Low Expression of the E3 Ubiquitin Ligase CBL Confers Chemoresistance in Human Pancreatic Cancer and Is Targeted by Epidermal Growth Factor Receptor Inhibition

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Abstract

Purpose: Expression of CBL, an ubiquitin ligase, is decreased in 60% of human pancreatic ductal adenocarcinomas (PDAC) and is associated with shorter overall survival. We sought to determine how low CBL directly contributes to clinically more aggressive PDAC.

Experimental Design: Human PDACs were stained for CBL, pEGFR, and EGFR. CBL-low was modeled in PDAC cells (Panc-1, L3.6pl, and AsPC-1) via transient transfection (siRNA) or stable knockdown (shRNA). Cell viability and apoptosis were measured by MTT assays and FACS. Immunoblot and a phospho-receptor tyrosine kinase (pRTK) array were used to probe signal transduction. NOD-scid-IL2Rγcnull mice were subcutaneously implanted with PDAC or PDACCBL-low cells on opposite flanks and treated with gemcitabine ± erlotinib for ≥2 weeks.

Results: There was an inverse correlation between CBL and pEGFR protein expression in 12 of 15 tumors. CBL knockdown increased PDAC resistance to gemcitabine and 5-fluorouracil (5-FU) by upregulating pEGFR (Y1068), pERK, and pAKT. A pRTK array of PDACCBL-low cells revealed additional activated tyrosine kinases but all to a much lower magnitude than EGFR. Increased chemoresistance from low CBL was abrogated by the EGFR inhibitor erlotinib both in vitro and in vivo. Erlotinib + gemcitabine–treated PDACCBL-low cells exhibited greater apoptosis by cleaved PARP, caspase-3, and Annexin V/PI.

Conclusions: Low CBL causes chemoresistance in PDAC via stress-induced EGFR activation that can be effectively abrogated by EGFR inhibition. These results suggest that dysregulation of ubiquitination is a key mechanism of EGFR hyperactivation in PDAC and that low CBL may define PDAC tumors likely to respond to erlotinib treatment. Clin Cancer Res; 21(1): 157–65. ©2014 AACR.

Introduction

Over the past decade, the number of people who die annually from pancreatic ductal adenocarcinoma (PDAC) has been slowly increasing in the United States. This trend is in strike contrast to the decreasing death rates for other major cancers (1). If the current incidence and mortality continue, PDAC will become the second leading cause of cancer-related deaths in the United States by 2020 (2). A main contributor to this poor prognosis is PDAC’s notorious unresponsiveness to cytotoxic and targeted therapies. Identification of distinct patient subgroups, by well-defined biomarkers, who are likely to respond to specific therapies has been less successful in PDAC than other solid tumors due to the presence of only a few high-prevalence, unifying molecular changes (3, 4). However, there are two notable examples that reveal this strategy may still work to improve treatment responses. First, three distinct molecular subtypes of PDAC were identified, only one of which was responsive to gemcitabine treatment (5). Second, from the phase III clinical trial comparing gemcitabine plus the EGFR inhibitor erlotinib to gemcitabine alone, subgroup analysis identified those who developed a severe skin rash achieved nearly double the overall survival with combination therapy than those who did not (6). In light of these findings, there has been renewed interest in the identification of biomarkers to identify PDACs likely to respond to these established therapies. The identification and validation of such biomarkers is an unmet clinical need in PDAC (7).

