Oncogenic Fusion Gene CD74-NRG1 Confers Cancer Stem Cell–like Properties in Lung Cancer through a IGF2 Autocrine/Paracrine Circuit

Takahiko Murayama1,2,3, Takashi Nakaoku4, Masato Enari5, Tatsunori Nishimura1, Kana Tominaga3, Asuka Nakata1, Arinobu Tojo3, Sumio Sugano2, Takashi Kohno4, and Noriko Gotoh1,3

Abstract

The CD74-Neuregulin1 (NRG1) fusion gene was recently identified as novel driver of invasive mucinous adenocarcinoma, a malignant form of lung cancer. However, the function of the CD74-NRG1 fusion gene in adenocarcinoma pathogenesis and the mechanisms by which it may impart protumorigenic characteristics to cancer stem cells (CSC) is still unclear. In this study, we found that the expression of the CD74-NRG1 fusion gene increased the population of lung cancer cells with CSC-like properties. CD74-NRG1 expression facilitated sphere formation not only of cancer cells, but also of nonmalignant lung epithelial cells. Using a limiting dilution assay in a xenograft model, we further show that the CD74-NRG1 fusion gene enhanced tumor initiation. Mechanistically, we found that CD74-NRG1 expression promoted the phosphorylation of ErbB2/3 and activated the PI3K/Akt/NF-kB signaling pathway. Furthermore, the expression of the secreted insulin-like growth factor 2 (IGF2) and phosphorylation of its receptor, IGF1R, were enhanced in an NF-kB–dependent manner in cells expressing CD74-NRG1. These findings suggest that CD74-NRG1–induced NF-kB activity promotes the IGF2 autocrine/paracrine circuit. Moreover, inhibition of ErbB2, PI3K, NF-kB, or IGF2 suppressed CD74-NRG1–induced tumor sphere formation. Therefore, our study provides a preclinical rationale for developing treatment approaches based on these identified pathways to suppress CSC properties that promote tumor progression and recurrence.

Introduction

Cancer stem cells (CSC) are thought to be responsible for tumor, recurrence, and drug resistance (1). It is also believed that many cancer cells are actually differentiated cells generated from CSCs, similar to how normal tissues are derived from tissue–specific stem cells (1). By definition, CSCs represent a distinct cell population with self-renewal capacity that can be prospectively isolated. This population of cancer cells was initially identified in acute myeloid leukemia in 1997 (2). Since then, several properties of CSCs have been described, and cancer cells that exhibit some CSC properties have been detected in many solid tumors, including lung cancer and breast cancer (3–6). Because CSCs are thought to be resistant to various stressful conditions such as treatment with chemotherapy and molecular targeted drugs, they may survive regardless of tumor shrinkage. After some time, the small number of therapy-resistant CSCs may start to grow, leading to recurrence associated with drug resistance. Therefore, targeting molecules that play a critical role in maintenance of CSCs is an important therapeutic strategy to eradicate tumors and prevent recurrence.

Recently, oncogenic fusion genes have been discovered in solid tumors, especially in lung cancer. In lung adenocarcinomas, a major type of lung cancer, oncogene fusions frequently occur and it may act as driver gene aberrations as well as EGFR or KRAS oncogene mutations. The ALK, RET, and ROS1 fusion genes have already been reported to be involved in cancer development (7–10). Crizotinib, an inhibitor of ALK kinase, is clinically available and has been shown to be effective in lung adenocarcinomas with EML4-ALK fusion. Much effort has been devoted to developing targeted drugs against the tyrosine kinases in the fusion protein for improving therapeutic strategies. However, major concerns regarding recurrence and resistance to the targeted drugs against the tyrosine kinases have emerged, resulting in poor prognosis in cancer patients (11). In fact, it is largely unknown whether the fusion genes are functional in terms of initiation and maintenance of CSCs. If such mechanisms exist, novel therapeutic strategies based on these could be developed.

We and other researchers recently identified the CD74-Neuregulin1 (NRG1) fusion gene in a portion of invasive mucinous adenocarcinomas (IMA) of the lung (12, 13). IMA is a highly malignant type of lung adenocarcinoma that is mainly caused by KRAS mutations. However, this fusion gene is found in cancers

Note:

T. Kohno and N. Gotoh contributed equally to this article. T. Murayama and T. Nakaoku contributed equally to this article.

