DNA Damage and Repair

Mcl-1 Mediates TWEAK/Fn14-Induced Non-Small Cell Lung Cancer Survival and Therapeutic Response

Timothy G. Whitsett1, Ian T. Mathews1, Michael H. Cardone5, Ryan J. Lena5, William E. Pierceall5, Michael Bittner2, Chao Sima2, Janine LoBello3, Glen J. Weiss1,4, and Nhan L. Tran1

Abstract

Insensitivity to standard clinical interventions, including chemotherapy, radiotherapy, and tyrosine kinase inhibitor (TKI) treatment, remains a substantial hindrance towards improving the prognosis of patients with non–small cell lung cancer (NSCLC). The molecular mechanism of therapeutic resistance remains poorly understood. The TNF-like weak inducer of apoptosis (TWEAK)–FGF-inducible 14 (TNFRSF12A/Fn14) signaling axis is known to promote cancer cell survival via NF-xB activation and the upregulation of prosurvival Bcl-2 family members. Here, a role was determined for TWEAK–Fn14 prosurvival signaling in NSCLC through the upregulation of myeloid cell leukemia sequence 1 (MCL1/Mcl-1). Mcl-1 expression significantly correlated with Fn14 expression, advanced NSCLC tumor stage, and poor patient prognosis in human primary NSCLC tumors. TWEAK stimulation of NSCLC cells induced NF-xB–dependent Mcl-1 protein expression and conferred Mcl-1–dependent chemo- and radioresistance. Depletion of Mcl-1 via siRNA or pharmacologic inhibition of Mcl-1, using EU-5148, sensitized TWEAK-treated NSCLC cells to cisplatin- or radiation-mediated inhibition of cell survival. Moreover, EU-5148 inhibited cell survival across a panel of NSCLC cell lines. In contrast, inhibition of Bcl-2/Bcl-xL function had minimal effect on suppressing TWEAK-induced cell survival. Collectively, these results position TWEAK–Fn14 signaling through Mcl-1 as a significant mechanism for NSCLC tumor cell survival and open new therapeutic avenues to abrogate the high mortality rate seen in NSCLC.

Implications: The TWEAK–Fn14 signaling axis enhances lung cancer cell survival and therapeutic resistance through Mcl-1, positioning both TWEAK–Fn14 and Mcl-1 as therapeutic opportunities in lung cancer. Mol Cancer Res; 12(4); 550–9. ©2014 AACR.

Introduction

Lung cancer is the leading cause of cancer-related mortality in the United States and throughout the world, with a 5-year survival rate for advanced, non–small cell lung cancer (NSCLC), the most common class of lung cancer, below 10%, in part due to intrinsic and acquired resistance to standard therapeutics (1). Although targeted therapies have shown promise in small subsets of patients, the majority of lung cancer patients rely on platinum-derived chemotherapeutics and radiotherapy in the absence of more effective targeted therapeutics. Acquired resistance to these treatments remains a significant barrier to reducing mortality in patients with NSCLC (2, 3). A deeper understanding of the molecular events leading to therapeutic resistance would identify novel therapeutic targets to improve patient prognosis in advanced NSCLC.

The TNF-like weak inducer of apoptosis (TWEAK)–fibroblast growth factor-inducible 14 (Fn14; TNFRSF12A) signaling axis has been implicated in a number of solid tumor types and can affect tumor cell proliferation, apoptosis, cell invasion, and cell survival (4). In NSCLC, Fn14 is overexpressed in primary tumors, correlated with activated EGFR, and promoted tumor cell migration and invasion (5). In glioblastoma, TWEAK exposure resulted in enhanced tumor cell invasion through Rac1 and NF-xB activation (6). In addition, TWEAK–Fn14 signaling promoted glioblastoma cell survival, primarily through Akt2 phosphorylation, NF-xB activation, and upregulation of Bcl-2 family members such as Bcl-xl and Bcl-w (7, 8). The role and mechanism(s) of TWEAK-mediated tumor cell survival in NSCLC has not been described.

