MAPK Kinase 3 Is a Tumor Suppressor with Reduced Copy Number in Breast Cancer

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Abstract

Cancers are initiated as a result of changes that occur in the genome. Identification of gains and losses in the structure and expression of tumor-suppressor genes and oncogenes lies at the root of the understanding of cancer cell biology. Here, we show that the mitogen–activated protein kinase (MAPK) MKK3 suppresses the growth of breast cancer, in which it varies in copy number. A pervasive loss of MKK3 gene copy number in patients with breast cancer is associated with an impairment of MKK3 expression and protein level in malignant tissues. To assess the functional role of MKK3 in breast cancer, we showed in an animal model that MKK3 activity is required for suppression of tumor growth. Active MKK3 enhanced expression of the cyclin-dependent kinase inhibitors p21Cip1/Waf1 and p27Kip1, leading to increased cell-cycle arrest in G1 phase of the cell cycle. Our results reveal the functional significance of MKK3 as a tumor suppressor and improve understanding of the dynamic role of the MAPK pathway in tumor progression. Cancer Res; 74(1); 162–72. ©2013 AACR.

Introduction

Since its initial description, endogenous suppression of tumorigenesis has been a cornerstone and topic of intensive investigation in cancer research (1). Today, we appreciate that cells use a growing assortment of genes to restrict proliferation and prevent tumor growth, including those that function in cell-cycle checkpoints and mitogenic signaling (2–4). Identification of changes to the genetic material encoding critical regulators of these processes is a central theme in efforts toward understanding cancer development, as all cancers carry tumorigenic somatic mutations (5, 6).

Current thought on tumor suppressor loss suggests a more fluid continuum model, in which subtle, but critical, changes in tumor suppressor levels can have drastic effects on the development of cancer, rendering haploinsufficiencies and partial losses just as tumorigenic as “two hits” (7). Chromosome 17 has emerged as a lightning rod of cancer. In a model of breast cancer, active MKK3significantly enhanced the growth of malignant mammary epithelial cells (11), adding weight to the pursuit of mechanistic insight into the functional role of MKK3 activity in breast cancer.

Breast cancer is the most commonly diagnosed cancer in women and second-leading cause of cancer-related deaths, statistics that strongly advocate for a better understanding of the mechanisms that underlie mammary carcinogenesis (12). In this report, we show that MKK3 expression is impaired in malignant mammary tissues and identify a significant copy-number loss of genomic MKK3 in human patients with breast cancer. In a model of breast cancer, active MKK3 significantly restricted tumor growth both in vivo and in an in vitro cell line expression system, whereas impaired MKK3 signals led to dramatically enhanced tumor growth. Cyclin-dependent kinase (CDK) inhibitors p21Cip1/Waf1 and p27Kip1, mediators of G1 cell-cycle arrest, were both significantly upregulated in an MKK3 activity–dependent mechanism, resulting in inhibition of cell-cycle progression in breast cancer cells. These findings identify new molecular functions for MKK3-dependent signaling, and position MKK3 as a novel tumor suppressor that is altered in human breast cancer.

Materials and Methods

Pathology samples from patients with breast cancer

The Ethics Committee of Chinese PLA General Hospital in Beijing approved this study, and informed consent was obtained from the patients. All pathology samples and clinical information were collected in accordance with institutional guidelines and regulations.
Animals

Immunodeficient Rag1\(^{-/-}\) mice were from The Jackson Laboratory (B6.129S7-Rag1\(^{tm1Mom}\)/J). Protocols were approved by the University Committee on Laboratory Animals, Dalhousie University, in accordance with the guidelines of the Canadian Council on Animal Care.

Antibodies and reagents

Antibodies to CDK inhibitors p21, p27, p16, p15, p18, and p57 as well as phospho-ATF2, phospho-pS3 (Ser6, Ser9, Ser15, Thr81, Ser20, Ser33, Ser37, Ser46, and Ser392), phospho-Akt, total Akt, and c-Jun were purchased from Cell Signaling Technology, Inc. Antibodies for MKK3 (C-19), actin, and horseradish peroxidase–linked secondary antibodies were purchased from Santa Cruz Biotechnology. Antibody for phospho-p21 (Ser130) was from Biorebyt. Fluorescein isothiocyanate (FITC)–conjugated antibodies to Flag were from Sigma. Alexa 594–conjugated goat anti-rabbit secondary was from Invitrogen. Recombinant stem-cell factor (SCF) was from PeproTech, Inc.