Corresponding Authors: Noriko Gotoh, Division of Cancer Cell Biology, Cancer Research Institute, Kanazawa University, Kakuma-machi, Kanazawa city, Ishikawa 920-1192, Japan. E-mail: ngotoh@ims.u-tokyo.ac.jp; and Takashi Kohno, Division of Genome Biology, National Cancer Center Research Institute, Tokyo, Japan.

doi: 10.1158/0008-5472.CAN-15-2135

©2016 American Association for Cancer Research.
pathway by targeting a single molecule or several molecules in function at the level of CSCs. Thus, inhibition of this signaling study reporting that oncogenic fusion gene products indeed

Production were cultured in DMEM: nutrient mixture with

Cell lines and cell culture
Lung cancer cell line H322 and breast cancer cell line BT20 were purchased from the ATCC. Cells were cultured in RPMI1640 with 10% FBS (Gibco) and 1% penicillin-streptomycin (P/S; Nacalai). HEK293T cells (ATCC) for lentivirus production were cultured in DMEM: nutrient mixture with 10% FBS and 1% P/S. The cells were maintained in a humidified incubator with 5% CO₂ at 37°C.

Materials and Methods

Cell lines and cell culture
Lung cancer cell line H322 and breast cancer cell line BT20 were purchased from the ATCC. Cells were cultured in RPMI1640 with 10% FBS (Gibco) and 1% penicillin-streptomycin (P/S; Nacalai). HEK293T cells (ATCC) for lentivirus production were cultured in DMEM: nutrient mixture with 10% FBS and 1% P/S. The cells were maintained in a humidified incubator with 5% CO₂ at 37°C.

Western blot analysis
Immunoblotting was performed using standard procedures as described (19). Anti-ErbB2, p-ErbB2, p-ErbB3, Akt, p-Akt, Nanog, Oct-4, Sox2, IKKα, IKKβ, p-IKKα/β, JcBo, p-JcBo, IGF1R (receptor for IGF2), and p-IGF1R antibodies were purchased from Cell Signaling Technology. Anti-ErbB3 and actin antibodies were purchased from Millipore. Anti-NRG1 and CD74 antibodies were purchased from Thermo Scientific and Abcam, respectively. Proteins were detected with horseradish peroxidase–conjugated antimouse or anti-rabbit antibodies (GE Healthcare Life Sciences).

Sphere formation assay
Sphere formation assay was performed as described (19). Briefly, cells were plated as single cells on ultralow attachment 24-well plates (2,000–5,000 cells/well). They were grown in SCM, which consisted of serum-free DMEM/F-12 medium (Gibco) supplemented with 20 ng/mL EGF (Millipore), 20 ng/mL basic fibroblast growth factor (bFGF; PeproTech), B27 (Gibco), and heparin (Stem Cell Technologies) or in DMEM/F-12 medium with or without inhibitors or antibodies. LY294002 and anti-IGF2 antibody were purchased from Cell Signaling Technology. Lapatinib and dasatinib were purchased from Selleck Chemicals. DHMEQ was a kind gift from K. Umezawa (Aichi Medical School, Aichi, Japan). Spheres with a diameter >75 μm were counted after 4 to 7 days.

Proliferation assay
Cells were seeded in a 12-well plate at low density (5,000 cells/well), and cultured in RPMI1640 with 10% FBS and 1% P/S. After 4 to 6 days, cells were harvested and counted.

Construction of lentiviral vectors for expression of CD74-NRG1
Expression vectors were constructed as described previously (12). Briefly, full-length cDNAs were amplified from tumor cDNA by PCR and then inserted into pLenti-6/V5-DEST plasmids (Invitrogen). By using Sanger sequencing, the integrity of integrated cDNA was verified.

Viral infection
H322 cells, BT20 cells, and small airway epithelial cells (SAEC) at 60% to 70% confluence were infected with empty lentiviruses or CD74-NRG1–expressing lentiviruses, and then treated with 500 μM 5-iododeoxyuridine (5-IDU) (Invitrogen). By using X-Gal staining, the integration of lentiviral vectors was verified.

