Synergistic Effects of Metformin Treatment in Combination with Gefitinib, a Selective EGFR Tyrosine Kinase Inhibitor, in LKB1 Wild-type NSCLC Cell Lines

Floriana Morgillo1, Ferdinando Carlo Sasso2, Carminia Maria Della Corte1, Donata Vitagliano1, Elena D’Aiuto3, Teresa Troiani1, Erika Martinelli1, Ferdinando De Vita1, Michele Orditura1, Raffaele De Palma3, and Fortunato Ciardiello1

Abstract

Purpose: EGFR receptor (EGFR) tyrosine kinase inhibitors (TKI) have been found to be effective against lung cancer, but clinical resistance to these agents has developed as their usage has increased. Metformin is a widely used antidiabetic drug and also displays significant growth-inhibitory and proapoptotic effects in several cancer models, alone or in combination with chemotherapeutic drugs.

Experimental Design: The effects of gefitinib, a selective EGFR-TKI, and metformin on a panel of non-small cell lung cancer (NSCLC) cell lines were assessed by using MTT, bromide assay, flow cytometry, anchorage-independent growth, coimmunoprecipitation, and Western blot analysis.

Results: The combination of metformin with gefitinib induced a strong antiproliferative and proapoptotic effect in NSCLC cell lines that harbored wild-type LKB1 gene. Treatment with metformin as single agent, however, induced an activation and phosphorylation of mitogen-activated protein kinase (MAPK) through an increased C-RAF/B-RAF heterodimerization. The inhibition of EGFR phosphorylation and of downstream signaling by adding gefitinib to metformin treatment abrogated this phenomenon and induced a strong apoptotic effect in vitro and in vivo.

Conclusions: Metformin and gefitinib are synergistic in LKB1 wild-type NSCLC cells. However, further studies are required to investigate better the effect of metformin action on the RAS/RAF/MAPK pathway and the best context in which to use metformin in combination with molecular targeted agents.

Introduction

Non–small cell lung cancer (NSCLC) is the major cause of cancer-related deaths worldwide (1). Platinum-based combination regimens offer a modest but significant survival advantage to patients with NSCLCs with advanced or metastatic disease, although most patients eventually experience disease progression (2).

Advances in the understanding of the molecular biology of cancer have enabled the discovery of several potential molecular targets with the development of novel targeted therapies. The EGFR receptor (EGFR) is involved in the development and the progression of several human cancers including NSCLCs. Two EGFR tyrosine kinase inhibitors (TKI), gefitinib (ZD1839, Iressa) and erlotinib (OSI774, Tarceva), represent the first examples of molecularly targeted agents developed in the treatment of NSCLCs and are, currently, used in the management of patients with advanced NSCLCs who progressed on previous chemotherapy or in the treatment of those patients harboring specific activating somatic EGFR gene mutations (3).

Despite impressive clinical successes with different kinase-targeted therapies, most, if not all, patients with cancer with an initially responsive disease eventually experience relapse as a result of acquired drug resistance to these agents. Consequently, it is critical to define the mechanisms by which drug resistance develops for the identification of therapeutic strategies to avoid and/or to overcome cancer cell acquired resistance (4).

Metformin (N′,N′-dimethylbiguanide) belongs to the biguanide class of oral hypoglycemic agents and is a widely used antidiabetic drug now prescribed to almost 120 million people in the world for the treatment of type II diabetes.
Metformin and Gefitinib in NSCLC

Translational Relevance
The combination of metformin with gefitinib, a molecular targeted agent blocking the EGF receptor (EGFR), has been shown to be particularly synergistic, in vitro and in vivo, in those non–small cell lung cancer (NSCLC) cell lines harboring an LKB1 wild-type gene. In addition to its antiproliferative effects in NSCLC cell lines, we observed also an increase in the level of activated phosphorylated mitogen-activated protein kinase (MAPK) after metformin single-agent treatment, which is mediated by an increased heterodimerization between C-RAF and B-RAF. This could be therapeutically relevant, as we have shown that while exerting antiproliferative and proapoptotic effects, single-agent metformin treatment could enhance pro-proliferating signals through the RAS/RAF/MAPK pathway. At the same time, treatment with both metformin and gefitinib can avoid aberrant signals through the RAS/RAF/MAPK pathway and could explain, at least in part, the mechanism of such significant synergism. These findings open new possibilities for the treatment of patients whose cancers become refractory to initially effective molecular targeted agents. Future perspective studies are required in patients with NSCLCs to investigate better the effect of metformin action on the RAS/RAF/MAPK pathway and the best context in which to use metformin in combination with molecular targeted agents.

