as a signaling molecule and its role in melanoma metastasis, we conducted a cDNA microarray analysis, following MUC18 silencing, in 2 metastatic melanoma cell lines and identified inhibitor of DNA binding-1 (Id-1) as a downstream target of MUC18. Id-1 is a part of the Id protein family ("Inhibitor of differentiation" or "Inhibitor of..."
DNA binding) of helix-loop-helix (HLH) proteins that heterodimerize to basic HLH (bHLH) transcription factors and inhibit their activity (11–13). It has been suggested that Id proteins, particularly Id-1, function as oncogenes in several malignancies. Upregulation of Id-1 expression has been shown in primary human cancers including melanoma (14, 15).

Herein, we establish that signaling through MUC18 regulates Id-1 expression via modulation of ATF-3 expression and binding to the Id-1 promoter. Id-1, in turn, regulates the expression of MMP-2. Collectively, our studies have identified a novel mechanism by which MUC18 contributes to the acquisition of the malignant phenotype of melanoma.

Materials and Methods

Cell lines

The generation and maintenance of A375SM, SB-2, and C8161-c9 cell lines were previously described (16,17). Briefly, A375SM and SB-2 cell lines were maintained in cell culture as monolayers in Eagle’s minimal essential medium supplemented with 10% FBS. C8161-c9 cells were maintained in Dulbecco’s modified Eagle’s medium-F12 (DMEM-F12) supplemented with 5% FBS (17). The 293FT cells (Invitrogen) used to produce the lentiviral short hairpin RNA (shRNA) were supplemented with 5% FBS (17). The 293FT cells (Invitrogen) used to produce the lentiviral short hairpin RNA (shRNA) were maintained as previously described (16). All cell lines used in our studies were tested prior to their usage for authentication by DNA fingerprinting using the short tandem repeat (STR) method.

Western blot analysis

To detect the expression of ATF-3, Id-1, MUC18, MMP-2, Ets-1, and Sp1, 20 μg of protein lysates were loaded on SDS-PAGE as previously described (16). Blots were incubated with primary antibodies (1:1,000, anti–ATF-3 or anti–Id-1; 1:10,000, anti–Ets-1, anti–Sp1; Santa Cruz Biotechnology; 1:1,000 anti–MMP-2; Cell Signaling Technology; 1:1,000 anti–MUC18; BD Bioscience). For detecting Ets-1, nuclear extracts were prepared using a nuclear extraction kit (Panomics). Densitometry was carried out by using ImageJ software (NIH).

Chromatin immunoprecipitation assay

Chromatin immunoprecipitation (ChIP) assay was carried out by using the ChIP-IT Express Kit from Active Motif as described previously according to the manufacturer’s protocol (16). Protein–DNA complexes were pulled down with anti–ATF-3 antibody (sc-188: Santa Cruz), anti–Sp1 antibody (sc-14027X: Santa Cruz), anti–Ets-1 antibody (sc-5581X: Santa Cruz), anti–AP-2α antibody (sc-184X: Santa Cruz), anti–CREB antibody anti-p53 antibody (sc-126X: Santa Cruz). See Supplementary Materials and Methods for primer sequences.

siRNA/shRNA

MUC18 targeting shRNA 5′-TGATATCGCTGCTGAGTGA-3′ and a nontargeting (NT) shRNA 5′-TTCTCCGAACGCTTTCGTCAGCTG-3′ were cloned into the lentivector, pLVTHM, and transfected into 293FT (human embryonic kidney cell) to generate lentiviral particles. The lentivirus system and cell transduction were generated as described previously (18, 19) and were kindly provided by Didier Trono (Ecole Polytechnique Fédérale de Lausanne). Id-1 siRNA (Hs 01_00246328) was purchased from Sigma and transfected into SB-2 cells overexpressing MUC18 by using HiPerFect Transfection Reagent (QIAGEN) according to the manufacturer’s instructions.