Flow cytometry analysis
To identify the breast CSC population, cells were stained with Alexa fluor 647–labeled anti-human CD24 and APC-H7–labeled anti-human CD44 antibodies by FACS and then inserted into pLenti-6/V5-DEST plasmids (Invitrogen). By using FlowJo, the integrity of integrated cDNA was verified.

Quantification of NF-κB activity by ELISA
Nuclear extracts were prepared with a Nuclear Extract Kit (Active Motif), and NF-κB subunit p65-DNA binding activity was measured with a TransAM NF-κB p65 Transcription Factor Assay Kit (Active Motif). All procedures were performed according to the manufacturer's protocol.
Measurement of IGF2 concentration in culture medium

Cells were seeded in 60-mm dishes and cultured in RPMI medium with 10% FBS. At 60% to 70% confluence, the medium was changed to 1.5 mL of RPMI without FBS. After 24-hour incubation, the medium was collected for IGF2 measurement assay. We concentrated 500 µL culture medium to 50 µL by using a microcon (Millipore) and then measured the IGF2 concentration with the IGF2 Human ELISA Kit (Mediagnost). All procedures were performed according to the manufacturer’s protocol.

Xenografts

Cells were admixed with 50 µL Matrigel (BD Biosciences) and the cell mixture was injected into the right flank of 8-week-old nude mice. Tumors larger than 200 mm³ were counted. Tumor volume was measured two times a week using the following formula: \( V = \frac{1}{2}(L \times W^2) \), where \( L \) equals length, and \( W \) equals width.

Statistical analysis

All data are presented as the mean ± SE. The unpaired Student t test was used to compare differences between two samples and values of \( P < 0.01 – 0.05 \) (*), \( P < 0.001 – 0.01 \) (**), or \( P < 0.001 \) (*** ) were considered significant. Tumor-initiating frequency was calculated using the ELDA Software (25).

Study approval

Mice were handled according to the guidelines of National Cancer Center Research Institute, Institute of Medical Science, the University of Tokyo and Kanazawa University. The experiments were approved by the Committees for Animal Research.
at National Cancer Center Research Institute, Institute of Medical Science, the University of Tokyo and Kanazawa University.

Results

CD74-NRG1 protein induces sphere formation of cancer cells

We first examined whether the CD74-NRG1 fusion protein induces sphere formation by lung cancer cells. To evaluate the sphere-forming ability of CD74-NRG1–expressing cells, we infected lentivirus encoding cDNA for the CD74-NRG1 fusion gene, C6;N6 and C8;N6 variants, as reported by Nakaoku and colleagues (12), into H322 lung cancer cells (Fig. 1A and B). These two variants are different in the breakpoints of CD74. We chose H322 cells for this study because they have no KRAS mutations. When we cultured these cells in conventional SCM containing EGF, bFGF, and B27 supplement, they generated spheres with similar efficiency as cells infected with lentivirus carrying a control vector (Fig. 1C and D). Intriguingly, CD74-NRG1–expressing cells also generated spheres when cultured in medium without EGF, bFGF, or B27 supplement, whereas control cells did not (Fig. 1C and D). Because CSC-related function of NRG1 protein was originally identified in breast cancer cells (19), we constructed CD74-NRG1–expressing BT20 breast cancer cells to investigate the mammosphere-forming ability (Fig. 1B). CD74-NRG1–expressing breast cancer cells formed mammospheres even when cultured in a medium without EGF, bFGF, or B27 supplement (Fig. 1E and F). These findings indicate that the CD74-NRG1 fusion protein induces tumor sphere-forming ability in lung and breast cancer cells.