TissueScan cDNA arrays and quantitative PCR

Quantitative PCR (qPCR) cDNA arrays were conducted using cDNA arrays (Origene; Cancer Survey cDNA Array 96-1, lot number 0312) according to the manufacturer’s instructions. Primer sequences were MKK3, For 5\'-CTTGGTGACCATCTCA-’ and Rev 5\'-CTTCTGCTCCTGTGAGTTCACG -3’, and PPIA, For 5’-ACCGCCGAGGAAAACCGTGT-3’ and Rev 5’-CTGTCTTTGGGACCTTGTCTGCAA-3’. For correlative analysis, total RNA was extracted from clinical tumor sample tissue using Trizol and reverse transcribed using Reverse Transcriptase M-MLV (TaKaRa), according to the manufacturer’s instructions. The primers used in qPCR for MKK3 and PPIA were as noted earlier and for glyceraldehyde-3–phosphate dehydrogenase (GAPDH) were For 5’-ACATCATTCCCTGCTCTTACTG-3’ and Rev 5’-ACCACCTGGTGCTCAGTGTAG-3’. For additional detail see Supplementary Materials and Methods.

Immunohistochemistry

Slides with sections of formalin-fixed paraffin-embedded (FFPE) normal mammary tissues and patient-derived tumor tissues (Origene and study patients) were incubated in 10 mmol/L citrate–tween buffer at 97°C for 20 minutes for antigen unmasking. Specimens were blocked in 2% goat serum/5% bovine serum albumin (BSA) in PBS–tween for 2 hours, and incubated overnight at 4°C in rabbit anti-MKK3 (C-19; Santa Cruz Biotechnology) at 1:100 in 5% BSA PBS–tween. Slides were then washed and incubated with Alexa 594–conjugated goat anti-rabbit (Invitrogen) at 1:2,000 in blocking buffer. Specimens were mounted in 4’,6–diamidino–2–phenylindole (DAPI; VECTASHIELD) and imaged using equivalent settings on a Nikon E600 microscope equipped with ×20 or ×40 objective lens using ACT-1 software (Nikon).

qPCR assessment of genomic MKK3 in clinical tumor samples

Human genomic DNA was isolated from random breast cancer patient tumor samples at SinoGenoMax Co., Ltd. Normal female genetic DNA samples were from a random control panel (Sigma; HRC1). \(C_v\) values for two distinct genomic sites in the MKK3 gene and five reference genomic sites (BCMA, SDC4, NUDT6, FGF2, and MYOD1) were determined for each DNA sample. Seg-1 and NCI-H774 (American Type Culture Collection, ATCC) cell lines were used as internal controls as NCI-H774 cells have a previously reported double deletion of the MKK3 gene (13). A 1:1 mixture of Seg-1 and NCI-H774 is thus expected to have a half level of genomic MKK3. For additional detail see Supplementary Materials and Methods.

Fluorescence in situ hybridization

Slides with sections of FFPE patient-derived tumor tissues (study patients) were analyzed using the Histology FISH Kit (Dako) according to the manufacturer’s instructions. Probe with specificity for the MKK3 gene (SureFISH Chr17 CEP, Red, Human Chr17: 20893971-21327887; Agilent Technologies) was used according to the manufacturer’s instructions (Dako). For additional detail see Supplementary Materials and Methods.

Generation of stable cell lines

MDA-MB-468 cells were obtained via the ATCC, resuscitated from early passage liquid nitrogen vapor stocks as needed, and cultured in Dulbecco’s Modified Eagle Medium (DMEM) supplemented with 10% FBS. Cells were cultured for less than 3 months before reintroducing cultures and were routinely inspected microscopically for stable phenotype. A concentration of 0.8 mg/mL G418 was used to generate stable lines. MDA-MB-468 cells were transfected with Flag-MKK3dn or Flag-MKK3ca plasmids (Addgene) using Lipofectamine 2000 (Invitrogen). Stable colonies of cells were plated under selection by limiting dilution to isolate stable clones. Plates were incubated for 3 weeks allowing colonies to form.

Immunofluorescence

Cells were grown on glass coverslips, fixed with 4% formaldehyde for 20 minutes, and permeabilized with a 0.2% solution of Triton-X in PBS for 10 minutes. Samples were blocked with 10% BSA (Sigma) for 30 minutes, followed by a 2-hour incubation with anti-Flag antibody (1:500) in a 3% BSA solution in PBS and finally with Alexa 594–conjugated goat anti-mouse immunoglobulin G (IgG) F(ab)\(_2\) (Molecular Probes) at 1:200 for 1 hour. Coverslips were mounted with DAPI-containing VECTASHIELD (Vector Laboratories).

