β-Catenin Contributes to Lung Tumor Development Induced by EGFR Mutations

Sohei Nakayama1, Natasha Sng1, Julian Carretero2, Robert Weiner3, Yuichiro Hayashi3, Mihoko Yamamoto1, Alistair J. Tan1, Norihiro Yamaguchi1, Hiroyuki Yasuda1, Danan Li4, Kenzo Soejima4, Ross A. Soo5,6, Dan B. Costa1, Kwok-Kin Wong4, and Susumu S. Kobayashi1,8

Abstract

The discovery of somatic mutations in EGFR and development of EGFR tyrosine kinase inhibitors (TKI) have revolutionized treatment for lung cancer. However, resistance to TKIs emerges in almost all patients and currently no effective treatment is available. Here, we show that β-catenin is essential for development of EGFR-mutated lung cancers. β-Catenin was upregulated and activated in EGFR-mutated cells. Mutant EGFR preferentially bound to and tyrosine phosphorylated β-catenin, leading to an increase in β-catenin-mediated transactivation, particularly in cells harboring the gefitinib/erlotinib-resistant gatekeeper EGFR-T790M mutation. Pharmacologic inhibition of β-catenin suppressed EGFR-L858R-T790M mutated lung tumor growth, and genetic deletion of the β-catenin gene dramatically reduced lung tumor formation in EGFR-L858R-T790M transgenic mice. These data suggest that β-catenin plays an essential role in lung tumorigenesis and that targeting the β-catenin pathway may provide novel strategies to prevent lung cancer development or overcome resistance to EGFR TKIs. Cancer Res; 74(20); 5891–902. ©2014 AACR.

Introduction

Lung cancer is the leading cause of cancer death worldwide (1). The conventional treatment of advanced lung cancer is unsatisfactory; however, the discovery of EGFR somatic kinase mutations provided the first glimpse of aberrant tyrosine kinase oncogene function in non–small cell lung cancer (NSCLC). Activating EGFR mutations (i.e., exon 19 deletions or the exon 21 L858R) are present in 10% to 40% of NSCLCs depending on race, gender, and smoking status (2). These mutations trigger the EGFR signaling pathway and promote EGFR-mediated prosurvival and antiapoptotic signals (2). Most NSCLCs with activating EGFR mutations respond dramatically to gefitinib and erlotinib, which are reversible EGFR tyrosine kinase inhibitors (TKI). However, almost all patients demonstrate progressive tumors within 2 years of continued drug exposure. The secondary EGFR-T790M mutation accounts for more than 50% of acquired resistance to gefitinib and erlotinib (2). Irreversible and second-generation EGFR inhibitors can partially overcome NSCLCs with T790M in vitro (3). This knowledge has spawned clinical trials of neratinib (4) and afatinib (5) in this patient population. However, these "second-generation" inhibitors alone have not led to significant control of tumors with acquired resistance to gefitinib/erlotinib (4, 5). Thus, novel strategies to overcome the acquired resistance caused by T790M either by developing inhibitors specific to EGFR-T790M (6) or by developing inhibitors of T790M downstream targets are sorely needed.

β-Catenin plays two major roles in normal cell homeostasis: it is a component of cell–cell adhesion structures and also a key player in the Wnt/β-catenin signaling pathway. As a cell adhesion molecule, membranous β-catenin links E-cadherin to α-catenin. In the nucleus, β-catenin acts as a transcriptional activator in conjunction with the TCF/LEF DNA-binding proteins and regulates its target genes that are responsible for cellular proliferation and differentiation (7). In the absence of Wnt/β-catenin signaling, β-catenin is degraded by the destruction complex consisting of adenosomatous polyposis coli (APC), axin, and glycogen synthase kinase 3β (GSK-3β). However, aberrant activation of the Wnt/β-catenin pathway can trigger tumorigenesis in several organs. In patients with familial adenomatous polyposis, mutations in APC lead to loss of APC function, stabilization of β-catenin, and constitutive activation of the Wnt/β-catenin pathway (8). In lung cancer, there is accumulating evidence that Wnt/β-catenin...
may be activated; however, mutations in APC are uncommon (9). Recently, it has been shown that this pathway plays an important role in lung adenocarcinoma metastasis (10), but the role of β-catenin signaling in NSCLC initiation/progression is not well understood.

In addition to serine/threonine phosphorylation, β-catenin can be tyrosine phosphorylated by several tyrosine kinases including Src (11, 12) and EGFR (13). In physiologic conditions, tyrosine-phosphorylation of β-catenin leads to dissociation of β-catenin/α-catenin/E-cadherin complexes, its stabilization with subsequent nuclear translocation, and finally increased transactivation of β-catenin (14). Moreover, it has been shown that β-catenin can also be tyrosine-phosphorylated by oncogenic Bcr-Abl or FLT3-mutant proteins, leading to its increased protein stability and transcriptional signaling activity (15, 16). These data strongly suggest that constitutively activated oncogenic kinases may contribute to cancer initiation and/or progression by increasing β-catenin activity.