Materials and Methods
Cell lines, drugs, and chemicals
The human NSCLC H1299, H1975, A549, H460, GLC82, H460, and CALU-3 cell lines were provided by the American Type Culture Collection and maintained in RPMI-1640 supplemented with 10% FBS (Life Technologies) in a humidified atmosphere with 5% CO₂. CALU-3 GEF-R is a cell line obtained in vitro as previously described (15). Briefly, over a period of 12 months, human CALU-3 lung adenocarcinoma cells were continuously exposed to increasing concentrations of gefitinib. The starting dose was the dose causing the inhibition of 50% of cancer cell growth (IC₅₀; gefitinib, 1 μmol/L). The drug dose was progressively increased to 15 μmol/L in approximately 2 months, to 20 μmol/L after other 2 months, to 25 μmol/L after additional 2 months, and, finally, to 30 μmol/L for a total of 12 months. The established resistant cancer cell lines were then maintained in continuous culture with the maximally achieved dose of each TKI that allowed cellular proliferation (30 μmol/L for each drug). Gefitinib was provided by AstraZeneca; metformin was purchased from Sigma-Aldrich. Primary antibodies against EGF (Tyr1068), EGFR, p-MAPK44/42 (Thr202/Tyr204), MAPK44/42, p-AKT (Ser473), AKT, C-RAF, BRAF, AMPK, p-AMPK (thr172), S6, p-S6 (ser 235-236), P70S6K, p-P70S6K (Thr389/421), 4EBP1, p-4EBP1 (Thr37/46), acetyl-CoA carboxylase (ACC), p-ACC (Ser79), and β-actin were obtained from Cell Signaling Technology. All other chemicals were purchased from Sigma-Aldrich.

Cell proliferation assays
Cancer cells were seeded in 96-well plates and were treated with different doses of gefitinib, metformin or both for 72 hours. Cell proliferation was measured with the MTT assay. The IC₅₀ values were determined by interpolation from the dose–response curves. Results represent the median of 3 separate experiments each conducted in quadruplicate. The results of the combined treatment were analyzed according to the method of Chou and Talalay by using the CalcuSyn software program (Biosoft; ref. 16). The resulting combination index (CI) is a quantitative measure of the degree of interaction between different drugs. If CI = 1, it denotes additivity; if CI > 1, it denotes antagonism; and if CI < 1, it denotes synergism.

DNA synthesis was measured by 5-bromo-2′-deoxyuridine (BrdUrd) labeling and detection kit (Roche Diagnostics). Cells were seeded onto glass coverslips and treated with metformin for 72 hours. Then, cells were incubated for 1 hour with BrdUrd (10 mmol/L) and fixed. Coverslips were incubated with anti-BrdUrd and secondary fluorescein-conjugated antibody. The fluorescent signal was visualized with an epifluorescent microscope (Axiovert 2, Zeiss) interfaced with the image analyzer software KS300. Cell nuclei were counterstained with Hoechst. The average results ± SD of 3 independent experiments in which at least 500 cells were counted are shown.

Western blotting
Following treatment, cancer cells were lysed with Tween-20 lysis buffer (50 mmol/L HEPES, pH 7.4, 150 mmol/L NaCl, 0.1% Tween-20, 10% glycerol, 2.5 mmol/L EGTA, 1 mmol/L EDTA, 1 mmol/L dithiothreitol, 1 mmol/L phenylmethylsulfonylfluoride, and 10 μg/mL of leupeptin and aprotinin) and sonicated. Equal amounts of protein were analyzed by SDS-PAGE. Thereafter, proteins were...
transferred to nitrocellulose membranes and analyzed by specific primary antibodies, as indicated in the experiment. Proteins were detected via incubation with horse-radish peroxidase-conjugated secondary antibodies and ECL chemiluminescence detection system.