The CBL (named after Casitas B-lineage lymphoma) family of proteins is composed of c-CBL, CBL-b, and CBL-c (hereafter collectively referred to as CBL). c-CBL and CBL-b are ubiquitously expressed and function as E3 ubiquitin-protein ligases and multifunctional adaptor proteins involved in regulation of signal transduction, lymphocyte signaling, and the actin cytoskeleton (8, 9). CBL-c is a truncated form that is expressed predominantly in epithelial cells, its in vivo functions are poorly understood (10).
The E3 ligase domain of CBL mediates the formation of a covalent bond between ubiquitin and protein substrates leading to their trafficking to the endosome for lysosomal degradation. Homozygous deletions or missense mutations in regions affecting the ubiquitin-related function of CBL are commonly found in myeloid neoplasms and are oncogenic. CBL’s ubiquitin targets are commonly tyrosine kinases (TK), including epidermal growth factor receptor (EGFR; 8). In a survival-based whole-genome multidimensional array analysis of 25 human PDACs with high tumor cell content (and low stromal volume), we have reported zygous deletions or missense mutations in regions affecting the levels (deincreased, undergoes CBL-mediated ubiquitination, and is targeted for destruction in lysosomes. EGFR has been previously shown to undergo endoplasmic reticulum stress by binding to extracellular protein ligands that leads to autophosphorylation of the intracellular domain, homo- or heterodimerization with other ERBB family members, and downstream signaling predominantly through the MAPK and AKT pathways (12). To maintain physiologic signaling levels, ligand-activated EGFR is internalized, undergoes CBL-mediated ubiquitination, and is targeted for destruction in lysosomes. EGFR is a cell-surface receptor that is activated by binding to extracellular protein ligands that leads to autophosphorylation of the intracellular domain, homo- or heterodimerization with other ERBB family members, and downstream signaling predominantly through the MAPK and AKT pathways (12). To maintain physiologic signaling levels, ligand-activated EGFR is internalized, undergoes CBL-mediated ubiquitination, and is targeted for destruction in lysosomes. EGFR dysregulation in PDAC is not due to genome level changes, as it is neither amplified (as seen in breast and gastric cancers) nor mutated (as seen with lung cancer). Rather, recent work in PDAC has confirmed previous findings in other solid tumors that EGFR is (hyper-)activated by autocrine ligand production in response to cytokine therapy (16). To our knowledge, CBL has not been previously explored as a possible mechanism of EGFR dysregulation leading to cell autonomous chemoresistance.

The objective of this study was to determine the mechanism whereby low CBL might directly contribute to worse patient survival. We hypothesized that CBL functions as an important negative feedback mechanism to EGFR signaling in PDAC that when suppressed results in enhanced tumor growth and chemoresistance. We found that erlotinib abrogates the chemoresistance afforded by low CBL in vitro and in vivo.

Materials and Methods

Patients and samples

This study was approved by the University of California Los Angeles (UCLA; Los Angeles, CA) Institutional Review Board and the UCLA Office of Animal Research Oversight.

Immunohistochemistry

Archival formalin-fixed, paraffin-embedded human tumor samples were incubated at 60°C for 1 hour, deparaffinized in xylene, and rehydrated with graded alcohol washes. Antigen retrieval was performed by heating in 0.1 mol/L sodium citrate buffer at 100°C for 15 minutes (CBL), or in Tris–EDTA buffer at 95°C for 30 minutes (pEGFR, EGFR), followed by quenching of endogenous peroxidase with 3% hydrogen peroxide. After blocking for 1 hour with 5% donkey serum in phosphate-buffered saline (PBS) at room temperature, primary antibody was added to serial sections, pEGFR at 1:100, EGFR at 1:100 (Cell Signaling Technology), and CBL at 1:50 (Abcam) and incubated overnight at 4°C. A 1:250 biotin-conjugated anti-rabbit secondary antibody (Jackson ImmunoResearch Laboratories, Inc.) was subsequently added and developed using the Elite Vectastain ABC Kit (Vector Laboratories).

Cell culture

Human pancreatic cancer cell lines, Panc-1 and AsPC-1, cells were obtained in 2005 from the American Type Culture Collection (ATCC). L3.6pl cells were obtained in 2010 from Hong Wu (UCLA). Since receipt, the cells have not been subsequently authenticated. Panc-1 and L3.6pl cells were maintained at low passage in DMEM (Gibco, Life Technologies) and CBL at 1:50 (Abcam) and incubated overnight at 4°C. A 1:250 biotin-conjugated anti-rabbit secondary antibody (Jackson ImmunoResearch Laboratories, Inc.) was subsequently added and developed using the Elite Vectastain ABC Kit (Vector Laboratories).

siRNA knockdown of CBL

Experimentally validated CBL siRNA was purchased from Qiagen. Using the RNAi Human/Mouse Starter Kit (Qiagen), optimization of the fast-forward transfection protocol was performed in each cell type. For each experiment, 3 × 10⁴ cells in 6-well (Western) or 2 × 10⁵ cells in 96-well (MTT assay) were plated from a single-cell suspension, then 5 nmol/L CBL or 5 nmol/L AllStars Negative Control (neg con) siRNA with HiPerfect Transfection Reagent was added. After overnight incubation, the transfection media was changed to fresh media and transfection efficiency was qualitatively assessed by fluorescent imaging (CBL; siRNA-3′-FAM; AllStars Negative Control siRNA-Alexa Fluor 555). Cells were then incubated for 24 hours at optimal growth conditions, before start of assays involving serum-deprivation, chemotherapy.