Prosurvival members of the Bcl-2 family, including Bcl-2, Bcl-xL, Bcl-w, and Mcl-1, are elevated in numerous cancer types and contribute to cancer cell survival and resistance to...
RNA impaired colony formation
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induced cell survival. Similarly, EU-5148, a pharmacologic
NF-

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Materials and Methods
Cell culture conditions
Human lung adenocarcinoma cell lines H1975 and H2073 (American Type Culture Collection) were main-
tained in RPMI-1640 media (Invitrogen) plus 10% heat-
treated in RPMI-1640 plus 10% FBS with 50 µmol/L β-mercaptoethanol added to 1863 and 1780 cells. In all
assays treated with TWEAK, cells were cultured in
reduced serum (0.5% FBS) for 16 hours before stimulation
with TWEAK at 100 ng/mL in RPMI + 0.1% bovine serum albumin for the indicated times.

Immunohistochemistry
Protein expression by immunohistochemistry was performed on a tissue microarray as previously described (5) and
immunohistochemical (IHC) analysis for Fn14 has been previously described in our laboratory (5). Mcl-1 staining
was performed using an antibody specific for the long form
of Mcl-1 (Santa Cruz Biotechnology). A scoring system
for each chromophore comprised of staining intensity and
extensiveness captured the outcome: 0, negative; 1, weak;
2 moderate; 3, strong. A two-sided Kendall tau test was
carried out on scores of Mcl-1 and Fn14 for samples in which
both were evaluated and scored.

Antibodies, reagents, and immunoblotting
Mcl-1, Bcl-2, Bcl-xL, phospho-p65 (Serine residue 536),
Bak, GAPDH, and cleaved-PARP antibodies were obtained
from Cell Signaling Technology Inc., and α-tubulin anti-
body was obtained from Millipore. Human recombinant
TWEAK was purchased from PeproTech, and cisplatin
was obtained from TZS Chemical via BIOTANG Inc.. The
Mcl-1–specific inhibitor EU-5148 (20) was kindly provided
by Eutropics Pharmaceuticals. The chemical scaffold of EU-
5148 is shown in Supplementary Fig. S1 and fully described
(http://patentscope.wipo.int/search/en/detail.jsf?docId¼
WO2012122370&t PMCNum=2&o office¼&queryString¼F-
P%3A%28Eutropics%29&prevFilter¼&sortOption¼
Pub+Date+Desc&maxRec=7). ABT-737 was obtained from Selleck Chemicals. Immunoblot analysis was performed
as previously described (5, 8).

Quantitative real-time PCR
mRNA expression was determined by quantitative real-
time PCR (qPCR) as previously described (21). Briefly,
total RNA was extracted from cell lines using the mirVana
isolation kit (Ambion) according to the manufacturer’s
directions. cDNA was synthesized from total RNA
using SuperScript III First-Strand Synthesis SuperMix
(Life Technologies) according to the manufacturer’s
protocol. qPCR analyses of Mcl-1 (forward: 5′-GGAC-
TGCTTAGTTAAAAAGAGG-3′; reverse: 5′-CITTTAGATATGCCAAAACCAGCTC-3′), Bcl-xL (BCL2L1; forward:
5′-GCTTAGTACCGGCATCC-3′; reverse: 5′-TTCTGAAAGGAGAGAAAGATTCC-3′) and histone
H3 (forward: 5′-CCACTAICTTCTGATCCGC-3′; reverse: 5′-GCCTGCTAGCTGATGTCTT-3′) were
carried out in triplicate in a 384-well plate using a Light-
Cycler 480 (Roche Applied Sciences) and analyzed as
previously described (22).

