Targeting Epithelial-to-Mesenchymal Transition with Met Inhibitors Reverts Chemoresistance in Small Cell Lung Cancer

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Abstract

**Purpose:** Met receptor phosphorylation is associated with poor prognosis in human small cell lung cancer (SCLC). The aim of our work was to investigate the effects of hepatocyte growth factor (HGF)/Met–mediated epithelial-to-mesenchymal transition (EMT) in SCLC and to evaluate the role of Met inhibition in mesenchymal/chemoresistant SCLC models.

**Experimental Design:** SCLC models of HGF-induced EMT were evaluated in vitro and in vivo (subcutaneous xenografts in BALB/c nude mice) for chemosensitivity and response to Met inhibition with PF-2341066 (crizotinib). Human SCLC samples at diagnosis (N = 87) and relapse (N = 5) were evaluated by immunohistochemistry and immunofluorescence for EMT markers and Met status and these were correlated with patient outcome.

**Results:** We identified that the activation of the Met receptor through HGF induced expression of mesenchymal markers, an aggressive phenotype, and chemoresistance. Blockade of this process with the Met inhibitor resensitized cells to chemotherapy in vitro and in vivo. Moreover, mesenchymal markers in human SCLC specimens were associated with Met activation, predicted worse survival, and were upregulated in chemoresistant disease.

**Conclusion:** These results provide novel evidence on an important role of Met-dependent EMT in the adverse clinical behavior of SCLC and support clinical trials of Met inhibitors and chemotherapy in this fatal disease. *Clin Cancer Res; 20(4); 938–50. ©2013 AACR.*

Introduction

Small cell lung cancer (SCLC) accounts for approximately 15% of lung cancers. Its tight association to tobacco carcinogens' exposure explains the high number of genetic alterations described in this disease (1, 2). First-line treatment with platinum plus etoposide results in a high percentage of responses. Despite this, early chemoresistant relapse causes short survival of patients with SCLC. So far, no trial evaluating targeted therapies in SCLC has shown benefit when compared with standard chemotherapy. Our group has previously described an association between the Met pathway and outcome in patients with SCLC (3), supporting a potential therapeutic interest of Met inhibitors in this disease.

Epithelial-to-mesenchymal transition (EMT) is a cellular process characterized by loss of epithelial markers and acquisition of a mesenchymal phenotype, which enables cancer cells to invade surrounding tissues and generate distant metastasis (4). Repression of E-cadherin defines the main hallmark of EMT. This process is initiated by Snail1 transcriptional factor, a key inducer of this conversion. Although Snail1 is induced at the early phases of EMT, repression is not maintained in most mesenchymal cells; instead, E-cadherin silencing is dependent on other transcriptional repressors induced by Snail1, such as Zeb1 and 2 (5). Mesenchymal features are associated with poor prognosis and chemoresistance in different tumor models (6–8). EMT can be induced by growth factors; among them, hepatocyte growth factor (HGF), the natural ligand of Met tyrosine kinase receptor, has been reported to be a potent inducer of EMT (9, 10). PF-2341066 (crizotinib) is a small molecule that specifically inhibits Met and Alk kinases acting as an ATP.

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Subcutaneous tumorigenesis

HGF cells. Continuous exposure to HGF was able to induce EMT in blotting were performed at days 3, 6, and 10 to study if study by light microscopy and a molecular study by Western was added every 48 hours during 14 days. A morphologic medium containing 10% FBS. After 24 hours, HGF was added at 40 ng/mL. Fresh culture medium containing HGF and administered at a dose of 12 mg/kg in one daily intraperitoneal injection on days 1 to 3 of treatment. PF-2341066 was diluted in water and administered daily by oral gavage at 100 mg/kg for 14 days. This dose was selected on the basis of previous literature (16), suggesting that at this dose, Met is inhibited >90%, which potentially translates in tumor responses in a Met-dependent model. Control animals received 0.9% NaCl and water as vehicles. Mice were euthanized and tumors measured with calipers. Part of the tumors were fixed in 4% formalin and embedded in paraffin for immunohistochemical studies.

Human samples and immunohistochemistry

The following antibodies were used for immunohistochemical studies: Met (SP44) mouse mAb (monoclonal antibody; Ventana-Roche), p-Met Y1234/35 (130H2) rabbit mAb, p-Met Y1349 (130H2) rabbit mAb, p-Met Y1349 (130H2) rabbit mAb (Cell Signaling Technology), E-cadherin (NCH-38) mouse mAb, NCAM (123C3) mouse mAb (Dako), Snail1 (EC3) mouse mAb, vimentin (V9) mouse mAb (Dako), and CD31 (SP38) rabbit mAb (Spring Bioscience).