Flow cytometry

Cells (5 \(\times\) 10\(^6\)) were collected using trypsin (Invitrogen), fixed, and permeabilized using Cytofix/Cytoperm buffer (BD Biosciences) for 20 minutes. Cells were stained in 100 μL with FITC-conjugated Flag antibody (1:1,000 or 1 μg/mL) for 2 hours, washed, and analyzed on a FACSARia (BD Biosciences).

Tumor growth in vivo

For xenotransplantation studies, 1 \(\times\) 10\(^7\) log-phase growing untransfected, M KK3dn, or MKK3ca MDA-MB-468 cells were trypsinized, washed twice in PBS, and injected into immunocompromised Rag1-deficient mice at the mammary fat pad (200 μL/injection in PBS). At endpoint, tumors were surgically
excised, collected, and imaged using an iPhone 4S (Apple). Tissue specimens were fixed in 10% buffered formalin, embedded in paraffin, sectioned, and stained with hematoxylin and eosin (H&E).

Thymidine incorporation and WST-1 assay

Of note, 5 × 10^4 cells were seeded in quadruplicate in a 96-well plate. Forty-eight hours later, cells were pulsed with 0.25 μCi of ^3H-thymidine for 3 hours. Incorporation was measured on a Wallac 1420 scintillation β counter. For WST-1 assays, cells were cultured as earlier for 4 days and WST-1 proliferation reagent (Clontech) was added at 1:10 dilution. Plates were read 90 minutes later.

Quantitative real-time PCR array

Of note, 1 to 2 × 10^6 cells were collected and processed using TRIzol (Invitrogen) and purified using RNeasy (Qiagen). Breast Cancer RT-PCR (real-time PCR) Arrays (Qiagen) were conducted in triplicate according to the manufacturer’s protocol and qPCR was performed using an ABI 7000 Sequence detector (PE Applied Biosystems). For additional detail see Supplementary Materials and Methods.

Western blotting and p53 siRNA

Cells were lysed in RIPA buffer supplemented with a cocktail of protease and phosphatase inhibitors. For siRNA knockdown of p53, wild-type (WT) MDA-MB-468 and MKK3-mutant cells were used in reverse transfection (Life Technologies, Ambion; TP53 s607 and s605) according to the manufacturer’s instructions. For additional detail see Supplementary Materials and Methods.

Chromatin immunoprecipitation

WT MDA-MB-468 and MKK3dn, or MKK3ca transfected cells were plated in 10-cm dishes. The following day, chromatin–protein complexes were prepared according to the manufacturer’s instruction (ChIP-IT Express Enzymatic; Active Motif). For additional detail see Supplementary Materials and Methods.

Cell-cycle analysis

Cell-cycle staging was conducted using Vybrant DyeCycle Green (Invitrogen) by flow cytometry according to the manufacturer’s instructions. Data were analyzed using WinList 5.0 software.

Nuclear protein preparation and electrophoretic mobility shift assay

Nuclear protein extracts were isolated using a nuclear extract kit (Active Motif) according to the manufacturer’s protocol. Electrophoretic mobility shift assay (EMSA) was performed as previously described (14). Double-stranded oligonucleotides for AP-1 and SP-1 consensus binding sequences were from Promega.

Statistical analysis

The paired Student t test was used for statistical evaluation of data. Results were considered significant when P<0.05. Data are expressed as means ± SEM unless otherwise indicated.

Results

MKK3 expression and genomic copy number is reduced in human breast cancer

To assess the mRNA expression level of MKK3 in primary tumor tissues compared with normal tissues, a cDNA array with nine tumor and three normal tissues from eight types of cancer was used in a qPCR assay. MKK3 gene expression was significantly downregulated in the tumor tissue in five of eight cancers examined, including breast, colon, liver, lung, and thyroid cancer, and was decreased in kidney cancer, whereas prostate and ovary tumor tissues showed normal MKK3 expression (Fig. 1A). This is the first report of widespread MKK3 expression loss as a feature in several types of cancer, most notably in breast and liver cancers. Following up on this, we examined MKK3 protein levels in cancerous versus normal mammary tissue by immunohistochemistry. A similar remarkable impairment in MKK3 protein expression in cells of the ductal walls was detected in breast tumor tissues (Fig. 1B).