Nontargetable MUC18 expression vector

Five silent point mutations were introduced into the MUC18 expression vector at the region targeted by the MUC18 shRNA, using the QuikChange II XL site-directed mutagenesis kit (Stratagene) and the following primers: forward, 5′-CAGGGCCTGGACTTGGACACCATGATTTCCCTTCTACGGAACACAGAATCGTTGGT-3′; reverse, 5′-CACCTGTAGCTCCTGTTGGTCTCGTGAGGAAATCATGTTGTCTCAAAGCCGCCCTG-3′. The amplified mutated sequence was ligated into the pLVX-DsRed-Monomer-C1 vector (Clontech) replacing the red protein coding sequence of DsRed generating the final rescue lentiviral vector.

To rescue MUC18 expression in stably transduced MUC18-silenced cells, the cells were transduced with the virus containing either the nontargetable MUC18 expression vector or empty vector control. Cells were selected with growth medium containing 50 μg/mL puromycin.

Luciferase assay

A375SM, C8161, and SB-2 were plated in a 24-well plate. Transfections of 0.8 μg luciferase reporter plasmids (pGL3-Id-1, pGL3-Id-1 mutant promoter, pGL3-MMP-2 and pGL3-MMP-2 mutant promoter) were carried out 48 hours after cells were plated using Lipofectamin-2000 (Invitrogen) as described previously (16).

Zymography

To determine MMP-2 activity zymography assay was carried out as described previously (9, 10).

Matrigel invasion assay

Invasion assay was carried out using BioCoat Matrigel invasion chambers (BD Biosciences) as described previously (16).

Immunohistochemistry

Immunohistochemistry was carried out as described previously (16). Slides were incubated with anti–MMP-2 (1:400; Chemicon), anti–Id-1 (polyclonal, 1:50; Santa Cruz), or anti–Ki67 (1:100; Abcam). For MUC18 staining, 1X Diva Decloaker (Biocare Medical) was used for antigen retrieval. Fragment blocking was used overnight at 4°C with Affini fragment blocking anti-mouse antibody (1:10; Jackson Immunoresearch). Slides were incubated overnight at 4°C with anti–MUC18 (1:50; BD Biosciences). Pictures were taken at ×20 magnification using a Leica DFC 320 R2. Terminal deoxynucleotidyl transferase–mediated dUTP nick end labeling (TUNEL) and CD31 staining were described previously (16).

Quantitative real-time PCR

RNA was harvested using the RNAqueous kit (Ambion) according to the manufacturer’s instructions and as described previously (18, 19).
previously (16). The primers were obtained from Applied Biosystems (MMP-2: Assay ID Hs01548727_m1). Reaction components for reverse transcription PCR and amplifications were described previously (16).

Animals, tumor growth, and metastasis

Female athymic BALB/c nude mice were purchased from the National Cancer Institute-Frederick Cancer Research and Development Center and housed in specific pathogen-free conditions. All studies were approved and supervised by The University of Texas MD Anderson Cancer Center, Institutional Animal Care and Use Committee (IACUC). Subcutaneous tumors and experimental lung metastases were produced as described previously (16). Briefly, 5 × 10^5 A375SM cells or 2.5 × 10^6 C8161 cells were injected into the right flank of each mouse (n = 7/group). Mice were sacrificed (according to guidelines of IACUC). To determine metastatic potential, 5 × 10^5 A375SM cells and 3.75 × 10^6 C8161 cells were injected into the tail vein of nude mice (n = 7/group). Mice were sacrificed 35 days after injections.

cDNA microarray

Total RNA was isolated from NT A375SM cells and MUC18-silenced A375SM cells using the Clontech Advantage RT-for-PCR kit according to the manufacturer’s instructions. A human genome U133 Plus 2.0 array (Affymetrix) was used for the microarray analysis. The microarrays were produced in the microarray core facility of Codon Bioscience. Affymetrix software was used to analyze the results as described previously (20).

Statistical analysis

Student t test was used to evaluate the statistical significance of differences for the in vitro data. Statistical analysis of the results of the animal studies was carried out using the Mann–Whitney U test. Values for tumor growth are given as a mean volume ± SEM, and P < 0.05 was considered statistically significant.

