Impact of the Integrin Signaling Adaptor Protein NEDD9 on Prognosis and Metastatic Behavior of Human Lung Cancer

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Abstract

**Purpose:** In a substantial population of non–small cell lung cancer (NSCLC), expression and activation of EGF receptor (EGFR) have been reported and is regarded as a novel molecular target. A growing body of evidence has shown the signaling crosstalk between EGFR and integrins in cellular migration and invasion. NEDD9 is an integrin signaling adaptor protein composed of multiple domains serving as substrate for a variety of tyrosine kinases. In the present study, we aimed at elucidating a role of NEDD9 in the signaling crosstalk between EGFR and integrins.

**Experimental Design:** Using NSCLC cell lines, we conducted immunoblotting and cellular migration/invasion assay *in vitro*. Next, we analyzed metastasis assays *in vivo* by the use of xenograft transplantation model. Finally, we retrospectively evaluated clinical samples and records of patients with NSCLCs.

**Results:** We showed that tyrosine phosphorylation of NEDD9 was reduced by the inhibition of EGFR in NSCLC cell lines. Overexpression of constitutively active EGFR caused tyrosine phosphorylation of NEDD9 in the absence of integrin stimulation. By gene transfer and gene knockdown, we showed that NEDD9 plays a pivotal role in cell migration and invasion of those cells *in vitro*. Furthermore, overexpression of NEDD9 promoted lung metastasis of an NSCLC cell line in NOD/Shi-scid, IL-2Rγnull mice (NOG) mice. Finally, univariate and multivariate Cox model analysis of NSCLC clinical specimens revealed a strong correlation between NEDD9 expression and recurrence-free survival as well as overall survival.

**Conclusion:** Our data thus suggest that NEDD9 is a promising biomarker for the prognosis of NSCLCs and its expression can promote NSCLC metastasis. **Clin Cancer Res;** 18(22); 6326–38. ©2012 AACR.

Introduction

Lung cancer is the leading cause of cancer-related mortality in men worldwide (1). Non–small cell lung cancer (NSCLC) constitutes more than 80% of lung cancer, whereas small cell lung cancer being around 13%. While surgical intervention is the therapeutic option in limited stage NSCLCs, relapse rate is very high, being around 40% within 5 years after surgical intervention with curative intent. Moreover, the prevalence rate of NSCLCs continues to grow, and 5-year survival rate after diagnosis is only 15% to 25%.

Large randomized trials showed that platinum-based adjuvant chemotherapy has modest survival advantage (HR, 0.6–0.8) for carefully selected patients with NSCLCs (2). Prognostic factor is a powerful tool to determine patients who may benefit from adjuvant chemotherapy, as well as the type of treatments which may benefit the patients. Besides tumor–node–metastasis (TNM) staging, which is the most important clinical prognostic factor for NSCLCs, several studies have examined gene expression profiles of NSCLCs, identifying molecular subtypes associated with patient outcome.

The EGF receptor (EGFR)/human epidermal receptor (HER) 1 is one such gene signature which has received increasing attention over the last decade. EGFR is a receptor tyrosine kinase (RTK; ref. 3) that frequently is overexpressed or harbors constitutively active mutations in NSCLCs. Its activation promotes tumor proliferation, invasion, and metastasis (4). The small molecule tyrosine kinase inhibitors (TKI) gefitinib and erlotinib target the ATP-binding
**Translational Relevance**

EGF receptor (EGFR) is regarded as a novel molecular target in non–small cell lung cancer (NSCLC). In this study, we focused on the interaction of NEDD9 and EGFR, as NEDD9 is a docking protein downstream of β1-integrins, which closely associates with EGFR. We showed the following findings.

1. EGFR is involved in tyrosine phosphorylation of NEDD9.
2. NEDD9 mediates EGFR–β1-integrin–induced migration and invasion of NSCLC cell lines.
3. In a murine xenograft model, NEDD9 promotes lung metastasis of an NSCLC cell line.
4. NEDD9 expression in primary lesion of NSCLCs strongly correlates with recurrence-free survival or overall survival of the patients with NSCLCs.

Our results suggest that NEDD9 is a useful biomarker for the prognosis of NSCLCs, and its expression can promote NSCLC metastasis. This is the first study to show the clinical importance of NEDD9 as a potential prognostic factor as well as the crosstalk between EGFR and NEDD9 signaling pathways in NSCLCs.

NEDD9 is phosphorylated at its tyrosine residues by integrins and other stimuli. Ligation of T- and B-cell antigen receptors (19, 20) caused tyrosine phosphorylation of NEDD9, resulting in the association of Crk, Crk-L, and C3G. Integrin- or integrin/TCR-elicited tyrosine phosphorylation of NEDD9 was mediated by focal adhesion kinase (FAK) and Src family tyrosine kinases (21, 22). Ectopic expression of NEDD9 conferred T cells with enhanced motility on the co-engagement of TCR/CD3 complex and β1-integrins (23, 24), suggesting a pivotal role of tyrosine-phosphorylated NEDD9 in TCR- and integrin-mediated cell motility. Recent work showed that NEDD9 expression correlates with metastatic behavior of several malignancies, including lung cancer, head and neck cancer, melanoma, and breast cancer (25–31).