Genomic copy-number variation has emerged as a pervasive phenomenon and an important consideration in a broad range of diseasecausality including breast cancer (15, 16), resulting in gene copy-number imbalances or LOH that can ultimately lead to altered gene expression and protein function (8). To investigate the copy-number status of MKK3 in clinical samples from patients with breast cancer, we designed a qPCR assay to assess relative genomic MKK3 content in patient-derived samples. DNA from the NCI-H774 cell line was used to evaluate specificity and create an internal assay control as NCI-H774 cells have a natural double deletion of the MKK3 gene (13). Remarkably, our analysis revealed a significantly decreased genomic MKK3 level in 8 of 10 patients with breast cancer (Fig. 1C). Additional patient tumor data from clinical evaluation of common relevant breast cancer markers are provided in Supplementary Table S1. Comparison of genomic and mRNA levels for MKK3 in patients suggests a positive correlation between gene loss and gene expression level (Supplementary Fig. S1). Further evaluation of tissues from these patients by FISH confirmed that MKK3 copy number was heterogeneously reduced, reflecting intratumoral genomic heterogeneity at the MKK3 locus (Fig. 1D). These results are the first to identify a specific MKK3 copy-number deficiency and strongly suggest that copy-number loss may contribute to reduced MKK3 expression in breast cancer. These findings prompted us to pursue the functional role of MKK3 activity in breast cancer.

MKK3 activity regulates tumor growth in vivo via differential regulation of cell proliferation

To determine the function of MKK3 signaling activity in breast cancer, we used the human breast cancer cell line, MDA-MB-468, which had a relative genomic MKK3 level of 1.44 by qPCR, similar to those patients who displayed genomic loss in Fig 1C. This cell line was transfected plasmids encoding either a dominant negative (MKK3dn) or constitutively active (MKK3ca) Flag-tagged mutant MKK3 gene, in which the activation site is mutated at two amino acids, rendering the resulting protein either permanently inactive or active (17). Colonies were selected and assessed for degree of expression and purity by immunofluorescence and flow cytometry and
Figure 1. Loss of MKK3 expression in human patients with breast cancer. A, MKK3 gene expression was evaluated by qPCR of normal tissue and tumor tissue using cDNA arrays. Data are expressed relative to the three normal controls ± SEM for n = 9 tumor samples per tissue type. Significant P values were as follows: breast, P = 0.0006; colon, P = 0.029; liver, P = 0.000009; lung, P = 0.024; and thyroid, P = 0.042. B, sectioned specimens of normal mammary tissue or tumor tissue were analyzed for MKK3 protein level by immunohistochemistry using anti-MKK3 antibodies (red) and DAPI (blue) to visualize nuclei. Representative images from n = 4 tumor specimens and a normal mammary tissue specimen are shown. C, human genomic DNA from breast cancer patient tumor samples and normal female control samples were analyzed by qPCR to assess copy number. DNA from Seg-1 and NCI-H774 cell lines (alone or mixed 1:1) were used as an internal assay control. Data are expressed as ±SEM for n = 10 tumor and nine normal controls; P = 0.009 between groups. D, breast cancer patient–derived tissues were analyzed for MKK3 gene copy-number variation by FISH. Red punctuations, genomic copy of MKK3; cell nuclei are stained blue with DAPI. A representative image from patient number 9 in C is shown, confirming that patient tumor cells display a heterogeneous loss of MKK3 genomic DNA. Evaluation of five fields of view had an average of 1.10 copies per nuclei. Boxed area is magnified from the original ×1,000 magnification.
were monitored weekly for stable expression (Supplementary Fig. S2). To assess the role of MKK3 activity on tumor growth in vivo, we used an immunodeficient (Rag1−/−) mouse model permitting xenotransplantation studies with our human cell lines. MKK3dn, MKK3ca, and untransfected MDA-MB-468 breast cancer cell lines were transplanted subcutaneously at the mammary fat pad of female Rag1-deficient mice. Interestingly, a significant and opposing effect on tumor growth was observed in MKK3-mutant tumors. Whereas MKK3ca tumors developed faster (Fig. 2A). Also noteworthy was that although all mice that received MDA-MB-468 cells and MKK3dn cells developed tumors, only 50% (P = 0.049) of mice receiving MKK3ca cells developed a palpable tumor. At experimental endpoint, tumor tissues were surgically excised and three representatives from each group are shown (Fig. 2B). Following the trend in tumor growth, a remarkable MKK3 activity–dependent difference in the density of intratumoral MDA-MB-468 cells was observable by histologic staining (Fig. 2C). These results indicate that MKK3 activity is suppressive of breast cancer tumor growth, and, conversely, that impaired MKK3 signals lead to significantly enhanced breast cancer tumor growth.