The CSC population increased in CD74-NRG1–expressing cells

Next, we examined expression levels of the stem cell marker proteins, Nanog, Oct-3/4, and Sox2 (26). These stem cell markers were expressed at higher levels in CD74-NRG1–expressing H322 cells than in control cells (Fig. 2A). Also, in CD74-NRG1–expressing BT20 cells, expression levels of the stem cell markers were higher than in control cells (Fig. 2B). In breast cancer, the CD44high/CD24low cell population is enriched with cancer cells with stem-like properties (3, 27). When we investigated the proportion of CD44high/CD24low CSC-enriched cells by flow cytometry, the percentages of the CD44high/CD24low population increased from 1.94% to 9.47% (C6;N6 variant) or 8.21%

Figure 2.
The CD74-NRG1 fusion protein increases the proportion of CSCs.
A, expression levels of Nanog, Oct3/4, and Sox2 in H322 cells with each vector were determined by immunoblotting. B, expression levels of Nanog, Oct3/4, and Sox2 in BT20 cells with each vector were determined by immunoblotting. C, vector- or CD74-NRG1–transduced BT20 cells were stained with CD44 and CD24 antibodies and then subjected to flow cytometry analysis. D and E, H322 cells (D) or BT20 cells (E) with each vector were seeded in a 12-well plate (5,000 cells/well). Cells were cultured in 10% FBS and then harvested and counted after 4 or 6 days (n = 4). F, H322 cells were seeded as described in D. Cells were starved in 0.5% FBS and then harvested and counted after 6 days (n = 4).
These data further support the idea that the CD74-NRG1 fusion gene can enhance CSC properties. On the other hand, the proliferation assay revealed that the CD74-NRG1 protein did not significantly induce cell growth in adherent cultures (Fig. 2D and E) in the medium containing 10% FBS or the starvation medium with 0.5% FBS (Fig. 2F).

The CD74-NRG1 protein activates the PI3K/Akt pathway and controls sphere formation ability

Because the CD74-NRG1 fusion protein contains the functional domain of NRG1, we hypothesized that activation of the ErbB2/ErbB3–regulated pathway contributes to sphere formation by CD74-NRG1–expressing cells. To test this hypothesis, we examined the phosphorylation levels of ErbB2, ErbB3, and Akt. Expression of the CD74-NRG1 fusion protein increased the phosphorylation levels of ErbB2, ErbB3, and Akt compared with vector control cells (Fig. 3A). Similar results were observed in CD74-NRG1–expressing BT20 cells (Fig. 3B). These data show that the CD74-NRG1 fusion protein activates ErbB2 and ErbB3 heterodimer receptors, leading to PI3K/Akt pathway activation. Then, to investigate whether activation of the ErbB signaling pathway is important for tumor sphere formation, we checked the effect of lapatinib, an inhibitory protein, in the cytoplasm (28). IκKα/β are the upstream kinases involved in the phosphorylation of IκBα, which results in its ubiquitination, proteasome-mediated degradation, and the subsequent release of NF-κB. The released NF-κB translocates to the nucleus and binds to the κB sequence, where it promotes the transcription of various genes. We compared phosphorylation levels of these proteins in CD74-NRG1–expressing cells and control cells. In CD74-NRG1–expressing cells, phosphorylation levels of IκKα/β and IκBα were increased (Fig. 4A). To examine the DNA-binding activity of NF-κB subunit p65 in CD74-NRG1–expressing cells, we quantified the intensity of the p65/DNA complex formation by ELISA. Expression of CD74-NRG1 fusion protein led to a marked increase in the DNA-binding activity of p65 (Fig. 4B and C). Thus, the CD74-NRG1 protein-stimulated ErbB2/ErbB3 signaling pathway appears to activate PI3K/Akt, leading to NF-κB activation. To test whether activation of PI3K or NF-κB is involved in the sphere-forming ability of CD74-NRG1–expressing cells, we treated these cells with LY294002 and DHMEQ, specific inhibitors of PI3K and NF-κB.