Results

Effect of MUC18 silencing on melanoma tumor growth and metastasis

To establish the role of MUC18 in promoting tumor growth and metastasis of human melanoma, we stably silenced MUC18 expression in 2 metastatic human melanoma cell lines, A375SM and C8161, using a lentiviral vector. MUC18 protein expression decreased by 90% and 80% in MUC18-silenced A375SM and C8161 cells, respectively, as compared with the NT shRNA–transduced cells (Fig. 1A).

We have previously shown that blocking MUC18 with the fully human antibody, ABX-MA1, significantly decreases both tumor growth and experimental lung metastasis (10). To corroborate these results and further determine the effect of MUC18 silencing on melanoma tumor growth, we injected both MUC18-silenced melanoma cell lines s.c. MUC18 silencing resulted in a significant decrease in tumor growth in both cell lines, as compared with mice injected with the NT shRNA–transduced cells; mean tumor volume at day 35 was 621.4 mm^3 in mice injected with NT A375SM cells, whereas in mice injected with MUC18-silenced A375SM cells it was 233.6 mm^3 (*, P < 0.05; Fig. 1B). Similar results were observed with NT shRNA and MUC18-silenced C8161 cells; mean tumor volume was 662.3 mm^3 versus 221.9 mm^3 (*, P < 0.001; Fig. 1B).

Immunohistochemical staining of the s.c. tumors showed that MUC18 expression decreased in tumors derived from MUC18-silenced A375SM and C8161 (Fig. 1C), as compared with tumors from NT shRNA–transduced cells. The decreased expression of MUC18 was sustained until the end of the experiment at day 35.

Although silencing of MUC18 resulted in decreased tumor growth in vivo, we did not observe any difference in cell proliferation in vitro for either cell line (data not shown). However, immunohistochemical staining showed reduced tumor cell proliferation (Ki67), accompanied by enhanced apoptosis (TUNEL) and diminished vessel size and number (CD31) in tumors obtained from MUC18-silenced cells (Supplementary Fig. S1), suggesting the importance of the tumor microenvironment in regulation of MUC18-mediated tumor growth in vivo.

To determine the effect of MUC18 silencing on melanoma metastasis, MUC18-silenced A375SM and C8161 cells were injected i.v. into nude mice. Lung metastasis was significantly decreased in mice injected with MUC18-silenced A375SM and C8161 cells, as compared with NT-transduced cells (median = 78 vs. 279 for A375SM and 133 vs. 290 for C8161; *, P < 0.05; Fig. 1D).

MUC18 silencing decreases in vitro cell invasion

We have previously shown that MUC18 contributes to melanoma cell invasion through regulation of MMP-2 activity (10). In the present study, we also observed decreased MMP-2 activity in MUC18-silenced A375SM and C8161 cells (Fig. 2A). Real-time PCR showed decreased MMP-2 mRNA expression, following MUC18 silencing, by more than 2-fold in A375SM cells and 3-fold in C8161 cells (Fig. 2B). Furthermore, a significant decrease of MMP-2 promoter activity was observed in MUC18-silenced A375SM cells (*, P < 0.01; Supplementary Fig. S2). Reduced MMP-2 expression was also confirmed in vivo by immunohistochemical analysis of tumor samples obtained from mice 35 days after injection with MUC18-silenced cells as compared with NT-transduced cells (Fig. 2C). Furthermore, Matrigel invasion assays showed a greater than 2-fold significant decrease in the invasive capability of MUC18-silenced cells (*, P < 0.05; Fig. 2D).

Id-1 is a downstream target of MUC18 in melanoma

To determine the mechanism by which MUC18 contributes to melanoma tumor growth and metastasis, we carried out cDNA microarray analysis comparing the gene expression pattern of NT-transduced cells and MUC18-silenced cells. Our analysis revealed a great number of genes differentially expressed following MUC18 silencing (partial list in Supplementary Table S1). We decided to focus our studies on the differential expression of transcriptional regulators and found that Id-1 was downregulated by 5.6-fold after MUC18 silencing.
silencing. Western blot validated the cDNA microarray results, illustrating that Id-1 was downregulated by 80% in MUC18-silenced A375SM cells and by 70% in MUC18-silenced C8161 cells, as compared with NT shRNA-transduced A375SM or C8161 cells. These results were obtained when cells were grown in 10% FBS. In serum-free medium, following a 48-hour incubation, lower levels of Id-1 were observed (data not shown). Moreover, immunohistochemical analysis of tumor samples after 35 days showed decreased Id-1 expression in MUC18-silenced tumors (Fig. 3B).