In this study, we investigated the biologic significance of the link between NEDD9 and EGFR signaling pathway in NSCLCs by in vitro and in vivo approaches. Furthermore, we evaluated the clinical significance of NEDD9 expression in primary NSCLC tumor samples through a retrospective analysis. We showed that NEDD9 plays a pivotal role in cell metastasis and invasion of NSCLC cells, and expression of NEDD9 appears to be a promising biomarker for NSCLC prognosis.

**Materials and Methods**

**Reagents and antibodies**

Gefitinib was purchased from Biaffin GmbH & Co KG. Recombinant human EGF was purchased from R&D systems, Inc. Monoclonal antibodies (mAb) against FAK and BCAR1 were purchased from BD. Rabbit anti-phospho-FAK (Tyr-397) polyclonal antibody (pAb) was from Invitrogen. Mouse mAb against NEDD9 (2G9) was purchased from BD. Rabbit pAb against NEDD9 was produced by MBL by immunizing synthetic peptide EYPSRYQKVY-DIPPSh. Anti- phosphotyrosine antibody (4G10) and anti-c-myc tag mAb (9E10) were produced from the hybridoma center Hospital, Tokyo, Japan) and were maintained as described previously (32).

**Cells, plasmids, and transfection procedures**

293T cells and A549 cells were obtained from American Type Culture Collection. PC-9 cells harboring the gefitinib-sensitizing deletion mutation (ΔE746-A750) and PC-14 were kindly provided by Dr. F. Koizumi (National Cancer Center Hospital, Tokyo, Japan) and were maintained as described previously (32).

The plasmid vector pBabe puro EGFR wild-type and its constitutively active mutants EGFR (del3) L747-E749del, A750P, EGFR G719S, EGFR D770-N771 insNPG, EGFR L858R, and its kinase dead mutant EGFR D837A were described previously (33). The plasmid vector pSRc c-myc tagged NEDD9 WT (wild-type) was used for transient expression. For stable expression, the following vectors were used: BCMG hygro c-myc NEDD9 WT (wild-type), NEDD9...
ΔSH3 (lacking aa 1–60), NEDD9ΔSD (lacking aa 63–401), NEDD9 ΔC (lacking aa 406–834), NEDD9ΔDYVYHL (lacking aa 629–834), NEDD9ΔCC (lacking aa 637–834), NEDD9ΔHL (lacking aa 707–834), and NEDD9F in which Y629 and Y631 were mutated into F. The plasmids were transfected into cells using Lipofectamine 2000 (Invitrogen) or FuGENE6 (Roche Applied Science) according to the manufacturer's instructions. In experiments using BCMG hygro vectors, transfected cells were selected in 0.2 mg/mL hygromycin B to establish stable transformants. The expression vector pMX-luc.neo for firefly luciferase was described elsewhere (34).

Gene knockdown by siRNA
To deplete endogenous NEDD9 or BCAR1, Stealth RNAi siRNAs were obtained from Life Technologies. The target sequence of siRNA for NEDD9 is 5′-UCCCAUCCAGGAGACUUCCGUCC-3′ and that for BCAR1 is 5′-GCCUCCGUCCGUUGGGAACGU-3′. As a control, we used Stealth RNAi siRNA negative control. The siRNAs were transfected using Lipofectamine RNAiMAX transfection reagent according to the manufacturer's instructions (Life Technologies).

Protein extraction, immunoprecipitation, and immunoblotting
Cells were serum-starved for 24 hours before the treatment with EGF (at a final concentration of 10 ng/mL). For suspension culture, HydroCell low cell binding culture dish (CellSeed Inc.) was used with serum-free medium. Cytoplasmic protein extracts were prepared by detergent lysis (1% Triton X-100) containing phosphatase and protease inhibitors. For immunoprecipitation, cell lysates were incubated with the appropriate first antibody at 4°C overnight and then with protein A Sepharose beads for 4 hours. After wash with lysis buffer, the beads were boiled in the SDS-PAGE loading buffer. The immunoprecipitates and cell lysates were separated by 8% SDS-PAGE gels and electrophoretically transferred onto polyvinylidene difluoride membranes. After blocking, the membranes were incubated serially with the primary antibody and horseradish peroxidase (HRP)-conjugated secondary antibody and then developed by enhanced chemiluminescence system (GE Healthcare).

Cell migration and invasion assays
Cell migration assay was conducted as described previously using Transwell inserts (8-µm pore size; Corning Incorporated; ref. 24). Cells were placed in the upper chamber at 1 × 10^5 cells/mL in 100 µL of 0.6% bovine serum albumin (BSA)/RPMI-1640 medium. After 6 hours, the inserts were fixed and stained with Diff-Quick. The cells that had not migrated were removed from the upper surface of the inserts using cotton swabs. Images of 3 different high-power fields were captured from each insert, and the number of migratory cells was counted. To determine invasive potential, Matrigel invasion chamber (BD BioCoat) was used.