For the siRNA transfection, NSCLC cells in the logarithmic growth phase in 6-well plates (5 × 10^3 cells/well) were transfected with 10 μL of 20 μmol/L LKB1 siRNA (Si-LKB1 Qiagen S102665383) or control scrambled siRNA (Dharmacon Research) using Lipofectamine 2000 (Invitrogen), according to the protocol of the manufacturer. LKB1 DNA transfection (Myc-DDK–tagged STK11) was conducted using Lipofectamine LTX according to the manufacturer’s specifications.

Immunoprecipitations were done using 1 μg protein from the total cell lysates and 1 μg mouse monoclonal anti-C-RAF antibody, mouse monoclonal anti-B-RAF antibody, or healthy preimmune serum anti-mouse for the negative control and by incubating overnight at 4°C. The immunocomplexes were precipitated with protein-G agarose (Pharmacia-LKB Biotechnology). The immunoprecipitates were resolved on 6% SDS-PAGE gels, followed by Western blotting as described elsewhere (17).

**Growth in soft agar**

Cells (10^5 cells per well) were suspended in 0.5 mL 0.3% Difco Noble agar (Difco) supplemented with complete culture medium. This suspension was layered over 0.5-mL 0.8% agar-medium base layer in 24-multiwell cluster dishes (Becton Dickinson) and treated with different concentrations of metformin, gefitinib, or both in combination. The medium was changed daily during this period, at the end of which, tumor cell colonies measuring at least 80 μm were counted using a dissection microscope. Assays were conducted in triplicate.

**Assessment of apoptosis**

Apoptosis was detected by flow cytometry via the examination of altered plasma membrane phospholipid packing by lipophilic dye Annexin V as described elsewhere (18). Briefly, treated cells were harvested by trypsin, washed twice with PBS, and then resuspended in binding buffer at a concentration of 1 × 10^5 cells/mL according to the manufacturer’s instruction. Thereafter, 5 μL of Annexin V-FITC and 5 μL of propidium iodide were added into 100 μL of cell suspension and incubated for 30 minutes at room temperature in the dark. After adding 400 μL of binding buffer, labeled cells were counted by flow cytometry within 30 minutes. All early apoptotic cells (Annexin V–positive, propidium iodide–negative), necrotic/late apoptotic cells (double positive), as well as living cells (double negative) were detected by FACScalibur flow cytometer and subsequently analyzed by Cell Quest software (Becton Dickinson). Argon laser excitation wavelength was 488 nm, whereas emission data were acquired at wavelength 530 nm (FL-1 channel) for fluorescein isothiocyanate (FITC) and 670 nm (FL-3 c3 channel) for propidium iodide.

**Tumor xenografts in nude mice**

Four- to 6-week-old female balb/c athymic (nu−/nu−) mice were purchased from Charles River Laboratories. The research protocol was approved and mice were maintained in accordance with the Institutional Guidelines of the Second University of Naples Animal Care and Use Committee. Mice were acclimatized for 1 week before being injected with cancer cells and injected subcutaneously with 10^7 H1299 and CALU-3 GEF-R cells that had been resuspended in 200 μL of Matrigel (Collaborative Biomedical Products). When established tumors of approximately 75 mm^3 in diameter were detected, mice were left untreated or treated with oral administrations of metformin (200 mg/mL metformin diluted in drinking water and present throughout the experiment), gefitinib (150 mg/kg daily orally by gavage), or both for the indicated time periods. Each treatment group consisted of 10 mice. Tumor volume was measured using the formula π/6 × larger diameter × (smaller diameter)^2. Tumor tissues were collected from the xenografts and analyzed by Western blotting for the expression and activation of EGFR, AMPK, mitogen-activated protein kinase (MAPK), and S6.

**Statistical analysis**

The Student t test was used to evaluate the statistical significance of the results. All P values represent 2-sided tests of statistical significance. All analyses were conducted with the BMDP New System statistical package version 1.0 for Microsoft Windows (BMDP Statistical Software).