In this study, we show that β-catenin is stabilized and activated through tyrosine-phosphorylation by mutant EGFRs. Inhibition of β-catenin was shown to suppress tumour growth in vitro and in vivo. Conditional deletion of the β-catenin gene (Ctnnb1) inhibited lung tumor formation induced by EGFR-L858R-T790M in transgenic mice. These data indicate that β-catenin plays an essential role in mutant EGFR-induced lung tumorigenesis.

Materials and Methods

Cell culture

A427, A549, NCI-H125, NCI-H1395, NCI-H1299, and NCI-H460 were purchased from the American Type Culture Collection, NCI-H1650, NCI-H3255, NCI-H1975, HCC827, PC9, and BEAS-2B cells were provided by Drs. Pasi Jänne and Geoffrey Shapiro (Dana-Farber Cancer Institute, Boston, MA). 293T cells and COS7 cells were provided by Dr. Daniel G. Tenen (Beth Israel Deaconess Medical Center, Boston, MA). These cells were regenotyped on a regular basis to confirm the presence of known EGFR mutations by standard Sanger sequencing.

Mice

The studies were approved by the Institutional Animal Care and Use Committee at Beth Israel Deaconess Medical Center. EGFR-L858R-T790M (EGFR<sup>RTK</sup>)/CCSP-rtTA bi-transgenic mice and tet-o-Cre transgenic mice were previously reported (17, 18). Ctnnb1 floxed mice (19) and TOPGAL reporter mice (20) were purchased from the Jackson Laboratory. To induce EGFR<sup>RTK</sup> expression and excise Ctnnb1, mice were fed with a doxycycline diet (Harlan Laboratories).

Plasmid constructs

FLAG-tagged and non-tagged pcDNA3-β-catenin plasmids were provided by Drs. Daniel G. Tenen and Akinobu Matsu moto (Beth Israel Deaconess Medical Center), respectively. pCG-LEF1 was provided by Rudolf Grosschedl (Max Planck Institute, Germany). Tyrosine to phenylalanine point mutations of β-catenin was generated using the QuikChange site-directed mutagenesis kit (Agilent technologies). pcDNA3.1 or MigR1 EGFR-mutant constructs were generated as described previously (21, 22).

Stable cell lines

Stable BEAS-2B cells expressing wild-type EGFR and EGFR mutants were generated by retroviral infection using MigR1-EGFR constructs as described previously (22). β-Catenin knockdown NCI-H1975 cells were generated by retroviral infection using pGIPZ constructs and GFP-positive cells were sorted. shRNA sequences were 5'-GCTTCTAACCCGGAGGTCTT-3' (control), 5'-TAAGGCTGACGTTATGGTCCA-3' (Ctnnb1 #1), 5'-TTACCACTCAGAAGGAG-3' (Ctnnb1 #2), and 5'-TACTGTCCATCAATATCG-3' (Ctnnb1 #3).

Real-time PCR assay

The mRNA levels of genes were measured as previously described (23). Primers for AXIN2 were 5'-TGTCACCAAAACTCTGAGG-3' (forward) and 5'-GTGCAAAGACATAGCCAGAAC-3' (reverse). Primers for GAPDH were 5'-CCAATACGTGCTCAGACACACT-3' (forward) and 5'-CCAGCGGCCCAATACG-3' (reverse).

Luciferase reporter gene assay

293T cells (1 × 10<sup>5</sup> cells) in 24-well plates were transfected by Lipofectamine 2000 (Invitrogen) with 200 ng of TCF-reporter constructs (pTOPFLASH/pPOFFLASH; ref. 24), and 100 ng of pcDNA3.1-EGFR, 100 ng of pCG-LEF1, and 500 ng of nontagged pcDNA3-β-catenin. Cells were incubated overnight and cultured for another 24 to 28 hours in the presence of 100 ng/mL EGFR. Luciferase activity was measured using Dual-Luciferase Reporter Assay System (Promega).

Western blotting and immunoprecipitation

Cells lysates were prepared as previously described (23, 25). Nuclei and cytoplasmic protein were isolated as previously described (26). Protein lysates were subjected to centrifugation, washed three times with PBS, and then suspended in sample buffer. Protein lysates were subjected to centrifugation, washed three times with PBS, and then suspended in sample buffer. The antibodies used were: α-tubulin (Millipore); β-actin (Sigma-Aldrich); axin2 (Abcam); β-catenin (Santa Cruz Biotechnology); EGFR (Cell Signaling Technology); FLAG (Sigma-Aldrich); total-GSK3β (Cell Signaling Technology); phospho-Ser9-GSK3β (Cell Signaling Technology); lamin B (Abcam); and phospho-tyrosine (Cell Signaling Technology).