The study population consisted of 87 patients diagnosed with SCLC at any stage from whom we had clinical and follow-up information. Specimens were retrospectively retrieved from Parc de Salut Mar Biobank (MARBiobanc, Barcelona, Spain) and Fundacion Jimenez Diaz Biobank (Madrid, Spain). This study was approved by the institutional review board of each participating center. Three-μm tissue sections from formalin-fixed and paraffin-embedded samples were obtained, mounted onto charged slides, and then deparaffinized in xylene and hydrated.

After heat antigen retrieval was performed at a high-pH solution using PT Link platform (Dako), slides for immunohistochemistry were incubated with primary antibody for 1 hour at a dilution of 1:1 for Met mAb, 1:20 for p-Met Y1349, and 1:50 for p-Met Y1234/35, 1:5 for Snail1, 1:100 for E-cadherin, 1:100 for NCAM (neuronal adhesion molecule), 1:100 for vimentin, and 1:200 for CD31. Then, sections were incubated with the specific polymer EnVision FLEX+ (Dako) and revealed with 3,3’-diaminobenzidine (DAB) as chromogen. In situ hybridization was done by deproteinization using proteinase K digestion for 5 minutes at room temperature and incubation with a set of specific digoxigenin-labeled probes for mRNA SPARC (agaaaatgggtagggattgag); competitor. Crizotinib is approved for the treatment of patients with Alk-positive non–small cell lung cancer (NSCLC; ref. 11) and has also shown activity in tumors with Met activation (12).

Selection of the correct patient population for molecular treatment has become increasingly relevant for the impact of these targeted drugs in patients’ outcomes (13). This is particularly challenging for biomarkers that may not be the drivers of tumor progression, but play an important role in tumor aggressiveness or resistance to therapies, such as Met (14). Experience with Met inhibitors in the treatment of NSCLC illustrates the difficulty of selection of patients according to biomarker status (i.e., Met expression levels) for the success of Met-targeting therapies (15).

We hypothesized that Met activation by HGF may cause EMT and, as a consequence, induce chemoresistance in SCLC. On the basis of this hypothesis, the objectives of our work were (i) to explore in vitro and in vivo and in clinical specimens, the Met-induced EMT phenomena in SCLC; (ii) to test in vitro and in vivo, the effects of Met inhibition to revert EMT; and (iii) to search for predictive biomarkers that discriminate patients with SCLC who would benefit from anti-Met therapies.

Materials and Methods

HGF-induced EMT

We seeded 6.7 × 10^5 cells in 60-mm² dishes with culture medium containing 10% FBS. After 24 hours, HGF was added at 40 ng/mL. Fresh culture medium containing HGF was added every 48 hours during 14 days. A morphologic study by light microscopy and a molecular study by Western blotting were performed at days 3, 6, and 10 to study if continuous exposure to HGF was able to induce EMT in H69 cells.

Subcutaneous tumorigenesis

Five-week-old male BALB/c nude mice were purchased from Charles River Laboratories and hosted in the patho-
performed using a Dako Autostainer. Staining was evaluated at room temperature. Fluorescence assays were performed using same primary antibodies and conditions as described. Vimentin and SPARC were quantified when detected in the cytoplasm of tumor cells. A semiquantitative histoscore (H-score) was calculated, determined by estimation of the percentage of tumor cells positively stained with low, medium, or high staining intensity for each marker. The final score was determined after applying a weighting factor to each estimate. The formula used was: H-score = (low%) + 2 × (medium%) + 3 × (high%), and the results ranged from 0 to 300. The tumors in the present study were classified as p-MET–negative when the H-score was 0, versus p-MET–positive for any positive H-score. In our prior work, we defined as negative, any case with H-score of 5 or less, but because only one tumor had this criteria in this series and there was a continuous distribution of positive H-scores, we chose this new cutoff as per the statistical criteria. Measurement of microvascular density was determined as the mean number of vessels by quantification of the CD31-expression vascular structures using the ImageJ (NIH) software to recognize contiguous stained tubular vessels, as described previously (17). Double immunofluorescence for coexpression analysis was performed on tissue sections using same primary antibodies and conditions as described. Snail1, p-Met, and vimentin were detected using appropriate Alexa Fluor 568 and 488–conjugated goat anti-rabbit IgG and anti-mouse IgG antibodies (Life Technologies; diluted 1:700). Sections were counterstained with 4′,6-diamidino-2-phenylindole dihydrochloride (DAPI; Abbott Molecular) to visualize cell nuclei. All incubations were performed at room temperature. Fluorescence assays were performed using a Dako Autostainer. Staining was evaluated by two investigators (F. Rojo and S. Zazo) using a CRI Nuance FX Multispectral Imaging System (PerkinElmer).