**Results**

**Effect of metformin alone and in combination with gefitinib on NSCLC proliferation and anchorage-independent colony-formation ability**

To evaluate the antiproliferative effects of different doses of metformin, alone and in combination with gefitinib, we did an MTT assay on a panel of 7 NSCLC cell lines with different sensitivity to gefitinib. Treatment with metformin, ranging from 0.1 to 20 mmol/L as single agent for 72 hours, resulted in a dose-dependent inhibition of growth with an IC_{50} value between 2 and 2.5 mmol/L in H1299, GLC82, H1975, CALU-3, and CALU-3 GEF-R cell lines. H460 and A549 cell lines displayed a limited metformin-induced inhibition of cell proliferation (Table 1A), with an IC_{50} over 20 mmol/L. Treatment with gefitinib alone lead to an inhibition of CALU-3 and GLC82 cell proliferation, with an IC_{50} of 2 μmol/L, according to previous reports (15). H1299, H460, H1975, CALU-3 GEF-R, and A549 cancer cell lines showed a limited sensitivity to gefitinib treatment with about 80% to 90% cells surviving at 5 μmol/L dose of EGFR inhibitor (Table 1A).

We then assessed the growth-inhibitory effects of combinations of metformin with gefitinib. As shown in Table 1B and Supplementary Fig. S1, a 72-hour exposure to metformin and gefitinib resulted in a clear synergism in CALU-3, CALU-3 GEF-R, H1975, H1299, and GLC82, with a CI between 0.001 and 0.1 (Table 1B and Supplementary Fig. S1). Of interest, the synergism was evident also in H1975, H1299,
CALU-3 GEF-R, and H1299 cell lines, which are strongly resistant to the EGFR inhibition, indicating that metformin can revert resistance to gefitinib in some cancer cell lines. In contrast, no synergistic effect was observed by the combination of metformin and gefitinib in A549 and H460 cell lines. However, as metformin is known to disrupt mitochondrial respiration, which may affect the MTT assay results, we measured inhibition of cell proliferation also by using the BrdUrd incorporation. To this end, we used the IC50 dose of metformin 2.5 mmol/L alone and in combination with gefitinib. Results confirmed a strongest inhibitory efficacy by adding metformin to gefitinib in H1975, CALU-3, CALU-3 GEF-R, H1299, and GLC82 cell lines (Fig. 1A).

We then tested the effects of metformin alone and in combination with gefitinib on anchorage-independent colony formation of NSCLC cells. As shown in Fig. 1B, CALU-3, CALU-3 GEF-R, H1299, and GLC82 cells showed greater sensitivity to single-agent metformin treatment at dose of 5 mmol/L than A549 and H460, and sensitivity was even greater when metformin was combined with 1 μmol/L gefitinib, with the reduction of the anchorage-independent colony forming ability to less than 10% of untreated control cells.

### Effects on apoptosis by combined treatment of metformin and gefitinib

We further asked whether the increased antiproliferative effect induced by metformin alone and in combination with gefitinib would be the result of an increased apoptosis. Therefore, we analyzed the induction of apoptosis in CALU-3, CALU-3 GEF-R, and in H1299 human NSCLC cell lines after 72-hour treatment with metformin as single agent or in combination with gefitinib. As shown in Fig. 1C, flow cytometric analysis of CALU-3 cells revealed that 19% of gefitinib-treated cells and 21% [95% confidence interval, 14.3%–28.6%; \( P < 0.05 \)] of metformin-treated cells underwent apoptosis. In contrast, combined treatment with both gefitinib and metformin significantly enhanced the apoptotic cell percentage to 65% (95% confidence interval, 55.4%–75.8%; \( P < 0.001 \); Fig. 1B). Similar results were observed in CALU-3 GEF-R and H1299 cells, with respectively a 5% and 4% apoptotic rate in gefitinib-treated cells, 20% and 26% in metformin-treated cells, and 68% and 78% of apoptotic cells after the combined treatment with gefitinib and metformin (\( P < 0.001 \); Fig. 1B). These results were confirmed by Western blot analysis: metformin single agent was able to induce the cleavage of the 113-kDa PARP to the 89-kDa fragment in all tested cell lines. Single-agent gefitinib

### Table 1. Effects of metformin, gefitinib, and their combination on NSCLC cell lines

<table>
<thead>
<tr>
<th>Cancer cell line</th>
<th>Metformin IC50, mmol/L</th>
<th>Gefitinib IC50, μmol/L</th>
</tr>
</thead>
<tbody>
<tr>
<td>A. Evaluation of the cell growth-inhibitory effects of metformin or gefitinib given as single agents</td>
<td></td>
<td></td>
</tr>
<tr>
<td>CALU-3</td>
<td>1</td>
<td>2</td>
</tr>
<tr>
<td>CALU-3 GEF-R</td>
<td>2</td>
<td>&gt;10</td>
</tr>
<tr>
<td>H1299</td>
<td>2.5</td>
<td>&gt;10</td>
</tr>
<tr>
<td>GLC82</td>
<td>1.5</td>
<td>2</td>
</tr>
<tr>
<td>A549</td>
<td>&gt;20</td>
<td>&gt;10</td>
</tr>
<tr>
<td>H460</td>
<td>&gt;20</td>
<td>&gt;10</td>
</tr>
<tr>
<td>H1975</td>
<td>1.5</td>
<td>&gt;10</td>
</tr>
</tbody>
</table>

