Oncogenic Ras and B-Raf Proteins Positively Regulate Death Receptor 5 Expression through Co-activation of ERK and JNK Signaling

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**Background:** The oncogene Ras induces DR5 expression with undefined mechanism. Results: Both Ras and B-Raf induce DR5 expression through co-activation of ERK and JNK signaling and subsequent cooperative effects among CHOP, Elk1, and c-Jun. Conclusion: Co-activation of ERK and JNK signaling accounts for Ras-induced DR5 expression. Significance: A novel function of DR5 in Ras- or B-Raf-mediated oncogenesis may be suggested.

Oncogenic mutations of ras and b-raf frequently occur in many cancer types and are critical for cell transformation and tumorigenesis. Death receptor 5 (DR5) is a cell surface pro-apoptotic death receptor for tumor necrosis factor-related apoptosis-inducing ligand and has been targeted in cancer therapy. The current study has demonstrated induction of DR5 expression by the oncogenic proteins Ras and B-Raf and revealed the underlying mechanisms. We demonstrated that both Ras and B-Raf induce DR5 expression by enforced expression of oncogenic Ras (e.g. H-Ras12V or K-Ras12V) or B-Raf (i.e. V600E) in cells and by analyzing gene expression array data generated from cancer cell lines and from human cancer tissues. This finding is further supported by our results that knockdown of endogenous K-Ras or B-Raf (V600E) reduced the expression of DR5. Importantly, we have elucidated that Ras induces DR5 expression through co-activation of ERK/RSK and JNK signaling pathways and subsequent cooperative effects among the transcriptional factors CHOP, Elk1, and c-Jun to enhance DR5 gene transcription. Moreover, we found that the majority of cancer cell lines highly sensitive to the DR5 agonistic antibody AMG655 have either Ras or B-Raf mutations. Our findings warrant further study on the biology of DR5 regulation by Ras and B-Raf, which may provide new insight into the biology of Ras and B-Raf, and on the potential impact of Ras or B-Raf mutations on the outcome of DR5-targeted cancer therapy.

Ras proteins, including H-Ras, K-Ras, and N-Ras, share similar structure and function and can become constitutively activated by mutation. Mutant Ras proteins are resistant to down-regulation by GAP-mediated hydrolysis of bound GTP and, therefore, signal persistently (1). It has been documented that activating mutations in ras genes are present in 15% of all cancers and perhaps as many as 30% of metastatic human cancers (2). The mutant Ras proteins typically activate the Raf/MEK/extracellular signal-regulated kinase (ERK) kinase cascade, which is often associated with the promotion of cell proliferation, and the phosphatidylinositol 3-kinase (PI3K)/Akt signaling pathway, which functions to suppress apoptosis and contributes to oncogenic transformation (1, 3, 4).

Moreover, Ras has been suggested to promote apoptosis. One mechanism accounting for this process involves the association of activated Ras with a Nore1-RASSF1-Mst1 complex (4, 5). In addition, it has been shown that protein kinase C-mediated phosphorylation of the K-Ras membrane-anchoring domain can trigger K-Ras release from the plasma membrane and relocation onto the outer mitochondrial membrane to interact with Bcl-X	extsubscript{L}, resulting in induction of apoptosis (6, 7). This apoptosis-inducing activity of Ras may exert a suppressive effect on Ras-induced oncogenesis by preventing survival of transformed cells.

Death receptor 5 (DR5	extsuperscript{3}; also called TRAIL-R2 or killer/DR5) is one of the death domain-containing cell surface receptors for tumor necrosis factor-related apoptosis-inducing ligand (TRAIL), a tumor-selective apoptosis-inducing cytokine with potential as a cancer therapeutic agent. When overexpressed or ligated with its ligand, TRAIL, DR5 becomes oligomerized (trimerized) and rapidly activates the extrinsic apoptotic pathway. This process involves trimerized DR5 interacting specifically with the adaptor protein Fas-associated death domain via death domain interaction and subsequent recruitment of caspase-8 through the death effector domain between Fas-
Ras Regulation of DR5 Expression

Expression Constructs and Transfection—CHOP and Elk1 expression constructs were described previously (15). c-jun expression plasmid (pCMV-c-Jun) was obtained from Dr. M. J. Birrer (NCI, NIH) and used in our previous study (25). HA-tagged human wild-type (WT) and constitutively activated (G12V) and dominant-negative (S17N) H-ras expression plasmids in pcDNA3.1 vector were obtained from UMR cDNA Resource Center (Rolla, MO) and provided by Dr. F. J. Shu (Emory University). WT EGFP-K-ras or B-ras constructs were obtained from Dr. H. Fu (Emory University). Mutant K-ras (12V, 12C, 12D, or 13D) and B-ras (V600E) expression constructs were generated by site-directed mutagenesis method using the QuikChange XL site-directed mutagenesis kit (Stratagene, La Jolla, CA). Cell transfection with the given plasmids was conducted using Lipofectamine™ 2000 (Invitrogen) according to the manufacturer’s protocol.