IHC analysis and X-gal staining

The studies were approved by the Institutional Review Boards at Beth Israel Deaconess Medical Center, Keio University School of Medicine, and National University Health System in Singapore. A tissue microarray was constructed from tumor tissues of 148 patients with NSCLC obtained at the National University of Singapore as previously described. For
conventional IHC analyses, four EGFR-mutated NSCLC patients (L858R and exon 19 deletion) with acquired gefitinib resistance were analyzed. They underwent CT-guided pre- and posttreatment biopsies of their tumors at Keio University Hospital and Beth Israel Deaconess Medical Center. All tissues were embedded in paraffin, sectioned, and stained with hematoxylin and eosin (H&E). IHC staining was performed on formalin-fixed paraffin sections. All cases for quantitation of nuclear β-catenin staining were reviewed in a blinded fashion. For murine studies, mice were sacrificed and lungs were fixed in 10% neutral buffered formalin. The antibodies used were: β-catenin (human, R&D Systems or DAKO; mouse, BD Transduction Laboratories); axin2 (Abcam); and TTF1 (Abcam). X-gal staining was performed as described (28).

**Immunofluorescence analysis**

Cells were plated in 6-well plates overnight and transfected with 1.5 μg pcDNA3.1-EGFR and 1.5 μg FLAG-tagged pcDNA3-β-catenin. Cells were incubated overnight and trypsinized the following day. Cells were then plated into the 2-well chamber slides, incubated overnight, and stained with the following antibodies: FLAG (Sigma-Aldrich); β-catenin (BD Transduction Laboratories); Alexa 594-mouse and 488-rabbit (Invitrogen).

**In vitro and in vivo drug treatment**

For cell culture studies, both afatinib (LC Laboratory) and ICG-001 (Selleck Chemicals) were reconstituted in DMSO and used at the indicated concentrations. For in vivo studies, ICG-001 was suspended in 0.5% (w/v) methylcellulose (Sigma-Aldrich) and administered intraperitoneally at 150 mg/kg/day. The stock solution was reconstituted every week and stored at 4°C. The same mice were imaged by MRI to determine the reduction in tumor volume after 2 to 3 weeks during the respective treatments.

**Cell proliferation assay**

Growth inhibition was assessed by CellTiter 96 AQueous One solution proliferation kit (Promega) according to the manufacturer’s instruction.

**Colony formation assay**

Anchorage-independent growth was assayed as previously described (29). A total of 5,000 cells were plated and colonies were counted after 14 days.

**MRI scanning**

All MRI was performed with a 4.7 Tesla Biospec 47/40 spectrometer using a birdcage radio-frequency coil with an inner-diameter of 30 mm (Bruker Instruments). Detailed procedure of MRI scanning was described previously (17). On each MRI image, areas indicating the pulmonary tumor were manually segmented and measured to calculate tumor volumes using NIH ImageJ software (version 1.46; http://rsb.info.nih.gov/ij/).

**Statistical analysis**

Differences between the experimental groups were tested with Fisher exact test, Student t test, or Wilcoxon signed-rank test. P values of less than 0.05 were considered statistically significant. The Kaplan–Meier method was used to estimate overall survival. We performed our statistical analyses with STATA version 12.1 (STATA Corp).

**Results**

**β-Catenin is overexpressed in cells with EGFR activating mutations**

We previously identified cyclin D1 as one of the major effectors downstream of EGFR with activating mutations (23). As cyclin D1 is one of the target genes of the Wnt/β-catenin signaling pathway (7), we asked whether the pathway is activated in EGFR mutant cells. As shown in Fig. 1A, expression of β-catenin was increased in all EGFR-mutant cells at similar levels to A427 cells carrying a β-catenin stabilizing mutation (30), compared with cells harboring wild-type EGFR. In addition, immunofluorescence studies using confocal laser scanning microscopy showed much brighter signals in cells with EGFR mutations (NCI-H1650 and NCI-H1975; Fig. 1B) as compared with A549 cells, which carry wild-type EGFR. Interestingly, β-catenin was detected not only on the cell membrane, but also in the cytoplasm and nucleus in cells with EGFR mutants. Conversely, it was localized on the cell surface and sites of cell–cell contact in A549 cells (Fig. 1B). These results prompted us to determine expression and localization of β-catenin in mutant EGFR-driven tumors in vivo. We have previously established the lung-specific conditional EGRF-L858R-T790M (EGFRritic) transgenic mice containing seven direct repeats of the tetracycline (tet)-operator sequence. These mice were crossed with CCSP-rtTA mice, which specifically express the reverse tetracycline transactivator protein (rtTA) in CCSP expressing cells (17). Consistent with our previous report (17), lung tumors were detected in EGFRitt/CPS-rtTA mice treated with doxycycline but not in CCSP-rtTA mice (Fig. 1C: I and V). These tumors were positive for thyroid transcription factor-1 (TTF-1; Fig. 1C: VI). More than 70% of tumor cells were positive for cytoplasmic β-catenin, whereas nuclear β-catenin was positive in approximately 20% of tumor cells (Fig. 1C: VII; arrows). Interestingly, cytoplasmic Axin2, which is a direct target gene of the Wnt/β-catenin pathway (31), was detected in almost all tumor cells (Fig. 1C: VIII), which indicates that β-catenin is indeed activated in EGFR-mutant tumor cells.