To further analyze the mechanism of Id-1 regulation by MUC18, we cloned the Id-1 promoter in front of a luciferase reporter gene and evaluated Id-1 promoter activity in both A375SM and C8161 MUC18-silenced cells. We found that Id-1 promoter activity decreased by more than 2.5-fold in MUC18-silenced A375SM cells (*, \( P < 0.01 \)) and by more than 2-fold in MUC18-silenced C8161 cells (**, \( P < 0.001 \)), as compared with NT-transduced cells (Fig. 3C). These experiments revealed that MUC18 transcriptionally regulates Id-1 expression.

**ATF-3 represses Id-1 promoter activity in MUC18-silenced cells**

Having shown that MUC18 regulates Id-1 at the transcriptional level, we next wanted to determine the mechanism of Id-1 regulation by MUC18 by analyzing the Id-1 promoter for potential transcription factor binding sites. We found an ATF/CREB family transcription factor binding site located 1,016 bp upstream of the transcription initiation site (Fig. 4A, top). Interestingly, ATF-3 was upregulated by nearly 7-fold after MUC18 silencing in our cDNA microarray analysis (Supplementary Table S1). Previous studies have shown that ATF-3 can act as a repressor of Id-1 expression through increased binding to the Id-1 promoter (21, 22). Western blot analysis corroborated the cDNA microarray results and showed that, as compared with NT-transduced cells, ATF-3 was upregulated by more than 9-fold in both MUC18-silenced A375SM and C8161 (Fig. 4A, bottom).

We then sought to determine whether there is differential binding of ATF-3 to the Id-1 promoter. ChIP analysis revealed increased binding of ATF-3 to the Id-1 promoter in both MUC18-silenced A375SM and C8161 cells (Fig. 4B). Together, these data suggest that MUC18 regulates ATF-3 expression and its differential binding to the Id-1 promoter.

To further delineate whether ATF-3 acts as a repressor of Id-1 expression, we exogenously expressed ATF-3, along with the Id-1 promoter, in MUC18-silenced and NT-transduced A375SM cells and then measured the promoter-driven luciferase activity. ATF-3 overexpression resulted in a significant decrease of Id-1 promoter activity (*, \( P < 0.05 \); Fig. 4C). In contrast, mutation of the Id-1 promoter at the ATF-3 binding site (depicted in Fig. 4A, top) significantly increased Id-1 promoter activity (*, \( P < 0.05 \)). Furthermore, stable overexpression of ATF-3 in parental A375SM and C8161 cells resulted in decreased expression of endogenous Id-1 protein.
by 90% and 70%, respectively (Fig. 4D). Collectively, MUC18 silencing resulted in enhanced ATF-3 expression and increased binding of ATF-3 to the Id-1 promoter. Accordingly, we conclude that ATF-3 acts to repress Id-1 transcription and protein expression.

Rescue of MUC18 in MUC18-silenced cells reverts the expression of Id-1 and ATF-3

To ascertain that the differential expression of Id-1 and ATF-3 are not off-target effects of MUC18, we used a nontargetable MUC18 expression vector to rescue MUC18 expression in MUC18-silenced cells. Figure 5A shows that MUC18 expression was rescued in both MUC18-silenced cells. MUC18 rescue subsequently resulted in increased Id-1 expression and decreased ATF-3 expression (Fig. 5B), thereby showing that both Id-1 and ATF-3 were indeed specifically regulated by MUC18.