Western Blot Analysis—Whole cell protein lysates were prepared and analyzed by Western blotting as described previously (26).

Reporter Plasmids and Luciferase Activity Assay—All DR5 reporter constructs used in this study were described previously (15, 27). Plasmid transfection and luciferase assays were the same as described previously (27).

Gene Silencing Using siRNA—Gene silencing was achieved by transfecting siRNA using HiPerFect transfection reagent (Qigen, Valencia, CA) following the manufacturer’s instructions. Control (i.e. non-silencing), CHOP, Elk1, and ERK1/2 siRNA and RSK2 shRNA were described previously (15, 27). shRSK1 (RHS3979–9569862) was purchased from Open Biosystems (Huntsville, AL). c-Jun (#6205) and JNK (#6234) siRNAs were purchased from Cell Signaling Technology. K-Ras (for both WT and mutant genes) siRNA, which targets the sequence of 5′-AGCAATAGTAATGGATGGAG-3′, and B-Raf (V600E) siRNA, which targets the sequence of 5′-TCTAGTACAGAGAAATCTCG-3′, were synthesized from Qigen. Gene silencing effects were evaluated by Western blot analysis as described above.

Oligonucleotide Pulldown Assay—The WT and mutant oligonucleotides corresponding to the human DR5 promoter region (−334 to −253) harboring Elk1 and CHOP binding sites, with biotin added to their 5′-ends were synthesized by Integrated DNA Technologies, Inc. (Corvallis, IA). The sequences for WT oligonucleotides were biotin-5′-CAGGGCGAAGGT-TAGTTCGGTCCCTTCTCCCTCCTCCGCCTGAGG-3′ and B-Raf (V600E) biotin, which targets the sequence of 5′-TCTAGTACAGAGAAATCTCG-3′, were synthesized from Qigen. Gene silencing effects were evaluated by Western blot analysis as described above.

EXPERIMENTAL PROCEDURES

Reagents and Cell Lines—Rabbit HA tag antibody was purchased from Abgent (catalog no. AP1012, San Diego, CA). Mouse Anti-Ras antibody (clone RAS10; catalog no. 05-512) was purchased from Millipore (Billerica, MA). B-Raf antibody was purchased from Cell Signaling Technology (Beverly, MA). Other antibodies were the same as described previously (15). The human monoclonal DR5 agonistic antibody, AMG655 (Conatumumab), was supplied by Amgen (Thousand Oaks, CA). HEK-293T cells were provided by K. Ye (Emory University, Atlanta, GA). The human lung cancer cell lines A549, H1792, H157, and Calu-1 were described previously (24). The rest of the cancer cell lines were provided by Dr. P. Giannakou (Weill Medical College of Cornell University, New York, NY).

associated death domain and caspase-8, leading to caspase-8 activation and ultimately, apoptosis (8).

DR5 expression can be induced by enhancing its transcription. The transcriptional factors p53 (9, 10), NF-kB (11, 12), C/EBP homologous protein (CHOP; also known as growth arrest and DNA damage-inducible protein 153 (GADD153)) (13, 14), Elk1 (15), and YY1 (16) have been suggested to be involved in this process. Interestingly, the oncogenic Ras was previously shown to induce DR5 expression and to sensitize cells to TRAIL-induced apoptosis (17, 18). However, the detailed mechanism underlying Ras-induced DR5 expression has not been elucidated.

The Raf/MEK/ERK kinase cascade represents the predominant and best studied effector pathway downstream of Ras and is critical for Ras-induced oncogenesis (1, 4). The Raf proteins, including A-Raf, B-Raf, and C-Raf/Raf-1, are a family of serine/threonine kinases and can bind to and are activated by GTP-bound Ras. Raf activation results in activation of the MAPK cascade through phosphorylation of MEK which, in turn, phosphorylates ERK. Following phosphorylation, ERK translocates to the nucleus where it activates various transcription factors or directly phosphorylates 90-kDa ribosomal S6 kinase (RSK), another conserved serine/threonine kinase, which can also translocate to the nucleus and activates transcription through direct phosphorylation (1, 19, 20). Activation of Raf/MEK/ERK signaling is generally associated with stimulation of cell proliferation, including promoting cell survival by suppression of apoptosis; however, a growing number of studies also suggest that activation of this signaling pathway can promote cell death, including apoptosis (19, 21–23).

