

# New Pathway Links From Cancer-Progression Determinants to Gene Expression of Matrix Metalloproteinases in Breast Cancer Cells

GREGORY S. DELASSUS, HYOJIN CHO, JANICE PARK, AND GEORGE L. ELICEIRI\*

Department of Pathology, Saint Louis University School of Medicine, St. Louis, Missouri

AP-2 $\alpha$ , interleukin-4 (IL-4), E-cadherin, fibulin 1D, p16<sup>INK4 $\alpha$</sup> , PTEN, RKIP, and S100A4 are determinants (suppressors, except for S100A4) of cancer cell invasiveness and other traits of cancer progression, which are located upstream of matrix metalloproteinases (MMPs) in cell signaling pathways. We will refer to them as upstream cancer-progression determinants (UCPDs, for brevity). MMP-1, MMP-2, MMP-9, MMP-11, MMP-13, MMP-14, MMP-16, and MMP-19 are enhancers of cancer cell invasiveness and other traits of cancer progression, in MDA-MB-231 breast cancer cells. We are interested in pathway links from UCPDs to gene expression of cancer cell MMPs in MDA-MB-231 cells. To test models about these links, wild-type copies of UCPDs were transiently overexpressed and then MMP mRNAs were measured by reverse transcription real-time PCR. The present results show that each of eight UCPDs is linked to the gene expression of a unique set of MMPs. This indicates that the effects are sequence-specific and that each UCPD reaches these MMP expressions through different sets of signaling pathways. We have detected 20 new pathway links, 11 are downregulatory and nine are upregulatory; 15 are new links in any cell, and five are new links in breast cancer. In seven links, three cancer-progression suppressing UCPDs unexpectedly enhance the gene expression of five cancer-progression promoting MMPs.

J. Cell. Physiol. 217: 739–744, 2008. © 2008 Wiley-Liss, Inc.

Cancer traits tend to depend on cell signaling pathways rather than a specific member of each pathway (Vogelstein and Kinzler, 2004; Wang et al., 2007). For restorative genetic and epigenetic therapy of a given type of metastatic cancer, it is a high priority to identify the highest number of cell signaling pathways which determine the progression of that cancer because they are potential targets for therapy. This overview information is needed to design alternative therapies, as the metastatic cancer becomes resistant to standard therapies. Much is unknown about these signaling pathways, particularly in MDA-MB-231 cells. We chose to work with these cells because they are well characterized to be human, metastatic, invasive, cancer cells (Neve et al., 2006).

Several cancer cell matrix metalloproteinases (MMPs), such as MMP-1, MMP-2, MMP-9, MMP-11, MMP-13, MMP-14, MMP-16, and MMP-19, enhance MDA-MB-231 cancer cell invasiveness (Ramos-DeSimone et al., 1999; Jiang et al., 2005, 2006; Wyatt et al., 2005; Merrell et al., 2006; Muñoz-Nájjar et al., 2006; Hegedüs et al., 2008). Activator protein-2 $\alpha$  (AP-2 $\alpha$ ), E-cadherin, fibulin 1D, interleukin 4 (IL-4), KAI1, p16<sup>INK4 $\alpha$</sup> , phosphatase and tensin homolog (PTEN), and raf kinase inhibitor protein (RKIP) suppress, and S100A4 enhances, cancer cell invasiveness and other cancer progression traits, in MDA-MB-231 breast cancer cells and cells from other types of cancers (Uchiyama et al., 1996; Chintala et al., 1997; Qing et al., 1997; Hayashido et al., 1998; Twal et al., 2001; Adachi et al., 2002; Fu et al., 2003; Wong and Gumbiner, 2003; Zheng et al., 2003; Schuierer et al., 2004; Sumigama et al., 2004; Hjelmeland et al., 2005; Saleem et al., 2006; Chen et al., 2007;). They are located upstream of MMPs in cell signaling pathways. The term “upstream cancer-progression determinants” (UCPDs, for brevity) will be used for them in this text.