Rescue of Id-1 expression in MUC18-silenced cells increases the invasive phenotype

Recent studies have shown that Id-1 plays a role in tumor invasion (23–25). Having established that MUC18 expression promotes melanoma cell invasion and enhanced MMP-2 expression and activity (Fig. 2A and B; refs. 8, 10), we assessed whether MUC18 contributes to melanoma cell invasion through Id-1. We therefore overexpressed Id-1 in MUC18-silenced A375SM and C8161 cells and subsequently observed an upregulation of Id-1 expression by 2.5- and 3.3-fold, respectively, as compared with control cells (Fig. 6A).

The invasive capacity of MUC18-silenced cells overexpressing Id-1 was then compared with that of MUC18-silenced cells expressing an empty vector control. As seen in Fig. 6B, ectopic expression of Id-1 in MUC18-silenced A375SM and C8161 cells resulted in increased MMP-2 expression and activity, compared with MUC18-silenced cells expressing empty vector

Figure 2. Effect of MUC18 silencing on melanoma cell invasion and MMP-2 expression. A, zymography shows decreased MMP-2 activity after MUC18 silencing in both A375SM and C8161, compared with NT-transduced cells. Control of zymography gel shows equal loading of samples as indicated by silver staining. Images are representative of 3 experiments. B, quantitative real-time PCR validates diminished MMP-2 expression following MUC18 silencing in both A375SM and C8161, compared with NT-transduced cells (*, P < 0.001). Expression values are illustrated as fold change of mean values ± SEM of 3 independent experiments in each cell line, relative to the NT-shRNA cells, after normalization with 18s RNA. C, immunohistochemical staining showing downregulation of MMP-2 expression in MUC18-silenced tumors 35 days after injections, as compared with NT-transduced A375SM and C8161 cells. Images are shown at ×20 magnification. D, Matrigel invasion assay shows a significant decrease in invasion following MUC18 silencing in both A375SM and C8161 (*, P < 0.05). Data are expressed as mean ± SEM of 3 experiments.
control (Fig. 6C and D, respectively). These data confirm that MUC18 modulates MMP-2 expression and activity via Id-1.

Id-1 regulates MMP-2 transcription

Because melanoma cell invasiveness, as well as MMP-2 expression and activity, was rescued in MUC18-silenced cells overexpressing Id-1, we sought to determine the role of Id-1 in regulating MMP-2 expression and melanoma cell invasion. To that end, Id-1 was stably overexpressed in SB-2 melanoma cells, which do not express endogenous MUC18 and express low levels of Id-1 (Fig. 7A).

We then assessed the function of Id-1 in melanoma cell invasion. SB-2 cells overexpressing Id-1 exhibited a significant increase in cell invasion through Matrigel-coated filters by greater than 3-fold, compared with control cells (Fig. 7B). Moreover, overexpression of Id-1 in SB-2 cells resulted in a significant increase in MMP-2 mRNA levels (*, P < 0.001) and protein expression as compared with empty vector control-transduced cells (Fig. 7C and D).

To ascertain the mechanism of MMP-2 regulation by Id-1, we cloned the MMP-2 promoter in front of a luciferase reporter gene and evaluated its activity in SB-2 cells overexpressing Id-1. MMP-2 promoter-driven luciferase activity was increased by 2.2-fold in SB-2 cells overexpressing Id-1, compared with control SB-2 cells (*, P < 0.001; Fig. 7E). These data show that Id-1 transcriptionally regulates MMP-2 expression.

To determine whether Id-1 regulates MMP-2 transcription via differential binding of transcription factors, we used the ChIP assay. Previous studies have shown that several transcription factors can positively regulate MMP-2 transcription (26–28). Figure 7F is a schematic of the MMP-2 promoter, depicting potential transcription factor binding sites. Specific primers were designed to amplify the potential transcription binding sites of p53, CREB, Ets-1, Sp1, and AP-2. ChIP assays showed that Id-1 overexpression in SB-2 cells resulted in increased binding of both Ets-1 and Sp1 to the MMP-2 promoter, compared with control cells expressing an empty vector (Fig. 7G). However, no effect on AP-2, p53, and CREB binding was observed (Fig. 7G and data not shown). Additionally, Western blot analysis revealed increased expression of Ets-1 and Sp1 after Id-1 overexpression in SB-2 cells (Fig. 7H). Moreover, a luciferase assay showed that in SB-2 cells overexpressing Id-1, MMP-2 promoter activity was significantly decreased following deletion of the Ets-1 binding site or mutation of the Sp1 binding site (*, P < 0.01; **, P < 0.001; Supplementary Fig. S3A and B). These results suggest that Id-1 regulated MMP-2 transcription by affecting both the expression and binding of Ets-1 and Sp1 transcription factors to the MMP-2 promoter.