**Results**

**HGF-induced EMT in SCLC cells is reverted and prevented by PF-2341066**

We exposed H69 SCLC cells to HGF (40 ng/mL) for 10 days. At day 6, HGF-treated cells grew as single cells partially attached to the plate (Fig. 1A, left). Because HGF-induced EMT is a dynamic process, we tested for EMT markers at various time points. Western blot analysis revealed that HGF promoted a partial downregulation of Met protein, stimulation of phosphorylated Met and ERK1/2, increase in Snail1 at day 6, and downregulation of E-cadherin at day 10 (Fig. 1A, right, and Supplementary Fig. S1A), but not in NCAM (data not shown).

We assessed whether PF-2341066 prevented HGF-induced effects. PF-2341066 was added to fresh medium upfront and every 48 hours along with HGF. As observed in Fig. 1A, the inhibitor prevented the disruption of cell clusters induced by HGF, as well as Met protein downregulation, ERK1/2 activation, Snail1 increase, or E-cadherin downregulation. We performed the experiment adding PF-2341066 at day 6, once the EMT phenotype was detectable. The Met inhibitor reversed the HGF-induced morphologic (Fig. 1B, left) and molecular changes (Fig. 1B, right).

To further demonstrate that the observed effect was a result of Met inhibition, we performed the same experiments with PHA-665752, which inhibits Met but not Alk, obtaining similar results (Supplementary Fig. S1B–S1D; ref. 18). Furthermore, we screened the cell lines used in this study for ALK translocation by FISH and all were negative (data not shown).

These data confirm that HGF, via Met activation, induced morphologic and molecular changes in H69 consistent with EMT, which are reversed or prevented by Met inhibition.

We stably knocked down the endogenous expression of Snail1 in H69 cells (shSnailH69). We observed an almost complete downregulation of the protein compared with cells transfected with the control short hairpin RNA (shRNA; shctH69; Fig. 1C, left). We then exposed shctH69 and shSnailH69 to HGF. We observed scattering of the shctH69 cells that grew partially attached to the plate (Fig. 1C, right) on day 6. In contrast, in shSnailH69 cells, no morphologic changes were observed under HGF exposure for 10 days. Detailed kinetic analysis showed that HGF induces Snail1 expression at day 3 in shctH69 but decayed at longer time points (day 6; Fig. 1C, left).

**A mesenchymal cell type is generated in vitro from SCLC cells treated with HGF**

Upon prolonged treatment with HGF, we observed a small pool of H69 cells with a mesenchymal (spindle-shaped) morphology that grew attached to the plates (Fig. 2A). This phenomenon was reproduced in six independent experiments. We isolated this subpopulation (H69-mesenchymal, H69M) and compared it with the parental H69 cells. H69M cells were phenotypically stable, maintaining the same mesenchymal morphology in the absence of HGF stimulation. A study of the karyotype showed the same chromosomal characteristics than H69 cells ruling out a potential contamination by another cell line (Supplementary Fig. S2A). As shown in Fig. 2B, left, H69M cells showed Met basal activation shown by phosphorylation of Tyr1349, and mesenchymal features characterized by the upregulation of fibronectin and downregulation of NCAM and E-cadherin. We then treated the H69M cells with HGF for 15 minutes to assess if...
they were still sensitive to HGF stimulation. We observed a higher increase in Met phosphorylation when compared with the increase observed in H69, and in the downstream molecules GAB1 (pTyr 307) and ERK1/2, indicating that these cells were more sensitive to exogenous HGF stimulation than parental H69.

One interesting observation is that differences in the intensity of baseline phosphorylation of Tyr1234/35 and Tyr1349 and in response to HGF were found in these experiments. This could be due to the performance of antibodies under our experimental conditions and/or to the different role of each phosphorylation site in response to HGF. Upon HGF binding, Met receptor is activated through dimerization and phosphorylation of Tyr1234/35 on the catalytic domain. Subsequently, phosphorylation of docking site Tyr1349 occurs with recruitment of downstream molecules as previously reported (19). Despite this, both were consistently upregulated upon HGF stimulation and expression decreased by Met inhibitors.

A global transcriptome analysis of H69 and H69M showed clear differences in mRNA expression. We found 9,712 genes that were differentially expressed (GEO accession number: GSE45120; Supplementary Fig. S2B). According to Ingenuity Pathway Analysis, the top altered functions in the comparison were "Cell movement," "Cell morphology," "Cellular growth and proliferation," and "Cell

![Figure 1](https://example.com/figure1.png)