A very large number of proteins determine invasiveness and other cancer progression traits (Uchiyama et al., 1996; Twal et al., 2001; Wong and Gumbiner, 2003; Zheng et al., 2003; Schuierer et al., 2004; Sumigama et al., 2004; Saleem et al., 2006). The progression of different types of cancers depends on

different profiles of cell signaling pathways (Walsh and King, 2007; Cybulski et al., 2008). In order to begin the identification of a cell signaling pathway between two factors, it is essential to have detected first a pathway link between them. The present study of some UCPDs and gene expression of some cancer progression-promoting MMPs showed 20 pathway links in MDA-MB-231 cells. We have found that different types of cancers have distinct pathway links from these UCPDs to the gene expression of these MMPs (manuscript in preparation). Thus, the cumulative number of cell signaling pathways involved in the progression of various types of cancers is expected to be high. Identification of signaling pathway is labor intensive. Therefore, strategically it makes sense to obtain first an overview of the pathway links. This overview is important to prioritize the pathway links whose signaling pathway should be identified first regarding potential therapeutic value.

Therapy does not require identification of all of the signaling pathways now. Thus, it is reasonable to focus first on mRNA measurements to detect pathway links because it is faster, less expensive, more sensitive and more quantitative to measure gene expression by reverse transcription by real-time PCR than to measure protein levels (Bakalova et al., 2005; Pérez-Ruiz et al., 2007). In addition, we have found that some cancer cell proteins whose mRNA levels are very low, are important for invasiveness (Hegedüs et al., 2008).

The goals of the present study were to find out: (a) whether there are any pathway links from any of these UCPDs to the

\*Correspondence to: George L. Eliceiri, Department of Pathology, Saint Louis University School of Medicine, 1402 South Grand Boulevard, St. Louis, MO 63104-1028. E-mail: eliceiri@slu.edu

Received 21 May 2008; Accepted 25 June 2008

Published online in Wiley InterScience  
(www.interscience.wiley.com.), 23 July 2008.  
DOI: 10.1002/jcp.21548

gene expression of any of these MMPs in MDA-MB-231 cells; (b) if so, whether each UCPD is linked to the same or a unique set of MMP gene expressions; and (c) whether the links are up- or down-regulatory. We found several connections from UCPDs to gene expression of various downstream MMPs. The results show that several UCPDs belong to signaling pathways which up- or down-regulate the gene expression of unique profiles of cancer cell MMPs. Surprisingly, some of cancer progression inhibitors stimulated the gene expression of some cancer progression enhancers.

## Materials and Methods

### Cells

MDA-MB-231 metastatic human breast cancer cells were obtained from the U.S. National Cancer Institute, and were grown in DMEM supplemented with 10% fetal bovine serum and maintained at 37°C in a humidified 10% CO<sub>2</sub> incubator.

### Plasmids

The following plasmids were used: pCMV-PTEN-WT for PTEN, provided by Donald Tindall; pCEP4mp16 for p16<sup>INK4α</sup>, from Laura Taylor; pcDNA-(+)-ssRKIP for RKIP, from Evan Keller; pSG5-neo-AP-2α for AP-2α, from Michael Tainsky; pCMV-KAI1 for KAI1, from J. Carl Barrett; pcDHull-4 for (IL-4), from Nancy Magnuson; hEcad/pcDNA3 for E-cadherin, from Barry Gumbiner; pSV2neo.S100A4 for S100A4, from Barry Davies; pcDNANeo-fibulin-ID for fibulin ID, from W. Scott Argraves; pEGFP-C1 (Becton Dickson, Franklin Lakes, NJ) for green fluorescent protein (eGFP); and pcDNA3.1 (Invitrogen, Carlsbad CA) was the empty vector control (Yokota et al., 1986; Buettner et al., 1993; Davies et al., 1994; Dong et al., 1995; Gottardi et al., 2001; Huang et al., 2001; Twal et al., 2001; Fu et al., 2003).