To directly determine the role of MKK3 activity on tumor cell proliferation, in vitro studies were conducted using five independently derived MKK3dn and MKK3ca cell lines. MKK3 activity had a significant impact on basal proliferation, with MKK3ca cells at 64% and MKK3dn cells at 229% of the proliferative rate of untransfected cells (Fig. 3A). These results were further confirmed using a WST-1 proliferation assay (Fig. 3B) and by counting equivalently seeded cells in culture (Fig. 3C–D). In accordance with our observations on in vivo tumor growth, these findings indicate that MKK3 activity inhibits tumor cell proliferation, and, conversely, that a lack of MKK3 signaling may enhance breast cancer tumor growth via enhanced tumor cell proliferation.

**MKK3 activity promotes p21 and p27 expression in breast cancer cells**

To investigate the mechanism of MKK3 activity–dependent impairment of cell proliferation, a qPCR array was used to assess the expression of 84 breast cancer-related genes in these cells. Of the nine genes found to be differentially oppositely regulated in MKK3dn and MKK3ca cells, the most significantly oppositely regulated was CDK inhibitor 1A (CDKN1A), the gene encoding the inhibitor of cell-cycle progression p21Cip1/Waf1 (Fig. 4A). Quantitative analysis showed that CDKN1A expression in MKK3ca was 2.56-fold, whereas that of MKK3dn cells was 0.66-fold compared with control cells (Fig. 4A). The full array data set is presented in Supplementary Table S2.

To confirm our gene expression analysis at the protein level, Western blot analyses were conducted to analyze the expression of a panel of CDK inhibitors. Indeed, opposing expression of p21 protein was detected in MKK3-mutant cell lines in accordance with mRNA levels detected by qPCR (Fig. 4B). Notably, another CDK inhibitor, p27kip (CDKN1B), was similarly oppositely deregulated in mutant MKK3 cell lines (Fig. 4B). Expression of family member p16 (CDKN2A) was in accordance with qPCR data and, as in the case of p15 (CDKN2B), was not significantly oppositely regulated by MKK3 (Fig. 4B), whereas remaining members p18 and p57 were not detectable (data not shown). Phosphorylation of p21 in a p38-dependent mechanism has been reported to stabilize p21 protein (18). We analyzed p21 at Ser130 in our cell lines and could not detect any phosphorylation at this site, suggesting that this mechanism is not playing a role in our system.

**MKK3 activity regulates CDK inhibitors independently of p53 and AP-1**

These results prompted an investigation into the mechanism of MKK3 activity–dependent expression of p21 and p27. It
is well established that MKK3 signaling through the p38 MAPK protein family culminates in the activation of downstream transcription factors, including activating transcription factor 2 (ATF2; ref. 19). Monitoring of ATF2 phosphorylation confirmed constitutive activity in MKK3ca cells and impaired signaling in MKK3dn cells, detectable in cells stimulated for activation of the MAPK pathway through the SCF receptor c-kit (Fig. 5A). The tumor suppressor p53 is a major regulator of p21 and p27 gene expression; however, p53-dependent and p53-independent mechanisms are known (20–22). Notably, however, MDA-MB-468 cells express a mutant p53 protein with the R273H mutation, which results in defective DNA contact and binding, suggesting that the MKK3 activity-dependent effect is unlikely to be mediated by p53 (23), but to confirm this was case, we conducted further analysis of p53 activation. To determine if MKK3 signaling activity modifies p53 phosphorylation and activation in MKK3ca cells, Western blotting for activation of the p53 protein was conducted. No MKK3-dependent activation of p53 consistent with activation of p21 and p27 was detectable. In fact, MKK3 signals led to dephosphorylation of p53 at Ser9, and in general, inconsistent with a p53-dependent mechanism, total p53 protein expression was slightly enhanced in MKK3dn cells (Fig. 5B). In addition to those shown in Fig. 5B, phosphorylation analysis was also conducted at Ser6 and Thr81, but no phosphorylation was detected at these sites. These results suggest that MKK3 activity regulates p21 and p27 expression independent of p53 phosphorylation.

We then further examined the role of p53 in our MKK3-transfected cell lines by siRNA-mediated knockdown of p53. Knockdown of p53 resulted in enhanced expression of both p21 and p27 in all cell lines, and did not impair the enhanced p21 and p27 expression in MKK3ca cells (Fig. 5C). Overall enhanced expression in the knockdowns is likely an effect of removal of the dominant negative and/or gain-of-function effects exerted by the mutant protein on basal p53 target gene expression. These results suggest that in our cell lines, mutant p53 is inhibitory to basal expression of p21 and p27, and that MKK3 can direct p21 and p27 expression in the absence of functional p53. Finally, we examined our cell lines by chromatin immunoprecipitation (ChIP) to determine if MKK3ca cells might yet have enhanced p53 association with the p21 promoter via another mechanism. However, our findings show similar p21 promoter binding in WT and MKK3ca cells, and an enhancement in binding in the MKK3dn cells. It is worth noting, however, that the level of binding to the p21 promoter in this