In this study, we further studied Ras-induced DR5 expression in a comprehensive way by enforced expression of oncogenic Ras in cells and by analyzing gene expression array data generated from cancer cell lines and from human cancer tissues. Moreover, we also demonstrated for the first time that oncogenic B-Raf induces DR5 expression. Most importantly, we have revealed the mechanisms by which Ras or B-Raf induces DR5 expression. Our results show that the cooperative interaction between CHOP, Elk1, and c-Jun activated by the ERK/RSK and c-Jun N-terminal kinase (JNK) signaling pathways mediates Ras-induced DR5 expression.
500 μl of whole cell protein lysate was mixed with biotinylated double-stranded oligonucleotides and ImmunoPure streptavidin-agarose beads (Thermo Scientific/Pierce, Rockford, IL). The mixture was incubated at 4 °C for 16 h with shaking. The beads were then pelleted and washed with cold lysis buffer for four times. Bound proteins were finally separated by SDS-PAGE followed by Western blot analysis to detect proteins of interest with specific antibodies.

Cell Survival Assay—Cells were seeded in 96-well cell culture plates and treated the next day with the tested agent. The viable cell number was determined using sulforhodamine B assay as described previously (29).

Data Source for Analysis of ras and B-raf Mutation and DR5 Expression in Cancer Cell Lines—The NCI-60 U133 microarray data on DR5 (i.e. TNFRSF10B) expression (including probe sets 209295_at, 209292_x_at, and 210405_x_at) were obtained from National Institutes of Health/NCI Cancer Genome Anatomy Project (available on-line at cgap.ncl.nih.gov/Microarray/MicroarrayAccessions?ORG=Hs&CID=521456). The ras (including K-ras and H-ras) and B-raf mutation information on the analyzed cancer cell lines was obtained from the Wellcome Trust Sanger Institute Cancer Genome Project (www.sanger.ac.uk/perl/genetics/CGP/core_lineviewer?action=nci60_list).

DR5 expression in Affymetrix U133 + 2.0 microarray data from human mammary epithelial cells infected with adenovirus expressing either human c-Myc, activated H-Ras, human c-Src, human E2F3, or activated β-catenin, activated K-Ras, human c-Src, human E2F3, or activated β-catenin was extracted from the Gene Expression Omnibus (GSE3151) (30). DR5 expression in Affymetrix U133A microarray data from cancer cell lines with and without B-raf V600E mutation before and after an 8-h treatment with the MEK1/2 inhibitor PD325901 (31) were extracted from the Gene Expression Omnibus (GSE10086).

Data Source for Analysis of K-ras Mutation and DR5 Expression in Human Cancer Tissues—Microarray data from 80 metastatic colorectal cancer patients were downloaded in series matrix format from Gene Expression Omnibus record GSE5851. The data were log2-transformed, and probe sets corresponding to DR5 were extracted (209295_at, 209294_x_at, and 210405_x_at). The highest signal intensities were associated with probe sets 209295_at, whereas probe set 210405_x_at did not yield high signal intensity in any sample. The K-ras gene mutational status corresponding to these samples was extracted from the study published by Khambata-Ford et al. (32).

Statistical Analysis—The statistical significance of differences in DR5 expression between the two groups was analyzed with two-sided unpaired Student’s t tests or Fisher’s exact test by use of InStat 3 software (GraphPad, San Diego, CA). Results were considered to be statistically significant at p < 0.05.

RESULTS

Oncogenic Ras and B-Raf Activate DR5 Promoter and Induce DR5 Expression—We first examined the effects of H-Ras on DR5 transcriptional activity and expression. To this end, we co-transfected WT or mutant H-ras gene with a DR5 luciferase reporter construct carrying −522 bp of the DR5 promoter region and then analyzed luciferase activity. As presented in Fig. 1A, enforced expression of the WT and constitutively active mutant (12V) H-Ras, but not dominant-negative mutant (S17N) H-Ras, increased DR5 promoter activity. However, H-Ras12V induced the greatest increase in DR5 promoter activity. In agreement, enforced expression of H-Ras12V, but not H-RasS17N, substantially increased DR5 protein levels (Fig. 1B). Time course analysis showed that H-Ras12V expression was detected at 36 h post-transfection and sustained up to 60 h. In parallel, DR5 induction was observed within the same time range (Fig. 1C). We also analyzed DR5 expression in publicly available gene expression array data generated from human mammary epithelial cells following adenovirally enforced expression of H-Ras, E2F3, c-Myc, c-Src, or activated β-catenin, with GFP as a control (30). As presented in supplemental Fig. S1, only infection with activated Ras appreciably and significantly induced expression of DR5 (p < 0.0001). These data taken together clearly indicate that oncogenic H-Ras induces DR5 expression.

Furthermore, we analyzed the effect of the oncogenic K-Ras12V on DR5 expression and found that its enforced expression increased DR5 promoter activity and DR5 expression (supplemental Fig. S2, A and B). Similar to K-Ras12V, other cancer-derived K-Ras mutants, including 12C, 12D, and 13D, could also transactivate the DR5 promoter and elevate DR5 expression (supplemental Fig. S2, C and D).