<table>
<thead>
<tr>
<th>Cancer cell line</th>
<th>CI at fa50</th>
<th>CI at fa75</th>
<th>CI at fa90</th>
</tr>
</thead>
<tbody>
<tr>
<td>A. Evaluation of the growth-inhibitory effects by the combined treatment with metformin and gefitinib</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>CALU-3</td>
<td>0.001</td>
<td>0.005</td>
<td>0.11</td>
</tr>
<tr>
<td>CALU-3 GEF-R</td>
<td>0.039</td>
<td>0.038</td>
<td>0.037</td>
</tr>
<tr>
<td>H1299</td>
<td>0.001</td>
<td>0.005</td>
<td>0.065</td>
</tr>
<tr>
<td>GLC82</td>
<td>0.001</td>
<td>0.007</td>
<td>0.012</td>
</tr>
<tr>
<td>A549</td>
<td>1.4</td>
<td>1.5</td>
<td>1.3</td>
</tr>
<tr>
<td>H460</td>
<td>1.7</td>
<td>2</td>
<td>1.4</td>
</tr>
<tr>
<td>H1975</td>
<td>0.001</td>
<td>0.005</td>
<td>0.04</td>
</tr>
</tbody>
</table>

**NOTE:** A. The evaluation of the cell growth-inhibitory effects of metformin or gefitinib, given as single agents, was done by MTT bromide assay. IC50 values for each drug were calculated by carrying out dose–response experiments. Cells were treated for 72 hours with metformin (0.01–20 mmol/L) or with gefitinib (0.01–20 μmol/L) for 72 hours. B. Evaluation of the growth-inhibitory effects by the combined treatment with metformin and gefitinib using an MTT bromide assay. Treatment combinations and sequences are described in Materials and Methods. CI values were calculated according to the Chou and Talalay mathematical model for drug interactions using the CalcuSyn software for different fractions affected (fa). CI is a quantitative measure of the degree of interaction between different drugs. If CI = 1, it denotes additivity; if CI > 1, it denotes antagonism; if 1 < CI > 0.7, it denotes slight synergism; if CI = 0.7–0.3, it denotes synergism; if CI < 0.3, it denotes strong synergism. Results are the median of 3 independent experiments, each done in 8 replicate wells for experimental point.
induced an increased cleavage of procaspase-3 only in CALU-3 cell line. However, the combination of metformin and gefitinib was accompanied by a sustained cleavage of procaspase-3 and 113-kDa PARP in CALU-3, CALU-3 GEF-R, and H1299 cell lines (Fig. 1C). Similar data were obtained with GLC82 cancer cell lines (data not shown). These findings suggest that metformin blocks proliferation and/or survival mechanisms in NSCLC cancer cells in which EGFR is blocked by gefitinib or is no longer the principal driver of growth.

Role of LKB1 as mediator of metformin anticancer activity

We therefore asked what could be the reason of the different response to metformin treatment among the NSCLC cell lines examined. Metformin interferes with the energetic metabolism of the cell by disrupting mitochondrial respiration, leading to an increase in the intracellular ratio of AMP:ATP, which in turn leads to activation of AMPK by LKB1 (19). Thus, loss of function of LKB1 can reduce the sensibility to metformin. Somatic inactivation of LKB1 gene

![Figure 1](image-url)
is a common event in NSCLCs, especially in lung adenocarcinoma cells (20). Previous reports show that among the panel of NSCLC cell lines, A549 and H460 are deficient in LKB1 expression (20). We confirmed and extended these results by conducting Western blot analysis for LKB1 protein expression. In Fig. 2A the levels of LKB1 protein in the panel of NSCLC cell lines tested are reported. LKB1 protein in A549 and in H460 cells was not detectable. To confirm a role of LKB1 as mediator of metformin anti proliferative activity, we then tested the effects of metformin on H1299 NSCLC cell line, in which LKB1 expression was inhibited by siRNA transfection. As shown in Fig. 2B, a significant reduction in the antiproliferative effects of metformin on H1299 cells transfected with a vector or LKB1 expression plasmid with the indicated concentrations of metformin for 3 days. Bottom, Western blotting for evaluation of LKB1 and phospho-AMPK after transfection.