Finally, to further validate that MUC18 indeed regulates melanoma cell invasion and MMP-2 expression via Id-1, we overexpressed MUC18 and silenced Id-1 expression in SB-2 cells (Supplementary Fig. S4A and B). Id-1 silencing in these
cells resulted in decreased cell invasion as well as MMP-2 mRNA levels (*, $P < 0.001$; Supplementary Fig. S4C and D).

We conclude that MUC18 contributes to melanoma progression by increasing the expression of the transcriptional regulator Id-1 (via ATF-3), which results in positive regulation of MMP-2 expression and activity, thus promoting melanoma cell invasion.

**Discussion**

The adhesion molecule MUC18 plays an important role in promoting melanoma tumor growth and metastasis (4, 8–10, 29, 30). Previous studies have shown that MUC18 contributes to melanoma progression by promoting both homo- and heterotypic adhesion of melanoma cells either to each other or to endothelial cells. Remarkably, little is known of what lies downstream of MUC18. We, therefore, further elucidated the downstream molecular events of MUC18 that promote the metastatic phenotype of melanoma.

To that end, we stably silenced MUC18 expression using lentiviral shRNA in 2 metastatic melanoma cell lines and validated that MUC18 silencing decreased both tumor growth and metastasis of human melanoma cell lines in nude mice. MUC18-silenced melanoma cells were subjected to gene expression profiling to identify potential target genes regulated by MUC18. cDNA microarray analysis identified Id-1 as a novel downstream target gene of MUC18. Id-1 is a regulator of gene transcription that binds to bHLH transcription factors to inhibit their transactivation function (11). The oncogenic role of Id-1 has been suggested because it is widely expressed in human cancers, functioning as a regulator of pleiotropic cellular processes, including cell growth, cellular senescence, apoptosis, angiogenesis, and invasion (14). Notably, in melanoma, Id-1 expression has been shown to be associated
with inhibition of p16/Ink4a transactivation. Furthermore, increased Id-1 expression was noted in metastatic melanoma cells lines and lesions (31, 32). Using melanoma tissue arrays, Straume and Akslen have shown that enhanced Id-1 expression is associated with increased melanoma tumor thickness and decreased patient survival (33). These results correlate with previous data showing the association between MUC18 and increased melanoma tumor thickness and metastatic progression (5, 7). We confirmed that Id-1 expression is indeed decreased in MUC18-silenced cells as well as in tumor xenographs, thereby establishing a link between MUC18 and Id-1. Furthermore, using a luciferase-driven Id-1 promoter, we show that MUC18 regulates Id-1 at the transcriptional level. Previous studies have linked ATF-3 to transcriptional inhibition of Id-1 (21, 22). Interestingly, we also identified ATF-3 as a MUC18 downstream target in our cDNA microarray.