Animals
Five- to 6-week-old female NOD/Shi-scid, IL-2R<sup>−/−</sup> mice (NOD mice; ref. 35) were supplied from Central Institute for Experimental Animals (Kawasaki, Japan) and maintained in a specific pathogen-free facility. All experiments were approved by and carried out following the guidelines of the Institute Animal Care and Use Committee of the University of Tokyo (Tokyo, Japan).

In vivo bioluminescence imaging
Human NSCLC cell line PC-14 was transplanted subcutaneously into the lumbar region on the dorsal side of NOD mice. On days 21 and 28, progression of the transplanted tumors was monitored by the following bioluminescence imaging (BLI) technique. β-Luciferin (Beetle Luciferin, Promega) was used as the substrate for the luciferase expressed by PC-14 cells. The mice received an intraperitoneal injection of 150 mg/kg β-luciferin and placed in the light tight chamber of a cooled CCD camera system (IVIS Imaging System 100; Xenogen) in the prone position under isoflurane anesthesia. Dorsal, left lateral, ventral, and right lateral images were acquired from 10 minutes after β-luciferin injection with the CCD camera system. All luminescent images were collected with an exposure time of 1 minute and binning of 8.

Gross and microscopic pathology
The NOG mice undergoing xenograft transplantation were euthanized with carbon dioxide on day 28 after BLI. Major organs were examined for grossly visible changes. Lung tissues and the primary tumors were removed into 10% neutral-buffered formalin for histology. After formalin fixation, samples were processed into paraffin wax, sectioned at a nominal thickness of 5 µm, stained with hematoxylin and eosin (H&E), and examined by light microscopy.

Clinical specimens and immunohistochemical staining
Upon approval from the Institutional Review Board of Keio University (Tokyo, Japan), we selected 60 consecutive patients with lung adenocarcinoma treated with curative surgery resection between 1999 and 2001 from the Keio University Hospital (IRB number: 16–90). Immunohistochemical studies were conducted on 5-µm sections of formalin-fixed, paraffin-embedded tissue section of the primary tumors of lung. Antigen retrieval was conducted with 0.01 mol/L of boiled citrate buffer (pH 9.0) for 10 minutes. The slides were stained on the Dako Autostainer (Dako) using the EnVision (Dako) staining reagents. The sections were first blocked for endogenous protein binding and peroxidase activity with Dual Endogenous Block (Dako) for 10 minutes. The sections were serially incubated with a polyclonal antibody against NEDD9 (2 µg/mL) and EnVision+ Dual Link reagent for 30 minutes. The sections were then treated with 3,3′-diaminobenzidine (DAB) and hydrogen peroxide. A toning solution (DAB Enhancer, Dako) was used to enrich the final color. The sections were counterstained with hematoxylin, dehydrated, and
cells were cultured in the presence or absence of gefitinib (0.2 μmol/L) for the indicated time period and then the cells were lysed by scraper in the lysis buffer. Lysates were immunoprecipitated with anti-NEDD9 pAb. The lysates and immunoprecipitates were subjected to SDS-PAGE and immunoblotting with the indicated antibodies. Combination of the vectors is as follows: Vec/Vec, pSR a NEDD9/pBabe puro; WT/NPG, pSR a EGFR NPG (constitutively active); WT/D837A, pSR a EGFR D837A (kinase dead); (–)/(–), no plasmids (FuGENE6 alone).

