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**Table 1.** Therapeutic effect of oral treatment with E7080 on the multiple organ metastasis produced by non-EGFR mutant lung cancer cell lines in immunodeficient mice

| Cell line | Treatment | Liver | | | Lung | | | Kidney | | | Bone |
|---|---|---|---|---|---|---|---|---|---|---|---|
| | | Weight, g | No. of metastasis | | Weight, mg | No. of metastasis | | Weight, mg | No. of metastasis | | No. of metastasis |
| | | | All nodules | >2 mm[a] | | All nodules | >2 mm | | All nodules | 2 mm | |
| SBC-5 ($N = 5$) | Control | 2.0 (1.1–2.7)[b] | 89 (58–95) | 64 (35–73) | 195 (162–212) | 66 (46–101) | All 0 | N/A | | | 11 (8–11) |
| | E7080 | | | | | | | | | | |
| | 1 mg/kg | 1.1 (0.9–1.4)[c] | 59 (29–78) | 30 (14–52)[c] | 189 (176–204) | 50 (37–85) | All 0 | | | | 11 (8–11) |
| | 3 mg/kg | 1.1 (0.8–1.3)[c] | 50 (30–56) | 20 (9–24)[c] | 222 (140–276) | 66 (41–89) | All 0 | | | | 6 (5–7) |
| | 10 mg/kg | 1.1 (1.0–1.4)[c] | 71 (30–107) | 12 (7–37)[c] | 190 (183–206) | 70 (46–85) | All 0 | | | | 6 (5–7) |
| PC14PE6 ($N = 8$) | Control | N/A | | | 558 (477–740) | 86 (85–108) | 65 (54–76) | N/A | | | N/A |
| | E7080 | | | | | | | | | | |
| | 1 mg/kg | | | | 240 (208–311)[c] | 77 (42–91) | 20 (8–41)[c] | | | | |
| | 3 mg/kg | | | | 260 (206–285)[c] | 79 (56–86) | 19 (10–24)[c] | | | | |
| | 10 mg/kg | | | | 205 (195–232)[c] | 69 (26–113) | 11 (2–29)[c] | | | | |
| H1048 ($N = 8$) | Control | 1.6 (1.0–2.3) | 77 (2–113) | 24 (0–86) | N/A | | | 490 (300–1,020) | 52 (18–85) | 40 (19–77) | 6 (3–10) |
| | E7080 | | | | | | | | | | |
| | 1 mg/kg | 1.3 (1.0–1.7) | 59 (17–122) | 17 (4–25) | | | | 485 (310–670) | 67 (52–83) | 45 (33–63) | 7 (4–9) |
| | 10 mg/kg | 0.9 (0.7–1.2) | 33 (3–91) | 6 (0–11)[c] | | | | 245 (200–450)[c] | 47 (27–69) | 15 (10–53)[c] | 4 (0–6)[c] |

Abbreviation: N/A, not applicable.

[a]Number of metastatic nodules larger than 2 mm in diameter.

[b]Median (range).

[c]$P < 0.05$.

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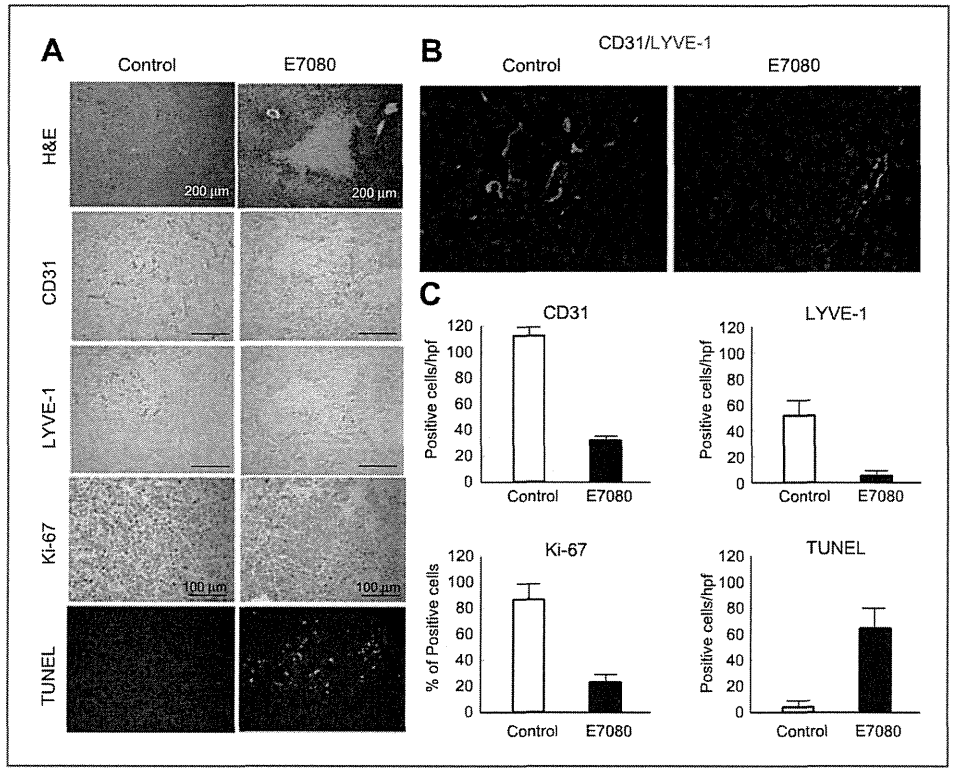


Figure 4. E7080 inhibition of angiogenesis and lymphangiogenesis in liver metastases of SBC-5 cells. A, liver metastatic nodules produced by SBC-5 cells with or without E7080 (10 mg/kg) treatment were stained for hematoxylin and eosin (H&E), endothelial cells (CD31), lymph endothelial cells (LYVE-1), proliferating human tumor cells (Ki-67), and apoptotic cells (TUNEL). Bars indicate 200 μm for H&E, CD31, and LYVE-1, and 100 μm for Ki-67 and TUNEL. B, the same nodules were double stained for CD31 (red) and TUNEL (green) to detect apoptotic endothelial cells. C, number of cells positive for CD31, LYVE-1, Ki-67, and TUNEL in 5 areas (×200). Bars indicate SDs.

PC14PE6 cells were intravenously inoculated into NK cell–depleted SCID and nude mice, respectively, and, beginning 14 days later, the mice were treated with E7080 (10 mg/kg). While all SBC-5–bearing mice treated with distilled water died within 40 days, treatment with E7080 significantly prolonged survival (median survival: 35 vs. 42 days; $P = 0.0001$; Fig. 5). Similarly, all PC14PE6-bearing mice treated with distilled water died within 42 days, whereas treatment with E7080 significantly prolonged survival (median survival: 37 vs. 65 days; $P = 0.0001$). These results clearly indicate that E7080 treatment has survival benefit in mice bearing metastases of nonmutant *EGFR* lung cancer cells.

## Discussion

Lung cancer has been subdivided clinically into SCLC and NSCLC because these 2 subgroups have quite different clinical characteristics, such as speed of growth/spread and responses to cytotoxic chemotherapy and radiotherapy (2). The prognosis of patients with lung tumors bearing *EGFR* mutations has been markedly improved by treatment with the EGFR tyrosine kinase inhibitors, gefitinib and erlotinib (3, 4), resulting in a paradigm shift in therapeutic strategy, based on *EGFR* mutation status, in these patients (28). Prognosis remains poor, however, in patients with tumors bearing nonmutated *EGFR*. We have shown here that a multiple kinase inhibitor, E7080, suppressed the production of hematogenous metastasis into multiple organs and prolonged the survival of mice bearing lung cancer cells with nonmutated *EGFR*. Because E7080 treatment was started after the establishment of micrometastases or macrometastases, our results indicate that E7080 can suppress the enlargement of established metastases. Our results also suggest that the major mechanism by which E7080 inhibited established metastases was inhibition of tumor cell growth due to angiogenesis inhibition. The angiogenesis inhibition was caused by suppression of VEGFR-2 expressed in endothelial cells. Angiogenesis inhibitors indirectly inhibit tumor growth via inhibition of angiogenesis which is essential for supplying the oxygen and nutrition to cancer cells (6). Here, E7080 inhibited the phosphorylation of VEGFR-2 in endothelial cells even at low doses ($IC_{50}$ = 0.3 nmol/L) but did not directly inhibit the *in vitro* proliferation of tumor cells at high doses ($IC_{50}$ > 1,000 nmol/L). In addition, E7080 dramatically decreased the density of CD31-positive vessels, and decreased the number of proliferating tumor cells, in the metastatic nodules.

We also found that E7080 treatment inhibited lymphangiogenesis. E7080 decreased the number of LYVE-1–positive lymph endothelial cells in the metastatic nodules produced by SBC-5 cells, although this effect was less than its effect on angiogenesis. Although lymphangiogenesis is thought to facilitate lymph node metastasis (7, 10, 11), the impact of lymphangiogenesis on the production of experimental hematogenous

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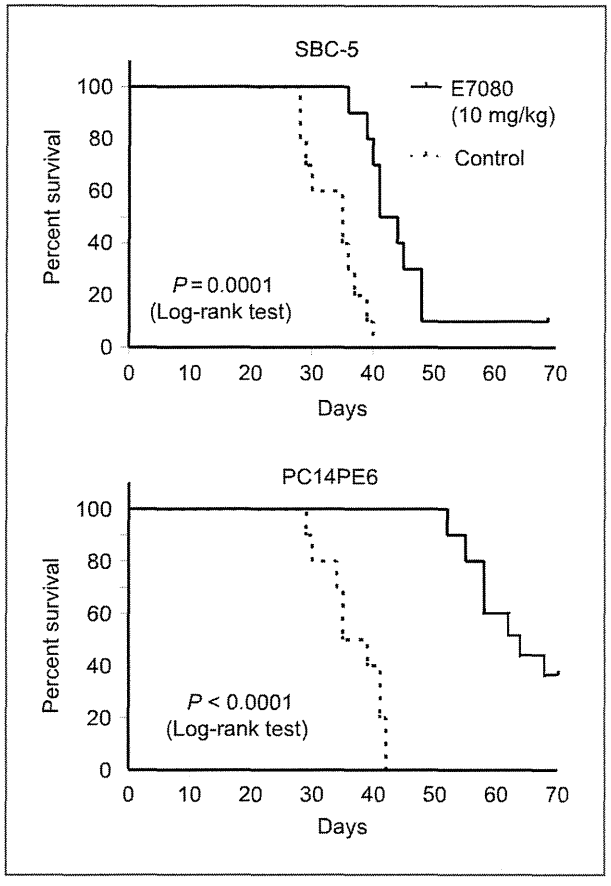


Figure 5. E7080 prolongation of the survival of mice bearing metastases of lung cancer cells bearing nonmutant EGFR. SBC-5 (A) and PC14PE6 (B) cells were intravenously inoculated into NK cell–depleted SCID mice and nude mice, respectively. The mice received distilled water or E7080 (10 mg/kg) orally, starting 14 days after tumor cell inoculation until they became moribund.

metastases in our models remains unclear. Interestingly, SBC-5 cells expressed VEGFR-3 but not its ligands, VEGF-C and VEGF-D. One possible explanation for lymphangiogenesis in SBC-5 tumors is that VEGF-C and/or VEGF-D production by tumor cells was induced *in vivo* (29), or the host microenvironment produced VEGF-C and VEGF-D (30) and activated VEGFR-3 on lymph endothelial cells. Another possibility is that VEGF produced by SBC-5 cells as well as host cells stimulated VEGFR-2, inducing not only angiogenesis but lymphangiogenesis (31). Further investigations on the role of lymphangiogenesis in our models may provide greater understanding of the mechanism by which E7080 inhibited lymphangiogenesis.