Expression plasmids and transfection
Cytomegalovirus plasmid backbones (pCMV) con-
taining genes for human wild-type IκBα or IκBβ with
serine-to-alanine mutations at residues 32 and 36 were purchased from Addgene and transfected into the human
adenocarcinoma cell lines using the Effective Transfec-
tion Reagent (Qiagen) kit according to the manufact-
urer’s protocol.
Small interfering RNA preparation and transfection

Small interfering RNA (siRNA) oligonucleotides specific for GL2 Luciferase were previously described (23). Validated siRNA sequences for Mcl-1 full-length transcripts (Mcl-1-1 and Mcl-1-2 target oligo sequences: 5'-CCGCGCAATTT-CATTAAATT-3', 5'-CCCTAGGAACCATGGGGA-3', respectively) and Bcl-xL sequence: 5'-CTGCT-TGGGATAAAGATGCAA-3' were purchased from Qiagen. Transient siRNA transfection was carried out as previously described (23). All siRNA transfections were done at 20 nmol/L siRNA using Lipofectamine RNAi MAX reagent (Invitrogen) and no cytotoxicity was observed 24 hours after transfection. Maximum inhibition of protein levels was achieved approximately 72 hours after transfection.

Clonogenic assay

Observations of colony-forming capacity following cytotoxic insult were performed as previously described (24). Briefly, cells were transfected with either luciferase or Mcl-1 siRNA, or treated with EU-5148 at 7.5 μmol/L for 24 hours, followed by serum reduction (0.5% FBS) for 16 hours before the addition of TWEAK for 24 hours. For cisplatin treatment, cells were pretreated with TWEAK for 4 hours before the addition of cisplatin (1 μmol/L) for 20 hours. For radiation treatment, cells were pretreated with TWEAK and incubated for 24 hours before exposure to 2 Gy ionizing irradiation using an RS-200 (Rad Source). Cells were then trypsinized, quantified, and equally dispersed in triplicate in 6-well cell culture dishes at 250 cells per well. Plates were incubated until colonies reached an approximate size of 50 cells (1–2 weeks) before being fixed briefly in a 10% (v/v) methanol 10% (v/v) glacial acetic acid solution, stained with a 0.5% (w/v) crystal violet solution and washed with deionized water. Apparent colonies were counted. All cell lines and treatments were run in triplicate. Statistical significance, defined as a P value of <0.05, was determined by ANOVA analysis with Bonferroni posttests in Graphpad Prism.

Immunoprecipitation

For immunoprecipitation, cells were treated with TWEAK, 7.5 μmol/L EU-5148, or TWEAK and EU-5148 simultaneously. After 24 hours of treatment, cells were lysed on ice for 10 minutes in a buffer containing 10 mmol/L Tris-HCl (pH 7.4), 0.5% Nonidet P-40, 150 mmol/L NaCl, 1 mmol/L phenylmethylsulfonyl fluoride, 1 mmol/L EDTA, 2 mmol/L sodium orthovanadate, 20 mmol/L sodium fluoride, 10 μg/mL aprotinin, and 10 μg/mL leupeptin. Equivalent amounts of protein (500 μg) were precleared and immunoprecipitated from each lysate using Bak antibody as indicated or a control isotype-matched antibody and then washed with lysis buffer followed by TXX-100 buffer (10 mmol/L HEPES (pH 7.4), 150 mmol/L NaCl, 2 mmol/L EDTA, 2 mmol/L EGTA, 20 mmol/L sodium fluoride, and 0.5% Triton X-100). Immunoprecipitated samples were then reconstituted in 2x SDS buffer containing protease and phosphatase inhibitors and immunoblotted with the indicated antibodies as described.

PrestoBlue assay

Cell killing was measured by PrestoBlue cell viability reagent after incubating cells with compound for 48 hours. EU-5148 and dimethyl sulfoxide (DMSO) were diluted in serum-free RPMI-1640 media and dispensed to a cell culture-treated 384-well plate (Griener Bio-One). Cells in culture were counted and centrifuged, then resuspended in RPMI-1640, 10% FBS, 1% penicillin-streptomycin. Cells were added to the plate containing drug dilutions (5,000 cells/well) and incubated at 37°C for 48 hours. PrestoBlue cell viability reagent (Invitrogen) was added to the plate and fluorescence was measured after 1 hour at excitation/emission 535/595 nm. Cell killing curves were made in GraphPad Prism 5.