NF-κB activation contributes to sphere formation by CD74-NRG1–expressing cells

The NF-κB transcription factor complex, a downstream target of Akt, is activated by the NRG1-stimulated ErbB2/ErbB3 signaling pathway (19). We then investigated whether NF-κB signaling is activated in CD74-NRG1–expressing cells. The NF-κB transcription factor complex is usually inactive and bound to IκBα, an inhibitory protein, in the cytoplasm (28). IκKα/β are the upstream kinases involved in the phosphorylation of IκBα, which results in its ubiquitination, proteasome-mediated degradation, and the subsequent release of NF-κB. The released NF-κB translocates to the nucleus and binds to the κB sequence, where it promotes the transcription of various genes. We compared phosphorylation levels of these proteins in CD74-NRG1–expressing cells and control cells. In CD74-NRG1–expressing cells, phosphorylation levels of IκKα/β and IκBα were increased (Fig. 4A). To examine the DNA-binding activity of NF-κB subunit p65 in CD74-NRG1–expressing cells, we quantified the intensity of the p65/DNA complex formation by ELISA. Expression of CD74-NRG1 fusion protein led to a marked increase in the DNA-binding activity of p65 (Fig. 4B and C). Thus, the CD74-NRG1 protein-stimulated ErbB2/ErbB3 signaling pathway appears to activate PI3K/Akt, leading to NF-κB activation. To test whether activation of PI3K or NF-κB is involved in the sphere-forming ability of CD74-NRG1–expressing cells, we treated these cells with LY294002 and DHMEQ, specific inhibitors of PI3K and NF-κB.
respectively (29). LY294002 or DHMEQ suppressed sphere formation at the similar levels in both H322 and BT20 cells (Fig. 4D and E). These data indicate that PI3K/Akt/NF-κB pathway induces tumor sphere-forming ability.

IGF2 plays important roles in sphere formation induced by the CD74-NRG1 fusion protein

We have recently found that IGF2 is a downstream target of NF-κB upon stimulation with NRG (Tominaga K, Murayama T, and colleagues; unpublished data). We next measured secreted IGF2 protein in culture medium. The amount of IGF2 protein was increased by CD74-NRG1 expression: 0.91 ng/mL and 0.98 ng/mL in cells expressing C6;N6 and C8;N6 variants of CD74-NRG1, respectively, compared with 0.71 ng/mL in control cells (n = 2).

To investigate whether secreted IGF2 is involved in sphere formation, we added IGF2-neutralizing antibody to the medium and measured sphere-forming efficiency in H322 cells and BT20 cells. The IGF2-neutralizing antibody greatly decreased sphere-forming efficiency in cells expressing either variant of CD74-NRG1 but not in control cells (Fig. 5A and B). To check whether IGF1R, a receptor for IGF2, is activated by secreted IGF2 that is induced by CD74–NRG1–NF-κB pathway, we treated H322 cells expressing C8;N6 variants of CD74-NRG1 with or without DHMEQ and examined phosphorylation of IGF1R. We found that the phosphorylation levels of IGF1R were increased by expression of CD74-NRG1 protein (Fig. 5C). The increased phosphorylation levels of IGF1R...
The CD74-NRG1 protein induces sphere formation of normal lung epithelial cells

Finally, we extended our analysis to noncancerous cells. Using the lentivirus system, we created CD74-NRG1–expressing SAECs, which are immortalized normal lung epithelial cells (30). We analyzed the efficiency of sphere formation by these cells in serum-free medium without EGF, bFGF, or B27 supplement. We found that CD74-NRG1–expressing SAECs formed spheres, but control SAECs formed no spheres. These results support the notion that CD74-NRG1 initiates CSCs in lung tissues without requiring paracrine factors such as growth factors, indicating that this fusion gene is a strong driver gene (Fig. 6B and C).

Discussion

In this study, we provide evidence that the CD74-NRG1 fusion gene appears to play critical roles in the initiation and maintenance of CSC properties. Moreover, we clarified the signaling pathways controlled by the CD74-NRG1 protein. The CD74-NRG1 protein activates the ErbB/PI3K/NF-κB pathway, which leads to activation of the IGF2-autocrine/paracrine circuit. Thus, oncogenesis may occur at the level of CSCs. It is reasonable to hypothesize that the CD74-NRG1 protein confers CSC properties on a few immature, progenitor-like cells rather than on the terminally differentiated cancer cells. This finding is important, because therapy targeting a single molecule or several molecules in combination in this pathway may eradicate tumors and prevent recurrence (Fig. 6D).