**Figure 1.** HGF stimulation induces EMT in the H69 cell line and PF-2341066 prevents and reverts this process. A, cell morphology by light microscopy of H69 treated with HGF (40 ng/mL) or the combination of HGF and PF-2341066 (200 nmol/L) during 14 days. Photomicrographs at days 6 and 10. Scale bars, 100 μm (left). Western blot analysis of H69 cells treated with HGF (40 ng/mL) or HGF and PF-2341066 (200 nmol/L) during 6 and 10 days for p-Met (Y1234/1235, Tyr1349), Met, p-ERK1/2, Snail1, E-cadherin, and tubulin (right). B, cell morphology by light microscopy of H69 treated with HGF (40 ng/mL) during 6 days or with HGF and PF-2341066 during 48 hours after 6 days of HGF stimulation. Photomicrographs at days 6 and 8. Scale bars, 100 μm (left). Western blot analysis of H69 cells treated for 6 days with HGF (40 ng/mL) or the combination of HGF and PF-2341066 (200 nmol/L) for p-Met (Y1234/1235), Met, p-ERK1/2, Snail1, E-cadherin, and tubulin (right). C, Western blot analysis showing stable knockdown of Snail1 in H69 cells transduced with shRNA targeting Snail1 versus H69 cells transduced with scrambled shRNA after 3 and 6 days of HGF stimulation (left). Cell morphology by light microscopy of shCTH69 and shSnailH69 cells treated with HGF (40 ng/mL) during 10 days. Photomicrographs at day 6. Scale bars, 100 μm (right).
Figure 2. HGF-induced EMT results in the appearance of a mesenchymal subpopulation. A, cell morphology by light microscopy of H69 cells treated with HGF during 14 days showing the appearance of an adherent cell subpopulation. Scale bars, 100 μm. B, Western blot analysis of H69 and H69M cells treated with PF-2341066 (200 nmol/L) for 3 hours and stimulated with HGF (40 ng/mL) for 15 minutes (left) and heat map of altered genes in H69M cells compared with H69 (right). Horizontal rows, individual genes; vertical columns, individual samples. Color intensity means degree of gene expression modulation. Blue, upregulation; yellow, downregulation. Black, no change. C, qRT-PCR of selected genes. Expression values were normalized to the levels of a control RNA (RPLP0). Relative mRNA levels were normalized to the expression of the control sample (left); HGF production in H69 and H69M culture supernatants measured by ELISA (right). D, cell growth of H69 and H69M cells treated with PF-2341066 (200 nmol/L) during 10 days. Cell number was assessed by Scepter Automated Cell Counter. The number of viable cells in each treatment was plotted as percentage of control (left); invasion assay of H69 and H69M cells treated with PF-2341066 (100 nmol/L) during 24 hours. Each data point represents the mean ± SD percentage cell invasion of three independent experiments, compared with controls at 100% (middle); clonogenic assay of H69M cells cultured with or without PF-2341066 at 50 or 200 nmol/L during 14 days. Each data point represents the mean ± SD percentage clonogenic growth of three independent experiments, compared with controls at 100% (right).
HGF-mediated EMT enhances tumorigenesis in SCLC cells

H69 and H69M cells were injected in the flanks of immunodeficient mice (n = 10) to establish tumor xenografts. We observed that tumors generated by H69M were larger (median volume, 1.5 x 10^3 mm^3) compared with the tumors generated by H69 (median volume, 0.57 x 10^3 mm^3; Fig. 3A). Moreover, H69M were more invasive locally (surrounding soft tissue infiltration), showing foci of infiltrating cells in 9 of 10 mice compared with 1 of 10 mice for H69 cells (Fig. 3B). To study whether the results occurred in other subpopulations, we performed an in vitro experiment with a different mesenchymal subpopulation derived from H69 obtained by prolonged exposure to HGF (H69M2). This cell line presented a mesenchymal phenotype by Western blotting and secreted higher levels of HGF compared with H69. We confirmed the increased tumorigenic capacity of this mesenchymal subpopulation (Supplementary Fig. S3).

We then analyzed H69M xenografts compared with those generated by H69 cells. Histologic characteristics of both tumor xenografts were similar, suggesting that H69M were able to recapitulate the original round-small cell morphology of the parental H69 (Fig. 3C, hematoxylin and eosin).

Immunohistochemical studies revealed that H69M cells presented increased Met phosphorylation, expression of Snail1, vimentin, and SPARC and decreased expression of E-cadherin and NCAM. We also found increased vascularization of H69M-derived tumors (Fig. 3C). Multiplexing assays with Snail1 and p-Met antibodies demonstrated that Snail1 was expressed in cells with upregulated Met activity (Fig. 3D).

We repeated these assays using a lower number of cells, 100 (N = 5) and 500 (N = 5). For 100 cells, we observed tumor formation in 5 of 5 mice with H69M injection and in 3 of 5 mice for H69 (median tumor volume, 165 vs. 79 mm^3, respectively). When injecting 500 cells, 5 of 5 mice with H69M formed tumors, whereas 3 of 5 mice did it for H69 cells (median tumor volume, 384 vs. 82 mm^3, respectively).