**EGFR mutants increase expression and activity of β-catenin**

Next, we investigated the effects of mutant EGFR on stability and localization of β-catenin. When 293T cells were cotransfected with constructs containing β-catenin and either wild-type EGFR, EGFR-L858R, or EGFR-L858R-T790M, expression of cytosolic and nuclear β-catenin was highest in cells transfected with EGFR-L858R-T790M (Fig. 2A). Lower expression of β-catenin was detected in cells transfected with EGFR-L858R, but the expression was still at higher level compared with cells transfected with wild-type EGFR (Fig. 2A). Next, to examine the effect of EGFR mutants on β-catenin localization, we generated stable cell lines expressing either wild-type EGFR, EGFR-L858R, or EGFR-L858R-T790M (Fig. 2B) using human immortalized...
bronchial epithelial cells (BEAS-2B; ref. 32). Confocal microscopy analysis demonstrated that expression of nuclear β-catenin was highest in BEAS-2B cells expressing EGFR-L858R-T790M. Although cytoplasmic β-catenin was increased in BEAS-2B cells expressing EGFR-L858R, expression of nuclear β-catenin was modest compared with BEAS-2B cells expressing wild-type EGFR (Fig. 2C). As nuclear translocation of β-catenin is required for its transcriptional activity, we attempted to determine whether activated EGFR mutants enhance transactivation using the TCF optimal promoter, luciferase reporter (*pTOPFLASH*; ref. 24). The luciferase reporter containing the mutant motif (*pFOPFLASH*) was used to measure background activity. As shown in Fig. 2D, the TCF/LEF transactivation was highest in cells transiently transfected with *EGFR*-L858R-T790M, whereas cells transfected with *EGFR*-L858R showed slightly, but significantly, enhanced transactivation compared with cells transfected with wild-type *EGFR*.

Furthermore, to detect transactivation of β-catenin directly in lung tumor, we crossed *EGFRTL/CCSP-rtTA* mice to *TOPgalactosidase* (*TOPGAL*) reporter mice (20). In this system, expression of β-galactosidase is mediated by TCF/LEF transactivation. IHC analysis showed that β-galactosidase was strongly positive in lung tumors isolated from *EGFRTL/CCSP-rtTA/TOPGAL* double transgenic mouse (V, VI, VII, VIII). Both animals were sacrificed after 20 weeks of doxycycline administration. Scale bar, 50 μm.

**Figure 1.** β-Catenin is highly expressed in cells with *EGFR* activating mutations. A, immunoblot analyses of extracts from cancer cell lines harboring wild-type or mutant *EGFR*. B, confocal images of A549, NCI-H1650, NCI-H1975 cells stained with anti-β-catenin antibody and visualized by Alexa Fluor 488. Scale bar, 10 μm. C, IHC analysis of lungs isolated from a CCSP-rtTA mouse (I, II, III, IV) and lung tumors from an *EGFRTL/CCSP-rtTA* double transgenic mouse (V, VI, VII, VIII). Both animals were sacrificed after 20 weeks of doxycycline administration. Scale bar, 50 μm.
Role of β-Catenin in Mutant EGFR-Induced Lung Cancer

β-Catenin is stabilized and activated by EGFR mutants. A, immunoblot analyses of fractionated extracts from 293T cells cotransfected with constructs containing FLAG-tagged β-catenin and either HA-tagged wild-type EGFR (WT), EGFR-L858R (LR), or EGFR-L858R-T790M (LR-TM). B, immunoblot analyses of whole extracts from BEAS-2B cells stably expressing HA-tagged wild-type EGFR (WT), EGFR-L858R (LR), or EGFR-L858R-T790M (LR-TM). BEAS-2B cells infected with MigR1 empty vector were used as a control. C, confocal images of stable BEAS-2B cells described in B. Cells were incubated with anti-β-catenin antibody and visualized by Alexa Fluor 488. Scale bar, 10 μm. D, transactivation of β-catenin measured by luciferase activity. Data represent mean ± SD from eight independent experiments. **, P < 0.01. E, IHC analysis of β-galactosidase (I, III, V) and X-gal staining (II, IV, VI). Lungs isolated from CCSP-rtTA/TOPGAL (I, II), EGFRTL/CCSP-rtTA (III, IV), and EGFRTL/CCSP-rtTA/TOPGAL (V, VI) are shown. Scale bar, 50 μm.