Cell viability assay

NSCLC cell viability was tested using the CellTiter-Glo Luminiscence Cell Viability Assay Kit (Promega) according to the manufacturer’s instructions. Cells were treated with EU-5148 for 48 hours before luminescence reading performed on a Victor3 1420 Multilabel Counter (PerkinElmer). All cell lines and treatments were performed in duplicate.

Results

Mcl-1 is overexpressed in human primary NSCLC tumors and correlates with Fn14

To determine the expression of MCL-1 protein in NSCLC, we utilized a NSCLC tissue microarray (TMA) as previously described. The protein expression of Mcl-1 was detected in the cytoplasm in the majority of NSCLC tumors (80% of adenocarcinomas and 58% of squamous cell carcinomas) demonstrated moderate to strong protein levels of Mcl-1. Because the correlation of Fn14 expression and prosurvival Bcl-2 family members has been previously reported, we next examined the relationship between these two markers. In both adenocarcinomas and squamous cell carcinomas, the protein levels of Mcl-1 were significantly correlated with the protein levels of Fn14 (Fig. 1). Publically available gene expression data (www.genesapiens.org) further showed a significant correlation between Mcl-1 and Fn14 mRNA levels in squamous cell lung cancer specimens (Supplementary Fig. S2). At the gene expression level (Bild Lung dataset; ref. 25; www.oncomine.org), mRNA levels of Mcl-1 significantly correlate with increasing stage of lung adenocarcinomas (Supplementary Fig. S3A) and with patient mortality at 1 year (Supplementary Fig. S3B). Thus, Mcl-1 is highly expressed in primary NSCLC tumors, correlates with Fn14 expression, and is associated with poor patient prognosis.

TWEAK stimulation induces Mcl-1 and other Bcl-2 family member expression through activation of NF-κB

TWEAK promotes cancer cell survival through phosphorylation of the p65 subunit of NF-κB, leading to increased expression of prosurvival Bcl-2 family members Bcl-xL and Bcl-w (8). We therefore investigated whether TWEAK stimulation induces prosurvival Bcl-2 members in NSCLC.
In the adenocarcinoma cell lines H1975 and H2073, TWEAK treatment led to the clear induction of phosphorylated p65 (P-p65), with concomitant incremental increases in protein expression of Mcl-1 and Bcl-xL over time. (Fig. 2A and B) The protein expression of Bcl-2 was also upregulated following TWEAK exposure in H1975, but was not expressed in H2073 (data not shown). To confirm TWEAK-induced expression of Bcl-2 family members, we measured mRNA expression by qPCR. TWEAK treatment induced mRNA levels of Mcl-1 and Bcl-xL in both H1975 and H2073 cells as early as 30 minutes post-TWEAK with maximal expression approximately 6 hours (10-fold increase in H1975 and 50-fold increase in H2073; Supplementary Fig. S4A and S4B).

To determine whether TWEAK-induced Mcl-1 expression is dependent on NF-κB activation, H2073 cells were transfected with wild-type IkBα (IkBα-wt), or a mutated IkBα super-repressor (IkBα-mt) expressing plasmid, and levels of Mcl-1 following TWEAK exposure were assessed.

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### Figure 1.
Mcl-1 expression in human NSCLC specimens correlates with Fn14 expression. A, Mcl-1 and Fn14 staining on representative samples from the same patient with lung adenocarcinoma (5× objective, Aperio GL Scanner). Tumor cell-specific Fn14 and Mcl-1 staining in each of the tumor punches was scored by a board-certified pathologist; a score of zero indicates staining level equal to adjacent nontumor cells. A nonzero score indicates increased staining (1 = minimum, 2 = moderate, 3 = strong positive). B, a total of 290 samples were scored for Mcl-1 and Fn14 expression and the correlation between the two stains was analyzed using the Kendall tau test.