Effects on intracellular signaling pathways following metformin treatment
To further elucidate the mechanism responsible for the cell growth-inhibitory effects of metformin, we next evaluated the effects of metformin on the expression of selected proteins and their activated forms, known to be important steps in the prosurvival and proliferation pathways, in CALU-3, CALU-3 GEF-R (Fig. 3A), and A549 cells. Furthermore, as metformin activates AMPK, we sought to examine whether pathways known to be influenced by AMPK activity might be affected in human tumor cells by metformin treatment. AMPK acts as a metabolic checkpoint inhibiting cellular growth. The most thoroughly described mechanism by which AMPK regulates cell growth is through the suppression of the mTORC1 pathway. mTOR exerts its effects by phosphorylating the eukaryotic initiation factor 4E-binding protein 1 (4EBP1) and via the ribosomal protein S6 kinase (S6K, formerly known as p70s6K; ref. 21). As the activation of AMPK correlates tightly with phosphorylation at Thr-172 (pAMPKα), we assessed the activation of AMPK by determining phosphorylation AMPKα and its primary downstream targeting enzyme, ACC, using immunoblots with specific phospho-Thr-172 and phospho-Ser-79 antibodies, respectively.
Treatment of CALU-3 and CALU-3 GEF-R cells with metformin (from 0.1 to 20 mmol/L) for 72 hours induced increased levels of activated phosphorylated AMPK without affecting total amount of AMPK protein (Fig. 3A). We tested also the ACC phosphorylation, which is a standard indicator of AMPK activity and resulted increased by metformin treatment. A significant decrease in the level of activated phosphorylated P70S6K and its principal target, S6, were evident after metformin treatment in a dose-dependent manner. Similar reduction was observed on the phosphorylation status of 4EBP1 at Thr37/46. In contrast, total amounts of P70S6K, 4EBP1, and S6 were not changed.

As the activated, phosphorylated forms of AKT and MAPK are key intracellular mediators of growth factor–activated cell survival and proliferation signals, investigating the activation state of these molecular pathways may be of interest in the understanding the mechanism of action of metformin in NSCLC cancer cells. Metformin treatment, at different dose levels, did not affect the protein levels of MAPK and AKT (Fig. 3A). While metformin treatment did not influence the activation status of AKT, it caused an unexpected increase in the levels of activated phosphorylated MAPK (p-MAPK) in CALU-3 and CALU-3 GEF-R cells. Similar results were obtained in H1299 cells untreated or treated with metformin (3 mmol/L) for 72 hours were immunoprecipitated (IP) with anti-C-RAF or anti-B-RAF antibodies. The immunoprecipitates were subjected to Western blot analysis (WB) with indicated antibodies. Control immunoprecipitation was done using control mouse preimmune serum (PS).

Figure 3. Effects on the downstream pathway by metformin treatment. A, Western blotting of AMPK, ACC, MAPK, AKT, p70S6K, S6, and 4EBP1 activation following treatment with the indicated concentration of metformin. β-Actin was included as a loading control. B, coimmunoprecipitation was done for the interaction between B-RAF and C-RAF. Whole-cell extracts from CALU-3, CALU-3 GEF-R, and H1299 cells untreated or treated with metformin (3 mmol/L) for 72 hours were immunoprecipitated (IP) with anti-C-RAF or anti-B-RAF antibodies. The immunoprecipitates were subjected to Western blot analysis (WB) with indicated antibodies. Control immunoprecipitation was done using control mouse preimmune serum (PS).
The activation of MAPK after metformin treatment.

Between C-RAF and B-RAF that could be responsible for suggest that metformin induces physical interaction binding than untreated cells (Fig. 3B). These results suggest that metformin induces physical interaction between C-RAF and B-RAF that could be responsible for the activation of MAPK after metformin treatment.