(Fig. 2E: VI), but not in EGFRTL/CCSP-rtTA mice (Fig. 2E: IV). Alveolar cells were weakly positive for both β-galactosidase and X-gal staining in CCSP-rtTA/TOPGAL mice (Fig. 2E: I and II, respectively). These results indicate that β-catenin is indeed activated in EGFR-mutated lung tumors and imply that EGFR mutants, particularly EGFR-L858R-T790M, increase expression and activity of β-catenin.

β-Catenin is upregulated in human lung tumors with EGFR mutations

Our in vitro results prompted us to examine expression of β-catenin in primary human lung cancer specimens. IHC analysis of tissue microarray composed of 148 human NSCLC samples (Fig. 3A and Supplementary Fig. S1) demonstrated that expression of nuclear β-catenin was significantly higher in lung tumor specimens with EGFR-L858R or exon 19 deletions than tumors expressing wild-type EGFR [19% (6/31) vs. 6.0% (7/117); P < 0.05, Fisher exact test]. However, this dataset did not include tumors harboring EGFRTL-T790M. As β-catenin expression (Fig. 2A and C) and activation (Fig. 2D) were higher in cells transfected with EGFRTL-L858R-T790M than EGFRTL-L858R, we next asked whether expression and/or localization of β-catenin are altered by emergence of T790M in human NSCLC. We obtained pre-and post-gefitinib biopsies from four patients who initially responded, but became resistant to TKIs due to development of T790M (Supplementary Table). Although cytoplasmic and nuclear β-catenin (Supplementary Fig. S2: red arrows) were detected in both pretreatment (Supplementary Fig. S2: I, III, V, VII) and posttreatment tissues (Supplementary Fig. S2: II, IV, VI, VIII), the cytoplasmic staining pattern was
more intense and there were significantly more nuclear staining-positive cells in posttreatment tumors than pretreated tumors (Fig. 3B). These results indicate that β-catenin is upregulated and activated in human NSCLC specimens and suggest that emergence of T790M may increase β-catenin activity.

Tyrosine phosphorylation of β-catenin is mediated by EGFR mutants and enhances its activity

To investigate the mechanism of β-catenin stabilization, we first examined whether EGFR mutants enhance GSK3β phosphorylation. Although levels of β-catenin were higher in cells transfected with mutant EGFR than in cells with wild-type EGFR, phosphorylation of GSK3β (serine 9) was not increased (Fig. 4A). These results suggest that GSK3β is not solely responsible for stabilization of β-catenin.

It has been shown that tyrosine-phosphorylation of β-catenin enhances its stabilization, nuclear translocation, and/or transcriptional activity (11–13). As EGFR-L858R and L858R-T790M show high levels of constitutive tyrosine kinase activity (3, 33), we first asked whether EGFR mutants tyrosine-phosphorylate β-catenin. Immunoprecipitation experiments demonstrated that EGFR mutants preferentially bound to and proportionally tyrosine-phosphorylated β-catenin (Fig. 4B). Phosphorylation and binding to EGFR were inhibited by both erlotinib and afatinib in cells transfected with EGFR-L858R, but only by afatinib in cells with EGFR-L858R-T790M (Fig. 4C). Given that irreversible inhibitors such as afatinib can inhibit phosphorylation of both EGFR-L858R and EGFR-L858R-T790M in vitro (3), these data indicate that EGFR mutants bind to and tyrosine-phosphorylate β-catenin. Furthermore, inhibition of EGFR-mediated tyrosine-phosphorylation of β-catenin by afatinib resulted in less accumulation of β-catenin in the nucleus (Fig. 4D and Supplementary Fig. S3), suggesting that tyrosine-phosphorylation of β-catenin by EGFR mutants, at least in part, contributes to its nuclear translocation.