### Figure 2.
TWEAK induces Mcl-1 in NSCLC cell lines in an NF-κB–dependent manner. Total cell lysates were prepared from serum-reduced (A) H1975 and (B) H2073 cell lines treated with TWEAK for the indicated times and immunoblotted with the indicated antibodies: Mcl-1, Bcl-xL, and phosphorylated-p65 (Ser536). Tubulin was used as a loading control. C, serum-reduced H2073 cells transfected ± IkBα mutant were treated with TWEAK for 24 hours. Cells were harvested, total cell lysates were prepared and immunoblotted with the indicated antibodies to both Mcl-1 and phospho-p65. All blots were run in duplicate and tubulin was used as a loading control.
The IκBα-mt is incapable of being phosphorylated and thus sequesters NF-κB in the cytoplasm. Mcl-1 protein expression increased with TWEAK treatment in IκBα-wt-expressing cells, but was inhibited in the presence of the IκBα-mt expression, in correlation with reduced p65 phosphorylation (Fig. 2C). These data suggest that NF-κB activation by TWEAK is necessary for the induction of Mcl-1 in NSCLC.

**TWEAK-induced NSCLC cell survival is dependent on Mcl-1 expression**

We next sought to characterize the functional role of Mcl-1 in TWEAK-induced tumor cell survival. The protein expression of Mcl-1 was depleted by targeted siRNA constructs in both H1975 and H2073 cells (Fig. 3A and B, respectively). Cell survival was assessed by colony-formation assay. In both H1975 and H2073, exposure to ionizing radiation or cisplatin significantly reduced NSCLC cell survival (Fig. 3C–F). siRNA-mediated depletion of Mcl-1 significantly enhanced sensitivity to either cisplatin or radiation compared with control cells expressing nontargeting siRNA oligonucleotides. TWEAK pretreatment significantly attenuated the effects of either cisplatin or radiation, back to untreated surviving fractions. Depletion of Mcl-1 via siRNA oligonucleotides completely abrogated the protective effects observed with TWEAK pretreatment. However, depletion of Bcl-xL could not fully rescue the TWEAK-induced cell survival as seen with Mcl-1 depletion (Supplementary Fig. S5A and S5B). Thus, TWEAK exposure may protect NSCLC cells from DNA-damaging therapies such as radiation and cisplatin; and this protective phenotype appears to be dependent on Mcl-1 function.

To confirm the effects of TWEAK signaling and the role of Mcl-1 in NSCLC cell survival, we assessed apoptosis through the induction of cleaved-PARP in H1975 cells exposed to cisplatin and radiation. Figure 4 demonstrates that exposure to cisplatin (Fig. 4A) or radiation (Fig. 4B) induces protein expression of cleaved-PARP over time (lanes 5 and 9 compared to 1). Pretreatment with TWEAK completely abrogates the induction of cleaved PARP (lanes 6 and 10 compared to lanes 5 and 9). The depletion of Mcl-1...
through siRNA results in enhanced induction of cleaved-PARP compared with cisplatin or radiation alone, an enhanced sensitivity that was not affected by TWEAK exposure.

**Mcl-1 pharmacological inhibitor EU-5148 decreases NSCLC cell survival**

Although inhibitors of Bcl-2/Bcl-xL have been well described, specific inhibitors of Mcl-1 are now being investigated (26–28). We explored the use of a Mcl-1–specific pharmacologic inhibitor designated EU-5148 (Supplementary Fig. S1) as an antagonist of NSCLC cell survival. Figure 5A demonstrates that exposure to EU-5148 specifically disrupts the protein–protein interaction of Mcl-1 and Bak, while not affecting the interaction of Bcl-xL and Bak. H1975 cells were treated with EU-5148 in the presence or absence of TWEAK. Cells were immunoprecipitated with anti-Bak antibodies and immunoblotted for Mcl-1, Bcl-xL, and Bak. Exposure to EU-5148 suppressed the protein interaction between Mcl-1 and Bak with or without TWEAK exposure. Conversely, exposure to EU5148 had no effect on the protein interaction of Bcl-xL and Bak. To further show Mcl-1 specificity for EU-5148, we employed cell lines deficient of Bax and Bim (DHL10; ref. 18) or driven by Mcl-1 (Mcl-1 1780) or Bcl-2 (Bcl-2 1863). Figure 5B shows that cells driven by Mcl-1 are most sensitive to EU-5148 (EC50 = 3.26 μmol/L), while cells deficient for Bax/Bim were less sensitive to EU-5148 (EC50 = 21.31 μmol/L). Furthermore, an ELISA-based competitive displacement assay demonstrated that EU-5148 was approximately 3.5-fold more disruptive of a Mcl-1-Bim protein interaction compared to a Bcl-xL-Bim protein interaction (Supplementary Fig. S6).