Immunoblots

To directly probe modulation of EGFR activation by EGF ligand with or without CBL knockdown, Panc-1 cells were first...
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were washed with PBS at 4°C, lysed with 2% SDS buffer containing phosphatase inhibitors and mechanical scraping, collected, and kept on ice. Data shown are for the 20-minute time point. Lysates were then sonicated for 5 seconds and Bradford assays were performed to measure protein concentrations for each sample. Thirty-five micrograms of protein was then loaded into each well of a 10% acrylamide gel. Samples were then resolved by SDS-PAGE and transferred to a polyvinylidenedifluoride (PVDF) membrane. Membranes were first blocked with 5% bovine serum albumin (BSA) in Tris-buffered saline and then incubated overnight at 4°C in 5% BSA in TBS containing primary antibody at 1:1,000 dilution unless otherwise noted: CBL, pAKT at 1:500, AKT, pEGFR (Y1068), pEGFR (Y1045), EGFR at 1:2,000, pERK, ERK (Cell Signaling Technology). β-Actin at 1:5,000 (Sigma) was used to normalize sample loading. After washing, anti-mouse at 1:10,000 or anti-rabbit at 1:5,000 HRP-conjugated secondary antibody (The Jackson Laboratory) in 5% milk was incubated for 1 hour at room temperature, again washed three times, before addition of Amersham ECL prime (GE Healthcare Life Sciences) and chemiluminescent imaging on a ChemiDoc XRS+ (Bio-Rad).

After siRNA treatment and with cells in the log phase of proliferation, we assessed CBL modulation of EGFR activation in the presence of cytotoxic chemotherapy agents gemcitabine (Gem; Sagent Pharmaceuticals) and 5-fluorouracil (PFU; APP Pharmaceuticals). These were added to Panc-1 and L3.6pl cell lines at their IC50 values [Panc-1, 1 and 10 μmol/L (17, 18); L3.6pl, 25 mmol/L and 1 μmol/L (19, 20), respectively] in serum-free media (SFM). After 48 hours in SFM ± chemotherapy, lysates were collected and analyzed via Western blot analysis as above. To broaden the scope from EGFR to other receptor tyrosine kinase (RTK) pathways, parallel samples were analyzed using the Proteome Profiler Human Phospho-RTK Array Kit (R&D Systems, Inc.). Blots of combination therapy, Gem/5-FU ± erlotinib 10 μmol/L (OSI Pharmaceuticals) were also performed.

Apoptosis was assessed via Western blot analysis of PARP and caspase-3 and their cleaved products (Cell Signaling Technology).

MTT assays

Cells were plated at equal density (2 x 104) in 96-well plates, treated with siRNA, then Gem/5-FU ± erlotinib were added in SFM at the concentrations above. At 24, 48, and 72 hours from the start of chemotherapy treatment, medium was aspirated from each well, and 12 mmol/L MTT (Life Technologies) was added in fresh phenol-red–free media and incubated for 4 hours at 37°C. Cells were then lysed in 10% SDS−0.01 mol/L HCl, and after 12 hours, the quantity of dissolved formazan was measured via automated plate reader at 570 mmol/L. All samples and controls were analyzed in triplicate, and each experiment was repeated twice. Shown are data from one representative experiment.

FACS

Using the Annexin V-FITC Apoptosis Detection Kit (BD Biosciences), cells were grown in 6-well plates, transfected with siRNA, then 48 hours in chemotherapy as above. Cells and media were collected, washed, and stained with FITC-Annexin V and PI in binding buffer along with appropriate controls. Total number of Annexin V- and PI-positive cells were counted using a FACScan flow cytometer (Becton Dickinson) and graphed as percentage of total cell number (FlowJo 9.3.2; TreeStar, Inc.). Error bars are the SEM for three independent experiments.

shRNA knockdown of CBL

Lentiviruses were produced by transfecting HEK293T packaging cells in polyethyleneimine (Polysciences) with a 3-plasmid system. Briefly, DNA for transfections was prepared by mixing PCKM-SS8.9, pCMV-VSVG with pLKO.1 plasmid, either as an empty vector or containing one of six unique sequences from the TRC library predicted to knockdown CBL (Open Biosystems, Thermo Scientific). Lentiviral supernatants were harvested at 24 hours after transfection, filtered, and frozen at −80°C for long-term storage.