Figure 1. A, EGF stimulation promotes phosphorylation of NEDD9 in human NSCLC cell lines. PC-9 cells and A549 cells were treated with EGF (10 ng/mL) for the indicated time period and then the cells were lysed by scraper in the lysis buffer. Lysates were immunoprecipitated with anti-NEDD9 pAb. The lysates and immunoprecipitates were subjected to immunoblotting with the indicated antibodies. IP, immunoprecipitate; NEDD9, anti-NEDD9 mAb; pEGFR, anti-phospho-EGFR pAb; pTyr, anti-phosphotyrosine mAb. B, inhibition of EGFR by gefitinib downregulates tyrosine phosphorylation of NEDD9 in NSCLC cell lines. PC-9 and A549 cells were detached by trypsin/EDTA and cultured in suspension with serum-starved condition. At 48 hours after transfection, the cells were lysed by scraper in the lysis buffer. The lysates were then subjected to immunoblotting with the indicated antibodies. BCAR1, anti-BCAR1 mAb; β-actin, anti-β-actin mAb; EGFR, anti-EGFR pAb; FAK, anti-FAK mAb; NEDD9, anti-NEDD9 mAb; pFAK, anti-phospho-FAK Ab. E, constitutively active EGFR tyrosine phosphorylates NEDD9 in 293T cells. 293T cells (6 × 10⁶ cells) were co-transfected with pBabe puro EGFR (wild-type or mutants) and pSR a NEDD9 (wild-type) by FuGENE6. At 24 hours after transfection, the cells were detached by trypsin/EDTA and cultured in suspension with serum-starved condition. At 48 hours after transfection, the cells were lysed and immunoprecipitated with anti-NEDD9 pAb. Treatment with gefitinib (0.2 μmol/L) was conducted during 2 hours before the cell lysis. The immunoprecipitates were subjected to immunoblotting with the indicated antibodies. D, inhibition of EGFR by gefitinib modulates FAK, NEDD9, and BCAR1 in PC-9 cells. PC-9 cells were treated with 0.2 μmol/L gefitinib for the indicated time period. The cells were lysed by scraper in the lysis buffer. The lysates were then subjected to immunoblotting with the indicated antibodies. BCAR1, anti-BCAR1 mAb; β-actin, anti-β-actin mAb; EGFR, anti-EGFR pAb; FAK, anti-FAK mAb; NEDD9, anti-NEDD9 mAb; pFAK, anti-phospho-FAK Ab. E, constitutively active EGFR tyrosine phosphorylates NEDD9 in 293T cells. 293T cells (6 × 10⁶ cells) were co-transfected with pBabe puro EGFR (wild-type or mutants) and pSR a NEDD9 (wild-type) by FuGENE6. At 24 hours after transfection, the cells were detached by trypsin/EDTA and cultured in suspension with serum-starved condition. At 48 hours after transfection, the cells were lysed and immunoprecipitated with anti-NEDD9 pAb or anti-EGFR pAb. The immunoprecipitates were subjected to SDS-PAGE and immunoblotting with the indicated antibodies. Combination of the vectors is as follows: Vec/Vec, pSR a NEDD9 (NEDD9 and/or pME18S Fyn (Fyn)) by FuGENE6. After 48 hours, the cells were lysed and immunoprecipitated with anti-NEDD9 pAb. Treatment with gefitinib (0.2 μmol/L) was conducted during 2 hours before the cell lysis. The immunoprecipitates were subjected to immunoblotting with the indicated antibodies. IP, immunoprecipitate; NEDD9, anti-NEDD9 mAb; pEGFR, anti-phospho-EGFR pAb; pTyr, anti-phosphotyrosine mAb. B, inhibition of EGFR by gefitinib downregulates tyrosine phosphorylation of NEDD9 in NSCLC cell lines. PC-9 and A549 cells were cultured in the presence or absence of gefitinib (0.2 μmol/L) for 2 hours and the cells were then treated in the same manner as A. C, gefitinib does not inhibit Fyn-mediated tyrosine phosphorylation of NEDD9 in 293T cells. 293T cells (6 × 10⁶ cells) were transfected with

Statistical analysis
The χ² analysis was applied for the comparison of dichotomous variables. The Kaplan–Meier estimate was used for recurrence-free survival (RFS) and overall survival (OS) analysis, and the log-rank test was used to compare the difference. The Cox proportional hazards model was applied in univariate and multivariate survival analysis to test independent prognostic factors. The control groups of all statistical analyses were usually the first groups in the panels unless specified otherwise in the figure legends. All the statistical analyses were conducted by SPSS Statistics 17 (IBM Corporation) at the 0.05 level of significance.

Clinical investigation was conducted according to Declaration of Helsinki principles. The written informed consent was received from patients before inclusion in this study.

Results
EGF enhances NEDD9 tyrosine phosphorylation
To examine the role of NEDD9 in EGFR signaling pathway in NSCLCs, we first used NSCLC cell lines PC-9 and A549. As shown in Fig. 1A, stimulation with EGF elevated the level of tyrosine phosphorylation of NEDD9 in both PC-9 and A549 cells. Because PC-9 harbors activating mutation of EGFR (ΔE746-A750), the basal level of tyrosine phosphorylation of endogenous EGFR was significantly higher than that of A549 cells with the wild-type EGFR. A TKI for EGFR, gefitinib, abolished the increase in tyrosine phosphorylation of NEDD9 induced by EGF in those cells (Fig.