In a panel of NSCLC cell lines, EU-5148 significantly diminishes cell viability 48 hours posttreatment compared with nontreated cells (Fig. 5C). Cell viability was reduced between 25%–87% across 13 NSCLC cell lines with 11 of the 13 lines showing >50% reduction in cell viability.

Finally, we sought to assess whether EU-5148 could suppress TWEAK-induced NSCLC cell survival. Exposure of H1975 cells to radiation significantly reduces cell survival, whereas exposure to the Mcl-1 inhibitor EU-5418 further enhances sensitivity to radiation (Fig. 6A). Pretreatment with TWEAK completely abrogates the reduction in cell survival induced by radiation exposure, but Mcl-1 inhibition restores radiation sensitivity, even with TWEAK exposure. Similar effects are observed with EU-5148 exposure in H1975 cells exposed to cisplatin and H2073 cells exposed to radiation or cisplatin (Supplementary Fig. S7). Although Mcl-1 inhibition abrogated TWEAK-induced cancer cell survival, exposure to ABT-737, a potent inhibitor of Bcl-2 and Bcl-xL, had a lesser effect on TWEAK-induced cell survival (Fig. 6B). Although ABT-737 did sensitize H1975 cells to radiation, the TWEAK-induced cell rescue was only minimally significant, suggesting a critical role for Mcl-1 in the TWEAK-induced cell survival effects in NSCLC.
Discussion

Prosurvival members of the Bcl-2 family are well-characterized antagonists of apoptotic signaling, mediating cell survival downstream of a variety of cytotoxic insults (29). Specifically, Mcl-1 plays an important prosurvival role in NSCLC by limiting cytotoxicity of chemo- or radiotherapy and TKI treatments (14), in addition to showing a significant role in evasion of apoptosis in a variety of solid tumors (17, 30). In this study, we demonstrated that Mcl-1 is regulated through the TWEAK–Fn14 signaling axis and is necessary to promote TWEAK-mediated NSCLC cell survival. Protein expression of Fn14 and Mcl-1 are significantly correlated in primary NSCLC tumors, and treatment with TWEAK induces expression of Mcl-1 through activation of NF-κB. Inhibition of Mcl-1 expression promotes chemoresistance and radiosensitivity and abrogates TWEAK-induced tumor cell survival. This work positions both the TWEAK–Fn14 pathway and Mcl-1 as potential therapeutic interventions targeting lung tumor evasion of apoptosis.

To date, the functional role of Fn14 in lung cancer remains poorly understood. We previously reported overexpression of Fn14 in primary NSCLC (5) and showed correlation of Fn14 with activated EGFR in NSCLC and a positive association with cell motility and metastasis. Activation of Fn14 signaling through TWEAK or receptor overexpression leads to enhanced tumor cell migration/invasion, angiogenesis, and tumor cell survival (4). In glioblastoma tumor cells, TWEAK stimulation promotes cell survival through Akt2 (7) and the NF-κB–dependent upregulation of prosurvival Bcl-2 family members (8). Our data support a TWEAK–Fn14 induced NSCLC cell survival by induction of prosurvival Bcl-2 family member, specifically Mcl-1, in a NF-κB–dependent manner. TWEAK exposure induced both protein and mRNA expression of Mcl-1 and...
Mcl-1 and TWEAK in NSCLC survival

Bcl-xL in NSCLC cell lines. We further demonstrated that protein and gene expressions of Fn14 and Mcl-1 were significantly correlated in primary lung tumor specimens. Thus, the TWEAK–Fn14 signaling axis and the prosurvival Mcl-1 gene may cooperate in NSCLC cell survival and represent potential therapeutic targets.