Next, we investigated whether tyrosine-phosphorylation of β-catenin leads to an increase in its activity. We focused on EGFR-L858R-T790M, as β-catenin was more efficiently phosphorylated and translocated into the nucleus in this model. Transactivation of β-catenin was inhibited by afatinib, which inhibits EGFR-L858R-T790M kinase activity (Fig. 4E). β-catenin is phosphorylated at Y86 by Src and oncogenic Bcr-Abl (15, 34) and at Y654 by activated wild-type EGFR (35) and oncogenic FLT3-ITD (16). On the basis of the structural similarity in the tyrosine kinase domain of various oncogenes (36), we hypothesized that Y86 and Y654 residues of β-catenin would be phosphorylated by EGFR mutants and affect activation of β-catenin. β-Catenin Y333, which has been shown to be phosphorylated by Src and bound to PKM, resulting in nuclear translocation of β-catenin (12), was also tested. We created single β-catenin Y-to-F mutants (Y86F, Y654F, and Y333F), plus the double-mutant Y86F+Y654F. All β-catenin Y-to-F mutants showed lower levels of tyrosine-phosphorylation (Supplementary Fig. S4) and decreased transactivation (Fig. 4F) compared with wild-type β-catenin, again suggesting that tyrosine-phosphorylation of β-catenin by EGFR mutants plays an important part for transactivation. Interestingly, Y333F had little impact on tyrosine-phosphorylation and transactivation of β-catenin (Fig. 4F). These results are consistent with the transactivation assay, which showed that SU6656, a Src inhibitor, failed to inhibit nuclear translocation (Fig. 4D) and transactivation of β-catenin (Fig. 4E). Taken together, these results suggest that tyrosine-phosphorylation of β-catenin by EGFR mutants, but not Src, contributes in part to its stabilization, translocation, and transactivation.

Inhibition of β-catenin suppresses tumor growth

On the basis of our observations that β-catenin is constitutively activated downstream of mutant EGFR-L858R-T790M, we hypothesized that inhibition of β-catenin would lead to suppression of tumor growth. To test this hypothesis, we generated β-catenin knockdown cells using NCI-H1975 cells harboring EGFR-L858R-T790M (Fig. 5A). Soft agar colony formation assay demonstrated that the number of colonies was significantly suppressed in β-catenin knockdown NCI-H1975 cells compared with control cells (Fig. 5B). Furthermore, we used ICG-001, a small molecule that specifically blocks the

![Figure 3](image-url)
Role of β-Catenin in Mutant EGFR-Induced Lung Cancer

CBP–β-catenin interaction (37). Treatment with ICG-001 led to suppression of AXIN2 (Fig. 5C) and suppressed cell growth in NCI-H1975 cells. ICG-001 failed to suppress NCI-H460 cell growth harboring wild-type EGFR (Fig. 5D). Interestingly, AXIN2 was not suppressed at this concentration in NCI-H460 cells (Fig. 5C). These in vitro results prompted us to model the effects of ICG-001 in lung tumors in the EGFR<sup>L858R-T790M</sup> mouse model in which Ctnnb1 can be conditionally deleted. We crossed EGFR<sup>L858R-T790M</sup>/CCSP-rtTA, teto-Cre (38) and conditional β-catenin knockout mice (Ctnnb1<sup>fl/fl</sup>; ref. 19). In the resultant mice, EGFR<sup>L858R-T790M</sup>/CCSP-rtTA/teto-Cre/Ctnnb1<sup>fl/fl</sup> mice (Fig. 6A; genotype is shown in Supplementary Fig. S6A), cre recombination, and induction of mutated proteins (EGFR-L858R-T790M) occurred selectively in pulmonary epithelial cells with doxycycline treatment (39). MRI studies demonstrated that no or significantly smaller tumors were detected in EGFR<sup>L858R-T790M</sup>/CCSP-rtTA/teto-Cre/Ctnnb1<sup>fl/fl</sup> mice compared with...
EGFR\textsuperscript{TL}/CCSP-rtTA/teto-Cre/Ctnnb1\textsuperscript{FY/+} mice (Fig. 6B) regardless of EGFR-L858R-T790M induction in both groups (Supplementary Fig. S6B). Lungs from EGFR\textsuperscript{TL}/CCSP-rtTA/teto-Cre/Ctnnb1\textsuperscript{FY/+} mice were more than 3-fold heavier than those from control mice, whereas lungs from EGFR\textsuperscript{TL}/CCSP-rtTA/teto-Cre/Ctnnb1\textsuperscript{F} mice showed no significant difference in weight compared with control CCSP-rtTA/Ctnnb1\textsuperscript{FY/+} mice (Fig. 6D). H&E stain demonstrated lung tumors consistent with adenocarcinoma in EGFR\textsuperscript{TL}/CCSP-rtTA/teto-Cre/Ctnnb1\textsuperscript{FY/+} (Fig. 6D, III). In contrast, deletion of Ctnnb1 in both alleles (EGFR\textsuperscript{TL}/CCSP-rtTA/teto-Cre/Ctnnb1\textsuperscript{FY/F}) significantly inhibited tumor formation (Fig. 6D, II). Complete deletion of Ctnnb1 showed no impact on normal lung structure (Fig. 6D, IV) with morphology indistinguishable from control mice (Fig. 6D, I) even after 11 weeks of doxycycline treatment. Interestingly, we observed histologically detectable small tumor clusters in 77% (17/22) of EGFR\textsuperscript{TL}/CCSP-rtTA/teto-Cre/Ctnnb1\textsuperscript{FY/F} mice when they were treated with doxycycline for more than 25 weeks (Supplementary Fig. S7A). Interestingly, when we isolated these histologically detectable tumors by laser capture microdissection in EGFR\textsuperscript{TL}/CCSP-rtTA/teto-Cre/Ctnnb1\textsuperscript{FY/F} mice, we found that \(\beta\)-catenin was not excised in most of these tumors [67% (8/12); Supplementary Fig. S7B]. Regardless of these small tumors, EGFR\textsuperscript{TL}/CCSP-rtTA/teto-Cre/Ctnnb1\textsuperscript{FY/F} mice showed significantly longer survival (\(P < 0.001\)) than EGFR\textsuperscript{TL}/CCSP-rtTA/teto-Cre/Ctnnb1\textsuperscript{F} mice (Fig. 6E). Taken together, these observations suggest that \(\beta\)-catenin is required for lung tumor initiation and/or development induced by EGFR-L858R-T790M.