Interestingly, H1048 cells did not produce lung metastasis though they originated from lung. This phenomenon was also observed in several SCLC (H69, H69/VP, and SBC-3) and NSCLC (RERF-LC-AI) cells in our metastasis model (20, 32). The reason why these lung cancer cell lines failed to produce lung metastasis in our model is unclear at present. As proposed by Paget as "seed and soil theory" (33), organ tropism of metastasis may be determined by cross-talk between cancer cells and host microenvironment. We previously reported that SBC-5 cells expressed different sets of genes in the different organs (34), suggesting heterogeneity of lung cancer cells and importance of interaction with microenvironment. We would like to explore the mechanisms in future.

Many chemotherapeutic agents show heterogeneity of therapeutic efficacy among organs (33). One of the advantages of our metastasis models is that therapeutic efficacy can be evaluated in multiple organs simultaneously (22–24). We found that E7080 showed therapeutic effects in almost all organs evaluated. For example, E7080 decreased the total number of osteolytic bone nodules, as well as the number of large nodules (>2 mm diameter) in the liver and kidney. This is consistent with the antiangiogenic mechanism of action of E7080 because angiogenesis is required for enlargement of nodules over 1 to 2 mm in diameter (35). The only exception was that E7080 had little effect on lung nodules produced by SBC-5 cells. However, lung lesions produced by SBC-5 cells were smaller than 2 mm in diameter and had few endothelial cells and lymph endothelial cells. In sharp contrast, PC14PE6 cells, which produce high amounts of VEGF, give rise to highly angiogenic and lymphangiogenic lung lesions greater than 2 mm in diameter (9, 25). E7080 decreased the number of endothelial cells, lymph endothelial cells, and proliferating cells in PC14PE6 lung lesions, but it did not in SBC-5 lung lesions with few endothelial cells and lymph endothelial cells (Supplementary Figs. S4 and 5). In addition, while E7080 did not decrease the total number of lung nodules, it did decrease the number of large nodules, similar to its effect against liver metastases of SBC-5 and H1048 cells (Table 1). Collectively, these results indicate that E7080 possesses antiangiogenic activity in various organs including the lungs.

Another serious problem in the management of patients with lung cancer is pleural effusion, which causes respiratory symptoms and decreases patient quality of life (36). We have reported previously that the VEGF–VEGFR-2 axis plays an essential role in the production of pleural effusion (9). To produce pleural effusion, tumor cells must invade the pleura, disseminate into the pleural cavity, and produce a large amount of VEGF in the thoracic cavity. This VEGF induces hypervascular permeability in the thoracic cavity, thereby causing pleural effusion (9). In addition to suppressing the enlargement of lung nodules by PC14PE6 cells, E7080 may inhibit vascular permeability by inhibiting VEGFR-2 activity. Therefore, E7080 may be also useful for controlling pleural effusion caused by lung cancers producing high amounts of VEGF.

We previously reported that 2 other VEGFR-2 tyrosine kinase inhibitors, PTK787 (37) and ZD6474 (vandetanib; refs. 25, 38), have therapeutic efficacy against multiple organ metastases induced by SBC-5 cells and/or against pleural effusion induced by PC14PE6 cells. The results

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presented here indicate that E7080 is much more active than these other compounds. The concentrations of E7080 required to inhibit endothelial proliferation was lower, as was the dose needed to show antimetastatic effects (10 vs. 50 mg/kg; refs. 25, 37, 38). Furthermore, we found that E7080 prolonged survival in mice bearing multiple organ metastases of SBC-5 cells those with pleural effusion caused by PC14PE6 cells, clearly indicating that E7080 is a highly active inhibitor of angiogenesis of lung cancers with nonmutant EGFR. Short-term (2 weeks) treatment with E7080 did prolong the mice bearing multiple organ metastases of SBC-5 or PC14PE6 cells, the duration was only 1 to 2 weeks (data not shown). Therefore, continuous treatment may be necessary for obtaining best therapeutic efficacy of this compound.

E7080 is currently being evaluated in clinical trials against a wide variety of solid tumors. Phase I studies have shown that treatment with E7080 induced partial responses in patients with colorectal cancer, melanoma, renal cell carcinoma, and sarcoma (39, 40). Based on these promising results, phase II clinical trials are currently ongoing.

In summary, we found that the multi tyrosine kinase inhibitor E7080 could inhibit angiogenesis and the enlargement of hematogenic metastatic nodules, thereby prolonging survival of mice bearing multiple organ metastases and pleural effusion induced by lung cancer cells with nonmutant EGFR. Further clinical evaluation of E7080 is warranted for treatment of lung cancer patients with nonmutant EGFR.

## Disclosure of Potential Conflicts of Interest

S. Sone received research support and lecture fee from Eisai Co. Ltd. The other authors declare no potential conflicts of interest. A. Tsuruoka and T. Uenaka are employed by Eisai Co. Ltd.

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*Tumorigenesis and Neoplastic Progression*

# Pleural Mesothelioma Instigates Tumor-Associated Fibroblasts To Promote Progression via a Malignant Cytokine Network

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**The tumor microenvironment is crucial to the progression of various malignancies. Malignant pleural mesothelioma (MPM), which originates from the pleura, grows aggressively in the thoracic cavity. Here we describe an orthotopic implantation SCID mouse model of MPM and demonstrate that α-SMA-positive fibroblast-like cells accumulate in the tumors produced by the human MPM cell lines MSTO-211H and Y-Meso-14. We assessed the interaction between MPM cells and their microenvironments, focusing on tumor-associated fibroblasts. MSTO-211H and Y-Meso-14 cells produced fibroblast growth factor-2 (FGF-2) and/or platelet-derived growth factor-AA (PDGF-AA); they also enhanced growth, migration, and production of hepatocyte growth factor (HGF) by human lung fibroblast MRC-5 cells. MRC-5 cells stimulated HGF-mediated growth and migration of MSTO-211H and Y-Meso-14 cells in an *in vitro* coculture system. In the orthotopic model, tumor formation by MSTO-211H and Y-Meso-14 cells was significantly inhibited by TSU-68, an inhibitor of FGF, VEGF, and PDGF receptors; imatinib, an inhibitor of PDGF receptors; and NK4, an antagonist of HGF. Histological analyses of clinical specimens from 51 MPM patients revealed considerable tumor-associated fibroblasts infiltration and expression of HGF, together with FGF-2 or PDGF-AA, in tumors. These findings indicate that MPM instigates tumor-associated fibroblasts, promoting tumor progression via a malignant cytokine network. Regulation of this cytokine network may be therapeutically useful for controlling MPM. *(Am J Pathol 2011, 179:1483–1493; DOI: 10.1016/j.ajpath.2011.05.060)***

Malignant pleural mesothelioma (MPM) is a unique form of tumor, the development of which is highly related to asbestos exposure.[1] Even after bans on asbestos were initiated in the 1970s, MPM remains a serious problem worldwide because of its long latency period (30 to 40 years) and high mortality rate. In the United States, 2000 to 3000 patients die of MPM every year. Deaths from this disease are expected to peak in 2020 to 2025, with more than 250,000 deaths expected to occur in Western Europe and Japan over the next 40 years.[2] MPM grows aggressively, with dissemination in the thoracic cavity, and frequently produces a malignant pleural effusion.[3] MPM is rarely diagnosed at an operable stage, and it is refractory to

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conventional chemotherapy and radiotherapy. Thus, the prognosis of patients with this disease is extremely poor, with median survival varying between 8 and 14 months after diagnosis, despite the recent development of a chemotherapy regimen combining cisplatin and an antifolate agent such as pemetrexed or raltitrexed.[4]

The tumor microenvironment is crucial for the progression and chemosensitivity of various malignant diseases.[5] For example, the tumor microenvironment mediates endocrine instigation of indolent metastatic tumor progression via osteopontin.[6] Moreover, EGFR-TKI resistance may be induced by microenvironmental fibroblasts in epidermal growth factor receptor mutant lung cancer.[7] Thus, innovative therapies may target the microenvironment. For example, antiangiogenic therapy targeting host endothelial cells and bisphosphonate targeting host osteoclasts have been successfully used to treat several malignant diseases, including colon cancer,[8] non-small cell lung cancer,[9,10] and metastatic bone tumors.[11]

In MPM, angiogenesis inhibition using an anti-VEGF antibody targeting endothelial cells can successfully control the progression of MPM cells that produce high concentrations of VEGF.[12] Tumor-associated fibroblasts (TAFs), also known as cancer-associated fibroblasts, are the major component of tumor microenvironments.[13] TAFs regulate tumor behavior through several mediators. Although recent studies show that many populations of MPM contain TAFs,[14] little is known about interactions between TAFs and MPM. We therefore investigated the molecular interaction between MPM and TAFs, using an orthotopic implantation SCID mice model and clinical specimens taken from MPM patients. We show here that MPMs produce fibroblast-growth factor 2 (FGF-2) and platelet-derived growth factor-AA (PDGF-AA), and that these growth factors stimulate TAFs to produce hepatocyte growth factor (HGF), thus promoting tumor progression through a malignant cytokine network.

## Materials and Methods

### Cell Lines and Reagents

We used the human MPM cell lines MSTO-211H, EHMES-10, and Y-Meso-14, established from patients with biphasic type MPM. MSTO-211H cells were purchased from the American Type Culture Collection (ATCC, Manassas, VA). EHMES-10 were kindly provided by Dr. Hironobu Hamada (Ehime University, Ehime, Japan) and Y-Meso-14 cells by Dr. Yoshitaka Sekido (Aichi Cancer Center Research Institute, Nagoya, Japan). Cells were cultured in modified Eagle's medium or in RPMI 1640 supplemented with 10% heat-inactivated fetal bovine serum (FBS) and gentamicin at 37°C in a humidified atmosphere of 5% $CO_2$ in air. The human embryonic lung fibroblast cell line MRC-5 and the mouse fibroblast cell line 3T3-Swiss were purchased from ATCC. MRC-5 (P 30–35) cells were maintained in Dulbecco's modified Eagle's medium with 10% FBS. The human endothelial cell lines HUVEC and HMVEC were cultured in HuMedia-MvG medium with growth supplements (Kurabo, Osaka, Japan).

TSU-68 was synthesized by Taiho Pharmaceutical (Tokyo, Japan). Imatinib was provided by Novartis Pharma (Basel, Switzerland). NK4 and anti-HGF antibody were produced as described previously[15,16] Mouse HGF and neutralizing antibodies for FGF-2 and PDGF were obtained from R&D Systems (Minneapolis, MN).