Overexpression of prosurvival Bcl-2 family members such as Mcl-1 is a well-characterized event in tumor progression, encouraging cell survival (29). Here, we demonstrate a role for Mcl-1 in NSCLC tumor survival as a critical downstream component of TWEAK/Fn14 signaling. The depletion of Mcl-1 through siRNA or pharmacologic inhibitor (EU-5148) was sufficient to abrogate the protective effects conferred on lung tumor cells by TWEAK/Fn14 signaling, whereas inhibition of Bcl-2 and Bcl-xL had a lesser effect. Despite similarities in transcriptional regulation of Mcl-1 and other prosurvival members of the Bcl-2 family, an increasing body of evidence indicates multiple tumor types have overdependence on Mcl-1 alone to negate apoptotic signaling (31). For example, IHC staining of Mcl-1 proved to be a better prognostic indicator of ovarian carcinoma progression in a group of patient biopsies compared to Bcl-2 or Bcl-xL (32).

Inhibition of Mcl-1 in multiple myeloma by antisense oligonucleotides induced apoptosis, where inhibition of Bcl-2 or Bcl-xL could not mimic this effect (33). Interestingly, resistance to inhibitors of Bcl-2 and Bcl-xL can be achieved through Mcl-1 expression (34). These data suggest nonoverlapping roles for the Bcl-2 prosurvival family members in cancer contexts, and position Mcl-1 as a critical regulator of tumor cell survival.

The complex molecular interactions between prosurvival and prodeath members of the Bcl-2 family are known to affect tumor survival/apoptosis. A shift in the interactions of prosurvival Bcl-2 members with prodeath members in response to survival stimuli is only beginning to be understood. Lopez and colleagues showed that DNA damage-induced apoptosis only occurred when Bcl-xL and Mcl-1 were inhibited (35). DNA damage induced a Noxa-Bcl-xL interaction that prompted cytochrome c release only when Mcl-1 was degraded. Bcl-xL and Mcl-1 have been shown to be inhibitors of apoptosis induced by TNF-related apoptosis-inducing ligand (TRAIL), with Noxa playing a critical role in sequestering Bcl-xL and Mcl-1 (36). ER stress or proteasome inhibition could induce a switch from Noxa-Mcl-1 to Noxa-Bcl-xL, most likely through degradation of Mcl-1. Here, we demonstrated that EU-5148 disrupts the protein interaction of Mcl-1 and Bak without affecting the Bcl-xL-Bak protein interaction. We further showed that Mcl-1 inhibition fully abrogated TWEAK-induced cell survival, while Bcl-xL depletion or Bcl-2/Bcl-xL inhibition only modestly affected TWEAK-induced cell survival. Other TNF ligands have shown preference towards Bcl-xL for cell survival. The suppression of Bcl-xL, but not Mcl-1 or Bcl-2, rendered cells sensitive to TNFα-induced apoptosis (37). These data support a complex relationship between Bcl-2 family interactions downstream of cell survival and apoptotic stimuli.

Inhibition of Mcl-1 has potential for clinical impact in NSCLC and a variety of other tumor types, although specific pharmacologic inhibition of Mcl-1 has been elusive. To date several pan-Bcl-2 inhibitors have been developed, such as ABT-737, and inhibit tumor growth and survival across a spectrum of tumor types (29, 38). Though progressing through clinical trials, ABT-737 does not inhibit Mcl-1 and expression of Mcl-1 leads to resistance to pan-Bcl-2 inhibitors (34). Obatoclax and sabutoclax are pan-Bcl-2 inhibitors that do target Mcl-1 and have shown inhibitory effects in a number of tumor cell lines (27, 39). Depletion or degradation of Mcl-1 as a consequence of targeted inhibitors has been recently reviewed (27). Proteasome inhibitors result in Mcl-1 degradation (40), while mTOR inhibition leads to Mcl-1 suppression in mutant kRas-driven colorectal cancer (41).