In addition, we performed an in vivo assay, injecting 10^6 H69M cells in the flank of mice and treating with control vehicle (PF-2341066 100 mg/kg from day 0 (N = 5 per condition). The Met inhibitor significantly decreased tumor growth (median volume, 1,047 mm^3 for untreated vs. 350 mm^3 for treated mice; P < 0.05; Supplementary Fig. S4A). We also found a significant decrease in local invasion in the treated mice. Immunohistochemical analysis of the xenograft confirmed that treatment with PF-2341066 significantly decreased p-Met, mesenchymal marker expression, and angiogenesis and increased epithelial marker expression (Supplementary Fig. S4B).

These results suggest that Met activation by HGF induces a mesenchymal transformation that translates in a more tumorigenic and aggressive behavior that can be blocked with a Met inhibitor.

HGF-mediated EMT in SCLC induces chemoresistance in vitro and in vivo and MET inhibition sensitizes cells to chemotherapy

Because EMT has been associated with apoptosis resistance in other cellular systems (22), we investigated if the mesenchymal phenotype caused increased chemoresistance in our model. We treated H69 and H69M with etoposide, a standard chemotherapeutic agent used in SCLC. MTS assays demonstrated that H69M were chemoresistant, compared with H69 (Supplementary Fig. S5A).

To elucidate if Met inhibition could revert chemoresistance, we performed a clonogenic assay with H69M cells with etoposide, PF-2341066, and the combination of both. We observed the highest inhibition rate with the combination of etoposide and PF-2341066, suggesting that Met inhibition by PF-2341066 conferred chemosensitivity (Supplementary Fig. S5B, left).

We confirmed this hypothesis in mouse heterotopic tumors. We xenografted H69M cells and treated mice with
etoposide, PF-2341066, or the combination. We did not observe a significant effect on tumor growth by any of the two drugs alone; however, the combination produced a significant decrease in tumor growth compared with either agent alone (\(P < 0.05\), Fig. 4A).

Of note, inhibition of p-Met by PF-2341066 of mesenchymal cells did not affect the expression of EMT markers in short term assays performed following 3 hours of drug exposure (Western blotting; Fig. 2B and Supplementary Fig. S3A). However, longer time exposure experiments in vitro (i.e., cell growth 8 days, invasive capacity 24 hours, and clonogenic growth lasting 14 days) demonstrated the cellular effects of Met inhibition (Fig. 2D). These effects and their correlation with molecular changes were more robustly demonstrated in vivo (>20-day experiments), suggesting that HGF-induced EMT is a dynamic process and inactivation of p-Met does not elicit phenotypic EMT changes until later time points (Fig. 4C).

We then evaluated effects of the different treatment strategies in H69-derived xenografts. Tumors originated from H69 were sensitive to etoposide; addition of PF did not significantly modify the response (Fig. 4B).

To further confirm the capacity of PF-2341066 of conferring chemosensitivity, we used the same experimental approach with another SCLC cell line, H841. This cell line was sensitive to HGF stimulation showing increased expression of p-MET (Supplementary Fig. S5C, left), and a mesenchymal phenotype. It secreted higher levels of HGF and its receptor c-Met expressing extraversion of adjacent soft tissues by tumor cells compared with H69 tumors. Dashed black lines indicate the edge of the tumor in H69 and invasion of muscle and adipose tissues in H69M. Scale bar, 100 mm.

Quantification of the number of invasive foci in complete H&E-stained section for each group (mean ± SD tumor volumes. B, hematoxylin and eosin (H&E) stained sections from heterotopic H69M xenografts revealed infiltration of adjacent soft tissues by tumor cells compared with H69 tumors. Dashed black lines indicate the edge of the tumor in H69 and invasion of muscle and adipose tissues in H69M. Scale bar, 100 mm. Quantification of the number of invasive foci in complete H&E-stained section for each group (mean ± SEM) and significance are displayed. C, staining for H&E, p-Met, E-cadherin, NCAM, Snail, vimentin, SPARC, and CD31 in H69 and H69M tumors. Scale bars, 75 μm. Quantification of expression for each marker between H69 and H69M tumors (mean H-score ± SEM) and significance are displayed. D, representative image of immunofluorescence staining in H69M tumor for Snail (red), p-Met (green), and DAPI (blue). Snail is detected in the nuclei (pink, red + blue) and p-Met in the membrane and cytoplasm (green). Scale bars, 15 μm.