L3.6pl and Panc-1 cells were transduced with lentivirus in the presence of 8 μg/mL polybrene (Sigma). Cells were incubated for 24 hours, and the media was changed to remove virus particles. Stable knockdown was achieved by 7-day selection in puromycin 1 μg/mL. After experimental validation of ~75% knockdown efficiency by qRT-PCR, the mature antisense sequence 5′-TACCTTATAATTTCACATCGGCC-3′ was chosen for in vivo studies.

qRT-PCR

Using the Qiagen system, total RNA was extracted from cells (RneNeasy Mini Kit), reverse transcribed (miScript II Reverse Transcription Kit) and then qRT-PCR was performed (miScript SYBR Green PCR Kit) with primers for CBL and RPL13A as a housekeeping control. The CBL primer sequences were referenced from the RTPrimerDB (21). RPL13A primers were designed with forward sequence 5′-CATCTGGCTAATAAGGTACTG-3′ and reverse 5′-GACAGACCTTGGAGGCCAGCC-5′. Primers were obtained from Integrated DNA Technologies.

Preclinical trial in NSG mice

After selection in puromycin, two transformed L3.6pl and Panc-1 cell lines, pLKO.1-CBL shRNA and pLKO.1-meg conv shRNA were expanded by serial passaging. After three passages, they were trypsinized, collected, and counted. pLKO.1-CBL shRNA cells (2 x 107) were injected into the right flank and 2 x 105 pLKO.1-meg conv into the left flank of NOD-scid-IL2Rγnull mice (n = 18) and randomly assigned to one of three groups. By the fourth day after injection, all mice had developed palpable tumors. At 7 days after injection, treatment began with gemicitabine 50 mg/kg administered by subcutaneous injection twice weekly (n = 6). A second treatment group received both gemcitabine + erlotinib 25 mg/kg by oral gavage daily (n = 6). Control animals received injections and oral gavage of PBS (n = 6). Gemcitabine-only–treated animals also received oral gavage PBS. Tumors were measured with digital calipers for length, width, and height every 3 to 4 days and volume estimated (22). At 22 days in the L3.6pl xenografts, several control animals had at least one tumor measuring ≥15 mm and were euthanized per protocol. At 28 days, L3.6pl gemcitabine-treated animals had met this same endpoint and this experiment was concluded. The Panc-1 xenografts were slower growing, and animals were survived out an additional 2 weeks until meeting study endpoints. Necropsies were performed and tumors were analyzed ex vivo for weight, volume, and
immunoblotting to verify stable CBL knockdown. To validate our findings, the entire experiment was then repeated, with similar trends in tumor growth characteristics and observed group differences. Shown are the data from the first experiment.

Statistical analysis
Statistical analysis was performed with SPSS 20.0.0.1 (IBM). The relationship between categorical variables was examined using the Pearson \(\chi^2\) test and difference between means were evaluated by the Student t test or one-way ANOVA as appropriate with significance defined as \(P < 0.05\). Image Lab software (Bio-Rad) was used for densitometry analysis of Western blot analyses. For ease of comparison, reported values were first normalized to \(\beta\)-actin as a loading control then multiplied by a constant to reach the lowest whole integer. Unless otherwise stated, error bars \(\pm\) SD.

Results
CBL expression in human PDAC is inversely correlated with EGFR expression and activation
Our previous in silico and in vitro published findings (11) of 67 human PDACs revealed that CBL miRNA expression is decreased in 60% of tumors and significantly correlated with patient survival (i.e., lower CBL was associated with shorter survival). EGFR is one of the most commonly reported CBL targets and is upregulated in at least 60% of human PDAC (13). Therefore, we hypothesized that low CBL leads to higher EGFR expression and activation in human PDAC. Staining of primary human PDAC tissues for CBL, pEGFR, and EGFR revealed an inverse correlation between CBL and pEGFR in 12 of 15 (80%; \(P = 0.01\)) tumors, and CBL and EGFR expression in 11 of 15 (73%; \(P = 0.03\)). Figure 1A shows representative images of strongly positive or negative CBL expression and its inverse correlation with pEGFR and EGFR in tumor cells. Notably, CBL, EGFR, and p-EGFR staining were low in the stroma.