There have been reports more recently of compounds that are Mcl-1–specific inhibitors. UMI-77 is a novel small-molecule inhibitor of Mcl-1, which showed antitumor activity against pancreatic cancer through disruption of Mcl-1-Bax and Mcl-1-Bak interactions (26). A recent article described a number of hydroxyquinoline-derived compounds with specific affinity for Mcl-1 over Bcl-xL (28).

Here, we show that EU-5148 specifically disrupts the Mcl-1-Bak protein interaction while not affecting the Bcl-xL-Bak interaction by immunoprecipitation, and demonstrate increased cell killing in cells driven by Mcl-1 compared with cells driven by Bcl-2 or cells deficient in Bax and Bim. EU-5148 decreased cell viability across a panel of NSCLC cell lines. As shown with specific siRNA depletion of Mcl-1,
EU-5148 abrogated TWEAK-induced radio- or chemoresistance in NSCLC cells, an inhibition not observed with ABT-737 exposure. Thus, specific inhibitors of Mcl-1 may be more effective in reducing tumor cell survival in contexts such as those involving TWEAK/Fn14 activation. Future work will characterize the use of EU-5148 in an in vivo setting both as a monotherapy and in combination with standard of care cytotoxic agents.

Mcl-1 may also play a critical role in progenitor/stem cell regulation in normal and tumor cells. A review by Perciavalle and Opferman highlighted the necessity of Mcl-1 for early embryonic development and the survival of multiple cell lineages (30). Tumor progenitor cells are associated with tumor self-renewal and therapeutic resistance (42, 43). Singh and colleagues recently demonstrated that NSCLC stem-like cells showed higher Mcl-1 expression compared with the main population of cells; and inhibition with obatoclax prevented self-renewal of resistant NSCLC cells (44). Overexpression of Mcl-1 in transgenic mice lead to lymphoma development with a progenitor cell phenotype, as well as lymphoid and myeloid cells highly resistant to a variety of cytotoxic agents (45). Future studies will be aimed at understanding the effect that Mcl-1-specific inhibitors (such as EU-5148) have on tumor progenitor cells, as well as the potential for pathways that induce Mcl-1 (such as TWEAK/Fn14) to affect progenitor cell populations.

In summary, our study showed that the TWEAK–Fn14 signaling axis promotes survival in NSCLC, via NF-xB-dependent induction of Mcl-1. Inhibition of Mcl-1 function enhanced chemotherapy- and radiosensitivity in NSCLC cells. This work positions the TWEAK–Fn14 signaling axis and Mcl-1 expression as important features in NSCLC cell survival and warrants further investigation into therapeutic avenues inhibiting these pathways towards reducing lung cancer mortality.

Disclosure of Potential Conflicts of Interest
M.H. Cardone is employed with and has ownership interest (including patents) in Eutropics Pharmaceuticals. R.J. Lena is a research associate at Eutropics Pharmaceuticals. W.E. Pierceall is Director of Oncology at Eutropics Pharmaceuticals. No potential conflicts of interest were disclosed by the other authors.

Authors’ Contributions
Conception and design: T.G. Whitsett, M.H. Cardone, N.L. Tran
Development of methodology: I.T. Mathews, W.E. Pierceall
Acquisition of data (provided animals, acquired and managed patients, provided facilities, etc.): I.T. Mathews, R.J. Lena, W.E. Pierceall, M. Bittner, J. Lobello, G.J. Weiss
Analysis and interpretation of data (e.g., statistical analysis, biostatistics, computational analysis): T.G. Whitsett, W.E. Pierceall, M. Bittner, C. Sima, J. Lobello, N.L. Tran
Writing, review, and/or revision of the manuscript: T.G. Whitsett, I.T. Mathews, M. Bittner, C. Sima, G.J. Weiss, N.L. Tran
Study supervision: T.G. Whitsett, J. Lobello, N.L. Tran

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