Figure 3. MKK3 activity directs proliferation of MDA-MB-468 cells. A, untransfected MDA-MB-468 cells and five independently derived lines for MKK3dn and MKK3ca cells (5 × 10³) were seeded in 96-well plates in quadruplicate. The following day, cells were pulsed with ³H-thymidine for 4 hours, incorporation was measured, and data were expressed as ±SEM. ***, P < 0.001; n = 5 independently derived clones each. B, untransfected MDA-MB-468 cells and five independently derived lines for MKK3dn and MKK3ca cells (5 × 10³) were seeded in 96-well plates in quadruplicate. Four days later, proliferation was measured by colorimetric WST-1 assay, expressed as the OD at 440 nm minus background. ***, P < 0.01; ***, P < 0.001; n = 5 independently derived clones each. C and D, untransfected MDA-MB-468, MKK3dn, and MKK3ca cell lines were seeded at 1 × 10⁵ cells per well and on days 2, 4, and 7, three wells per group were counted by trypan blue exclusion. *, P < 0.05; **, P < 0.01 for n = 3. Representative images of cells in culture at 48 and 96 hours are shown.
MKK3 activity promotes p21/p27–mediated G1 cell-cycle arrest, inhibiting tumor growth.

Cell-cycle regulators p21 and p27 inhibit cell-cycle progression at the G1 checkpoint (25), a considerably attractive mechanism to target in cancer (26–30). Recent studies in glioblastoma proliferation have shown that a natural plant product, β-elemene, inhibits tumor growth by arresting cells in the G0–G1 phase through a mechanism dependent on MKK3 activation (31). To determine if MKK3-mutant cells indeed have deregulated cell-cycle progression, flow cytometric analysis of cell-cycle staging was conducted. Consistent with enhanced p21 and p27 expression, MKK3ca cells showed significant cell-cycle arrest at the G1 phase, whereas MKK3dn cells had significantly reduced numbers in G1, indicating a more rapid entry into the S phase. Accordingly, MKK3ca cells had significantly fewer numbers in the G2–M mitotic phase, whereas MKK3dn cells had enhanced numbers in S and G2–M phase (Fig. 7A). Collectively, these results identify MKK3 as a novel tumor suppressor in breast cancer that is downregulated in a range of cancer types, and suggest that active MKK3 promotes G1 cell-cycle arrest and restricts tumor cell proliferation by enhancing p21 and p27 expression, resulting in suppressed tumor growth, whereas impaired MKK3 signals have the opposing effect on both gene expression and tumor growth (Fig. 7B).

Discussion

Addressing the significance of MKK3 in breast and other types of cancer has garnered increasing interest in recent years as efforts continue to decipher the elusive role of the MAPK pathway in carcinogenesis and tumor suppression (3). In this study, we have identified a new tumor-suppressive role for the mitogenic signaling protein MKK3 in the regulation of breast cancer tumor growth. We have characterized this function mechanistically to be mediated by MKK3 signaling activity-dependent regulation of the expression of cell-cycle inhibitors, p21 and p27, and subsequent restriction of cell-cycle progression, as shown in our proposed model (Fig. 7B). Importantly, we demonstrate that MKK3 expression is significantly impaired in breast cancer tissues, and describe a novel loss of MKK3 genomic copy number in patients with breast cancer. This is the first specific detection of MKK3 copy-number variation in human cancer, and suggests that MKK3 is a suppressor of mammary carcinogenesis with potential prognostic, predictive, and/or therapeutic value.

In breast cancer, inactivation of the MAPK phosphatase Wip1 inhibits mammary carcinogenesis. Wip1 functions to inactivate signals mediated by MKK3 through the p38 MAPK pathway in breast cancer. Wip1 functions to inactivate signals mediated by MKK3 through the p38 MAPK pathway in breast cancer.