### Transient transfections

Samples of  $1 \times 10^6$  MDA-MB-231 cells were electroporated with a mixture of 1 μg of pEGFP (green fluorescent protein) DNA and 1 μg of either plasmid wild-type cDNA of one of the factors indicated in Figures 1–3, or with empty pcDNA3 vector, using an Amaxa nucleofactor set at X-13. The cells were examined under fluorescence microscopy to assess transfection efficiency (eGFP

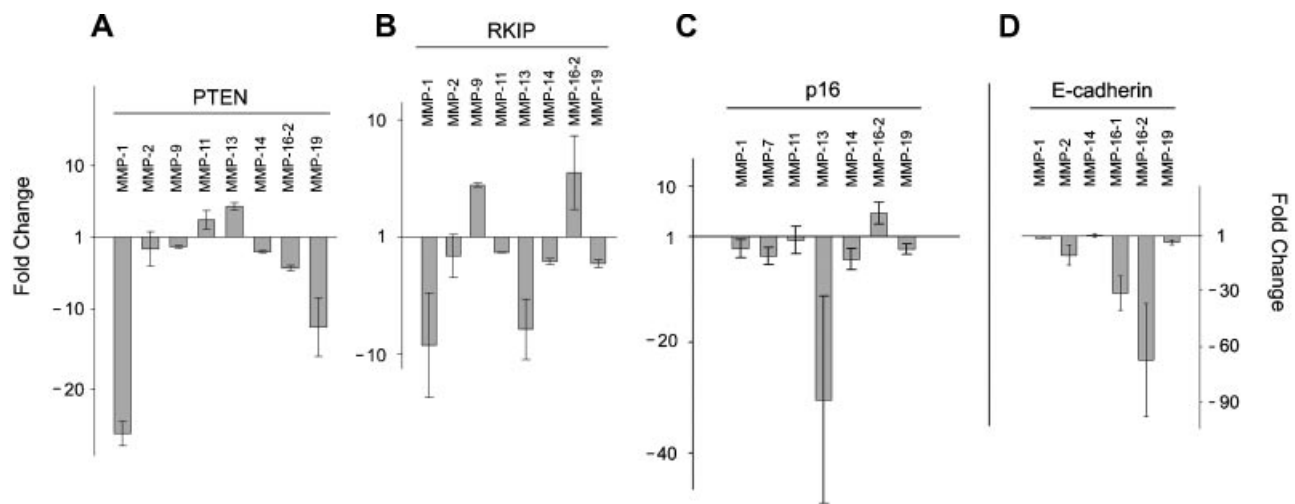
expression) 2 days after transfection, and they were harvested 4 days after transfection. All cell cultures whose mRNAs were measured were at least 70% eGFP-positive.