Because the activation of the ERK/RSK signaling mediates DR5 expression (15), we pondered whether the constitutively activated B-Raf mutant (V600E) would also induce DR5 expression. Therefore, we further analyzed the effect of B-Raf (V600E) on DR5 promoter activity and expression. Indeed, enforced expression of B-raf (V600E) increased both DR5 promoter activity and DR5 expression (Fig. 2, A and B). Therefore, not only H-Ras, but also K-Ras and B-Raf, up-regulate DR5 expression.

To further demonstrate whether DR5 expression is regulated by endogenous Ras or B-Raf, we used an siRNA approach to knock down K-Ras or mutant B-Raf (V600E) in a few cancer cell lines with K-ras (A549, H1792, H157, Calu-1, HCT15, and HCT116) or B-raf (V600E) (HT29, BCPAP, and LOXIMVI) mutation. As presented in Figs. 1D and 2C, knockdown of K-Ras or B-Raf (V600E) decreased the levels of p-ERK1/2 accompanied with reduction of DR5 expression in these cell lines, indicating that the Ras/B-raf signaling indeed positively regulates endogenous DR5 expression. These data provide further strong support for Ras and B-Raf regulation of DR5 expression.

Cancer Cell Lines and Tissues with ras and/or B-raf Mutations Exhibit Elevated DR5 Expression—To further explore the association between ras or B-raf mutations and DR5 expression, we asked whether DR5 expression is in general higher in cancer cell lines or cancer tissues with ras or B-raf mutations than those without these mutations. We took advantage of available published data warehoused in public domains and databases for this analysis. We first analyzed DR5 expression levels in microarray data generated from certain cancer cell lines that represent four types of cancers with high frequencies of K-ras and/or B-raf mutations (melanoma, colon cancer, non-small cell lung cancer, and breast cancer) (33), among the NCI-60 cancer cell line panel (NCI60_U133). The highest sig-
nal intensities in the microarray analyses were generated with probeset 209295_at in comparison with signals generated with two other probesets (210405_x_at and 209294_x_at). Thus we first compared DR5 expression between cancer cell lines with and without \( \text{ras} \) (i.e. \( \text{K-ras} \) and \( \text{H-ras} \)) and/or \( \text{B-raf} \) mutations. There were 21 cell lines with either \( \text{K-ras} \) (or \( \text{H-ras} \)) or \( \text{B-raf} \) mutation and 10 cell lines with WT genes among the cell lines analyzed. \( \text{DR5} \) mRNA levels were significantly higher in cell lines with mutant \( \text{ras} \) or \( \text{B-raf} \) than those with WT genes (\( p = 0.0073 \)) (supplemental Fig. S3A). We used an arbitrary cutoff value of 150 to define “high” \( \text{DR5} \) expression and observed that 81% of cell lines (17/21) with \( \text{ras} \) or \( \text{B-raf} \) mutation expressed a high level of \( \text{DR5} \) (i.e. \( >150 \)). In contrast, only 30% (3/10) of cell lines without these mutations expressed a high level of \( \text{DR5} \) (supplemental Fig. S3B). Collectively, these data clearly indicate that cancer cell lines harboring \( \text{ras} \) or \( \text{B-raf} \) mutation have elevated \( \text{DR5} \) expression.

Moreover, we extracted gene expression data and \( \text{K-ras} \) mutational status from a previously published cohort of 80 microarrays generated using metastatic tumor deposit in the liver from colorectal cancer patients (32) to test whether \( \text{DR5} \) gene expression is associated with \( \text{K-ras} \) mutational status in human cancer tissues. We found that \( \text{DR5} \) expression in \( \text{K-ras} \) mutant tumors was significantly higher than in those with WT \( \text{K-ras} \) when comparing the data generated from probeset 209295_at (\( p = 0.005 \)) (supplemental Fig. S3C), further demonstrating a strong association between \( \text{K-ras} \) mutation or activation and high \( \text{DR5} \) expression in human cancer tissues. A similar trend was observed using data generated with the probeset 209294_x_at and 210405_x_at.

FIGURE 1. Activated \( \text{H-Ras} \) transactivates the \( \text{DR5} \) promoter (A) and induces \( \text{DR5} \) expression along with activation of \( \text{ERK/RSK} \) and \( \text{JNK} \) signaling pathways and up-regulation of \( \text{CHOP} \) (B and C), whereas knockdown of \( \text{K-Ras} \) reduces \( \text{DR5} \) expression along with \( \text{ERK} \) inhibition (D). A, HEK293T cells were co-transfected with \( \text{DR5} \) promoter reporter plasmid and the indicated \( \text{H-ras} \) genes. After 36 h, the cells were harvested for measurement of luciferase activity. The data are means ± S.D. of triplicate determinations. B and C, HEK293T cells were transfected with the expression plasmids carrying the given \( \text{H-ras} \) genes for 40 h (B) or the indicated times (C). D, the indicated cell lines with mutant \( \text{K-ras} \) were transfected with control or \( \text{K-Ras} \) siRNA for 62 h. After the aforementioned transfections, the cells were harvested for preparation of whole cell protein lysates and subsequent Western blotting to detect the indicated proteins. NT, no transfection; V, vector; NS, nonspecific band; C, control.
Western blotting to detect the indicated proteins. Ctrl infected with control (or B-) cate determinations. and vector or the indicated B-, HEK293T cells were co-transfected with B raf V A, HEK293T cells were transfected with vector (naling pathways and up-regulation of CHOP (C), whereas knockdown of 12V gene (Fig. 1, H- ras p-Akt in cells transfected with either WT H- Ras, particularly H-ras12V (Fig. 1, B and C). Thus, oncogenic H-Ras also activates JNK/c-Jun signaling. Similarly, enforced expression of oncogenic K-ras12V or B-raf (V600E) increased the levels of p-ERK1/2, p-RSK, p-Elk1, p-JNK, and p-c-Jun (Fig. 2 A and supplemental Fig. S2A) (34) indicating that activated K-Ras and B-Raf also activate both the ERK/RSK and JNK signaling pathways in the tested cell system.