Figure 3. H69M cells are more tumorigenic and maintain mesenchymal features in vivo. A, photograph of a representative mouse with H69 and H69M cells subcutaneously inoculated at right and left flanks, respectively. Photograph of the excised tumors from the same animal (left) and tumor volume measurement after 25 days of injection (right). Each data point represents mean ± SD tumor volumes. B, hematoxylin and eosin (H&E) stained sections from heterotopic H69M xenografts revealed infiltration of adjacent soft tissues by tumor cells compared with H69 tumors. Dashed black lines indicate the edge of the tumor in H69 and invasion of muscle and adipose tissues in H69M. Scale bar, 100 mm. Quantification of the number of invasive foci in complete H&E-stained section for each group (mean ± SD) and significance are displayed. C, staining for H&E, p-Met, E-cadherin, NCAM, Snail, vimentin, SPARC, and CD31 in H69 and H69M tumors. Scale bars, 75 μm. Quantification of expression for each marker between H69 and H69M tumors (mean H-score ± SEM) and significance are displayed. D, representative image of immunofluorescence staining in H69M tumor for Snail (red), p-Met (green), and DAPI (blue). Snail is detected in the nuclei (pink, red + blue) and p-Met in the membrane and cytoplasm (green). Scale bars, 15 μm.
Figure 4. PF-2341066 increases sensitivity to etoposide (Et) in H69M-derived tumors. A and B, photograph of representative mice of each group of treatment with H69M (A) or H69 cells (B) subcutaneously inoculated at right flanks, and photograph of the excised tumors from the same animal. Graphs show changes in tumor volume of H69M (A) and H69 (B) xenograft treated with etoposide alone, PF-2341066 alone, or the combination of both treatments. Dose schedules were etoposide (12 mg/kg/i.p. on days 1 to 3 of treatment), PF-2341066 (100 mg/kg/oral gavage daily), and the combination of both. Each data point represents the mean ± SD tumor volume of each group of mice compared with control. C, p-Met, E-cadherin, NCAM, Snail, vimentin, SPARC, and CD31 staining in H69M tumors in control, PF 100 mg/kg, etoposide 12 mg/kg, and combination conditions of treatment. Met inhibition by PF alone or in combination with etoposide induces epithelial phenotype in tumor cells. Scale bars, 75 μm. Quantification of expression for each marker in the different treatment conditions (mean H-score ± SEM) and significance are displayed. *, P < 0.05 (PF arm compared with the combination). **, P < 0.05 (etoposide arm compared with the combination).
or amplification in MET (data not shown). In clonogenic assays, H841 and H69M cells presented a similar sensitivity to PF-2341066. It was also sensitive to etoposide, although the inhibitory effect was much greater when both drugs were combined (Supplementary Fig. S5C, bottom, right). Accordingly, PF-2341066 or etoposide alone did not significantly inhibit tumor xenograft growth when compared with the control group (Supplementary Fig. S5D). However, the combined therapy produced a significant decrease in tumor growth with respect to either group alone (P < 0.05; Supplementary Fig. S6A), suggesting that Met inhibition increased sensitivity of etoposide in chemotherapy H841-derived tumors (Supplementary Fig. S5D). The similar phenotypic response to chemotherapy and Met inhibition of H69M and H841 cell lines might be related to the presence of a mesenchymal phenotype in both cell lines in basal conditions as well as a common effect of exogenously added HGF in terms of induction of p-Met and downstream molecules p-GAB and p-ERK. However, differences in baseline phosphorylation of Tyr1234/35 and Tyr1349 do not seem to account for the effects observed in these mesenchymal-like cell lines (baseline phosphorylation is not present in H841). Furthermore, no common genetic alterations in the Met gene were detected. Of note, we tested another mesenchymal-like SCLC cell line, SHP77, which was chemo-resistant, did not express Met or p-Met with HGF addition, and was unresponsive to PF-2341066 (data not shown), suggesting that the mesenchymal phenotype per se is not sufficient to predict response to anti-Met therapy.

Immunohistochemical studies of H841-derived tumors in the different treatment groups, confirmed previously observed downregulation of p-Met and mesenchymal markers in xenografts treated with PF-2341066 (Supplementary Fig. S6B). Finally, in the H841-derived xenograft experiment, in the combined treatment group, we continued the experiment with 6 mice for 12 additional days, withdrawing the drugs in three cases. When the treatment was discontinued, the tumors significantly regrew compared with those that were kept treated (Supplementary Fig. S6C).

**Mesenchymal phenotype in human SCLC is associated with a worse outcome**

We retrospectively analyzed 87 SCLC specimens obtained at diagnosis between 2002 and 2012 with sufficient material for biomarker analysis and available clinical information. This series did not include patients from our previous publication (3). Supplementary Table S1 shows the patients’ characteristics. All the patients received standard first-line chemotherapy with platinum and etoposide and concomitant radiotherapy in cases if indicated. Mean follow-up time was 14 months (0.2–105 months). We determined Snail1, vimentin, SPARC, NCAM, Met, p-Met, and E-cadherin expression in these specimens. Figure 5A and Supplementary Table S2 show the pattern of expression of each biomarker. As observed, most of the cases were negative (no expression) for Snail1, vimentin, SPARC, and p-Met. There was not a relationship among the magnitude (intensity) of the signal in the positive cases (Supplementary Table S3). As no cutoff with clinical validity has been established for these biomarkers, we used the median as an arbitrary cutoff point. p-Met was expressed in 34% of patients, confirming our previous results. As dichotomous variables, we found direct association of p-Met expression with Snail1, vimentin, and Met and inverse correlation with E-cadherin (all P values < 0.001; Supplementary Table S4). There was a significant direct association between Snail1, vimentin, and SPARC and an inverse correlation between each of them and E-cadherin (all P values < 0.001). We found no association between Met and p-Met with clinical characteristics (Performance Status, stage).