### ELISA

Cells ($2 \times 10^5$) were cultured in 2 mL modified Eagle's medium (for EHMES-10 and MRC-5) or RPMI 1640 (for MSTO-211H) with 10% FBS for 48 hours. The culture supernatants were centrifuged and stored at −80°C. Tumor cells were lysed in cell lysis buffer containing a phosphatase and proteinase inhibitor cocktail (Sigma-Aldrich, St. Louis, MO), and their protein concentrations were determined using a BCA protein assay kit (Pierce; Thermo Fisher Scientific, Rockford, IL). The concentrations of VEGF, FGF-2 and PDGF in culture supernatants and cell lysates were determined using enzyme-linked immunosorbent assay (ELISA) kits according to the manufacturer's instructions (R&D Systems). HGF was quantified by ELISA (IMMUNIS HGF EIA; Institute of Immunology, Tokyo, Japan), according to the manufacturer's instructions. The detection limit for HGF was 0.1 ng/mL. All samples were run in triplicate.

### Growth of Tumor Cells and Fibroblasts

Cell growth was measured by the MTT dye reduction method, as described previously.[12] Briefly, MRC-5 or MSTO-211H cells ($2 \times 10^3$/200 μL per well), which had been plated in triplicate in 96-well plates, were incubated in culture medium for 24 hours, washed and incubated for 72 hours with TSU-68 or NK4 in fresh culture medium containing 5% FBS (for MRC-5) or 2.5% FBS (for MSTO-211H) in the presence or absence of FGF-2, PDGF-AA, HGF, or culture supernatants of MPM cells. A 50-μL aliquot of stock MTT solution (2 mg/mL; Sigma-Aldrich) was added to each well, and the cells were incubated for 2 hours at 37°C. The medium containing the MTT solution was removed, and the dark blue crystals were dissolved by adding 100 μL dimethyl sulfoxide. Absorbance was measured with an MTP-120 microplate reader (Corona Electric, Hitachinaka, Japan) at test and reference wavelengths of 550 and 630 nm, respectively. Percent growth was determined relative to untreated controls. Each experiment was performed at least three times, each with triplicate samples.

### Real-Time RT-PCR

Total cellular RNA was isolated using an RNeasy mini kit and an RNase-free DNase kit (Qiagen, Valencia, CA) according to the manufacturer's protocols. First-strand cDNAs were synthesized using SuperScript III reverse transcriptase (Invitrogen, Carlsbad, CA) with oligo$(dT)_{12-18}$ primers (R&D Systems). The primer sequences were as follows: human HGF, forward primer 5′-TTCATGATGTCCACGGAAGA-3′ and reverse primer 5′-GCCTGGCAAGCTTCATTAAA-3′; human GAPDH, forward primer 5′-GAGTCAACGGATTTGGTCGT-3′ and re-

verse primer 5′-GACAAGCTTCCCGTTCTCAG-3′. Quantitative PCR was performed on an ABI PRISM 7900HT sequence detection system (Applied Biosystems, Foster City, CA) using Power SYBR Green PCR master mix (Applied Biosystems).

### *Cell Migration Assay*

Cell migration assays were performed using the modified Boyden-chamber method,[17] with 8-$\mu$m pore filters separating the upper and lower Transwell chambers (BD Biosciences, Franklin Lakes, NJ). The cells were serum-starved for 24 hours before the assay. In some experiments, MSTO-211H cells ($10^5$/200 $\mu$L 10% FBS RPMI 1640) were added to the upper chambers, and MRC-5 cells ($10^4$/500 $\mu$L 10% FBS RPMI 1640), with or without 300 nmol/L NK4, were added to the lower chambers. After 24 hours incubation at 37°C, the cells that had not migrated were removed from the upper surface of the filters with cotton swabs. The cells that had migrated to the lower surface of the filters were fixed in methanol and stained with H&E. Migration was quantified by counting cells in six randomly selected fields on each filter under a microscope at ×200 magnification.

### *Coculture of MPM Cells with Fibroblasts*

Cells were cocultured in Transwell chambers separated by 8-$\mu$m-pore filters. MSTO-211H cells ($8 \times 10^3$/700 $\mu$L) were placed in each lower chamber, and fibroblasts ($10^4$/300 $\mu$L) were placed in each upper chamber, with or without 300 nmol/L NK4 in the lower chamber or 3 $\mu$mol/L TSU-68 in the upper chamber. After 72 hours, the upper chambers were removed, and cell growth was measured with a Cell Counting Kit-8 (Dojindo Molecular Technologies, Rockville, MD). Each experiment was performed at least three times, each with triplicate samples.

### *Antibodies and Western Blot Analysis*

Western blotting was performed as described,[18] using anti-MET, anti-phospho-MET, anti-phospho PDGFR$\alpha$, anti-phospho-FGFR (Cell Signaling Technology, Danvers, MA), and anti-G3PDH (R&D Systems) antibodies. Each experiment was performed in triplicate.

### *Orthotopic Implantation Model*

Cultured MSTO-211H cells were harvested by pipetting, washed twice, and resuspended in PBS, and $1 \times 10^6$ cells in 100 $\mu$L PBS were injected into the thoracic cavity of each SCID mouse.[19] The mice were treated with TSU-68 (200 mg/kg, oral gavage), imatinib (25 or 50 mg/kg, i.p.), or NK4 (3 or 9 mg/kg, i.p.) daily on days 7 to 20. At 3 weeks after tumor cell inoculation, the mice were sacrificed, their thoracic tumors were carefully removed and weighed, and the volume of pleural effusion was measured.

### *Immunofluorescence Analysis*

For bromodeoxyuridine (BrdU) staining, the mice were injected with BrdU solution (200 $\mu$L, i.p.; BrdU staining kit; Zymed Laboratories, South San Francisco, CA). The mice were sacrificed 2 hours later; thoracic tumors were collected and cut into 5-mm fragments and placed in buffered 10% formalin solution or optimum cutting temperature compound (Bayer, Pittsburgh, PA) and snap-frozen in liquid nitrogen. The frozen tissue sections (6 $\mu$m thick) were assayed for the presence of fibroblasts using mouse anti-$\alpha$-SMA antibody (1:500; Sigma-Aldrich) or goat anti-type I collagen antibody (1:200; SouthernBiotech, Birmingham, AL) and the proliferating cells were assessed by BrdU staining.

### *Histology and Immunohistochemistry*

Tumor biopsy specimens from MPM patients, obtained from Hyogo Prefectural Amagasaki Hospital, were fixed on formalin, and embedded in paraffin. The study was approved by the institutional review boards of Hyogo Prefectural Amagasaki Hospital and Kanazawa University.

Sections (5 $\mu$m thick) were deparaffinized in xylene and rehydrated in decreasing concentrations of ethanol. The sections were retrieved by microwave treatment for 10 minutes, with immersion in antigen retrieval medium (Immunosaver; Nissin EM, Tokyo, Japan). After blocking endogenous peroxidase activity with 3% aqueous $H_2O_2$ for 10 minutes, the sections were treated with 5% normal horse serum and subsequently incubated overnight at 4°C with rabbit polyclonal anti-HGF antibody,[15] goat anti-PDGF antibody (R&D), mouse anti-FGF-2 antibody (BD Biosciences), and rabbit polyclonal anti-MET antibody (IBL Immuno-Biological Laboratories, Gunma, Japan). After a PBS wash, the sections were incubated with biotin-conjugated anti-rabbit IgG, anti-goat IgG, or anti-mouse IgG (each 1:200) for 30 minutes at room temperature and subsequently with avidin-biotin-peroxidase complex (ABC) using a Vectastain ABC kit (Vector Laboratories, Burlingame, CA) for 30 minutes. Immunostaining was detected using 3,3′-diaminobenzidine tetrahydrochloride (DAB liquid system; DakoCytomation, Carpinteria, CA). Samples with primary antibodies omitted served as negative controls.

### *Quantification of Immunohistochemistry and Immunofluorescence*

The five areas containing the highest levels of staining within a section were selected for histological quantification under light or fluorescence microscopy at 40× magnification. The results were evaluated by two investigators (Q.L. and H.U.).

### *Evaluation of Immunohistochemical Results*

Immunoreactivities of antibodies to FGF-2, PDGF-AA, HGF, MET, and $\alpha$-SMA were scored as follows: −, complete absence of staining or staining of >5% of cells; 1+, staining of 5% to 50% of cancer cells; and 2+, staining of

51% to 100% of cancer cells or interstitial fibroblasts (α-SMA). Immunoreactivity was evaluated independently by two investigators (H.U. and Y.B.), with discrepancies decided by consensus after joint reevaluation.

### *Statistical Analysis*

Statistical significance was determined by *t*-test or one-way analysis of variance. All statistical analyses were performed using Prism software (version 4.01; GraphPad Software, San Diego, CA). All tests were two-sided. $P < 0.05$ was considered significant. Correlations between expression of different cytokines in patient specimens were evaluated by Pearson's correlation analysis. Data are reported as means with 95% confidence intervals.

## *Results*

### *MSTO-211H Cell-Derived FGF-2 and PDGF-AA Promote Growth of Fibroblasts*

Human MPM cells MSTO-211H and EHMES-10 produced different types of thoracic tumors when orthotopically inoculated into the thoracic cavities of SCID mice. EHMES-10 cells produced a few larger tumors, whereas MSTO-211H cells produced many smaller tumors, most with dispersed white nodes of diameter <5 mm.[12] A large number of α-SMA-positive fibroblast-like cells infiltrated the tumors produced by MSTO-211H cells, but not EHMES-10 cells (Figure 1A).

To explore the mechanism of fibroblast infiltration, we assessed the production by MPM cell lines of cytokines associated with fibroblast motility. Assays for production of VEGF, a potent motility factor for endothelial cells, showed that MSTO-211H and Y-Meso-14 cells secreted much lower levels of VEGF than did EHMES-10 cells (Figure 1B), as we have previously reported.[12] In contrast, lysates of MSTO-211H cells showed large amounts of FGF-2 protein, with the supernatants of these cells containing discernible levels of FGF-2, whereas FGF-2 levels in the lysates of Y-Meso-14 cells were relatively low and those in the supernatants were below the limit of detection. In addition, MSTO-211H and Y-Meso-14 cells secreted high concentrations of PDGF-AA (Figure 1B), but not PDGF-AB or PDGF-BB (data not shown).

When we assessed the effects of these cytokines on fibroblasts by using the human fibroblast cell line MRC-5, we found that FGF-2 ($P < 0.001$) and/or PDGF-AA ($P < 0.01$) significantly stimulated the growth of MRC-5 cells (Figure 1C). TSU-68, which targets the tyrosine kinases of FGFR1, PDGFR, and VEGFR, did not inhibit the baseline growth of MRC-5 cells, but it abrogated the effects of FGF-2 and PDGF-AA. In contrast, TSU-68, as well as exogenously added FGF-2 and PDGF-AA, had no effect on the growth of MSTO-211H cells, indicating that FGF-2 and PDGF-AA are not autocrine growth factors for MSTO-211H cells. The supernatant of MSTO-211H cells stimulated the growth of MRC-5 cells ($P < 0.001$), an effect completely abrogated by TSU-68. In addition, FGF-2 and PDGF-AA increased the migration of MRC-5 cells (see Supplemental Figure S1 at *http://ajp.amjpathol.org*). Western blot analysis showed that the supernatants of MSTO-211H cells activated FGFR1 and PDGFRα in MRC-5 cells, and that the phosphorylation of these receptors was inhibited by TSU-68 (Figure 1D). Taken together, these results suggest that FGF-2 and PDGF-AA produced by MSTO-211H cells promoted the growth and migration of fibroblasts via the activation of FGFR1 and PDGFRα.