**Oncogenic Ras Induces DR5 Expression through an ERK/RSK-dependent Mechanism**—We next determined whether the activation of ERK and RSK signaling is required for Ras-induced DR5 expression. To this end, we knocked down ERK1/2 expression with ERK1/2 siRNA to suppress Ras-induced ERK/RSK activation and then analyzed its impact on Ras-induced DR5 expression. As shown in Fig. 3A, transfection of ERK1/2 siRNA not only reduced the levels of total ERK1/2 but also the levels of p-ERK, p-RSK, and p-Elk1 induced by H-Ras12V compared with the control siRNA, indicating successful knockdown and blockage of Ras-induced activation of ERK/RSK signaling. We detected increased levels of DR5 in control siRNA-transfected but not in ERK1/2 siRNA-transfected cells (Fig. 3A). In agreement, we observed that H-ras12V increased DR5 promoter activity in cells transfected with the control siRNA but not in cells transfected with ERK1/2 siRNA (Fig. 3B). Moreover, we determined whether Ras activation is also involved in mediating Ras-induced DR5 expression. Expression of either shRSK2 or shRSK1 substantially reduced the levels of RSK2 or RSK1, respectively, indicating the successful knockdown of their expression. Enforced expression of H-Ras12V increased DR5 expression in the vector control cells (pLKO1) but failed to do so in cells expressing shRSK2 or shRSK1 (Fig. 3C), indicating that both RSK2 and RSK1 are involved in mediating Ras-induced DR5 expression. Similarly, H-Ras12V increased DR5 promoter activity in pLKO1-transfected cells but only minimally in cells transfected with either shRSK1 or shRSK2 (Fig. 3D). Collectively, these data clearly demonstrate that oncogenic Ras induces DR5 expression in an ERK/RSK-dependent manner.

The above findings led us to further analyze whether this paradigm held true in cancer cell lines harboring activated B-Raf (V600E) following chemical MEK inhibition with the compound PD325901. For this analysis, we extracted DR5 expression data from publicly available microarray data reported by Pratilas et al. (31). Consistent with the above-discussed data, B-Raf V600E cell lines demonstrated higher baseline expression of DR5 than B-Raf WT cell lines. MEK inhibition with PD325901 (8 h) significantly reduced DR5 gene expression in B-Raf V600E cell lines (p = 0.009), but not in B-Raf WT cell lines (p > 0.05) (supplemental Fig. S5). These data provide further support for the critical role of the MEK/ERK signaling in mediating DR5 expression induced by activated Ras or B-Raf.

**Oncogenic Ras Also Induces a JNK-dependent DR5 Expression**—Our previous studies suggest that JNK activation contributes to drug-induced DR5 up-regulation (35, 36). Because Ras activates JNK signaling in parallel with the activation of ERK/RSK signaling, we further asked whether JNK signaling is involved in Ras-induced DR5 expression. To address this question, we inhibited
JNK activation by knocking down JNK expression and then looked at its impact on Ras-induced DR5 expression. As shown in Fig. 4A, transfection of JNK siRNA drastically reduced the levels of JNK, confirming its successful knockdown. Correspondingly, we detected an increase in DR5 expression induced by H-ras12V transfection in control siRNA-transfected cells, but not in JNK siRNA-transfected cells, indicating that the activation of JNK signaling is also required for Ras-induced DR5 expression.

The Transcriptional Factors, CHOP, Elk1, and c-Jun, Are Involved in Mediating Ras-induced DR5 Expression—We have recently shown that CHOP and Elk1 cooperate to mediate ERK/RSK-dependent DR5 up-regulation induced by certain small molecules (15). Therefore, we determined whether CHOP and Elk1 are involved in Ras-induced DR5 expression. By analyzing the promoter region of the DR5 gene through deletion analysis, we found that the region between −373 and −240 bp was required for H-Ras12V to increase DR5 transcription, because H-Ras12V could increase luciferase activity of reporter constructs carrying −373 and −522 bp DR5 promoter regions but failed to do so in cells transfected with vector or H-ras12V. After 48 h, the cells were harvested for preparation of whole cell protein lysates and subsequent Western blotting for the indicated proteins. The data are means ± S.D. of triplicate determinations.