### RNA isolation, reverse transcription and real-time PCR

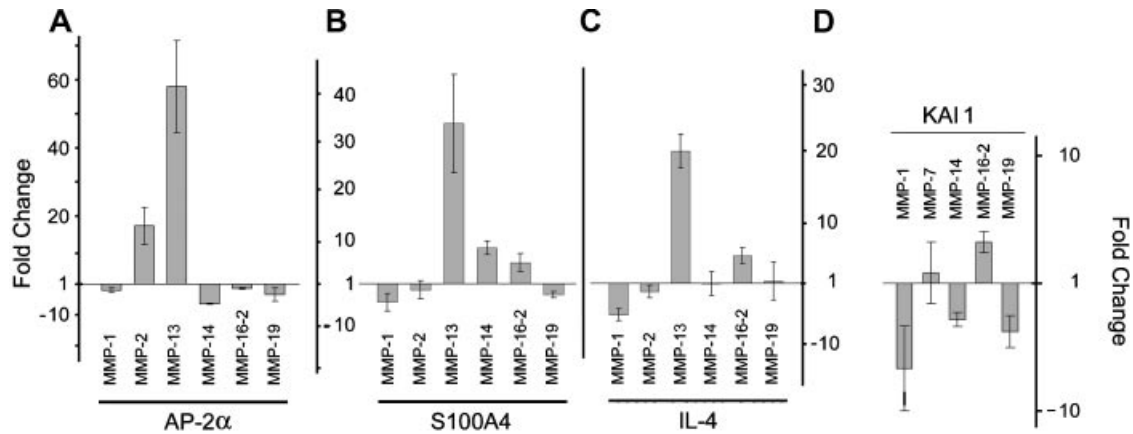
Whole cell RNA was extracted with Trizol (Invitrogen) and digested with RNase-free DNase (0.1 U/μg of RNA) in the presence of RNase inhibitor (0.5 U/μg of RNA). MMP-7 and MMP-11 mRNAs were reverse transcribed with avian myeloblastosis virus reverse transcriptase (14 U/μg of RNA), primed with oligo(dT), in the presence of RNase inhibitor (0.5 U/μg of RNA). Reverse transcription of other MMP mRNAs was done with Moloney murine leukemia virus reverse transcriptase (20 U/μg of RNA). Cell mRNA levels were measured by quantitative real-time PCR (qRT-PCR) of cDNA in the presence of SYBR Green I. The reverse transcription specific reverse primers and the PCR primers used were as indicated before (Hegedüs et al., 2008). All cell MMP mRNA levels were normalized by the GAPDH mRNA level in each sample. The MMP mRNAs analyzed in this study are (their common names and accession numbers are in parenthesis): MMP-1 (collagenase-1; NM\_002421); MMP-2 (gelatinase A; NM\_004530); MMP-9 (gelatinase B; NM\_004994); MMP-11 (stromelysin-3; NM\_005940); MMP-13 (collagenase-3; NM\_002427); MMP-14 (MT1-MMP, MT-MMP1; NM\_004995); 6,347-base long MMP-16 variant 1 mRNA (MT3-MMP, MT-MMP3; MMP-16-1 in this text; NM\_005941) that generates a membrane-inserted MMP-16; 1,800-base long MMP-16 variant 2 mRNA (NM\_022564) which produces a secreted MMP-16 (MMP-16-2 in this text); and MMP-19 (RASI-1, MMP-18; NM\_002429).

## Results

We wished to test three models in MDA-MB-231 cells. First, overexpression of cancer progression-suppressing UCPDs might or might not affect the gene expression of cancer progression-promoting, cancer cell MMPs. Second, each UCPD may affect the gene expression of either the same or different profile of MMPs. Third, the result of each effective cancer progression-suppressing UCPD may or may not be only downregulation of MMP gene expression. Gene expression was



**Fig. 1.** Effects of PTEN, RKIP, p16<sup>INK4α</sup> or E-cadherin overexpression on the gene expression of various MMPs in transfected MDA-MB-231 cells. Bars represent averages of measurements by RT-PCR of different transfections. Positive numbers represent increases in MMP:GAPDH ratios relative to vector-only transfected cells and negative numbers represent decreases in MMP:GAPDH ratios relative to vector-only transfectants, in linear scales. All of this set of MMPs were analyzed from each transfection, but only the conclusive, reproducible results are shown.



**Fig. 2.** Effects of AP-2 $\alpha$ , S100A4, IL-4, or KAI1 overexpression on the gene expression of various MMPs in MDA-MB-231 cells. Bars and positive and negative numbers represent the same as in Figure 1.

assayed by measuring mRNA rather than protein levels because reverse transcription qRT-PCR is about ten orders of magnitude more sensitive than immunoblotting (Bakalova et al., 2005; Pérez-Ruiz et al., 2007).