### *FGF-2 and PDGF-AA Enhance HGF Production by Fibroblasts*

We next assessed the role of infiltrating fibroblasts in MPM. We hypothesized that one or more cytokines pro-

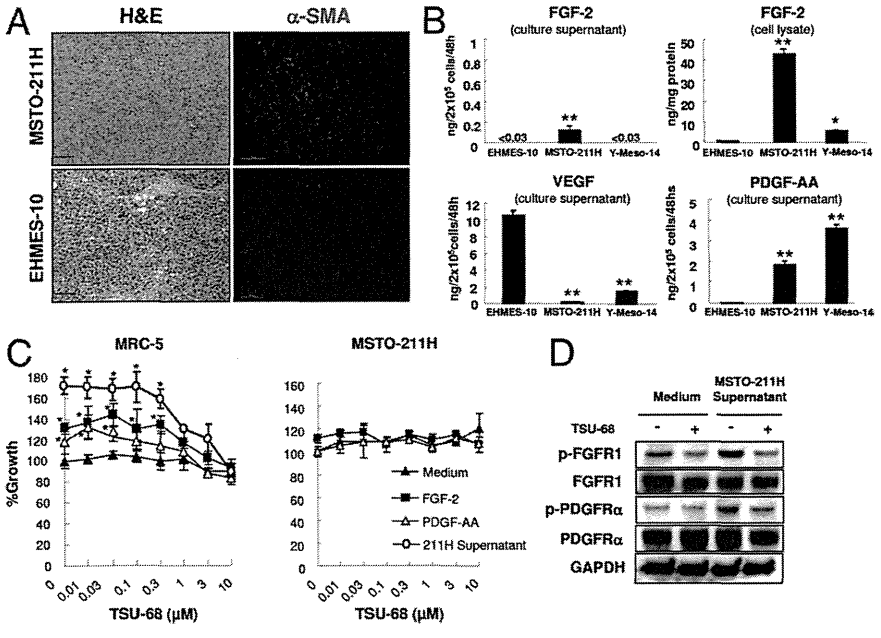


**Figure 1.** MSTO-211H cell-derived FGF-2 and PDGF-AA promote growth of fibroblasts. **A:** Thoracic tumors produced by MPM cells in SCID mice were stained with H&E and by immunofluorescence for α-SMA (red) and DAPI (blue). Scale bars = 100 μm. **B:** ELISA assays of FGF-2, VEGF, and PDGF-AA in the culture supernatant of MPM cells and of FGF-2 in cell lysates. $^{*}P < 0.05$, $^{**}P < 0.01$ versus EHMES-10. **C:** MRC-5 or MSTO-211H cells were cultured in the presence of FGF-2 (20 ng/mL), PDGF-AA (20 ng/mL), or the culture supernatant of MSTO-211H cells ($2 \times 10^5$/2 mL/48 hours), with or without TSU-68. After 72 hours, the growth of MRC-5 or MSTO-211H cells was determined by MTT assay. $^{*}P < 0.01$ versus medium alone. **D:** TSU-68 abrogates the phosphorylation of FGFR1 and PDGFRα induced by the supernatant of MSTO-211H cells. MRC-5 cells were incubated with or without TSU-68 (10 μmol/L) in the presence or absence of the supernatant of MSTO-211H cells for 15 minutes. The cells were lysed and proteins were detected by immunoblotting.

duced predominantly by fibroblasts might influence MPM behavior. We therefore compared the cytokine production profiles of MRC-5 and MSTO-211H cells using a cytokine antibody array (see Supplemental Figure S2 at *http://ajp.amjpathol.org*). Whereas both MSTO-211H and MRC-5 cells produced IL-6, IL-8, and the growth-regulated oncogenes IGFBP-1 and MCP-1, only MRC-5 cells produced high levels of hepatocyte growth factor/scatter factor (HGF). We therefore assayed the production of HGF by various cell lines. Although neither the MPM cell lines (MSTO-211H, Y-Meso-14, and EHMES-10) nor the endothelial cell lines (HUVEC and HMVEC) secreted discernible levels of HGF (Figure 2A), MRC-5 and IMR-90 cells and primary cultured patient fibroblasts (PF) produced high levels of HGF, as reported previously.[7,20] We also evaluated the effects of FGF-2 and PDGF-AA on fibroblast production of HGF. Both FGF-2 ($P < 0.05$) and PDGF-AA ($P < 0.01$) significantly stimulated HGF production of MRC-5, at both the protein (Figure 2B) and mRNA (Figure 2C) levels. Similarly, treatment of another human lung fibroblast cell line, IMR-90, with FGF-2 and PDGF-AA stimulated HGF production (see Supplemental Figure S3 at *http://ajp.amjpathol.org*). These results clearly indicate that FGF-2 and PDGF-AA secreted by MSTO-211H cells stimulated fibroblast growth and production of HGF.

## *HGF Derived from Fibroblasts Enhances the Growth and Motility of MPM Cells*

To clarify the role of HGF, which can be produced by fibroblasts, on the biological behavior of MPM cells, we assessed the effect of HGF on the growth of MSTO-211H cells. In contrast to FGF-2 or PDGF-AA, HGF enhanced the growth of MSTO-211H cells, an effect inhibited by anti-HGF antibody (Figure 2D). More importantly, the HGF antagonist NK4 abrogated the HGF-stimulated growth of MSTO-211H cells, as well as slightly inhibiting the constitutive growth of MSTO-211H cells (Figure 2D). Furthermore, the supernatant of MRC-5 cells, as well as HGF, stimulated the phosphorylation of MET, the specific receptor of HGF, in MSTO-211H cells, an effect inhibited by NK4 (Figure 2E). We therefore evaluated the effect of fibroblasts on the motility of MSTO-211H cells. HGF dramatically enhanced the motility of MSTO-211H cells, an effect blocked by NK4 (Figure 2F). In addition, HGF significantly stimulated the growth and motility of Y-Meso-14 cells, and these effects were blocked by NK4. In contrast, HGF stimulated neither growth nor motility of EHMES-10 cells (see Supplemental Figure S4 at *http://ajp.amjpathol.org*). These results indicate that fibroblast-derived HGF promotes the growth and motility of MSTO-211H and Y-Meso14 cells.

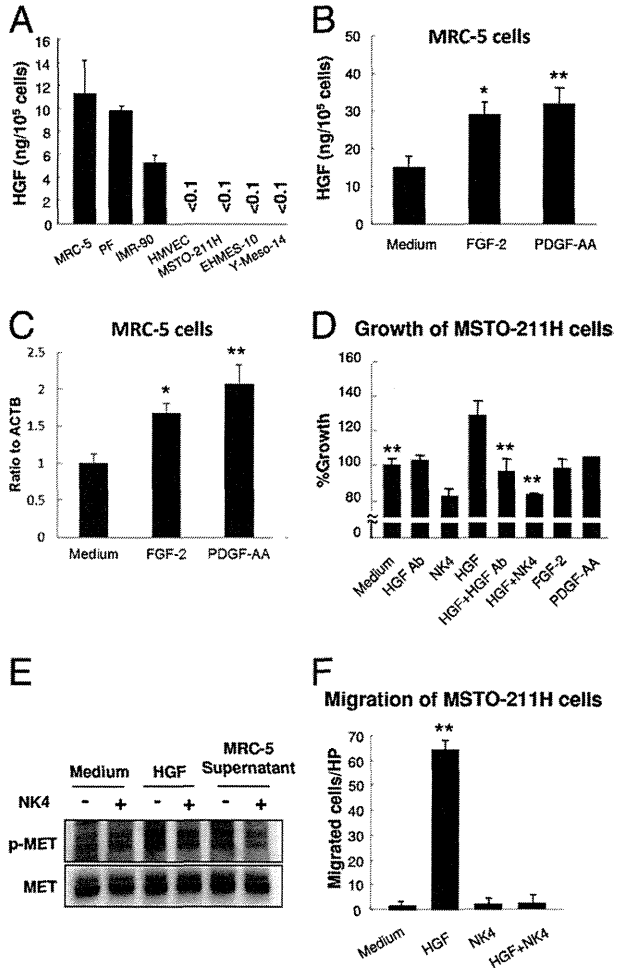


**Figure 2.** HGF derived from fibroblasts enhances the growth and motility of MPM cells. **A:** HGF production by MPM (EHMES-10, MSTO-211H), fibroblast (MRC-5 and IMR-90), Primary cultured patient fibroblast (PF), and endothelial (HMVEC) cell lines. Cells ($2 \times 10^5$/2 mL) were incubated in medium for 8 hours, the culture supernatants were harvested, and HGF concentrations were determined by ELISA. **B:** FGF-2 and PDGF-AA enhance HGF production by fibroblasts. MRC-5 cells ($2 \times 10^5$/2 mL) were cultured for 48 hours in the presence of FGF-2 (20 ng/mL) or PDGF-AA (20 ng/mL), and HGF concentrations in culture supernatants were determined by ELISA. $^*P < 0.05$; $^{**}P < 0.01$ versus medium alone. **C:** FGF-2 and PDGF-AA increase HGF mRNA expression in fibroblasts. HGF mRNA expression by MRC-5 cells pretreated with FGF-2 (20 ng/mL) or PDGF-AA (20 ng/mL) for 48 hours was determined by real-time RT-PCR. $^*P < 0.05$; $^{**}P < 0.01$ versus medium alone. **D:** HGF increases MPM cell growth. MSTO-211H cells were cultured with 20 ng/mL of HGF, FGF-2, or PDGF-AA in the presence or absence of NK4 (300 nmol/L) for 72 hours, and cell growth was determined by MTT assay. $^*P < 0.05$, $^{**}P < 0.01$ versus HGF. **E:** NK4 abrogates MET phosphorylation induced by fibroblast-derived HGF in MPM cells. MSTO-211H cells were treated with or without NK4 (300 nmol/L) in the presence or absence of HGF (20 ng/mL) or the supernatant of MRC-5 cells ($10^6$/mL/48 hours) for 30 minutes. The cells were lysed and proteins were detected by immunoblotting. The lower band (p145 MET) corresponds to the mature form of MET; the upper band (p170 MET) corresponds to the immature MET precursor. **F:** HGF induces the migration of MSTO-211H cells. The assay was performed in triplicate as described under *Materials and Methods*. $^*P < 0.05$, $^{**}P < 0.01$ versus medium alone.