FIGURE 4. Involvement of JNK (A) and c-Jun (B and C) in Ras-induced DR5 expression. A, HEK293 cells were transfected with control (Ctrl) or JNK siRNA, and 15 h later, were transfected with vector or H-ras12V. After 40 h, the cells were harvested for preparation of whole cell protein lysates and subsequent Western blotting for the indicated proteins. B, HEK293T cells were co-transfected with the indicated reporter constructs and vector or H-ras12V plasmids. After 42 h, the cells were lysed for luciferase activity assay. C, HEK293 cells were transfected with control (Ctrl) or c-Jun siRNA, and 15 h later, were transfected with vector or H-ras12V. After 40 h, the cells were harvested for preparation of whole cell protein lysates and subsequent Western blotting for the indicated proteins. The data are means ± S.D. of triplicate determinations.
induced DR5 transactivation; however, mutation of either the CHOP or Elk1 binding site attenuated Ras-mediated DR5 transactivation (Fig. 5B). These data suggest that both CHOP and Elk1 binding sites are important for Ras to transactivate the DR5 gene, implying that both CHOP and Elk1 are involved in this process.

In the aforementioned ras or B-raf transfection experiments, increased CHOP was detected in cells transfected with H-Ras12V (Fig. 1), K-ras12V (supplemental Fig. S2), or B-raf (V600E) (Fig. 2) in addition to an increase in Elk1. To further demonstrate the involvement of CHOP and Elk1 in Ras-induced DR5 expression, we knocked down Elk1 and CHOP expression individually, and then examined their impact on Ras-induced DR5 expression. As presented in Fig. 5 (C and D), H-Ras12V increased DR5 expression in control siRNA-transfected cells but not in cells transfected with either Elk1 siRNA (Fig. 5C) or CHOP siRNA (Fig. 5D). In agreement, the ability of H-Ras12V to increase DR5 promoter activity was also impaired or attenuated in cells where Elk1 or CHOP expression was silenced by siRNA (supplemental Fig. S6). Together, these data demonstrate that both Elk1 and CHOP are indeed critical for mediating Ras-induced DR5 expression.

Another transcriptional factor, c-Jun, was also up-regulated upon Ras activation in our cell system (Fig. 1 and supplemental Fig. S2). We explored whether c-Jun plays a role in regulation of DR5 expression, including Ras-induced DR5 expression. We first analyzed the effects of c-Jun expression on transactivation of the DR5 promoter. As presented in Fig. 4B, c-Jun indeed increased DR5 promoter activity. Mutation of the NF-kB site did not affect the ability of c-Jun to transactivate the DR5 gene; however, mutation of either the CHOP or Elk1 binding site attenuated its ability to increase DR5 promoter activity. These data suggest that c-Jun transactivates the DR5 gene through CHOP- and Elk1-mediated mechanisms. Furthermore, we knocked down c-Jun expression to block c-Jun up-regulation and then analyzed its effect on Ras-induced DR5 expression. As shown in Fig. 4C, knockdown of c-Jun substantially suppressed the increase in c-Jun expression induced by H-Ras12V. Consequently, knockdown of c-Jun not only reduced the basal levels of DR5, but it also abolished Ras-induced DR5 up-regulation. Hence, it is clear that c-Jun is also critical for Ras-induced DR5 expression.

**c-Jun Participates in CHOP- and Elk1-mediated Transcription of DR5 Gene**—Because the DR5 promoter region lacks an AP-1 binding site, we were interested in understanding how c-Jun contributes to Ras-induced DR5 expression. It was previously shown that CHOP interacts with c-Jun (or AP-1) to regulate gene expression through binding to the AP-1 consensus binding sequence in AP-1 target genes (37, 38). Thus we considered that c-Jun may interact with CHOP and even Elk1 to enhance CHOP- and Elk1-mediated gene transcription (Fig. 6A). To test this hypothesis, we conducted a oligonucleotide pulldown assay to test whether c-Jun binds to CHOP and/or Elk1 in the DR5 promoter. First, we determined whether the oligonucleotides with CHOP and Elk1 binding sites could pull down CHOP, Elk1, and c-Jun from protein lysates of cells co-transfected with CHOP, Elk1, and c-Jun expression plasmids in comparison with empty streptavidin beads (Fig. 6B). As presented in Fig. 6C, we could detect CHOP, Elk1, and c-Jun proteins in protein complexes pulled down by the oligonucleotides but not in protein complexes pulled down with the empty streptavidin beads (Fig. 6C). Moreover, we transfected H-ras12V into cells, and then incubated lysates with biotin-
labeled DR5 oligonucleotides or streptavidin beads for the oligonucleotide pulldown assay. Again we detected CHOP, Elk1, c-Jun, and p-c-Jun only in the complexes pulled down with the DR5 oligonucleotides from cell lysates expressing H-Ras12V (Fig. 6D). To robustly demonstrate this mechanism, we repeated the above experiments with a mutant oligonucleotide, in which both CHOP and Elk1 sites were mutated (Fig. 6B). Identical to the data presented in Fig. 6C, we found that the WT DR5 oligonucleotides, but not the mutant DR5 oligonucleotides or empty streptavidin beads, could pull down CHOP, Elk1, and c-Jun proteins from cells co-transfected with these three genes (Fig. 6E). Collectively, these data clearly suggest that c-Jun forms a complex with CHOP and/or Elk1 that binds to the DR5 promoter.