IMAs of the lung constitute 2% to 10% of all lung adenocarcinomas in Japan and the United States, and are regarded as more malignant than other more common types of lung adenocarcinomas (31–33). The KRAS mutation was the only driver aberration found in IMAs. However, to improve clinical outcomes, it is necessary to identify novel driver aberrations in IMAs. Following much effort, the CD74-NRG1 fusion gene was identified in IMAs in 2014 (12, 13). This fusion gene is mutually exclusive with KRAS mutations. In CD74-NRG1 fusion–positive tumors, enhanced expression of NRG1 is observed (13). CD74-NRG1 is regarded as a driver gene aberration in the development of IMA. As it has been recently reported that the fusion genes that include a part of NRG1 are found in ovarian cancer (15), the gene alteration involving NRG1 fusion may also occur in other types of tumors.

In breast cancer cells and tissues, breaks within NRG1 are frequently detected and may be responsible for NRG1 gene fusion (16, 17). In fact, DOC4-NRG1 fusion gene is observed in the MDA-MB-175 breast cancer cell line (18). In this cell line, NRG1 expression is enhanced because of the promoter activity of DOC4 and NRG1 is produced in the culture medium. It is, thus, reasonable that some breast cancers are caused by NRG1 gene fusion in a manner similar to that observed in CD74-NRG1 fusion–positive IMAs. We are currently trying to identify important gene fusion variants in breast cancers.
aberrations including gene fusions in breast cancer by using next-generation sequencing.

In this study, we showed that expression of the CD74-NRG1 protein not only induces sphere-forming ability \textit{in vitro} but also enhances the tumor-initiating ability \textit{in vivo}. These findings indicate that this fusion gene is involved in tumor development by inducing CSC properties and will be an effective therapeutic target for these tumors. Moreover, we showed that the CD74-NRG1 protein activates the PI3K/Akt/NF-\text{k}B signaling pathway, leading to IGF2 autocrine/paracrine circuit to initiate and maintain cells with CSC properties. Our findings provide a rationale for developing alternative treatment options, despite the emergence of

### Table 1. Results of limiting dilution assay of vector- or CD74-NRG1-transduced H322 cells

<table>
<thead>
<tr>
<th>Cells (per site)</th>
<th>H322 cells</th>
<th>Tumor-initiating cell frequency estimate</th>
<th>Probability</th>
</tr>
</thead>
<tbody>
<tr>
<td>Empty vector</td>
<td>1/6</td>
<td>3/6</td>
<td>6/6</td>
</tr>
<tr>
<td>CD74-NRG1 (C6,N6)</td>
<td>4/6</td>
<td>5/6</td>
<td>5/6</td>
</tr>
</tbody>
</table>

**Figure 6.**

The CD74-NRG1 fusion protein enhances the tumor-initiating ability of cancer cells. A, tumor growth curves of vector- or CD74-NRG1-transduced H322 cells when injected with 1 $\times$ 10^3 cells (n = 6). B and C, sphere formation assay with vector- or CD74-NRG1-transduced SAECs. (N.T., not treated; n = 4, “”, P < 0.001). Scale bar, 100 $\mu$m. D, The CSC maintenance signals. The CD74-NRG1 protein activates PI3K/Akt/NF-\text{k}B pathway to induce IGF2 autocrine/paracrine circuit for maintenance of CSCs. Blocking one or several molecules in the pathways would be effective for eradicating tumors.
acquired resistance. Because the major acquired resistance mechanisms have been reported to be additional mutations in the tyrosine kinase domain of the fusion gene, effective drugs targeting the mutant tyrosine kinases have been developed (34). Our findings suggest that targeting other molecules in this pathway, rather than the mutant tyrosine kinases themselves, for the initiation and maintenance of CSCs, may be equally effective.

It does not seem that expression of the CD74-NRG1 protein strongly stimulates cell growth in vitro and in vivo. It is thought that cells with CSC properties grow rather slower than other differentiated cancer cells (1). It is thus reasonable that the CSC properties conferred by expression of the CD74-NRG1 are not strongly associated with stimulation of cell growth. As the important characteristic of CSCs is the resistance to stressful conditions, the CD74-NRG1–expressing cancer cells may be more resistant to conventional chemotherapeutics than those without expression of the CD74-NRG1 protein.