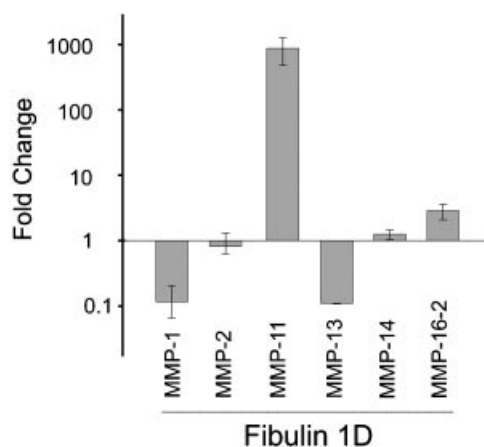
PTEN decreases MMP-1 promoter transcription in fibroblasts (Oh et al., 2006). In order to test its effects on MMP gene expression in a metastatic breast cancer cell, MDA-MB-231 cells were transfected to overexpress the PTEN gene or empty pcDNA vector as a control. Four days later cells were harvested and RNA was isolated and then analyzed by qRT-PCR to measure the levels of various MMP mRNAs in the control and PTEN-transfected cells. MMP-1 and MMP-19 mRNAs decreased in PTEN-overexpressing cells relative to control cells (Fig. 1A). These effects were sequence-specific because PTEN overexpression did not substantially alter MMP-2, MMP-9, MMP-13, MMP-14, or MMP-16-2 mRNA levels (Fig. 1A).

RKIP decreases MMP-13 gene expression in chondrocytes (Xu et al., 2007). RKIP overexpression reduced MDA-MB-231

cell MMP-1 and MMP-13 mRNA levels, increased MMP-9 gene expression, and had negligible effect on MMP-2, MMP-11, MMP-14, MMP-16-2, or MMP-19 mRNA levels (Fig. 1B). We do not know of any effect of p16<sup>INK4a</sup> on gene expression of any MMP in any cell. p16<sup>INK4a</sup> overexpression lowered MMP-13 gene expression in MDA-MB-231 cells (Fig. 1C). Cleaved E-cadherin upregulates MMP-2 gene expression in lung cancer cells (Nawrocki-Raby et al., 2003). E-cadherin overexpression decreased MDA-MB-231 cell MMP-2, MMP-16-1 and MMP-16-2 gene expression, without substantial change in MMP-1, MMP-14, or MMP-19 mRNA (Fig. 1D).

AP-2 $\alpha$  stimulates MMP-2 gene expression in endothelial cells (Park et al., 2007). AP-2 $\alpha$  overexpression induced a decrease in MDA-MB-231 cell MMP-14 mRNA, had no appreciable effect on the expression of MMP-1, MMP-16-2 or MMP-19 (suggesting sequence specificity) and, unexpectedly, increased MMP-2 and MMP-13 mRNAs (Fig. 2A). S100A4 promotes the expression of MMP-13 in fibroblasts (Senolt et al., 2006). S100A4 overexpression in MDA-MB-231 cells increased MMP-13 and MMP-14 mRNA, and did not substantially alter the expression of MMP-1, MMP-2, MMP-16-2, or MMP-19 (Fig. 2B). IL-4 suppresses gene expression of MMP-1 in fibroblasts (Leonardi et al., 2003) and of MMP-13 in chondrocytes (Tardif et al., 1999). IL-4 overexpression decreased MDA-MB-231 cell MMP-1 mRNA, increased MMP-16-2 mRNA, had no appreciable effect on MMP-2, MMP-14 or MMP-19 gene expression and, unexpectedly, increased MMP-13 mRNA (Fig. 2C). KAI1 overexpression did not have any discernable effect on the mRNA level of any of the MMPs tested in MDA-MB-231 cells (Fig. 2D).

We are not aware of any known effect of fibulin 1D on gene expression of any MMP in any cell. Fibulin 1D overexpression in MDA-MB-231 cells decreased MMP-1 and MMP-13 mRNA levels, had little effect on MMP-2, MMP-14 or MMP-16-2 and, surprisingly, not only increased MMP-11 gene expression levels but did it by nearly three orders of magnitude (Fig. 3).