## *Simultaneous Blockade of FGFR1 and PDGFRs Inhibits Growth of MPM Cells in a Coculture System*

Our findings suggested the presence of a malignant cytokine network (malignant crosstalk) involving MPM cells and fibroblasts (Figure 3A). We therefore used a coculture system to determine whether such a malignant network exists between MPM and fibroblast cells. Cocultured MRC-5 cells stimulated the growth of MSTO-211H cells, an effect blocked by both TSU-68 and the combination of anti-FGF-2 and anti-PDGF neutralizing antibodies (Figure 3B). This growth was also abrogated by either

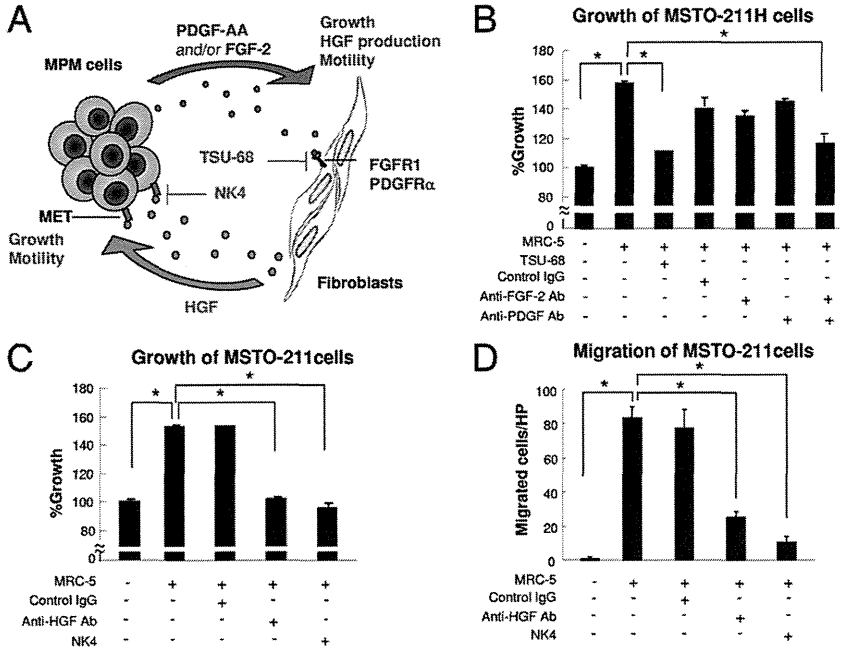


**Figure 3.** Simultaneous blockade of FGFR1 and PDGFRs inhibits the growth of MPM cells in a coculture system. **A:** Schema of the malignant cytokine network between MPM cells and stromal tumor-associated fibroblasts (TAFs). **B:** TSU-68 circumvents the growth of MPM cells induced by fibroblasts in the coculture system. MSTO-211H cells were cocultured with MRC-5 cells with or without TSU-68 (10 μmol/L), control IgG, anti-FGF-2 antibody, and/or anti-PDGF antibody (1 μg/mL) for 72 hours. MPM cell growth was determined using a Cell Counting Kit-8. **C:** Inhibition of HGF blocks the growth of MPM cells induced by fibroblasts in a coculture system. MSTO-211H cells were cocultured with MRC-5 cells with control IgG, anti-HGF neutralizing antibody (1 μg/mL), or NK4 (300 nmol/L) for 72 hours, and MPM cell growth was determined. **D:** Blockade of HGF prevents MSTO-211H cell migration induced by MRC-5 cells. The assay was performed in triplicate as described under *Materials and Methods*. $^*P < 0.01$.

anti-HGF antibody or NK4 (Figure 3C). Moreover, cocultured MRC-5 cells markedly induced the migration of MSTO-211H cells, an effect also inhibited by either anti-HGF antibody or NK4 (Figure 3D). Consistent with these observations, coculture with MRC-5 cells stimulated the growth of Y-Meso-14 cells, and this effect was blocked by TSU-68, NK4, or anti-HGF antibody. Either anti-HGF antibody or NK4 inhibited the migration of Y-Meso-14 cells induced by coculture with MRC-5 cells (see Supplemental Figure S5 at *http://ajp.amjpathol.org*). These findings clearly point to the existence of a malignant cytokine network between MPM cells and fibroblasts *in vitro*.

## *Malignant Cytokine Network between MPM Cells and Patient Fibroblasts or Mouse Fibroblasts*

To assess whether this malignant cytokine network is unique to MPM cells and MRC-5 human fibroblast cell lines, we cocultured MSTO-211H cells with either primary cultured patient fibroblasts or the mouse fibroblast cell line 3T3-Swiss. Similar to the effect on MRC-5 cells, the patient fibroblasts induced the migration of both MSTO-211H and Y-Meso-14 cells, and anti-HGF antibody or NK4 inhibited the migration induced by the patient fibroblasts (Figure 4A). Cocultured patient fibroblasts also stimulated growth of MSTO-211H and Y-Meso-14 cells. These effects were inhibited by TSU-68, NK4, or anti-HGF antibody (Figure 4, B and C). These results indicate that the cytokine network is not specific to the MRC-5 fibroblast cell line.

Moreover, similar to its effect on human fibroblasts, TSU-68 did not inhibit the growth of 3T3-Swiss cells. PDGF-AA, but not FGF-2, significantly up-regulated the growth of 3T3-Swiss cells ($P < 0.05$), an effect blocked by TSU-68 (Figure 4D). Both exogenous mouse HGF and the supernatant of 3T3-Swiss cells induced MET phosphorylation of MSTO-211H cells, effects abrogated by NK4 (Figure 4E), indicating that mouse HGF can activate human MPM cells. These results were consistent with previous findings showing that the activity of HGF is not always species-specific.[21] Although mouse HGF did not promote the growth of MPM cells (data not shown), 3T3-Swiss cells induced their migration, an effect inhibited by NK4 (Figure 4F). These findings suggest that MPM cells also stimulate mouse fibroblasts to promote the progression of MPM cells.

## *Presence of Malignant Cytokine Network between MPM and Microenvironment* in Vivo

We next examined whether the malignant cytokine network could promote the progression of MPM cells *in vivo*. To assess this possibility, MSTO-211H or Y-Meso-14 cells were inoculated orthotopically into the thoracic cavities of SCID mice and the mice were treated with TSU-68 (an inhibitor of FGFR1 and PDGFRs), imatinib (an inhibitor of PDGFRs), or NK4 (an inhibitor of HGF/MET). MSTO-211H cells produced thoracic tumors and a small volume of pleural effusion, whereas Y-Meso-14 cells produced thoracic tumors and large volumes of pleural effusion. We previously reported that treatment of these mice with the anti-VEGF antibody bevacizumab did not significantly inhibit the progression of MSTO-211H cells, suggesting that VEGF is not primarily responsible for progression in an MSTO-211H mouse model.[12] Although tumor concentrations of VEGF, PDGF-AA, and FGF-2 were not altered by either TSU-68 or imatinib (data not shown), both treatments significantly inhibited the growth of thoracic tumors (Table 1, experiments 1, 2, and 4; Figure 5A). Furthermore, either TSU-68 or imatinib significantly inhibited the production of pleural effusion by Y-Meso-14 cells (Table 1,

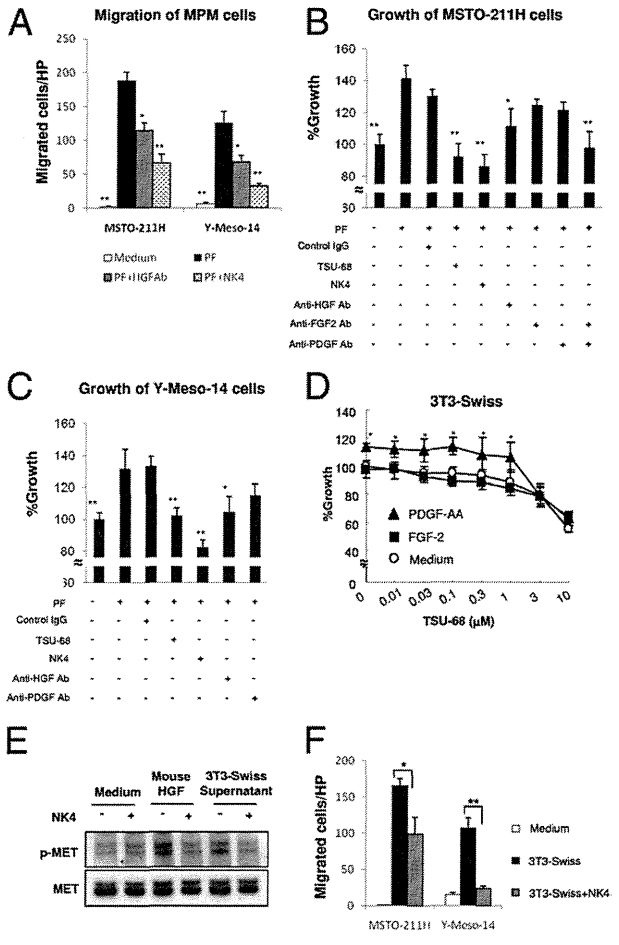


**Figure 4.** Malignant cytokine network between MPM cells and patient fibroblasts or mouse fibroblasts. **A:** Blockade of HGF prevents MSTO-211H or Y-Meso-14 cell migration induced by primary cultured patient fibroblasts (PF). The assay was performed in triplicate as described under *Materials and Methods*. $^{*}P < 0.05$, $^{**}P < 0.01$ versus PF. **B** and **C:** TSU-68, NK4, and anti-HGF antibody blocked the growth of MSTO-211H cells induced by PF in the coculture system. MSTO-211H (**B**) or Y-Meso-14 (**C**) cells were cocultured with PF cells with or without TSU-68 (10 μmol/L), control IgG, NK4 (300 nmol/L), anti-HGF antibody (1 μg/mL), anti-FGF-2 antibody, and/or anti-PDGF antibody (1 μg/mL) for 72 hours. MPM cell growth was determined using a Cell Counting Kit-8. $^{*}P < 0.05$, $^{**}P < 0.01$ versus PF. **D:** PDGF-AA (20 ng/mL), but not FGF-2 (20 ng/mL), enhances the growth of the mouse fibroblast 3T3-Swiss cell line, as determined by MTT assays. $^{*}P < 0.05$. **E:** NK4 abrogates MET phosphorylation induced by mouse fibroblast-derived HGF in MPM cells. MSTO-211H cells were treated with or without NK4 (300 nmol/L) in the presence or absence of mouse HGF (100 ng/mL) or the supernatant of 3T3-Swiss cells ($10^6$/mL/48 hours) for 30 minutes. The cells were lysed and proteins were detected by immunoblotting. **F:** NK4 decreases the migration of MPM cells induced by mouse fibroblasts. Migration of MSTO-211H cells and Y-Meso-14 cells in the presence or absence of NK4 (300 nmol/L) cocultured with 3T3-Swiss cells was assayed as described under *Materials and Methods*. $^{*}P < 0.05$, $^{**}P < 0.01$.

experiment 4). Histological analyses using BrdU staining to identify proliferating cells and antibodies to type I collagen or α-SMA showed that treatment with TSU-68 reduced the number of tumor-associated proliferating fibroblasts in tumors produced by both MSTO-211H and Y-Meso-14 cells (Figure 5B). These results suggest that inhibition of FGFR1 and PDGFRs suppressed the recruitment and/or growth of tumor-associated fibroblasts and thereby inhibited the growth of MPM tumors.

We also found that treatment with 9 mg/kg NK4 significantly inhibited the growth of thoracic tumors (Table 1, experiments 3 and 4; Figure 5A). NK4 also inhibited the production of pleural effusion by Y-Meso-14 cells. In NK4-treated tumors, the number of tumor-associated fibroblasts tended to be decreased, but the difference was not statistically significant. However, the numbers of proliferating cells, including MPM cells and fibroblasts, were markedly decreased (Figure 5B), indicating that, even though inhibition of HGF-MET signaling did not affect the recruitment and/or growth of tumor-associated fibroblasts, it suppressed the growth of MPM tumors. These results strongly suggest that MPM cells stimulate fibroblasts to promote progression *in vivo* via a malignant cytokine network consisting of FGF-2, PDGF-AA, and HGF.