Furthermore, we compared the effects of single, double, or triple transfection of CHOP, Elk1, and/or c-Jun on DR5 gene transactivation and expression. The triple expression of CHOP, Elk1, and c-Jun induced the highest levels of DR5 promoter activity and DR5 expression compared with either single or double transfection (supplemental Fig. S7), suggesting that these three transcriptional factors cooperate to enhance DR5 gene transcription.

**Mutation Status of ras or B-raf Impacts Cell Response to DR5 Agonistic Antibody**—Given that DR5 agonistic antibody exerts anticancer efficacy exclusively through binding to DR5 and inducing DR5-mediated apoptosis, we speculated that cancer cell lines with mutant ras or B-raf might be particularly susceptible to DR5-targeted cancer therapy due to elevated DR5 expression. Thus, we examined the effects of AMG655, a human monoclonal DR5 agonistic antibody, on the survival of 38 human cancer cell lines, which consist of several cancer types known to have high frequency of ras or B-raf mutations (e.g., melanoma, colon, lung, breast, and pancreatic cancer). These cell lines showed varied sensitivities to AMG655. Among them there were 12 cell lines that were highly sensitive to AMG655 (IC50 values < 300 ng/ml), 10 cell lines that were insensitive to AMG655 (<25% cell killing at 2000 ng/ml), and 16 cell lines showing intermediate sensitivity (IC50 values ≈ 1000 ng/ml) (Fig. 7A and supplemental Fig. S8). If we consider only the highly sensitive cell lines as responders, the response rate in cancer cell lines with ras or B-raf mutation was 44% (11/25), which was significantly higher than the 7.7% (1/13) in the cancer cell lines without these mutations (p = 0.03) (Fig. 7B). When we looked at the sensitive cancer cell line group alone, we noted that 91.7% (11/12) of the cancer cell lines had either a ras or B-raf mutation was 44% (11/25), which was significantly higher than the 7.7% (1/13) in the cancer cell lines without these mutations (p = 0.03) (Fig. 7B). When we looked at the sensitive cancer cell line group alone, we noted that 91.7% (11/12) of the cancer cell lines had either a ras or B-raf mutation was 44% (11/25), which was significantly higher than the 7.7% (1/13) in the cancer cell lines without these mutations (p = 0.03) (Fig. 7B).

**DISCUSSION**

In addition to overexpression approaches, as conducted by other investigators previously (17, 18), the current study has further demonstrated Ras-mediated DR5 regulation under physiological conditions by knocking down endogenous K-ras
expression in cancer cell lines (Fig. 1D). Thus, our current data provide robust evidence supporting that oncogenic Ras positively regulates DR5 expression. Moreover, our analysis of DR5 expression in a cohort of 80 metastatic human colon cancer tissues with known K-ras mutation status has shown significant elevation of DR5 expression in tissues with K-ras mutation compared with those with WT K-ras (supplemental Fig. S4), providing the first in vivo evidence that ras mutations impact DR5 expression in human cancer tissues.

Previous studies with chemical inhibitors suggested that MEK or ERK activation is involved in Ras-mediated DR5 up-regulation (17, 18). However, the precise mechanism by which Ras induces DR5 expression was unknown. Using specific siRNA and shRNA approaches, we confirmed ERK-dependent DR5 induction by Ras, by demonstrating that inhibition of ERK signaling by knocking down ERK1/2 expression abrogated Ras-induced activation of DR5 promoter and DR5 expression (Fig. 3). Moreover, we further showed that knockdown of RSK2 or RSK1, well known ERK substrates, also suppressed Ras-induced DR5 expression (Fig. 3). Thus, not only ERK- but also RSK-mediated signaling is involved in Ras-induced DR5 expression.