The effect of metformin was tested also on A549 and H460 cell lines, and no changes in the level of activated phosphorylated AMPK, P70S6k, 4EBP1, p-AKT, and p-MAPK were observed (Supplementary Fig. S2).

Taken together, these results suggest that activation of AMPK and inhibition of mTOR downstream signals are important to predict sensitivity to metformin treatment.

Effects on the intracellular signaling pathways following treatment with metformin and gefitinib

To determine whether the synergic growth inhibition effects obtained by the combination of metformin and the EGFR TKI, gefitinib, was due to a more effective inhibition of EGFR activation and the intracellular signaling through MAPK and/or AKT, Western blot analyses were done on protein extracts from CALU-3 and CALU-3 GEF-R NSCLC cells that were treated with 3 mmol/L of metformin, 1 µmol/L, gefitinib, or with combinations of both metformin and gefitinib. Treatment was conducted for 72 hours.

We selected these cells as they represent a model of sensitivity (CALU-3) and resistance (CALU-3 GEF-R) to treatment with anti-EGFR drugs as single agent. Figure 4 illustrates that gefitinib treatment, as single agent, although causing a decrease on EGFR phosphorylation, had a very little effect in inhibiting downstream mitogenic and prosurvival signals in CALU-3 GEF-R, as shown by the levels of activated phosphorylated AKT and MAPK and by little or no effect on the activation of p70S6k and S6.

Treatment with metformin in combination with gefitinib resulted in a more pronounced decrease in the levels of protein phosphorylation (p-MAPK, p-AKT). The combined treatment also affected the mTOR signaling as suggested by the sustained inhibition of the phosphorylation of S6 and of p70S6k.

Effects of the combined treatment with metformin and gefitinib on H1299 and CALU-3 GEF-R tumor xenografts

We finally investigated the in vivo antitumor activity of metformin in nude mice bearing H1299 or CALU-3 GEF-R cells that were grown subcutaneously as tumor xenografts. Treatment with metformin or gefitinib, as single agents, caused a slight decrease in tumor size as compared with control untreated mice. For example, at day 35 from the starting of treatment, the mean tumor volume in mice bearing H1299 tumor xenografts and treated with metformin and gefitinib were 78% and 70%, respectively, as compared with control untreated mice. Treatment with the combination of metformin and gefitinib induced a significant reduction in tumor growth (Fig. 5A). In this respect, at day 35 from the starting of treatment, the mean tumor volumes in the combination treatment group in mice bearing H1299 tumor xenografts ranged between 27% and 40%, as compared with control untreated mice. Similar results were reported for mice bearing CALU-3 GEF-R tumor xenografts (Fig. 5B). During our experiments, no obvious side effects were observed in mice treated with metformin. We then studied the effects of gefitinib, metformin, and their combination on the activation of AMPK, EGFR, MAPK, and S6 in vivo. According to Western blot analysis of total protein extracts harvested from the H1299 xenograft tumor tissues, 2 samples for each arm of treatment, the levels of pAMPK were increased by metformin. Interestingly, metformin treatment activated MAPK. In addition, combined treatment with gefitinib and metformin induced marked decrease in the levels of phosphoS6 (Fig. 5C).

Discussion

The correlation between diabetes and increased cancer risk has been supposed since 1910, by C.D. Maynard (24), and 100 years later, a Joint Conference of the American Diabetes Association and the American Cancer Society led to a Consensus Report that clearly indicated an association...
between diabetes and the incidence of cancers (25). Since the first report of Evans and colleagues (5), a series of studies have suggested that metformin is associated with a reduced risk of cancer, as compared with other antidiabetic treatments (sulfonylurea, insulin) in diabetic patients (26-29).

Metformin is a widely used antidiabetic drug now prescribed to almost 120 million people in the world for the treatment of type II diabetes. At the cellular level, metformin interferes with the energetic metabolism of the cell by disrupting mitochondrial respiration, leading to an increase in the intracellular ratio of AMP:ATP, which in turn leads to activation of AMPK by the LKB1 (19). Metformin-mediated AMPK activation leads to an inhibition of mTOR signaling, a reduction in phosphorylation of its major downstream effectors, the 4E-BPs and p70S6Ks, and an inhibition of global protein synthesis and proliferation in a number of different cancer cell lines (6-10). Several reports established a direct action of metformin on cancer cells with a significant and consistent antiproliferative action, in vitro and in vivo (6-10). In addition, previous reports showed an adjuvant role of metformin for other chemotherapeutic drugs, such as paclitaxel, carboplatin, and doxorubicin, however, without describing any mechanism to explain such synergism (10).