To further confirm CBL regulation of EGFR expression and activation, Panc-1 PDAC cells with or without siRNA-induced low CBL (hereafter referred to as Panc-1CBL-low or Panc-1 cells, respectively) were cultured in the presence or absence of EGFR ligand, EGF. In the absence of ligand, low CBL conferred only a mild increase in activation of EGFR at its autophosphorylation (Tyrosine 1068) site (Fig. 1B, columns 1 vs. 3). However, in the presence of ligand, low CBL significantly enhanced EGFR activation (Fig. 1B and C, columns 2 vs. 4). Moreover, EGF treatment of Panc-1CBL-low cells also resulted in increased activation of pERK and pAKT (Fig. 1B and C, columns 2 vs. 4); these downstream mediators were not activated in Panc-1CBL-low cells in the absence of exogenous ligand. These results suggest that low CBL increased ligand-dependent EGFR activation, as well as downstream MAPK and AKT signaling, which may lead to improved cell proliferation and survival.

Low CBL mediates chemoresistance through enhanced EGFR autoactivation
Considering that low CBL increased EGFR-dependent AKT and MAPK signaling, we next sought to determine the functional significance of low CBL on PDAC cells in culture. CBL siRNA treatment of Panc-1, L3.6pl, and AsPC-1 PDAC cell lines did not yield increased viability (Fig. 2A and Supplementary Fig. S1), soft agar growth, or invasion either alone or in the presence of exogenous EGF ligand (data not shown). Given that all of the patients in the previous survival analysis received adjuvant chemotherapy following surgical resection (11), we next tested the...
functional consequences of low CBL in the presence of chemo-
therapy. Panc-1CBL-low and L3.6plCBL-low had signi-
ificantly greater viability than isogenic cells with intact CBL expression when
treated with gemcitabine or 5-FU, two chemotherapeutic drugs
commonly used for PDAC (Fig. 2A). Phosphoproteomic com-
parison of gemcitabine- and 5-FU–treated Panc-1 cells reveals that EGFR is autoactivated at its canonical autophosphorylation site (Y1068) with
corresponding activation of downstream mediators Erk and Akt (columns 3 and 5 vs. 1). CBL knockdown further enhances autoactivation of EGFR at
Y1068 as well as the docking site for CBL binding Y1045, (columns 3 vs. 4 and 5 vs. 6). Relative densitometry values using β-actin as a loading control are
reported below each band. C, a human pRTK immunoblot array of L3.6pl cells in gemcitabine (25 nmol/L) reveals that pEGFR is highly expressed and
increased >2-fold with CBL knockdown.

CBL also downregulates many additional, non-EGFR, TKs
implicated in pancreatic tumorigenesis such as SRC (11), IGF-
1R (23), platelet derived growth factor receptor (PDGFR; ref. 24),
c-MET (25), and RON (26). The specificity of low CBL for EGFR
activation was evaluated using a phospho-TK screen (Fig. 2C and
Supplementary Fig. S3). Gemcitabine-treated L3.6plCBL-low cells
had >2× activation of EGFR than L3.6pl cells. Although at a much
lower magnitude (membrane exposure for 5 minutes), ErbB2, -3,
and -4, hepatocyte growth factor receptor (HGFGR), and PDGFR
had significantly greater activation in cells with low CBL. These
findings suggest that low CBL expression associated with shorter
survival in human PDAC may be due to chemoresistance resulting
from enhanced autoactivation of EGFR or other RTKs.

Erlotinib targets the CBL-mediated chemoresistance mechanism

To further determine whether EGFR autoactivation was the
principal mechanism responsible for chemoresistance in PDACs...
with low CBL, EGFR activation was blocked using the EGFR inhibitor erlotinib in vitro. Figure 3A reveals that the addition of erlotinib abrogates the viability advantage of L3.6plCBL-low cells as compared with L3.6pl cells in the presence of gemcitabine or 5-FU. Biochemically, erlotinib effectively inhibits EGFR autoactivation and the downstream mediators pAKT and pERK (Fig. 3B and C). Finally, erlotinib also increased gemcitabine-induced apoptosis in L3.6plCBL-low cells as evidenced by cleaved PARP and caspase-3 immunoblots (Fig. 3B) and Annexin V/PI flow cytometry (Fig. 3D). These results suggest that erlotinib abrogates the chemoresistance afforded by low CBL, implicating EGFR as a key functional target of CBL in human PDAC.