We then assessed coexpression of p-Met staining with Snail1 and vimentin in human samples. Figure 5B demonstrates that both markers are coexpressed and tumor cells with Snail1 and vimentin expression also presented Met phosphorylation. The percentage of tumor cells with coexpression for Snail1 and vimentin, Snail1 and p-MET, and p-MET and vimentin was estimated in a subset of specimens (N = 25) by double immunofluorescence. The mean of Snail1-positive cells coexpressing vimentin was 73% (±20% SD), Snail1-positive cells coexpressing p-MET was 74% (±17% SD), and p-MET–positive cells coexpressing vimentin was 80% (±13% SD).

For survival analysis, we first evaluated the association of classic prognostic factors for patients with SCLC. As expected, poor performance status (≥2) and stage IV disease were associated with worse outcome (P < 0.001). We first performed a univariate analysis of each biomarker with survival illustrated in Fig. 6A. All biomarkers were associated with outcome except for p-Met and E-cadherin that showed a trend toward statistical significance. In our previous work (3), p-Met was significantly (P < 0.001) associated with survival in univariate and multivariate analysis. In the present study, p-Met was of borderline significance in the univariate analysis and significantly associated with survival in multivariate analysis. The difference in the P values between the two studies by univariate analysis may be related to relatively small sample size (albeit large for a SCLC study), or minor differences in the cutoffs used for positivity due to intrinsic differences in both study populations. However, the independent significance observed in both studies by multivariate analysis strongly supports the role of p-Met expression in SCLC outcomes. In the multivariate analysis, Snail1, vimentin, and SPARC expression also correlated with poor prognosis (all P values < 0.05). In contrast, E-cadherin expression was a marker of better outcome (P < 0.05; Supplementary Table S5 and Supplementary Fig. S7).

**Mesenchymal features are enhanced in relapsed disease in human SCLC**

We prospectively obtained paired samples (biopsies or cytology block) from 11 patients before first-line treatment and at first relapse/progression. We sought to compare EMT markers and Met status in these samples to validate our
preclinical hypothesis. Only five paired cases were adequate for immunohistochemical analysis. Globally, we observed upregulation of mesenchymal markers and p-Met in the specimens obtained at relapse (Supplementary Table S6 and Fig. 6B).

Discussion

Here, we demonstrate using preclinical models that the activation of the HGF/Met pathway induces EMT phenotype in SCLC cells and generates a mesenchymal population, more tumorigenic and chemoresistant than the parental cells. More importantly, Met-specific inhibition, via modulation of these mesenchymal biomarkers reverses this mesenchymal transition and subsequently increases chemosensitivity in SCLC models. Of translational relevance, a mesenchymal phenotype is associated with Met activation in the same tumor cells. Importantly, these mesenchymal features and Met phosphorylation are predictive of poor survival in patients with SCLC and are upregulated in chemoresistant or relapsed tumors. Globally, these results suggest a potential therapeutic role for PF-2341066 in combination with chemotherapy in the treatment of Met-activated SCLC.

SCLC is a highly lethal disease. No improvements in the treatment outcome have occurred for many years, leaving “old agent” chemotherapy and radiotherapy as the backbone treatment for these patients. Moreover, resistance to available therapy is a typical feature of this tumor at relapse, a phenomenon that has been elusive to tackle, to date. We have previously observed that Met activation is an independent prognostic factor in SCLC (3), suggesting a potential role for Met-targeted therapies in this disease. HGF has been previously associated
with poor prognosis and tumor burden in patients with SCLC (23, 24). Because Met is a well-known inducer of EMT in other models, we hypothesized that this transition, when induced by HGF, could be responsible for resistance to chemotherapy. We confirmed this hypothesis using H69 cells treated with HGF. Upon HGF-chronic exposure, we isolated a mesenchymal chemoresistant and highly tumorigenic subpopulation mimicking chemoresistant SCLC. Interestingly, these cells showed an increased basal Met phosphorylation when compared with the parental H69 along with upregulation of mesenchymal markers in vitro and in vivo and increased angiogenesis. The role of HGF as an inducer of EMT (10, 25, 26) and angiogenesis (27, 28) has been reported previously.