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expression plasmid pSR a NEDD9 (NEDD9 and/or pME18S Fyn (Fyn)) by FuGENE6. After 48 hours, the cells were lysed and immunoprecipitated with anti-NEDD9 pAb. Treatment with gefitinib (0.2 μmol/L) was conducted during 2 hours before the cell lysis. The immunoprecipitates were subjected to immunoblotting with the indicated antibodies. D, inhibition of EGFR by gefitinib modulates FAK, NEDD9, and BCAR1 in PC-9 cells. PC-9 cells were treated with 0.2 μmol/L gefitinib for the indicated time period. The cells were lysed by scraper in the lysis buffer. The lysates were then subjected to immunoblotting with the indicated antibodies. BCAR1, anti-BCAR1 mAb; β-actin, anti-β-actin mAb; EGFR, anti-EGFR pAb; FAK, anti-FAK mAb; NEDD9, anti-NEDD9 mAb; pFAK, anti-phospho-FAK Ab. E, constitutively active EGFR tyrosine phosphorylates NEDD9 in 293T cells. 293T cells (6 × 10⁶ cells) were co-transfected with pBabe puro EGFR (wild-type or mutants) and pSR a NEDD9 (wild-type) by FuGENE6. At 24 hours after transfection, the cells were detached by trypsin/EDTA and cultured in suspension with serum-starved condition. At 48 hours after transfection, the cells were lysed and immunoprecipitated with anti-NEDD9 pAb or anti-EGFR pAb. The immunoprecipitates were subjected to SDS-PAGE and immunoblotting with the indicated antibodies. Combination of the vectors is as follows: Vec/Vec, pSR a NEDD9 (NEDD9 and/or pME18S Fyn (Fyn)) by FuGENE6. After 48 hours, the cells were lysed and immunoprecipitated with anti-NEDD9 pAb. Treatment with gefitinib (0.2 μmol/L) was conducted during 2 hours before the cell lysis. The immunoprecipitates were subjected to immunoblotting with the indicated antibodies. IP, immunoprecipitate; NEDD9, anti-NEDD9 mAb; pEGFR, anti-phospho-EGFR pAb; pTyr, anti-phosphotyrosine mAb. B, inhibition of EGFR by gefitinib downregulates tyrosine phosphorylation of NEDD9 in NSCLC cell lines. PC-9 and A549 cells were cultured in the presence or absence of gefitinib (0.2 μmol/L) for 2 hours and the cells were then treated in the same manner as A. C, gefitinib does not inhibit Fyn-mediated tyrosine phosphorylation of NEDD9 in 293T cells. 293T cells (6 × 10⁶ cells) were transfected with...
1B). To assess the specificity of EGFR-mediated tyrosine phosphorylation of NEDD9, we next used the human embryonic kidney cell line 293T cells. As shown in Fig. 1C, gefitinib did not alter the level of tyrosine phosphorylation of NEDD9 caused by exogenous Fyn, an Src family tyrosine kinase in 293T cells. Time course experiments showed that the treatment of PC-9 cells with gefitinib downregulated not only tyrosine phosphorylation of EGFR but also that of FAK. Interestingly, the protein amounts of EGFR, NEDD9, and NEDD9 homologue BCAR1 were also reduced following the addition of gefitinib (Fig. 1D).

In NSCLCs, a variety of activating mutations or deletions have been found in EGFR to correlate with poor clinical outcome. To evaluate the effect of such gene alterations on the tyrosine phosphorylation of NEDD9 in vitro, we next conducted co-transfection analysis using 293T cells in suspension culture with serum starvation. As a result, co-transfection of constitutively active mutant EGFR D770N771 (EGFR NPG) promoted significant level of tyrosine phosphorylation of NEDD9 despite its relatively low level of protein expression, whereas other EGFR constructs including wild-type EGFR and the kinase-negative mutant D837A did not alter the level of tyrosine phosphorylation of NEDD9 (Fig. 1E). However, immunoprecipitation and colocalization analysis revealed that these EGFR constructs and NEDD9 did not co-precipitate and co-localize only marginally (data not shown). These results therefore suggest that the EGFR signaling pathway may modulate tyrosine phosphorylation of NEDD9 in an indirect manner.

**Exogenous NEDD9 enhances migratory and invasive potential of NSCLC cell lines**

We previously showed that transfected NEDD9 upregulated the motility of Jurkat T cell line on fibronectin (FN) and/or anti-CD3 mAb (23). To determine the association between the expression level of NEDD9 and migratory or invasive behavior of NSCLCs, we used full-length construct for NEDD9, a point mutant NEDD9 F in which the Src SH2-binding motif YDYVHL was mutated to FDFVHL, and a mutant NEDD9 D in which the Src SH3-binding motif YDYHL was deleted from the C-terminus to YDYVHL. The set of NEDD9 mutants in the presence of EGF (Fig. 2G). As shown in Fig. 2C–F, gene transfer of the wild-type EGFR and the kinase-negative mutant D837A did not alter the level of tyrosine phosphorylation of NEDD9 (Fig. 1E). However, immunoprecipitation and colocalization analysis revealed that these EGFR constructs and NEDD9 did not co-precipitate and co-localize only marginally (data not shown). These results therefore suggest that the EGFR signaling pathway may modulate tyrosine phosphorylation of NEDD9 in an indirect manner.

Gene ablation of NEDD9 or BCAR1 reduces the migratory and invasive activity of NSCLC cell lines

To further confirm the enhancing effect of NEDD9 on cell motility and invasiveness of NSCLCs, we conducted gene knockdown experiments using endogenous NEDD9 and its related protein BCAR1 by transfecting PC-9 and A549 with their respective siRNA. Concerning to the off-targeting effect, we evaluated 3 siRNAs (siRNA-1: UCCCAUGGCGAGAGACUGCCUCCAGU, siRNA-2: UCCCAUGGCAACCGGAGUGAGACUGCCUCCAGU, and siRNA-3: CCUUAUAUGACAAUGUGAAGCUUCU, and siRNA-3: CCUUAUAUGACAAU-GUCCCAUGGCGAGAGACUGCCUCCAGU, and siRNA-3: CCUUAUAUGACAAU-GUCCCAUGGCGAGAGACUGCCUCCAGU) for NEDD9 in their inhibitory effects in cDNA rescue experiments and selected siRNA-1 (Supplementary Fig. S1).