## *High Immunoreactivity for FGF-2, PDGF-AA, and HGF in Tumors from MPM Patients*

To assess the clinical relevance of immunoreactivity for FGF-2, PDGF-AA, and HGF, we examined whether these cytokines could be detected in clinical specimens obtained from MPM patients. We analyzed 51 tumors from 51 MPM patients (Table 2; see also Supplemental Figure S6 at *http://ajp.amjpathol.org*). We found that 46 (90%), 40 (78%), and 50 (98%) tumors showed positive staining for FGF-2, PDGF-AA, and HGF, respectively. Moreover, all 51 (100%) tumors were positive for MET, including 47 (92%) showing high positivity (2+), indicating the importance of expression of the MET ligand (HGF) for controlling HGF-induced biological activity in MPM. Notably, of the 34 tumors highly positive (2+) for HGF, 20 (59%) were also highly positive (2+) for FGF-2 and/or PDGF-AA. Furthermore, tumors from three patients (3/51, or 9%) were highly positive (2+) for all three. Statistical correlation analysis showed that FGF-2 and PDGF-AA expression were correlated ($P < 0.05$), suggesting that these two cytokines are frequently expressed coordinately in MPMs, as in MSTO-211H cells.

Of the 51 tumors, 27 (53%) were highly positive (2+) for α-SMA. Of these 27 tumors, 17 (63%), 5 (19%), and 17 (63%) were highly positive (2+) for FGF-2, PDGF-AA, and HGF, respectively. Moreover, 10 of the 17 (59%) HGF-positive tumors were also positive for FGF-2 and/or PDGF-AA.

Taken together, these results strongly suggest that a local cytokine network between mesothelioma cells and fibroblasts is involved in the progression of a considerable proportion of MPM tumors.

## *Discussion*

The tumor microenvironment has been the subject of intensive investigation and has been shown to facilitate tumor growth and distant metastasis. For example, in breast and colon cancer models, the primary tumors have been reported to activate bone marrow in their systemic environment and to instigate the growth of indolent distant tumors, a process called systemic instigation.[6] In contrast, MPM is a locally aggressive disease with intrathoracic dissemination, and rarely causes distant metastases except at end stages. We have shown here that local instigation in MPM is mediated by malig-

**Table 1.** Therapeutic Efficacy of TSU-68, Imatinib, and NK4 on Production of Thoracic Tumor and Pleural Effusion Produced by MSTO-211H and Y-MESO-14 Cells in SCID Mice

| | | Thoracic tumor | | | Pleural effusion | | |
|---|---|---|---|---|---|---|---|
| | | | Weight (mg) | | | Volume (μL) | |
| Treatment†‡ | Dose (mg/kg) | Incidence | Median | Range | Incidence | Median | Range |
| | | | MSTO-211H | | | | |
| Experiment 1 | | | | | | | |
| Control (CMC) | | 10/10 | 378 | 132–773 | 5/10 | 40 | 0–400 |
| TSU-68† | 200 | 10/10 | 164** | 29–254 | 2/10 | <10 | 0–180 |
| Experiment 2 | | | | | | | |
| Control (saline) | | 5/5 | 187 | 94–327 | 3/5 | 30 | 0–140 |
| Imatinib | 25 | 4/5 | 83* | 0–155 | 2/5 | <10 | 0–180 |
| Imatinib | 50 | 4/5 | 76* | 0–143 | 1/5 | <10 | 0–30 |
| Experiment 3 | | | | | | | |
| Control (saline) | | 5/5 | 356 | 164–437 | 2/5 | <10 | 0–200 |
| NK4 | 3 | 4/5 | 336 | 0–448 | 3/5 | 40 | 0–320 |
| NK4 | 9 | 3/5 | 40* | 0–276 | 1/5 | <10 | 0–300 |
| | | | Y-Meso-14 | | | | |
| Experiment 4 | | | | | | | |
| Control (saline) | | 5/5 | 320 | 270–370 | 5/5 | 700 | 500–800 |
| TSU-68 | 200 | 5/5 | 140** | 130–160 | 5/5 | 200* | 50–400 |
| Imatinib | 25 | 5/5 | 60** | 10–150 | 3/5 | 50* | 0–350 |
| NK4‡ | 9 | 5/5 | 140** | 0–230 | 3/5 | 200* | 0–400 |

*$P < 0.05$; **$P < 0.01$, versus control group (two-tailed nonparametric *t*-test).
†MSTO-211H cells ($1 \times 10^6$) or Y-Meso-14 cells ($1 \times 10^6$) were inoculated into thoracic cavity of SCID mice on day 0. Mice were treated daily on days 7 to 20 (MSTO-211H) or days 7 to 27 (Y-Meso-14). All mice were sacrificed on day 21 (MSTO-211H) or day 28 (Y-Meso-14).
‡Route of administration: oral gavage for TSU-68 and intraperitoneal for imatinib and NK4.
CMC, carboxymethylcellulose-based vehicle solution.

nant cytokine network involving MPM and TAFs. MPM cells produce FGF-2 and PDGF-AA, which stimulate the growth and/or motility of fibroblasts and up-regulate their production of HGF. Fibroblast-derived HGF, in turn, stimulates the growth and/or motility of MPM cells. Importantly, the infiltration of TAFs and the simultaneous expression of three cytokines (FGF-2, PDGF-AA, and HGF) were detected in clinical specimens obtained from patients with MPM. These results indicate that MPMs recruit and activate TAFs by secreting FGF-2 and PDGF-AA, and that activated TAFs produce HGF, which promotes the dissemination of MPM in the thoracic cavity. These three cytokines may therefore be therapeutic targets in the treatment of MPM.

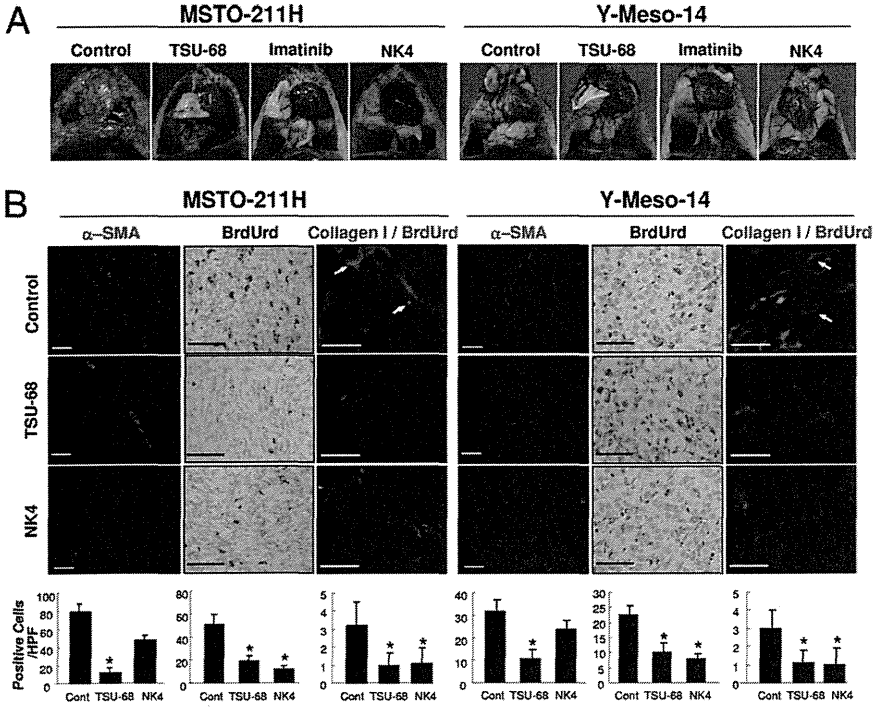


**Figure 5.** TSU-68, imatinib, and NK4 inhibit the production of thoracic tumors by MPM cells in an orthotopically implanted SCID mouse model. **A:** Macroscopic appearance of thoracic tumors caused by MSTO-211H or Y-Meso-14 cells treated with TSU-68, imatinib, or NK4. The thoracic tumors were evaluated as described under *Materials and Methods*. **B:** Histological analysis of the same tumors. The thoracic tumors were analyzed by immunohistochemistry (type I collagen and BrdU) and immunofluorescence (α-SMA and double staining of BrdU and type I collagen). In double staining, red fluorescence indicates BrdU and green fluorescence indicates type I collagen; **arrows** mark double-positive cells (proliferating fibroblasts). Scale bars = 50 μm. The corresponding graphs show the mean number of positive cells per high-power field (HPF), from five independent areas. *$P < 0.01$ versus control. Negative controls without primary antibodies did not show discernible staining for α-SMA, BrdU, or type I collagen (data not shown).

**Table 2.** Demographic Characteristics and Tumor Immunoreactivity for FGF-2, PDGF-AA, HGF, and MET in Malignant Pleural Mesothelioma Patients

| Characteristic | MPM patients |
|---|---|
| Sample size | $N = 51$ |
| Sex, no. (%) | |
| M | 42 (82) |
| F | 9 (18) |
| Age (years) | |
| Median | 67 |
| Range | 38–80 |
| Exposure to asbestos, no. (%) | |
| Yes | 18 (35) |
| No | 13 (25) |
| Unknown | 20 (39) |
| Histology, no. (%) | |
| Epithelial | 26 (51) |
| Biphasic | 15 (29) |
| Sarcomatoid | 10 (20) |
| Expression in tumors,* no. (%) | |
| FGF-2 | |
| – | 5 (10) |
| 1+ | 16 (31) |
| 2+ | 30 (59) |
| PDGF-AA | |
| – | 11 (22) |
| 1+ | 33 (65) |
| 2+ | 7 (14) |
| HGF | |
| – | 1 (2) |
| 1+ | 16 (31) |
| 2+ | 34 (67) |
| MET | |
| – | 0 (0) |
| 1+ | 4 (8) |
| 2+ | 47 (92) |
| $\alpha$-SMA | |
| – | 10 (20) |
| 1+ | 14 (27) |
| 2+ | 27 (53) |

*–, complete absence of staining or staining of <5% of cells; 1+, staining of 5% to 50% of cancer cells (or interstitial fibroblasts, $\alpha$-SMA); 2+, staining of 51% to 100% of cancer cells (or interstitial fibroblasts, $\alpha$-SMA).

F, female, M, male.

All three cytokines (FGF-2, PDGF-AA, and HGF) are ligands of receptor tyrosine kinases (FGFR1, PDGFR$\alpha$, and MET, respectively). Several studies have suggested that FGF-2 and PDGF-AA are involved in the pathogenesis of MPM.[22,23] Moreover, significant concentrations of HGF have been detected in pleural effusions obtained from patients with MPM.[24] Although FGF-2 and PDGFs have been reported to be growth factors for several MPM cell lines, neither FGF-2 nor PDGF-AA stimulated the growth of MPM cells, whereas HGF stimulated not only the migration but the growth of MSTO-211H and Y-Meso-14 cells, consistent with prior observations.[25] Meanwhile, although anti-FGF-2 antibody alone or anti-PDGF antibody alone only slightly inhibited the MPM proliferation up-regulated by MRC-5, combined use of both antibodies almost reversed the effect of MRC-5 (Figure 3B). These observations indicate that FGF-2 or PDGF-AA alone may be sufficiently functional to maintain the cytokine network, further suggesting functional redundancy between FGF-2 and PDGF in MRC-5 cells. Although the role of each cytokine has been evaluated individually, to our knowledge this is the first comprehensive analysis to show their association and the interaction between MPM and TAFs, using orthotopically implanted SCID mice and clinical specimens.