Raf proteins as a family of serine/threonine kinases mediate Ras-induced ERK activation (1). In this study, we further showed that the oncogenic B-Raf (V600E), a commonly mutated form in cancers, activated ERK/RSK signaling, increased DR5 promoter activity, and up-regulated DR5 expression (Fig. 2). Analysis of DR5 expression in publicly available microarray data also demonstrated that cancer cell lines with mutant B-raf (V600E) expressed significantly higher levels of DR5 in cell with WT B-raf (supplemental Fig. S5). In agreement, knockdown of mutant B-Raf (V600E) in cancer cells decreased DR5 expression (Fig. 2). Moreover, chemical inhibition of MEK with PD325901 significantly reduced DR5 expression levels only in cancer cell lines harboring the mutant B-raf gene (supplemental Fig. S5), indicating an MEK/ERK-dependent DR5 regulation by B-Raf. To our knowledge, this is the first study to show that B-Raf activation induces DR5 expression.

In addition to activation of the Raf/MEK/ERK signaling cascade, oncogenic Ras also activates the PI3K/Akt and JNK/Jun signaling pathways (3). In our cell system, we did not detect increased p-Akt levels in H-ras12V-transfected cells (Fig. 1), suggesting that PI3K/Akt signaling was not activated by Ras under the tested conditions. However, we did see substantially increased levels of p-JNK and/or p-c-Jun in cells transfected with H-ras12V or K-ras12V (Fig. 1 and supplemental Fig. S2), indicating that oncogenic Ras turns on JNK/Jun signaling. Knockdown of JNK with JNK siRNA inhibited Ras-induced DR5 expression (Fig. 4). Moreover, c-Jun transactivated the DR5 promoter, and siRNA-mediated knockdown of c-Jun abolished the ability of Ras to induce DR5 expression (Fig. 4). Together, these results indicate that JNK/c-Jun signaling is involved in mediating Ras-induced DR5 expression.

JNK signaling has been implicated in the regulation of drug-induced DR5 expression (35, 36). However, the underlying mechanism is unknown. DR5 promoter analysis from the current study suggests that the region between −373 and −240 is responsible for Ras-induced transactivation of the DR5 gene (Fig. 5). This region contains both CHOP and Elk1 binding sites, but it lacks an AP-1 binding site. Mutation of either the CHOP or Elk1 binding site attenuated the ability of Ras to transactivate the DR5 gene (Fig. 5), demonstrating that both binding sites are responsible for Ras-induced DR5 transactivation. Enforced expression of the oncogenic Ras (both H- and K-Ras) or B-Raf (V600E) increased the levels of p-Elk1 and CHOP along with DR5 induction (Figs. 1, 2, and supplemental Fig. S2). Moreover, knockdown of either Elk1 or CHOP expression inhibited Ras-induced DR5 gene transactivation (supplemental Fig. S6) and expression (Fig. 5), indicating that both CHOP and Elk1 are indeed critical mediators for Ras-induced DR5 expression. These results are consistent with our recent findings that CHOP and Elk1 cooperatively regulate DR5 expression induced by small molecule drugs (15), thus reinforcing the notion that CHOP- and Elk1-mediated gene transcription is critical for DR5 expression. The unaddressed question is the role of c-Jun in CHOP- and Elk1-mediated DR5 expression.
Ras Regulation of DR5 Expression

It has been documented that CHOP interacts with c-Jun (or AP-1) to regulate gene expression through binding to the AP-1 consensus binding sequence in AP-1 target genes (37, 38). This led us to hypothesize whether c-Jun interacts with CHOP and even Elk1 and consequently enhances CHOP- and Elk1-mediated gene transcription. Indeed, c-Jun could be co-precipitated with CHOP and Elk1 in the oligonucleotide pulldown assay when these three proteins were co-expressed or when H-Ras was activated (Fig. 6), suggesting that c-Jun does form a complex with CHOP and/or Elk1 that binds to the DR5 promoter region. Moreover, triple expression of CHOP, Elk1, and c-Jun induced the highest levels of DR5 promoter activity and DR5 expression compared with either single or double expression of these proteins (supplemental Fig. S7). Collectively these results demonstrate that c-Jun, likely as a co-activator, participates in CHOP- and Elk1-mediated DR5 transcription through interaction with CHOP and/or Elk1 (Fig. 8).

We noted that the levels of DR5 expression varied among different cell lines, although cancer cell lines harboring ras or B-raf mutation have significantly elevated DR5 expression (supplemental Fig. S3). This variation is likely due to other regulatory mechanisms of DR5 expression (e.g. p53, NF-κB, and YY1) (39).

It is well known that K-Ras mutation or activation is critical for cell transformation and cancer development, primarily through activation of the Raf/MEK/ERK and PI3K/Akt signaling pathways. However, Ras activation also leads to cell senescence and cell death (e.g. apoptosis), which may counteract its oncogenic function (4, 40–43). A recent mouse study has shown that deficiency of TRAIL receptor in mice (there is only one death receptor for TRAIL in mice) enhances metastasis without affecting primary tumor development (44), suggesting that TRAIL receptor or TRAIL-TRAIL receptor interaction may be critical for regulation of tumor metastasis. Thus, whether DR5 up-regulation plays a suppressive role in Ras-induced oncogenesis needs to be determined.

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