These cells endogenously expressed HGF, leading to an autocrine loop and constitutive activation of the pathway. This has been demonstrated in other tumor models (29, 30). The existence of autocrine loops has been shown to be common in mesenchymal cells participating in the stabilization of their phenotype (5).

PF-2341066, now crizotinib, is a dual Met/Alk inhibitor that has demonstrated a clear benefit in the treatment of patients with Alk-positive NSCLC (11). This drug is orally delivered and has a good safety profile. In our study, Met inhibition by PF-2341066 decreased the expression of Snail1, SPARC, and vimentin in SCLC xenografts. Although this was not sufficient to arrest tumor growth in vivo, there was a potent effect of PF-2341066 in resensitizing cells to chemotherapy, specifically to etoposide. In addition, in our

Figure 6. Met and EMT markers: association with survival in SCLC and changes after treatment. A, Kaplan–Meier curves for overall survival univariate analysis according to biomarker status. B, paired samples from SCLC patient #5 at diagnosis and relapse time points, stained for Met, p-Met, E-cadherin, Snail, vimentin (VIM), and SPARC. Upregulation of mesenchymal markers and downregulation in E-cadherin expression were detected in relapse sample. Scale bars, 75 μm.
patient population, there was a strong and independent correlation of this mesenchymal phenotype with Met activation and poor patient outcome. Without the data of untreated patients’ arm, it is not possible to specify whether these biomarkers are predictive or prognostic in this disease. However, 85% of patients in this series showed response to first-line treatment, and this was not associated with biomarker status (data not shown).

The mechanistic association between Met activation and mesenchymal features was supported by the coexpression of p-Met, Snail1, and vimentin in the same tumor cells and by the changes in EMT markers upon treatment with crizotinib. Upregulation of mesenchymal biomarkers and Met activation have both been associated separately with prognosis in several tumor types (6, 31–33) and coexistence of both markers with stemness (34). One could hypothesize that the presence of a subset of cells with these markers in SCLC at diagnosis could predict the enrichment of this chemoresistant population at progression after chemotherapy and, therefore, explain the poor prognosis of these patients in our study. This would be consistent with the greater antitumor effect observed when PF-2341066 is added upfront (Supplementary Fig. S4A) when compared with in vivo experiments using established H69M tumor xenografts (i.e., average tumor volume ~200 mm³). In the latter model, PF-2341066 alone did not significantly affect tumor growth albeit EMT markers and vasculogenesis were modified in the tumor specimens assayed at the time animals were sacrificed (Fig. 4). In contrast, PF-2341066 significantly reduced tumor growth and mesenchymal biomarkers when drug exposure was initiated before tumor xenografts were established (Supplementary Fig. S4). A possible explanation, beyond a potential greater effect of drug just based on lower tumor volume, is that a higher proportion of tumor cells at earlier time points is more mesenchymal than at later time points. Regardless of this, our data suggest that the inhibition of EMT and vasculogenesis markers plays a role in the sensitizing effects of PF-2341066 toward etoposide and we propose that the main role of Met inhibition would be to enhance chemotherapy activity instead of a role as a single-drug strategy.

However, the selection of patients who may benefit from this drug is crucial. Some researchers postulate that a selection according to Met expression by immunohistochemistry would be a good criterion for further evaluation of Met inhibitors (i.e., onartuzumab; ClinicalTrials.gov identifier: NCT01456325).

In our experience, Met levels (neither by mRNA or protein quantification) do not reflect Met activity and do not predict for Met inhibitor sensitivity; accordingly, Met phosphorylation would be a superior biomarker for pathway activation. However, p-Met antibodies have poor performance due to lack of sensitivity and specificity on routine clinical samples.

We previously reported that Met mutations or polymorphisms could be a marker of response to Met inhibitors. However, in the present work, we report that a Met-dependent cell line, H841, without any known Met mutation or polymorphism, but enriched with mesenchymal features, was also sensitive to Met inhibition. This novel observation suggests the potential benefit of Met inhibitors for patients with SCLC with mesenchymal features in the tumor.

We initially focused on Snail1 as it is the best-characterized inducer of EMT and its role in our SCLC models was confirmed by shRNA experiments. Because our ultimate goal was to explore an EMT phenotype of potential clinical interest, as assayed by robust epithelial and mesenchymal markers, but not to study EMT at the transcriptional level, we did not assay additional EMT transcriptional repressors such as Zeb1, Zeb2, Twist1, or Slug.

Our work suggests that the selection of patients according to mesenchymal biomarkers (SPARC, vimentin, and E-cadherin) in combination with Met expression is a good alternative for selecting patients with SCLC for clinical trials of Met inhibitors plus chemotherapy.

Disclosure of Potential Conflicts of Interest
E. Arriola is a consultant/ advisory board member of Pfizer, Inc. No potential conflicts of interest were disclosed by the other authors.

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