As shown in Fig. 3, introduction of NEDD9-specific siRNA abolished not only fibronectin-induced cell migration and invasion but also EGFR-induced cell invasion. The BCAR1-specific siRNA also reduced cell migration and invasion, although its inhibitory effect was less than that of NEDD9-specific siRNA in NSCLC cell lines.

Together, results of the gene transfer and gene knockdown experiments suggest that NEDD9 as well as BCAR1 seem to be indispensable factors for EGFR as well as integrin-mediated cell motility and invasiveness in NSCLCs.

Gene transfer of NEDD9 into an NSCLC cell line promotes lung metastasis in vivo

Our data showing the enhancing effects of NEDD9 on cell motility and invasion of NSCLC cell lines led us to evaluate a xenograft transplantation model using immunodeficient mice (NOG mice) and B16 (34). For this purpose, we used the poorly differentiated human lung adenocarcinoma cell line PC-14 which is negative for NEDD9 at the protein level (Fig. 4A). Figure 4B shows stable expression of transfected NEDD9 (wild-type) in PC-14 cells as long as 28 days after xenotransplantation into NOG mice. The bioluminescence images of xenograft-transplanted NOG mice revealed a positive signal in the lung region of mice transplanted with...
Figure 2. Exogenous NEDD9 enhances migratory and invasive potential of NSCLC cell lines. A, structure of NEDD9 and its mutants. The secondary structure of NEDD9 is graphically shown. From 5', closed oval, c-myc tag; SH3, Src homology 3 domain; SD, substrate domain; SR, serine-rich region; C, coiled-coil domain; H, helix-loop-helix domain; CT, C-terminal region. B, protein expression of NEDD9 and its mutants in A549 NEDD9 transfectants. A549 cells were transfected with the indicated NEDD9 constructs. After establishing stable transformants, the cell lysates were subjected to immunoblotting with the indicated antibodies (c-myc, anti-c-myc mAb). Vec, BCMG hygro. C–F, transfection of wild-type NEDD9 promotes migratory activity of NSCLC cell lines. PC-9 (C and E) and A549 cells (D and F) were transfected with either empty vector BCMG hygro (closed bar) or BCMG hygro c-myc NEDD9 WT (open bar). The stable transformants were subjected to cell migration assay (C and D) or cell invasion assay (E and F) in the presence or absence of the indicated reagents. NT (nontreated), fetal calf serum (FCS), 10% in the lower chamber; EGF, 10 ng/mL in the lower chamber; FN, inserts were coated with 0.5 mg/mL of fibronectin; Gef, gefitinib in both chambers at 0.2 μmol/L. Statistical significance was evaluated by comparison with NT. *, P < 0.01; **, P < 0.001; ***, P < 0.0001. G, motility-enhancing effect of a series of NEDD9 mutants. A549 NEDD9 transfectants were subjected to the cell migration assay in the presence of EGF (10 ng/mL). Statistical significance was evaluated by comparison with Vec (BCMG hygro).
PC-14 co-expressing luciferase and wild-type NEDD9 (Fig. 4C). A region of interest (ROI) of a fixed size was then set in the chest of these mice, and the mean signal intensity (photons/sec/cm²/steradian) in the ROI was determined. In particular, for the mice transplanted with PC-14 co-expressing luciferase and wild-type NEDD9, the mean signal intensity of the ROI was 5.69 × 10⁵ ± 0.64 for the right lung and 10.33 × 10⁵ ± 2.65 for the left lung, whereas the mean signal intensity of the ROI was 1.23 × 10⁵ ± 1.03 for the right lung and 1.42 × 10⁵ ± 0.66 for the left lung of mice transplanted with control PC-14 cells expressing luciferase alone, a greater than 3 times higher signal intensity in the case with the PC-14 NEDD9 transformant. These results suggest that overexpression of NEDD9 promotes in vivo lung metastasis of a xenograft-transplanted NSCLC cell line in NOG mice. We next conducted metastasis assays in NOG mice with PC-14 NEDD9 mutants (ΔSH3 and ΔC). We found that subcutaneous injections of these cell lines resulted in detectable tumors in NOG mice. However, the sizes of the primary tumors were less than tumors created by PC-14 vector transfectant and NEDD9 wild-type transfectant. Furthermore, by microscopic examination, we could not detect any metastatic lesions in the lungs of these mice, indicating that these NEDD9 mutants displayed a dominant-negative effect on cell metastasis as well as tumor growth (Fig. 4D and E).

Expression of NEDD9 in human NSCLCs is associated with poor prognosis in lung cancer patients

To determine the clinical relevance of NEDD9 expression in human NSCLCs, we evaluated NEDD9 expression in the primary lesions of human lung adenocarcinoma and also examined the available clinical information of 60 patients treated consecutively at Keio University Hospital with curative surgery between 1999 and 2001. Clinical characteristics of these patients are summarized in Supplementary Tables S1 and S2. By immunohistochemical method, significant expression of NEDD9 protein was identified in 46.7% (28
of 60) of primary human lung adenocarcinoma tissues (Fig. 5A). Overexpression of NEDD9 was associated with increasing invasion into mediastinal (N2) lymph node ($P = 0.01$), pathologic lymphatic invasion ($P = 0.03$), and pathologic venous invasion ($P = 0.03$; Fig. 5B). However, no other statistically significant correlation was found in lung cancer between NEDD9 expression and other clinical parameters, such as age, sex, smoking history, and the extent of primary tumor (Table 1).