ATF-3 is a stress-inducible protein and member of the ATF/CREB family of transcription factors induced by the p38 signaling pathway (34). It has been shown to act in a promoter-dependent manner, either as a transcriptional repressor or activator (35). A recent study has described ATF-3 as having a tumor suppressive role in melanoma by negatively regulating interleukin-6 (36). Moreover, Kang and colleagues have shown that in epithelial cells ATF-3 binds to the Id-1 promoter and represses its transcription due to a stress response of the cells (21). Our finding that MUC18 silencing increased the expression of ATF-3 further supports the tumor-suppressive role of ATF-3 in melanoma.
These results raised the possibility that MUC18 negatively regulates ATF-3 expression, possibly through inhibition of the p38 signaling pathway, to promote upregulation of Id-1. In this regard, promoter and ChIP analyses showed that indeed, in MUC18 silenced cells, upregulation of ATF-3 results in increased binding of ATF-3 to the Id-1 promoter and repression of Id-1 transcription. Additionally, stable overexpression of ATF-3 in 2 metastatic melanoma cell lines, A375SM and C8161, decreased endogenous Id-1 expression, thus further establishing the role of ATF-3 in repression of Id-1 expression. The possibility that other transcription factors are involved in Id-1 transcription is currently being investigated.
To further establish the link between MUC18, Id-1, and 
ATF-3, we rescued MUC18 expression in MUC18-silenced 
cells. The expression patterns of Id-1 and ATF-3 were 
reverted after rescue of MUC18 expression in both A375SM and C8161, 
confirming that the modulation of Id-1 and ATF-3 was not an 
off-target effect of MUC18 silencing.

Previous studies have shown the role of Id-1 in promoting 
tumor invasion and MMP-2 expression (14, 23). Herein, we 
propose that MUC18 promotes melanoma cell invasion 
through the regulation of MMP-2 expression and activity 
via Id-1. Our data show that Id-1 overexpression in MUC18-silenced 
cells significantly increased the invasive capacity of 
melanoma cells. Additionally, MMP-2 expression and activity 
were rescued by Id-1 in MUC18-silenced cells. This suggests 
that Id-1 is an intermediary in the regulation of melanoma cell 
invansion by MUC18.

Although Id-1 has been shown to increase MMP-2 expres-
sion, the mechanism of regulation of MMP-2 by Id-1 has not 
been elucidated. To assess the role of Id-1 in the regulation 
of MMP-2 expression and melanoma cell invasion, we over-
expressed Id-1 in a nonmetastatic melanoma cell line, SB-2, 
which lacks expression of MUC18 and expresses low levels of 
Id-1. Interestingly, we found that Id-1, alone, can drive 
melanoma cell invasion and positively regulate MMP-2 
transcription, as shown by enhanced MMP-2 promoter activity 
and mRNA levels. Although Id-1 functions as an 
inhibitor of DNA binding, it was recently shown by Qian and 
colleagues that it can act as a positive regulator of tran-
scription in human breast cancer cells (37). Thus, we further 
aimed to elucidate the mechanism by which it transcription-
ally regulates MMP-2 expression. Studies have shown that 
transcriptional regulation of MMP-2 is mediated by 
differential binding of several transcription factors, such as 
Sp1 and Ets-1, to the MMP-2 promoter (26, 27). Our studies 
reveal that Id-1 promotes MMP-2 expression through 
increased expression and binding of both Ets-1 and Sp1 
to the MMP-2 promoter. Although MMP-2 expression can be 
modulated by CREB, AP-2, and p53, these transcription 
actors do not seem to play a role in MMP-2 expression 
in our system, as no differential binding of these transcric-
tion factors was found following Id-1 overexpression in SB-2 
cells. Although we showed that Id-1 positively regulated the 
expression and binding of Ets-1 to the MMP-2 promoter, it 
should be noted that in other systems Id-1 has been shown 
to inhibit the function of Ets proteins as transactivators (32). 
It is possible that in our system increased expression of Ets-1 
promotes its interaction with other transcription factors or 
coactivators (i.e., c-Jun, c-Fos, and CBP/p300), rather than 
being inhibited by Id-1, thus competing with Id-1 and 
leading to transactivation of MMP-2.

Taken together, our data reveal a novel mechanism by 
which the adhesion molecule MUC18 contributes to melano-
ma metastasis. The current studies support the notion that 
MUC18 does not simply function to promote cell adhesion, 
but rather is involved in cellular signaling events that affect 
the expression of genes such as Id-1 and ATF-3. We further 
show that MUC18 promotes melanoma cell invasion by 
upregulating MMP-2 transcription and protein expression 
through Id-1, thus contributing to the malignant phenotype of 
melanoma.

Disclosure of Potential Conflicts of Interest

No potential conflicts of interest were disclosed.

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