Notably, mouse HGF induced MET phosphorylation and stimulated the motility, but not the growth, of human MPM cells, whereas human HGF stimulated both motility and growth. Regarding the effect of mouse HGF on human cells, results of previous reports are controversial. Burgess et al[26] showed that mouse HGF does not potently activate human MET signaling; however, Previdi et al[27] recently demonstrated that mouse HGF activated MET in human breast cancer cells. Taken together with our results, these findings suggest that i) MET signaling induced by mouse HGF is not as strong as that induced by human HGF, ii) MET signaling induced by mouse HGF is sufficient to stimulate the motility of human MPM cells, and iii) stronger MET signaling is required to stimulate the growth of human MPM cells. Although mouse HGF stimulated only motility, suppression of invasive growth by blockade of HGF/MET signaling had therapeutic value,[28] because MPM is an aggressive neoplasm characterized by extensive invasive growth.

Although human FGF-2 stimulated the growth of human fibroblasts, it did not stimulate the growth of mouse fibroblasts. Under the same experimental conditions, human PDGF-AA stimulated the growth of both human and mouse fibroblasts. Moreover, imatinib, which inhibits PDGFR signaling, markedly inhibited the progression of MSTO-211H and Y-Meso-14 cells in an orthotopic implantation model that mimics the MPM microenvironment in humans. Clinical trials of imatinib monotherapy in MPM have shown limited efficacy,[29,30] suggesting that, although the PDGF/PDGFRs axis is the signaling pathway responsible for fibroblast motility and growth in mice, the pathway in humans also involves the FGF-2/FGFR1 axis, which acts redundantly with the PDGF/PDGFR axis. Under these conditions, a multiple kinase inhibitor such as TSU-68 may control fibroblast motility and growth in humans. Further understanding of the crosstalk between tumors and their microenvironments, including TAFs, may lead to development of more effective therapeutic modalities.

The microenvironment of MPM consists of various components, including endothelial cells, fibroblasts, immune cells, mesothelial cells, and extracellular matrix. In MPMs producing large quantities of VEGF, the interaction with endothelial cells seems to be particularly important. VEGF produced by MPM cells activates endothelial cells and induces angiogenesis, promoting tumor progression.[12] In addition, VEGF activates endothelial cells and induces hypervascular permeability to produce pleural effusion.[31] Therapy targeting VEGF/endothelial cells may therefore be effective for MPM cells that produce large (EHMES-10) but not small (MSTO-211H) quantities of VEGF.[12] The results presented here suggest that therapy targeting TAFs and related molecules may be warranted for MPM with low VEGF expression and abundant TAFs, as in MSTO-211H cells.

The cytokine antibody array that we used is designed to scan for many cytokines at one time, but the array does

not include PDGF-AA (see Supplemental Figure S2 at *http://ajp.amjpathol.org*); instead, the array detects PDGF-BB. However, we could not detect PDGF-BB in the supernatant of MSTO-211H cells when quantified by ELISA. Instead, a high level of PDGF-AA was detected by ELISA. This mismatch between cytokine antibody array and ELISA may have been due to the relatively lower specificity of the cytokine antibody array. In addition to HGF, low concentrations of CXCL5 have been observed in the supernatants of MRC-5 but not MSTO-211H cells. CXCL5 (also known as epithelial-derived neutrophil-activating peptide 78, or ENA-78) was reported to be produced also by white blood cells, such as neutrophils and eosinophils, suggesting that CXCL5 may not be a specific fibroblast-derived cytokine that influences MPM function. Because the main issue under investigation in the present study was the interaction between MPM cells and fibroblasts, and the CXCL5 concentration in MRC-5 cells was much lower than that of HGF, we concentrated on HGF, which is produced abundantly by fibroblasts.

MPM is histologically classified into three types: epithelial, biphasic, and sarcomatous. Both cell lines used in the present study, MSTO-211H and EHMES-10, were established from patients with biphasic mesothelioma. However, these two cell lines show quite different characteristics, including different patterns of cytokine production and their content of TAFs in orthotopically implanted tumors. In addition, histological analyses of clinical specimens showed that the amount of TAFs did not correlate with MPM histological type. These findings suggest that histological differentiation and TAF accumulation in MPM may be regulated by different molecular mechanisms. We also detected simultaneous expression of FGF-2, PDGF-AA, and HGF in mesotheliomas with low numbers of TAFs, suggesting the need to analyze the role of these molecules in MPM tumors.

We have shown here that a malignant cytokine network between malignant pleural mesothelioma and tumor-associated fibroblasts, mediated through FGF-2, PDGF-AA, and HGF, exists in a population of MPM patients. Therefore, simultaneous inhibition of these three molecules may be clinically beneficial for patients with these tumors. Multiple targeted tyrosine kinase inhibitors may be appropriate for clinical trials of MPM patients, and treatments targeting the tumor microenvironment may also be beneficial in MPM.

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# Hepatocyte Growth Factor Expression in *EGFR* Mutant Lung Cancer with Intrinsic and Acquired Resistance to Tyrosine Kinase Inhibitors in a Japanese Cohort

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**Introduction:** This study was performed to determine the incidence rates of resistance factors, i.e., high-level hepatocyte growth factor (HGF) expression, epidermal growth factor receptor (EGFR) T790M secondary mutation, and *MET* amplification, in tumors with intrinsic and acquired EGFR tyrosine kinase inhibitor (TKI) resistance in *EGFR* mutant lung cancer.

**Methods:** Ninety-seven specimens from 93 *EGFR* mutant lung cancer patients (23 tumors with acquired resistance from 20 patients, 45 tumors with intrinsic resistance from 44 patients [nonresponders], 29 sensitive tumors from 29 patients) from 11 institutes in Japan were analyzed. HGF expression, *EGFR* T790M secondary mutation, and *MET* amplification were determined by immunohistochemistry, cycleave real-time polymerase chain reaction, and fluorescence in situ hybridization, respectively.

**Results:** High-level HGF expression, *EGFR* T790M secondary mutation, and *MET* amplification were detected in 61, 52, and 9% of tumors with acquired resistance, respectively. High-level HGF expression was detected in 29% of tumors with intrinsic resistance (nonresponders), whereas *EGFR* T790M secondary mutation and *MET* amplification were detected in 0 and 4%, respectively. HGF expression was significantly higher in tumors with acquired resistance than in sensitive tumors ($p < 0.001$, Student's $t$ test). Fifty percent of tumors with acquired resistance showed simultaneous HGF expression with *EGFR* T790M secondary mutation and *MET* amplification.

**Conclusions:** High-level HGF expression was detected more frequently than *EGFR* T790M secondary mutation or *MET* amplification in tumors with intrinsic and acquired EGFR-TKI resistance in *EGFR* mutant lung cancer in Japanese patients. These observations provide a rationale for targeting HGF in EGFR-TKI resistance in *EGFR* mutant lung cancer.

**Key Words:** EGFR-TKI, EGFR mutation, HGF, Acquired resistance, Intrinsic resistance.

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Epidermal growth factor receptor (EGFR)-activating mutations, in-frame deletion in exon 19, and L858 point mutation in exon 21 are selectively expressed in a population with lung cancer.[1,2] *EGFR*-activating mutations are detected considerably more frequently in nonsmokers, females, adenocarcinomas, and patients from East Asia, including Japan.[3–5] The reversible EGFR tyrosine kinase inhibitors (EGFR-TKIs) gefitinib and erlotinib show dramatic therapeutic efficacy, response rates of 70 to 80%, and significant prolongation of progression-free survival (PFS) compared

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with standard first-line cytotoxic chemotherapy in patients with *EGFR* mutant lung cancer.[6–9] However, patients almost always develop acquired resistance to EGFR-TKIs after varying periods.[6,9,10] In addition, 20 to 30% of patients with *EGFR*-activating mutations show intrinsic resistance to EGFR-TKIs.[4] Therefore, intrinsic and acquired resistance to EGFR-TKIs are major problems in management of *EGFR* mutant lung cancer.

Two genetically conferred mechanisms—*EGFR* T790M secondary mutation (T790M secondary mutation)[11,12] and *MET* gene amplification[13]—induce acquired resistance to EGFR-TKIs in *EGFR* mutant lung cancer. In addition, we recently demonstrated the occurrence of hepatocyte growth factor (HGF)-induced resistance.[14] HGF, a ligand of MET,[15] induces EGFR-TKI resistance by activating MET, which restores phosphorylation of downstream MAPK-ERK1/2 and PI3K-Akt pathways,[14] using Gab1 as an adaptor.[16] HGF may be involved in both intrinsic and acquired resistance to EGFR-TKIs in *EGFR* mutant lung cancer.[14]

T790M secondary mutation, *MET* amplification, and high-level HGF expression were detected in clinical specimens from *EGFR* mutant lung cancer patients who acquired resistance to EGFR-TKIs,[11–14,16–18] indicating the clinical relevance of all three resistance mechanisms in lung cancer. Although the number of cases in each study was limited (<30 cases/study), probably because of low availability of biopsy specimens from resistant tumors, *EGFR* T790M secondary mutation and *MET* amplification were estimated to have occurrence rates of 50%[11,12,17,19] and up to 20%,[13,16,17] respectively, in patients showing acquired resistance to EGFR-TKIs. Nevertheless, the incidence of HGF-induced resistance has not been determined. In addition, the incidence rates of these three resistance factors in intrinsic resistance (nonresponders) are unknown.

Here, we performed a large-scale study in 23 tumors with acquired resistance from 20 patients, 45 tumors with intrinsic resistance from 44 patients (nonresponders), and 29 sensitive tumors from 29 patients to determine the incidences of the three resistance factors not only in acquired resistance but also in intrinsic resistance (nonresponders) to EGFR-TKIs in Japanese patients with *EGFR* mutant lung cancer.

## MATERIALS AND METHODS

Patient details are described in the Supplementary information (http://links.lww.com/JTO/A197).

### Definition of Sensitivity to EGFR TKI

Here, tumors with *EGFR* mutation known to be associated with drug sensitivity (i.e., G719X, exon 19 deletion, and L858R) were obtained from patients before or after treatment with a single EGFR-TKI.[9]

Sensitive tumors were defined as those obtained from patients whose tumors showed a decrease in diameter of at least 30% (either documented partial response or complete response) associated with EGFR-TKI treatment in imaging studies (Response Evaluation Criteria in Solid Tumors [RECIST] version 1.0). Tumor specimens were obtained before EGFR-TKI treatment.

Tumors with acquired resistance were defined as described previously.[9] Briefly, cases showing objective clinical benefit from treatment with an EGFR TKI as defined by either documented partial or complete response (RECIST) or significant and durable (>6 months) clinical benefit (stable disease as defined by RECIST) and systemic progression of disease (RECIST), while on continuous treatment with gefitinib or erlotinib within the last 30 days were defined as showing acquired resistance. Tumor specimens were obtained after systemic progression of disease.

As intrinsic resistance (nonresponders) has not been clearly defined, tumors without response to treatment with an EGFR TKI, i.e., either documented stable disease or progressive disease (RECIST), were defined as showing intrinsic resistance (nonresponders). Tumor specimens were obtained either before or after EGFR-TKI treatment.

### Patients

Ninety-seven tumor specimens with EGFR mutations were obtained from 93 lung cancer patients, all of whom provided written informed consent, at 11 institutes in Japan. This study was approved by the Institutional Review Boards of each institute.