**Discussion**

EGFR TKIs have improved outcomes for patients with EGFR-mutated NSCLC; however, acquired resistance to TKIs is an inevitable consequence of tumor selection over
continuous drug pressure. The *EGFR-T790M* mutation has emerged as the major mechanism of resistance to erlotinib and gefitinib. Although irreversible EGFR inhibitors are effective in lung cancer cells with *EGFR-T790M* mutation in vitro (3), clinical trials of these same compounds, such as afatinib or neratinib, have been disappointing (4, 5). Therefore, in addition to ongoing efforts to develop *EGFR-T790M* selective inhibitors, elucidating the precise mechanisms by which oncogenic EGFR mutations initiate and induce progressive lung tumors should be part of the research strategy to overcome and prevent resistance to clinically available EGFR TKIs. In this study, we demonstrated that β-catenin is required for tumor development and progression induced by TKI-sensitive or -resistant EGFR mutants. Our results give strong evidence for crosstalk between the oncogenic EGFR signaling and Wnt/β-catenin signaling for lung tumorigenesis.

Our data show that β-catenin is upregulated and translocated into nucleus in cells harboring EGFR mutants, particularly *EGFR-T790M*. Nuclear translocation of β-catenin is a hallmark of activation of β-catenin signaling, and indeed, β-catenin is activated in EGFR-mutant cells in vitro (Fig. 2D) and in vivo (Fig. 2E). Our observations are supported by previous observations that β-catenin-TCF/LEF target genes such as cyclin D1 and c-Myc are upregulated in NSCLC harboring *EGFR-T790M* (23, 40). Inhibition of serine/threonine phosphorylation by GSK3β is a well-recognized mechanism of β-catenin stabilization (8). However, our data demonstrate that this may not be a sole mechanism of β-catenin...
The model of cooperation between EGFR mutants and β-catenin in lung tumors enhances the knowledge that the β-catenin pathway is involved in oncogene kinase-driven tumors. Mouse models of Kras G12D have demonstrated that activation of Wnt/β-catenin accelerates tumor development by converting bronchial Clara cells to more proliferative embryonic progenitor cells (47). In addition, activating mutations of Ctnnb1 and mutations of Egfrβ cooperatively induce lung tumors (48). Gene expression analysis of clinical lung cancer samples has identified that activation of Wnt/β-catenin is critical for tumor metastasis (10). Our own conditional knockout model clearly suggests that β-catenin plays a significant role on lung tumorigenesis induced by EGFR-L858R-T790M because both deletion of β-catenin gene and induction of EGFR-L858R-T790M occur in the same cells (Fig. 6). Given that expression of an activated β-catenin alone causes lung tumors in none (47) or only a small subset of mice (49), it is predicted that tumor initiation likely requires concomitant genetic alterations in addition to activation of Wnt/β-catenin signaling. One possible explanation is that activation of β-catenin by EGFR mutants may ‘prime’ pulmonary cells to be susceptible to other downstream signaling aberrations and subsequent transformation into tumor cells. Indeed, it has been shown that expression of activated β-catenin leads to expansion of lung-specific progenitor cells (50).