With a median follow-up time of 58.5 months (range, 7–91 months), the median RFS was significantly longer in the NEDD9-negative group (not reached) than in the NEDD9-positive group (23 months; $P < 0.001$; Fig. 5C). The HR for RFS was 4.24 [95% confidence interval (CI), 1.93–9.26] in the NEDD9-positive group. The median OS was also significantly longer in the NEDD9-negative group (not reached) than in the NEDD9-positive group (36 months; $P < 0.001$; Fig. 5C).

In univariate Cox analysis, the HR for OS was 5.35 (95% CI, 1.98–14.50) in the NEDD9-positive group. In addition, N2 invasion and pathologic lymphatic invasion were also significant predictors by univariate analysis. In multivariate Cox analysis, NEDD9 expression (HR, 3.88; 95% CI, 1.34–11.23; $P = 0.01$) and pathologic lymphatic invasion (HR,
4.94; 95% CI, 1.04–23.5; \( P = 0.04 \) were independent prognostic variables (summarized in Table 1). Taken together, these results suggest that the expression of NEDD9 closely correlates with venous and lymphatic invasion of cancer cells, and NEDD9 may also be a predictive biomarker for the recurrence and prognosis of human NSCLCs in the clinical setting.

Discussion

In the present study, we showed that tyrosine phosphorylation of NEDD9 was reduced by the inhibition of EGFR in NSCLC cell lines. A constitutively active mutant of EGFR promoted tyrosine phosphorylation of NEDD9 in the absence of integrin signaling. The gene transfer and gene knockdown studies revealed that NEDD9 plays a pivotal role in cell migration and invasion of NSCLC cell line. Overexpression of NEDD9 was shown to promote lung metastasis of an NSCLC cell line in a murine xenograft transplantation model. Finally, the evaluation of the clinical specimens of NSCLCs revealed a strong correlation between NEDD9 expression and RFS or OS, suggesting that NEDD9 is a promising prognostic biomarker in NSCLCs. This is the first study to show the clinical importance of NEDD9 as a prognostic factor as well as the crosstalk between EGFR and NEDD9 signaling pathways in NSCLCs.

Several protein tyrosine kinases (PTK) phosphorylate NEDD9, including FAK (21, 22), RAFTK/Pyk2 (20), Src family PTKs (20, 21), platelet-derived growth factor receptor (PDGFR; ref. 36), Abl (17), and Bcr-Abl (37), many of which are involved in cancer progression and growth. EGFR and PDGFR are RTKs (3) that crosstalk with integrins (8–10, 12), with EGFR physically associating with \( \alpha_5\beta_1 \) (38) and PDGFR with \( \alpha_v \beta_3 \) (39). Engagement of EGFR modulates tyrosine phosphorylation of BCAR1, mediated partly by Src (9), whereas engagement of integrins induces tyrosine phosphorylation of EGFR, mediated by BCAR1 and Src (40, 41). FAK is also a necessary component for EGFR- and PDGFR-induced cell motility (42). These reports suggest that RTKs and integrins form a macromolecular signaling complex at least transiently and have reciprocally compensatory roles in contributing to cell migration and invasion.

In this study, we show that NEDD9 may also be an integrator of EGFR and \( \beta_1 \)-integrin in phosphorylation-dependent signaling, leading to cell migration and invasion of NSCLCs. In this regard, it is possible that other molecules may be associated with EGFR in regulating NEDD9 tyrosine phosphorylation, and additional work is needed to further characterize the signaling complex involving NEDD9, EGFR, and \( \beta_1 \)-integrins in tumorigenesis and metastasis of NSCLCs.

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PC-9 cells used in this study harbors an in-frame deletion in EGFR which causes the receptor to be constitutively activated as a result of structural change proximal to the ATP-binding site (43). These cells and a significant population of NSCLC tumor cells are dependent on the constitutively activated EGFR, thus blockade of the signal by gefitinib results in apoptotic cell death (6, 7). In the context of oncogene involvement in tumor growth, of particular
interest is that blockade of EGFR signal caused not only
dephosphorylation but also a reduction in the protein levels
of focal adhesion resident proteins such as BCAR1 and FAK
as well as NEDD9. Because these proteins have been
reported to incur caspase-induced degradation in apoptosis
(44), the results observed in this study may reflect a gefitin-
nib-induced apoptotic process. Supporting this notion,
gene transfer of NEDD9 into PC-9 and A549 cells conferred
resistance to the chemotherapeutic reagents such as gefiti-
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gene transfer of NEDD9 into PC-9 and A549 cells conferred
resistance to the chemotherapeutic reagents such as gefiti-
nib, paclitaxel, and cisplatin (Supplementary Figs. S2 and
S3). Future in-depth studies will be conducted to expand on
these interesting data.