In this study, we have evaluated for the first time the effects of metformin and of the combination of metformin and gefitinib, a selective EGFR-TKI, in NSCLC cell lines and showed a significant potentiating of the antiproliferative and proapoptotic activity both in vitro and in vivo. Although we and others (6-10, 30) used doses of metformin higher than that observed in diabetic patients, where the metformin plasma concentration is between...
In the present study, we observed also an increase in the level of activated phosphorylated MAPK after metformin.
single-agent treatment (Fig. 3). Metformin is known to activate the phosphorylation of AMPK, thus activating TSC2 and consequently inhibiting Rheb/mTORC1 signaling (22). A recent study (23) showed a role of Rheb as inhibitor of C- and B-RAF kinase activity and their heterodimerization. Therefore, we supposed that the metformin-induced activation of AMPK could enhance the C-RAF/B-RAF dimerization through a downregulation of Rheb. Indeed, the results of the present study suggest that metformin treatment increases such association, thus potentiating the signaling from RAS to MAPK. This could be therapeutically relevant, as we have shown that, while exerting antiproliferative and proapoptotic effects, single-agent metformin treatment could enhance pro-proliferating signals through the RAS/RAF/MAPK pathway, that could in turn induce cell proliferation in those cell lines with constitutively activating RAS mutations (Fig. 6). The activation of MAPK by metformin treatment, which is reported for the first time in this work, is the new scenario that we have to consider when testing metformin as anticancer agent. In our cell model, the activation of MAPK is not enough strong to counteract the inhibitory effects of metformin on cell proliferation and survival. However, we have to ask what could happen in a system with a mutated and constitutively active RAS. This consideration opens new possibilities of treatment combination first of all, metformin and MEK inhibitors.

At the same time, treatment with both metformin and gefitinib can avoid aberrant signals through the RAS/RAF/MAPK pathway and could explain, at least in part, the mechanism of such significant synergism.

Future perspective studies are required in patients with NSCLCs to investigate better the effect of metformin action on the RAS/RAF/MAPK pathway and the best context in which to use metformin in combination with molecular targeted agents.

Disclosure of Potential Conflicts of Interest
No potential conflicts of interest were disclosed.

Authors’ Contributions
Conception and design: F. Morgillo, F. Ciardiello, F.C. Sasso
Development of methodology: F. Morgillo, D. Vitagliano, C.M. Della Corte
Acquisition of data (provided animals, acquired and managed patients, provided facilities, etc.): F. Morgillo, F. Ciardiello, F.C. Sasso, E. D’Aiuto, R. De Palma
Analysis and interpretation of data (e.g., statistical analysis, biostatistics, computational analysis): F. Morgillo, D. Vitagliano, C.M. Della Corte, E. Martinelli, T. Troiani
Writing, review, and/or revision of the manuscript: F. Morgillo, F. Ciardiello, F.C. Sasso
Grant Support
This research has been supported by a grant from the Associazione Italiana per la Ricerca sul Cancro (AIRC), Milan, Italy.

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

Received August 28, 2012; revised April 24, 2013; accepted May 11, 2013; published OnlineFirst May 21, 2013.

References
Synergistic Effects of Metformin Treatment in Combination with Gefitinib, a Selective EGFR Tyrosine Kinase Inhibitor, in LKB1 Wild-type NSCLC Cell Lines

Floriana Morgillo, Ferdinando Carlo Sasso, Carminia Maria Della Corte, et al.


Updated version
Access the most recent version of this article at:
doi:10.1158/1078-0432.CCR-12-2777

Supplementary Material
Access the most recent supplemental material at:
http://clincancerres.aacrjournals.org/content/suppl/2013/05/22/1078-0432.CCR-12-2777.DC1

Cited articles
This article cites 34 articles, 16 of which you can access for free at:
http://clincancerres.aacrjournals.org/content/19/13/3508.full#ref-list-1

Citing articles
This article has been cited by 5 HighWire-hosted articles. Access the articles at:
http://clincancerres.aacrjournals.org/content/19/13/3508.full#related-urls

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

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

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