**Fig. 3.** Effects of fibulin 1D overexpression on the gene expression of various MMPs in MDA-MB-231 cells. Bars and positive and negative numbers represent the same as in Figure 1, except that the scale is logarithmic.

## Discussion

It is well documented that the proteins studied in the present work are important in cancer progression. For example, MMPs play roles in cancer invasion, metastasis, growth regulation, immune evasion, apoptosis, and angiogenesis (Egeblad and Werb, 2002; Polette et al., 2004; Deryugina and Quigley, 2006). Cancer cell MMP-1, MMP-2, MMP-9, MMP-11, MMP-13,



TABLE 1. Effect of overexpression of the indicated UCPDs on gene expression of various MMPs in MDA-MB-231 cells

Overexpressed UCPD	Measured MMP mRNA																	
	1		2		9		11		13		14		16-1		16-2		19	
	Effect	F.E. <sup>1</sup>	Effect	F.E. <sup>1</sup>	Effect	F.E. <sup>1</sup>	Effect	F.E. <sup>1</sup>	Effect	F.E. <sup>1</sup>	Effect	F.E. <sup>1</sup>	Effect	F.E. <sup>1</sup>	Effect	F.E. <sup>1</sup>	Effect	F.E. <sup>1</sup>
AP-2 $\alpha$	●		Δ	2					Δ	1	▼	1			●			●
E-cadherin	●		▼	3							●		▼	1	▼	1		
Fibulin 1D	▼		●				Δ	1	▼	1	●				●			
Interleukin 4	▼	1	●						Δ	1	●				Δ	1		●
p16	●		●						▼	1	●				●			●
PTEN	▼	2	●		●						●				●			▼
RKIP	▼	1	●		Δ	1	●		▼	2	●				●			▼
S100A4	●		●						Δ	2	Δ	1			●			●

The symbols represent an increase (Δ), a decrease (▼), or no substantial change (●) in MMP gene expression relative to vector-only transfectants.

<sup>1</sup>F.E. (first evidence): to our knowledge, this is the first evidence of such an effect in any cell ("1"), in any cancer cell ("2") or in any breast cancer cell ("3").

focusing on the measurement of mRNA levels has the additional advantage of easily detecting a large number of pathway links.

The effects of the tested UCPDs on MMP gene expression could be mediated by any of the transcription factors or other downstream proteins which they are known to regulate, such as: (a) RKIP through p53, c-Jun/c-Fos, NF- $\kappa$ B, SRF, STAT, PEA3, or CREB; (b) PTEN through Akt or p53; (c) fibulin 1D through ZBTB16 or JNK; (d) E-cadherin through  $\beta$ -catenin or JNK; (e) IL-4 through Akt or MAPK; (f) AP-2 $\alpha$  through Sp1 or YBX1 or directly on MMP gene expression as a transcription factor; (g) p16<sup>INK4a</sup> through p53 or Rb; and (h) S100A4 through JNK or p53 (Fig. 4).

Cancer progression depends on many factors and signaling pathways (Uchiyama et al., 1996; Twal et al., 2001; Wong and Gumbiner, 2003; Zheng et al., 2003; Schuierer et al., 2004; Sumigama et al., 2004; Saleem et al., 2006). Our present results show many pathway links from some UCPDs to the gene expression of some cancer-progression enhancing MMPs. We have also found that different types of cancers have different pathway links from these UCPDs to the gene expression of these MMPs (manuscript in preparation). In view of this complexity, one of the next challenges will be to identify pathway links between other cancer-progression determinants and then to prioritize which of these links should first be studied further, in order to identify the signaling pathways involved.

## Acknowledgments

We thank Joseph J. Baldassare, Donald J. Tindall, Laura Taylor, Evan T. Keller, Michael A. Tainsky, J. Carl Barrett, DNAX Inc. (Palo Alto CA), Nancy Magnuson, Barry M. Gumbiner, Barry R. Davies, and W. Scott Argraves for their kind gifts of plasmids. We also thank Subhra Chakraborty and Shalini Thakran for preparation of plasmids.

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