Figure 4. MKK3 activity differentially regulates p21 and p27 CDK inhibitor expression in MDA-MB-468 cells. A quantitative real-time PCR array was used to examine cell lines for the expression of 84 breast cancer markers. A, list of all breast cancer array genes oppositely regulated by MKK3dn and MKK3ca-mutant proteins. *, P < 0.05; **, P < 0.01; ***, P < 0.001. Light gray indicates >1.5-fold decrease and dark gray indicates 1.5-fold increase compared with WT. Data are expressed as a summary of n = 3 experiments. ***, P < 0.001. Aside from CDKN1A/p21, additional analysis was conducted on Jun (c-Jun; Fig. 6), interleukin (IL)-6, and CST6. MKK3-dependent IL-6 production (48 hours) was measured by ELISA and was consistent with mRNA; however, MKK3-dependent IL-6 production did not remarkably alter cell-free culture supernatant levels (not shown), whereas CST6 protein was undetectable by Western blot analysis. B, cell lines were examined for expression of a panel of CDK inhibitors by Western blotting. CDK inhibitors p21 and p27 were similarly differentially regulated. Actin is shown as a loading control and MKK3–mutant protein expression is shown using a Flag antibody. Representative blots from n = 4 experiments are shown.

 assay was between 0.03% and 0.06% of input DNA, an extremely low overall level that indicates considerably weak interactions between p53 and the p21 promoter, which is not surprising, given a functionally defective p53. Altogether, these results suggest that MKK3 activity–driven expression of p21 and p27 is occurring via a p53–independent mechanism in our model.

The AP-1 transcription factor can also control p21 gene expression through activation of SP-1 promoter binding (24). Gene expression array data indicated that c-Jun, a component of AP-1, was oppositely regulated in MKK3-mutant cells, consistent with p21 (Fig. 4A). MKK3-dependent protein expression of c-Jun was confirmed by Western blotting (Fig. 6B). However, investigation of the DNA-binding activity of AP-1 and SP-1 revealed that their activities were not notably altered in the MKK3-mutant cells (Fig. 6C), suggesting that this mechanism is unlikely to be contributing to MKK3-directed p21 expression.

Table 1. Microarray analysis of gene expression in MDA-MB-468 breast cancer cells

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pathway, supporting a suppressive role for MKK3 signaling in breast cancer pathogenesis (32, 33). Our mechanistic results expand significantly on how MKK3 activity inhibits carcinogenesis, through promotion of cell-cycle arrest. Inhibition of cell-cycle progression is clearly an attractive mechanism to target and promote in the development of anticancer therapies, and the significance of p21 and p27 expression in this mechanism has not been understated in the literature (26–28, 34). In breast cancer, p21 and p27 have received considerable attention as clinical indicators and potential targets in therapeutic development (28–30). In agreement with the findings we present here, previous work in leukemia showed that impaired MKK3 signals enhanced prostaglandin PGJ2-induced proliferation, and described impaired p21 and p27 expression in treated THP-1 cells (35). In addition, a natural fungal product (FTY720) induced MKK3 activity and p21 expression in prostate cancer cells, leading to cell-cycle arrest (36), whereas studies in muscle cell differentiation have shown that dominant negative MKK3 inhibits p21 and p27 expression (37). Downstream of MKK3, p38 MAPK activity is linked to p27 expression, leading to contact inhibition in mouse embryonic stem cells (38, 39), and it is also well known that p38 can activate p53-dependent p21 expression (40), and further stabilize p21 protein by direct phosphorylation (18). Although these reports suggest that MKK3 signals are linked to p21 and p27 expression, we report the first direct evidence that active MKK3 is a vital regulator of these two cycle-cell inhibitors, independent of p53 activation, with ramifications in tumor progression, and may represent a novel approach to targeting cell-cycle inhibition in cancer.

Induction of p21 transcription and resultant cell-cycle arrest is associated with both p53-dependent and p53-independent mechanisms (20, 22, 34). The DNA damage response is known to activate p21 expression in a p53-dependent manner, inducing transient senescence preceding DNA repair or apoptosis (41), whereas p53-independent p21 induction is more associated with the induction of cellular senescence, differentiation, and development (20). The p38 MAPK, a direct substrate of MKK3, can itself activate p53 at Ser15, Ser33, and Ser46, leading to p21 transcription (3, 42, 43). To determine if MKK3