We and others previously reported that NEDD9 phos-
phorylation contributes to cell migration and invasion (22,
23, 36, 45). We now show the involvement of NEDD9 in
EGF-mediated cell migration and invasion of NSCLCs.
Consistent with previous reports, our studies indicated that
BCAR1 siRNA also caused significant reduction in EGFR-
muchinolected cell motility of NSCLCs. Another member of Cas
family, BCAR1/p130Cas, was independently identified as
the primary gene that confers breast cancer cells with
resistance to anti-estrogen (46). HER2/neu is a member of
the EGFR family and is a notable therapeutic target of breast
cancer, similar to EGFR in NSCLCs (47). Interestingly, a
double-transgenic mice of MMTV-BCAR1 and MMTV-
HER2/neu developed multifocal mammary tumors with a
significant shorter latency than the MMTV-HER2/neu trans-
genic mice (48). Because elevated expression of HER2
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| Table 1. Cox univariate and multivariate analysis of patients with NSCLCs |
|-----------------------------|-----------------------------|-----------------------------|
|                            | RFS                        | OS                         |
|                            | HR (95% CI)                 | P                          | HR (95% CI)                 | P                          |
| **Univariate analysis**    |                            |                            |                            |                            |
| NEDD9 (positive vs. negative) | 4.24 (1.93–9.26)           | <0.001                     | 5.35 (1.98–14.50)           | 0.001                      |
| Sex (male vs. female)      | 1.08 (0.53–2.20)           | 0.83                       | 1.3 (0.56–3.00)             | 0.54                       |
| Age (>65 y)                | 1.17 (0.58–2.38)           | 0.86                       | 1.11 (0.49–2.51)            | 0.8                        |
| Smoking history (smoker vs. non-smoker) | 1.19 (0.58–2.39) | 0.85                       | 1.25 (0.55–2.84)            | 0.59                       |
| pStage (III vs. I–II)      | 2.42 (1.20–4.91)           | 0.01                       | 3.1 (1.35–7.13)             | 0.01                       |
| N1 (positive vs. negative) | 1.45 (0.35–6.12)           | 0.61                       | 1.22 (0.16–9.09)            | 0.85                       |
| N2 (positive vs. negative) | 3.9 (1.91–7.97)            | <0.001                     | 4.8 (2.05–11.21)            | <0.001                     |
| Lymphatic invasion (positive vs. negative) | 5.83 (2.23–15.28) | <0.001                     | 10.1 (2.36–43.2)            | 0.002                      |
| Venous invasion (positive vs. negative) | 1.85 (0.85–4.06) | 0.12                       | 2.713 (1.17–6.29)           | 0.02                       |
| **Multivariate analysis**  |                            |                            |                            |                            |
| NEDD9 (positive vs. negative) | 3.08 (1.37–6.93)           | 0.006                      | 3.88 (1.34–11.23)           | 0.01                       |
| pStage (III vs. I–II)      | 0.78 (0.24–2.5)            | 0.67                       | 1.32 (0.38–4.47)            | 0.66                       |
| N2 (positive vs. negative) | 2.54 (0.76–8.46)           | 0.13                       | 1.84 (0.53–6.39)            | 0.34                       |
| Lymphatic invasion (positive vs. negative) | 4.84 (1.52–15.37) | 0.008                      | 4.94 (1.04–23.5)            | 0.04                       |
| Venous invasion (positive vs. negative) | 0.62 (0.26–1.44) | 0.26                       | 0.79 (0.31–1.99)            | 0.62                       |
identified pathologic prognostic factors. Expression of NEDD9 was associated with a significant increase in the risk of metastasis and recurrence, with a corresponding decrease in survival and worsened clinical outcome. Multivariate analysis also suggested that NEDD9 expression is an independent predictive factor for the recurrence of NSCLCs. To evaluate the NEDD9 expression in NSCLCs, we set 3 cutoff values (10%, 30%, 50%). Kaplan–Meier curves in the cases with 10% cutoff and 50% cutoff value are shown in Supplementary Fig. S4. When the cutoff value (% positive cells) was 10%, there was no statistically significant difference in OS and RFS. When the cutoff was 50%, the number of positive cases was only 6. When the cutoff was 30%, significant difference was observed in OS and RFS. It should be noted that these data were derived from a retrospective analysis and are likely to suffer from selection bias. Randomized control study or stratified analysis will be necessary in a future study to extend our present findings.

In conclusion, our present work suggests that NEDD9 is a predictive factor for recurrence and prognosis in NSCLCs. Although a variety of gene profiles have been reported to correlate with recurrence of NSCLCs, none has yet been definitely established (51). Because the clinical records evaluated in this study did not contain genetical information on EGFR mutation, KRAS mutation which may affect the sensitivity to gefitinib (52), further comprehensive analysis is necessary in the next step. Optimal strategies to prevent recurrence and metastasis of NSCLCs may need to incorporate NEDD9 expression as one of the promising predictive factors and NEDD9 itself may be a novel therapeutic target for future NSCLC treatment.

References


Impact of the Integrin Signaling Adaptor Protein NEDD9 on Prognosis and Metastatic Behavior of Human Lung Cancer

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