In this study, we used the EGFR-L858R-T790M inducible mouse model to show that β-catenin plays an essential role in lung tumor development in vivo. Although β-catenin was most stabilized (Fig. 4A) and activated (Fig. 2D) in cells harboring EGFR-L858R-T790M, EGFR-L858R was still a more potent activator of β-catenin (Fig. 2D) than wild-type EGFR. Therefore, the question remains as to whether activation of β-catenin is specific for EGFR-T790M or also important for tumor development by non-T790M mutants such as EGFR-L858R. Furthermore, it is still unclear whether β-catenin is activated in lung tumors driven by other oncogenic kinases. β-catenin can also be tyrosine-phosphorylated and activated by oncogenic Bcr-Abl or FLT3-mutant proteins in leukemia (15, 16). Therefore, it is possible that other oncogenic receptor tyrosine kinases such as EML4-ALK translocations may also activate β-catenin. Future studies are required to answer these questions.

In summary, we demonstrate that β-catenin is involved in and required for lung tumor formation induced by EGFR mutants. These results uncover the mechanisms by which EGFR mutants lead to lung tumorigenesis and suggest that modulation of the β-catenin activity could be a novel therapeutic approach not only to inhibit lung cancer development, but also to overcome resistance to EGFR TKIs.

Disclosure of Potential Conflicts of Interest

D.B. Costa is a consultant/advisory board member for Pfizer, Roche, and AstraZeneca. No potential conflicts of interest were disclosed by the other authors.

Authors’ Contributions

Conception and design: S. Nakayama, N. Sng, R. Welner, H. Yasuda, S.S. Kobayashi

Development of methodology: S. Nakayama, N. Sng, R. Welner, R.A. Soo, K.-K. Wong, S.S. Kobayashi

Downloaded from cancerres.aacrjournals.org on April 14, 2017. © 2014 American Association for Cancer Research.
Acquisition of data (provided animals, acquired and managed patients, provided facilities, etc.)


Analysis and interpretation of data (e.g., statistical analysis, biositats, computational analysis)


Writing, reviewing, and/or revising of the manuscript:


Administrative, technical, or material support (i.e., reporting or organizing data, constructing databases):


Study supervision:

S.S. Kobayashi

Acknowledgments

The authors thank Rudolf Grosschedl (Max Planck Institute, Germany), Daniel Tenen, and Akinobu Matsumoto (Beth Israel Deaconess Medical Center, Boston, MA) for providing DNA constructs; Hisako Watanabe (Dana Farber Cancer Institute, Boston, MA) and Balazs Halmos (Columbia University, New York) for critical reading the manuscript and helpful discussion; and Bhavin Thakkar (National University of Singapore, Singapore), Michelle Farley, and David Bennett (Beth Israel Deaconess Medical Center) for technical assistance.

Grant Support

This work was supported by NIH grants (R00CA126026 and R01CA169259 to S.S. Kobayashi, P50CA105978 to D.B. Costa and K.-K. Wong, and R01CA122794, CA140594, CA163896, CA166480, CA154303, and CA120964 to K.-K. Wong), a Lung Cancer Foundation of America-International Association to Study Lung Cancer grant (D.B. Costa), an American Cancer Society grant RSG 11-186 (D.B. Costa), Ronnie J. Addarna Lung Cancer Foundation grant (S. Nakayama), and the Singapore National Research Foundation and the Ministry of Education under the Research Center of Excellence Programme (R.A. Soo).

The costs of publication of this article were defrayed in part by the payment of page charges. This article must therefore be hereby marked advertisement in accordance with 18 U.S.C. Section 1734 solely to indicate this fact.

Received January 23, 2014; revised July 28, 2014; accepted August 11, 2014; published OnlineFirst August 27, 2014.
Nakayama et al.


β-Catenin Contributes to Lung Tumor Development Induced by EGFR Mutations

Sohei Nakayama, Natasha Sng, Julian Carretero, et al.


Updated version
Access the most recent version of this article at:
doi:10.1158/0008-5472.CAN-14-0184

Supplementary Material
Access the most recent supplemental material at:
http://cancerres.aacrjournals.org/content/suppl/2014/08/26/0008-5472.CAN-14-0184.DC1

Cited articles
This article cites 49 articles, 22 of which you can access for free at:
http://cancerres.aacrjournals.org/content/74/20/5891.full.html#ref-list-1

Citing articles
This article has been cited by 2 HighWire-hosted articles. Access the articles at:
/content/74/20/5891.full.html#related-urls

E-mail alerts
Sign up to receive free email-alerts related to this article or journal.

Reprints and Subscriptions
To order reprints of this article or to subscribe to the journal, contact the AACR Publications Department at pubs@aacr.org.

Permissions
To request permission to re-use all or part of this article, contact the AACR Publications Department at permissions@aacr.org.