Expression of CD74-NRG1 increased the percentage of CD44<sup>high</sup>/CD24<sup>−/low</sup> CSC-enriched cells from 1.9% to approximately 9.5%. The fact that CD44<sup>high</sup>/CD24<sup>−/low</sup> CSC-enriched cells are still a minor population indicates that expression of the CD74-NRG1 protein is not sufficient for conferring CSC properties on all cells. As the parental BT20 cells do not express the CD74-NRG1 gene, it is possible that the intrinsic CSC properties carried by a subpopulation of BT20 cells are conferred by other gene alterations. However, the increase in the population of BT20 cells with CSC properties by enforced CD74-NRG1 expression may indicate that the intrinsic CSC properties are conferred on more cells by the IGF2 autocrine/paracrine circuit. It is known that even within a cancer cell line, there are immature cell populations with CSC properties and other differentiated cancer cell populations (27, 35). It is thus possible that expression of the CD74-NRG1 protein shifts the cell population toward more cells with CSC properties than differentiated cells.

The mechanisms underlying the production of IGF2 by NF-κB are unclear. We recently found that NRG stimulates the transcription of IGF2 mRNA in an NF-κB–dependent manner (Tominaga K, Murayama T, and colleagues; unpublished data). Several binding site motifs for NF-κB are present in the IGF2 promoter sequence. Thus, increased NF-κB activity may lead to production of IGF2 at the transcriptional level.

In conclusion, our results suggest that PI3K/Akt/NF-κB/IGF2 signaling activated by the CD74-NRG1 fusion protein is involved in CSC maintenance and tumor initiation. Therefore, development of efficient inhibitors or antibodies targeting the molecules in this pathway is anticipated to improve the prognosis of IMA patients with the CD74-NRG1 fusion gene. Furthermore, establishment of effective diagnostic methods capable of detecting this gene aberration is necessary. A therapeutic strategy that targets cells with CSC properties by inhibiting PI3K/Akt/NF-κB may be useful in other types of cancers caused by NRG1 gene fusions, besides IMAs.

Disclosure of Potential Conflicts of Interest

No potential conflicts of interest were disclosed.

Authors’ Contributions

Conception and design: T. Murayama, T. Nakaoku, N. Gotoh

Acquisition of data (provided animals, acquired and managed patients, provided facilities, etc.): T. Murayama, N. Gotoh

Analysis and interpretation of data (e.g., statistical analysis, biostatistics, computational analysis): T. Murayama, T. Nakaoku, N. Gotoh

Writing, review, and/or revision of the manuscript (i.e., reporting and organizing data, constructing databases): M. Enan, A. Tojo, S. Sugano

Study supervision: S. Sugano, T. Kohn

Acknowledgments

The authors thank H. Nakauchi, Y. Ishii, and A. Fujita for their help with flow cytometry. The authors also thank A. Umezawa for his kind gift of DHMEQ.

Grant Support

This work was supported in part by Extramural Collaborative Research Grant of Cancer Research Institute, Kanazawa University, by Grant-in-Aid for Scientific Research on Innovative Areas from MEXT (13327601) and Grant-in-Aid for Scientific Research (B, 15548647) from JSPS (N. Gotoh), and for the Practical Research for Innovative Cancer Control (15ck0106012h00002) from the Japan Agency for Medical Research and Development (AmED, T. Kohn).

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 April 4, 2015; revised October 17, 2015; accepted October 26, 2015, published OnlineFirst February 2, 2016.

References

5. Tominaga K, Murayama T, and colleagues; unpublished data.


Oncogenic Fusion Gene CD74-NRG1 Confers Cancer Stem Cell–like Properties in Lung Cancer through a IGF2 Autocrine/Paracrine Circuit

Takahiko Murayama, Takashi Nakaoku, Masato Enari, et al.

Cancer Res 2016;76:974-983. Published OnlineFirst February 2, 2016.

Updated version
Access the most recent version of this article at:
doi:10.1158/0008-5472.CAN-15-2135

Cited articles
This article cites 35 articles, 9 of which you can access for free at:
http://cancerres.aacrjournals.org/content/76/4/974.full#ref-list-1

Citing articles
This article has been cited by 1 HighWire-hosted articles. Access the articles at:
http://cancerres.aacrjournals.org/content/76/4/974.full#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, use this link
http://cancerres.aacrjournals.org/content/76/4/974.
Click on "Request Permissions" which will take you to the Copyright Clearance Center's (CCC) Rightslink site.