**EGFR inhibition abrogates chemoresistance mediated by low CBL in vivo**

Expanding on the cell culture results, we next tested the synergy between erlotinib and gemcitabine on growth of PDAC<sub>CBL-low</sub> tumors in vivo. Lentiviral-mediated transduction of L3.6pl and Panc-1 PDAC cells with CBL shRNA yielded low CBL expression (Supplementary Fig. S4). These cell lines treated with empty vector (PDAC<sup>CBL-shRNA</sup>) or CBL shRNA (PDAC<sup>CBL-shRNA</sup>) were subcutaneously implanted into the opposite flanks of NOD-scid-IL2R<sup>gnull</sup> mice and left untreated, or treated with gemcitabine <sup>+</sup> erlotinib. As with the cell culture findings, CBL-low did not result in larger tumors than the negative controls in untreated mice (Fig. 4A and B). However, CBL-low did confer chemoresistance, as PDAC<sup>CBL-shRNA</sup> tumors were approximately twice the size as PDAC<sup>CBL-shRNA</sup> tumors in mice treated with gemcitabine. Strikingly, when CBL-low tumors were treated with combination erlotinib and gemcitabine, chemosensitivity to gemcitabine was completely restored as there was no significant difference between PDAC<sup>CBL-shRNA</sup> and PDAC<sup>CBL-shRNA</sup> tumor growth (Fig. 4A and B and Supplementary Fig. S5). Analysis of tumor explants via Western blot analyses confirmed that low CBL expression was maintained (Supplementary Fig. S4). In summary, the combined treatment of gemcitabine and erlotinib abrogates the chemoresistance in isogenic PDAC cell lines engineered with low CBL in vivo.

**Discussion**

The relative incidence of cancer-related deaths due to PDAC, as compared with other malignancies, is increasing in the United States (27). This disturbing trend can be partly attributed to PDAC’s resistance to treatment and particularly aggressive tumor biology (3, 4). To gain a better understanding of the rapid clinical progression, recent studies have focused not only on determining the genomic and transcriptomic makeup of this tumor but on identifying the specific changes that are associated with patient
Tumor cell intrinsic autoactivation of EGFR after treatment with cytotoxic chemotherapy has been previously shown to occur in many solid malignancies. Recently, in the context of PDAC using transgenic mice, Miyabayashi and colleagues (16) determined that EGFR activation was due to gemicitabine-induced cellular stress that led to activation of MAPK, leading to release of EGFR ligands. These findings are further supported by previous work revealing that the ligand-releasing enzyme, ADAM17/TACE, is expressed on the surface of 100% of human PDAC tissues and cell lines (30). Likewise, colon cancer cells treated with 5-FU in culture increase ADAM17 expression and release of EGFR-activating ligands: TGFα, amphiregulin, and heregulin (31). Interestingly, EGFR autoactivation may not be a generalized response to all cytotoxic chemotherapies, as only a subset of cancer cells treated with oxaliplatin developed EGFR activation (32). Our results reveal that EGFR is activated with both gemicitabine and 5-FU, the two most commonly used agents in PDAC.

CBL deletions and missense mutations are prevalent in myeloid malignancies (33). Functional studies of specific mutations reveal that CBL has both oncogenic and tumor-suppressor functions. The E3 ligase domain regulates RTK internalization through ubiquitination; mutations in this region are generally oncogenic. In contrast, the ring finger domain stabilizes the FAK (RTK)—SRC—actin cytoskeleton promoting cellular motility and AKT signaling, therefore mutations in this region are generally suppressive (8). Furthermore, oncogenic mutations are homozygous in all cases of CML; loss of the wild-type suppressive allele is required for transformation in cell culture and in vivo (34).

The net consequence of specific CBL mutations or loss of CBL expression is less defined in solid malignancies than for CML. This uncertainty is further fueled by the paradoxical finding that CBL mutations outside of the E3 ligase region yielded increased cellular viability and motility in lung cancer cells in culture (35). However, the functional significance of interrupting CBL-dependant processes on solid tumor progression has been implicated, as the addition of a proteasome inhibitor decreased gemcitabine-induced cell death in head and neck cancer cells (36). In the context of PDAC development, E3 ligases, of which CBL is a member, contain oncogenic mutations in a small subset of pancreatic cystic neoplasms (37). Our previous results identified that low CBL expression is common in human PDAC, as 60% of human tumors had low levels on qRT-PCR (11). Taken together, our previous study (11) and current results reveal that low CBL is oncogenic in PDAC. We found that patients with lower CBL expression have shorter overall survival. Loss of the RTK downregulating E3 ligase function had greater functional significance than loss of adaptor function, as chemoresistance afforded by low CBL was abrogated by EGFR inhibition with erlotinib.