Patients' characteristics are shown in Table 1. Eighty-seven patients had adenocarcinomas, one had large cell carcinoma, two had squamous cell carcinoma, two had adenosquamous carcinoma, and one had undifferentiated non-small cell carcinoma. As the first EGFR-TKI, gefitinib and erlotinib were given to 82 and 10 patients, respectively, and the dual inhibitor of EGFR and VEGFR2, vandetanib,[20] was given to 1 patient.

Exon 19 deletion and L858R point mutation in exon 21 of *EGFR* were detected in 40 and 57 of the 97 tumors, respectively (Table 1). Two of these tumors had both exon 19 deletion and L858R point mutation. Two tumors without exon 19 deletion or L858R had G719X. Twenty-three tumors with acquired resistance were obtained from 20 patients after EGFR-TKI treatment. Forty-five tumors with intrinsic resistance (nonresponders) were obtained from 44 patients either before (41 tumors from 41 patients) or after (four tumors from three patients) EGFR-TKI treatment. Twenty-nine sensitive tumors were obtained from 29 patients before EGFR-TKI treatment.

### Immunohistochemistry for HGF

Immunohistochemical staining was conducted on formalin-fixed, paraffin-embedded tissue sections (4 $\mu$m thick) of tumor specimens with microwave antigen retrieval in 0.01 M citrate buffer (pH 6.0). We used rabbit polyclonal antibody against HGF-$\alpha$ (IBL, Gunma, Japan) at 1:20 dilution as a primary antibody and EnVision/HRP Polymer Reagent (Dako, Glostrup, Denmark) and DAB (3,3′-diaminobenzidine tetrahydrochloride) Liquid (Dako) for detection.

### Evaluation of HGF Expression

The percentages of cancer cells with positive cytoplasmic and/or membrane HGF immunoreactivity were evaluated (0 to 100%), and the modal intensity of the positively staining cells on a scale ranged from 0 to 3+ (0, complete

**TABLE 1.** Patient Characteristics

| Number of Patients | Acquired Resistance ($n$ = 20) | Intrinsic Resistance ($n$ = 44) | Sensitive ($n$ = 29) | Total ($n$ = 93) |
|---|---|---|---|---|
| Age | | | | |
| Median | 59.5 | 65.5 | 65 | 64 |
| Range | 32–85 | 34–76 | 42–86 | 32–86 |
| Gender | | | | |
| Male | 6 | 26 | 10 | 42 |
| Female | 14 | 18 | 19 | 51 |
| Smoking history | | | | |
| Former/current Smoker | 3 | 21 | 11 | 35 |
| Never smoker | 17 | 23 | 18 | 58 |
| Histological type | | | | |
| Adeno | 19 | 39 | 29 | 87 |
| Large cell | 0 | 1 | 0 | 1 |
| Squamous cell | 0 | 2 | 0 | 2 |
| Undifferentiated non-small cell carcinoma, or adenosquamous | 1 | 2 | 0 | 3 |
| EGFR-TKI treatment | | | | |
| Gefitinib | 19 | 36 | 27 | 82 |
| Erlotinib | 1 | 7 | 2 | 10 |
| Vandetanib | 0 | 1 | 0 | 1 |
| **Number of Tumors** | **$n$ = 23** | **$n$ = 45** | **$n$ = 29** | **$n$ = 97** |
| *EGFR* mutation status | | | | |
| Exon 19 deletion | 12 | 14[a] | 14[a] | 40 |
| L858R | 11 | 30 | 16 | 57 |
| G719X | 0 | 2 | 0 | 2 |

[a] One patient's tumor had both exon 19 deletion and L858R point mutation.

absence of staining; 1+, weaker staining than normal bronchial epithelium; 2+, similar staining to normal bronchial epithelium; and 3+, clearly more intense staining than normal bronchial epithelium) (Supplementary Figure 1, http://links.lww.com/JTO/A197). The percentage and intensity were multiplied to give a scoring index ($H$ score) ranging from 0 to 300, according to a previously reported method with minor modifications.[16] Turke et al.[16] reported that HGF expression was significantly higher in specimens with acquired resistance (mean ± SD: 205 ± 106) compared with pretreatment (126 ± 112). On additional evaluation with specimens showing acquired resistance from patients whose tumors were obtained only after acquiring EGFR-TKI resistance, HGF expression was similar (176 ± 126) to that of specimens with acquired resistance in patients with paired tumor specimens; they concluded that these findings with clinical specimens supported the suggestion that HGF mediated resistance to EGFR-TKIs. Therefore, we defined high-level HGF expression as $H$ score ≥200 in this study. Evaluation was performed independently by two investigators (KT and MN) blinded to individual clinical information.

## Cycleave Real-Time Polymerase Chain Reaction Assay for T790M Mutation

Details of the cycleave real-time polymerase chain reaction (PCR) assay have been described previously.[21] Briefly, tumor cell-rich areas in hematoxylin and eosin-stained sections were marked under a microscope, and tissues were scratched from the area of another deparaffinized unstained section. Pieces of the scratched tissue were incubated with 1× PCR buffer containing 100 μg/mL proteinase K for 1 hour at 54°C. After heat inactivation at 95°C for 3 minutes, the solution was used directly as the template DNA for the assay. Then, exon 20 of the *EGFR* gene was amplified by real-time quantitative PCR assay on a SmartCycler (Cepheid, Sunnyvale, CA) using Cycleave PCR Core kits (TaKaRa Co. Ltd., Ohtsu, Japan) with a T790M-specific cycling probe and a wild-type cycling probe. This assay detected as few as 5% cancer cells with T790M mutation in a background of cells with wild-type T790M in *EGFR*.

## MET Amplification

Formalin-fixed, paraffin-embedded tissue sections (4 μm thick) were subjected to dual-color fluorescence in situ hybridization using a MET/CEP7 probe cocktail (Kreatech Diagnostics, Amsterdam, The Netherlands) according to the manufacturer's instructions. Staining was evaluated as reported previously.[22,23]

## Statistical Analysis

Statistical significance was determined by Student's $t$ test. All statistical analyses were performed using GraphPad

**TABLE 2.** Expression of HGF, T790M Secondary Mutation, and *MET* Amplification in EGFR-TKI-Resistant Tumors Obtained from *EGFR* Mutant Lung Cancer Patients

| | Acquired Resistance ($n$ = 23) | Intrinsic Resistance ($n$ = 45) | Sensitive ($n$ = 29) |
|---|---|---|---|
| High-level HGF expression | 14 (61%) | 13[a] (29%) | 3[b] (10%) |
| *EGFR* T790M secondary mutation | 12 (52%) | 0 | 0 |
| *MET* amplification | 2 (9%) | 2 (4%) | 0 |

[a] High-level HGF expression was detected in the stroma in two patients.
[b] High-level HGF expression was detected in the stroma in one patient.

Prism Ver. 4.01 (GraphPad Software, Inc., San Diego, CA). All tests were two sided, and $p < 0.05$ was taken to indicate statistical significance.

## RESULTS

### HGF Expression, T790M Secondary Mutation, and MET Amplification in Tumors with Acquired Resistance

Among 23 tumors with acquired resistance from 20 patients, *EGFR* T790M secondary mutation was detected in 12 tumors (52%) from 11 patients (60%) (Table 2). *MET* amplification was detected in two tumors (9%) from two patients (10%). As HGF is a soluble cytokine, evaluation of HGF is not as simple as that for genetically conferred T790M secondary mutation and *MET* amplification, which can be designated as plus or minus. As described in the Materials and Methods section, we defined high-level HGF expression as *H* score ≥200 in this study. High-level HGF expression was detected in 14 tumors (61%) from 13 patients (60%). In these 14 tumors, HGF was predominantly expressed in cancer cells.

The high HGF expression was simultaneously detected in 6 of 12 tumors positive for T790M secondary mutation (50%) (Table 3, Figure 1). High-level HGF expression was also detected simultaneously in one of two tumors positive for *MET* amplification (50%). These results suggested possible interactions among these three resistance factors, consistent with previous reports.[16,17]

### Expression of HGF, T790M Secondary Mutation, and MET Amplification in Tumors with Intrinsic Resistance (Nonresponders)

T790M secondary mutation was not detected in 45 tumors with intrinsic resistance from 44 patients (nonresponders), but *MET* amplification was detected in two tumors (4%) (Table 2). *EGFR* D761Y secondary mutation was detected in two tumors (4%) from one patient[24](Supplementary Table 1, http://links.lww.com/JTO/A197). In contrast, high-level HGF expression in cancer cells was detected in 11 tumors (24%) from 11 patients. In addition, HGF was detected at high levels in stromal cells in two tumors (4%) from two patients (data not shown). In total, high-level HGF expression was detected in 13 tumors with intrinsic resistance (29%). Notably, high-level HGF expression was simultaneously detected in one of two *MET* amplification-positive tumors (50%) (Table 2). These results suggested the involvement of HGF in intrinsic resistance to EGFR-TKIs in *EGFR* mutant lung cancer in Japanese patients.

### Expression of HGF, T790M Secondary Mutation, and MET Amplification in Sensitive Tumors

Neither *EGFR* T790M secondary mutation nor *MET* amplification was detected in 29 sensitive tumors from 29 patients. High-level HGF expression was detected in two tumors (7%) (Supplementary Table 2, http://links.lww.com/JTO/A197). High levels of HGF were detected in stromal cells in one tumor (3%). In total, a high level of HGF expression was detected in three sensitive tumors (10%). Thus, although high HGF expression level was detected even in sensitive tumors, the incidence of high HGF expression was much lower in sensitive tumors than in those with acquired or intrinsic resistance. In addition, mean *H* score of HGF in tumors with acquired resistance was significantly higher than that in sensitive tumors ($p < 0.001$, Student's $t$ test) (Figure 2). There was no significant difference in mean *H* score of HGF between tumors with intrinsic resistance (nonresponders) and sensitive tumors.

## DISCUSSION

Our previous studies[14,25,26] documented HGF-mediated resistance to EGFR-TKIs in *EGFR* mutant lung cancer, which was also confirmed by other groups.[16,27] Here, we demonstrated that a high level of HGF expression was detected most frequently in tumors with intrinsic and acquired resistance to EGFR-TKIs in *EGFR* mutant lung cancer in Japanese patients. Our data indicated that although T790M secondary mutation and *MET* amplification are predominantly responsible for acquired resistance, HGF may be responsible not only for acquired resistance but also for intrinsic resistance to EGFR-TKIs.

The mechanism of intrinsic resistance to EGFR-TKIs is not well understood. To our knowledge, this is the first study with more than 40 clinical specimens indicating the incidence of resistance factors in intrinsic resistance to EGFR-TKIs in *EGFR* mutant lung cancer. Here, we found that a high level of HGF expression was most frequently (29%) detected in tumors with intrinsic resistance, compared with T790M secondary mutation (0%) and *MET* amplification (4%). It is noteworthy that although the high HGF expression level was detected in cancer cells in tumors with acquired resistance, HGF expression was detected in both cancer cells (10/12 tumors) and host stroma cells (2/12 tumors) in tumors with intrinsic resistance (nonresponders). HGF was reported to be produced by not only cancer cells but also stromal cells.[15] Our data clearly indicated that both cancer cells and stromal cells are sources of HGF, which induces intrinsic EGFR-TKI resistance in *EGFR* mutant lung cancer. As HGF-induced resistance could be reversed by anti-HGF antibody and the natural HGF inhibitor NK4,[25,27] highly produced HGF in