Figure 5. MKK3-directed proliferation in MDA-MB-468 is p53-independent. A, Western blot analysis of MKK3 activity–dependent ATF-2 phosphorylation in MDA-MB-468 cells with actin as a total protein loading control. Cells were untreated (NT) or stimulated with SCF for 120 minutes to monitor downstream activation of the p38 MAPK pathway via ATF-2 activation. A representative of n = 4 experiments is shown. B, Western blot analysis of MKK3 activity–dependent p53 activation by phosphorylation at Ser 9, Ser 15, Ser 20, Ser 33, Ser 37, Ser 46, and Ser 392 and total MKK3 activity–dependent p53 protein expression in MDA-MB-468 cells, with actin as a loading control. Representative blots from n = 4 experiments are shown. C, knockdown of p53 by siRNA in WT, MKK3ca, and MKK3dn cells and subsequent Western blot analysis of p21 and p27 expression. Representative blots (p53 siRNA s607) from n = 4 experiments with two different p53 siRNAs showing similar results is shown with detection of p53 to confirm knockdown and actin as a loading control. D, ChIP was used to measure relative binding of p53 to the promoter of p21 in WT, MKK3dn, and MKK3ca cells. Data were calculated as percentage input and expressed as relative p21 promoter binding ± SEM for n = 3 independent experiments; *, P < 0.05.
activity–dependent p21 expression was regulated by p53, we examined p53 phosphorylation at a range of sites, including Ser46, Ser15, and Ser392, which are known to lead to p53-dependent p21 transcription (44–46), and found no altered p53 activation. Notably, total p53 protein was actually slightly enhanced in MKK3dn cells. We also examined the contribution of p53 by knockdown and by ChIP analysis of promoter association. Altogether, these results support a p53-independent transcriptional regulation of p21 by MKK3 activity. Interestingly, our results may have additional relevance in cases of p53 mutation, which occur in up to 50% of cancers, given that our results describe a scenario of p53 mutation in which p21 and p27 expression is actively repressed by the R273H-mutant p53.

Notably, p21 and p27 expression is known to be upregulated by inhibition of the PI3K/Akt signaling pathway leading to G1 cell-cycle arrest (47), and indeed MKK3ca MDA-MB-468 cells had impaired activation of this pathway when Akt phosphorylation was examined (Supplementary Fig. S3), suggesting that MKK3 signals can inhibit Akt activation, thereby supporting p21 and p27 expression. Aside from a transcription factor activation–mediated mechanism acting directly on the p21 and p27 promoters, an alternative mode of action could be through mRNA stability. MKK3 signaling is associated with increased mRNA stability of transcripts with adenosine/uridine–rich elements in the 3’ untranslated region (3’-UTR) in breast cancer cells (48), and p21 and p27 expression are known to be regulated through RNA stabilization mechanisms (49–51). It remains unclear precisely how MKK3 activity can direct p21 and p27 expression leading to cell-cycle arrest.

Despite extensive interest in a tumor-suppressive role for MAPK signaling, this study is, to our knowledge, the first direct assessment of MKK3 activity on tumor growth in an in vivo xenograft model. We report a novel p53-independent mechanistic regulation of cell-cycle inhibitors p21 and p27, dependent on MKK3 activity, leading to cell-cycle arrest at G1 and

![Figure 6. MKK3 activity regulates c-Jun expression, but not AP-1 or SP-1 transcription factor activity. A, Western blot analysis of MKK3-directed c-Jun protein expression with actin as a total protein loading control in cells untreated (NT) or stimulated with SCF for 120 minutes. A representative blot from n = 4 experiments is shown. B, EMSA analysis of MKK3 activity–dependent AP-1 and SP-1 transcription factor activity in MDA-MB-468 cells.](image)

![Figure 7. MKK3 activity is tumor suppressive in MDA-MB-468 cells by enhancing p21 and p27-mediated G1 cell-cycle arrest. A, MKK3 activity enhances cell-cycle arrest. Untransfected (control) MDA-MB-468, MKK3dn, and MKK3ca cells were analyzed for cell-cycle progression staging by flow cytometry following Vybrant DyeCycle Green staining. Data are expressed as percentage of total cells ± SEM for n = 3 experiments. *, P < 0.05; **, P < 0.01. B, model of MKK3 activity as a p53-independent tumor suppressor regulating p21 and p27 expression and subsequently leading to G1 cell-cycle arrest and inhibited breast cancer tumor growth.](image)
significantly impaired tumor growth in vivo. Moreover, we identify a prevalent loss of M KK3 genomic copy number in patients with breast cancer and significantly impaired gene and protein expression in malignant mammary tissues. Collectively, these results position M KK3 as a novel tumor suppressor that is altered in human breast cancer.

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

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Conception and design: A.J. MacNeil, S.-C. Jiao, T.-J. Lin
Acquisition of data (provided animals, acquired and managed patients, provided facilities, etc.): A.J. MacNeil, T.-J. Yang, A. Dennis, H. Yu, Z. Xu, J.S. Marshall
Analysis and interpretation of data (e.g., statistical analysis, bio statistics, computational analysis): A.J. MacNeil, S.-C. Jiao, L.A. McEachern, T.-J. Lin
Writing, review, and/or revision of the manuscript: A.J. MacNeil, L.A. McEachern, Z. Xu, T.-J. Lin

References

MAPK Kinase 3 Is a Tumor Suppressor with Reduced Copy Number in Breast Cancer


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