The mechanism underlying low CBL expression in PDAC has also not been identified. Our previous study (11) revealed that CBL mRNA expression was both decreased in 60% of patients and prognostically significant. Genomic deletions of the CBL locus were not present in the in silico arrayed tumors. Previous PDAC sequencing studies have not identified frequent CBL mutations (38). Taken together, these findings implicate an epigenetic or posttranscriptional process as one potential mechanism regulating CBL expression. microRNA 125a-3p was suggested (but not validated) in our previous study, as it was (i) predicted by sequence to bind CBL, (ii) anticorrelated with CBL expression across tumors, and (iii) prognostically significant. However, CBL...
protein expression was not examined in these 67 human PDACs, leaving open the possibility that regulation may also be occurring on the protein level.

Importantly, our current study revealed an inverse correlation with CBL expression and EGFR activation (pEGFR) in human PDACs. There are numerous proteins that have been implicated in PDAC tumorigenesis and previously shown to modulate CBL expression: SRC (11), c-MET (25), and PTEN (39). SRC activation, which was also a prognostically significant finding in our previous study, induces CBL destruction and enables EGFR to evade destruction (40). c-MET activation can also yield low CBL (41). PTEN loss destabilizes CBL–EGFR–ubiquitin ligase complexes, yielding increased EGFR activity in cancer cell lines (42).

Taken together, these candidate molecular and protein-level mechanisms of low CBL, previously implicated in PDAC tumorigenesis, further suggest that CBL may be an important node involved in PDAC progression. Future studies should be designed to identify the mechanisms involved in loss of CBL function in PDAC.

Although oncologists have become skeptical about the efficacy of EGFR inhibition in PDAC, we believe that it may still be an effective treatment approach. A close analysis of the phase III trial identifies that while the overall improvement in survival was minimal for all patients (6.37 vs. 5.95 months; P = 0.03), the subgroup who developed grade 2 skin rashes (compared with those who did not develop skin changes) derived among the best clinical benefit of all combination treatments that have been reported for this disease (median survival 10.5 vs. 5.3 months; P < 0.001; refs. 6, 43, 44). These observations shed hope on the efficacy of this drug for PDAC.

Our findings that erlotinib abrogates chemotherapy resistance associated with low CBL suggest that CBL may be a sensitive pretreatment negative predictive biomarker for erlotinib response. However, the specificity of CBL for erlotinib response may be limited by the diverse CBL target proteins that include other TKs and non-TK targets (8). This concern is further fueled by our phospho-TK array findings that identified enhanced activation of proteins in CBL-low cells in addition to EGFR. This concern is further fueled by our phospho-TK array findings that identified enhanced activation of proteins in CBL-low cells in addition to EGFR dysregulation and (ii) begin to de

Conclusions

In conclusion, our findings reveal that low CBL increases chemotherapy stress-induced EGFR activation in human PDAC, resulting in treatment resistance. Dual treatment with gemcitabine or 5-FU and erlotinib abrogated the chemoresistance of isogenic PDAC cells engineered with low CBL in cell culture and in vivo. These results are clinically significant for PDAC, as they (i) identify the importance of the lysosomal destruction process as a mechanism for EGFR dysregulation and (ii) begin to define low CBL expression as a predictive biomarker of response to the previously FDA-approved EGFR inhibitor, erlotinib.

Disclosure of Potential Conflicts of Interest

No potential conflicts of interest were disclosed.

Authors’ Contributions

Conception and design: B.E. Kadera, T.R. Donahue


Acquisition of data (provided animals, acquired and managed patients, provided facilities, etc.): B.E. Kadera, P.A. Toste, N. Wu, L. Li, A.H. Nguyen, D.W. Dawson, T.R. Donahue

Analysis and interpretation of data (e.g., statistical analysis, biostatistics, computational analysis): B.E. Kadera, P.A. Toste, N. Wu, L. Li, A.H. Nguyen, D.W. Dawson, T.R. Donahue

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Study supervision: T.R. Donahue

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References


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Epidermal Growth Factor Receptor Inhibition

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