ABSTRACT

The clinical efficacy of epidermal growth factor receptor (EGFR) kinase inhibitors is limited by the development of drug resistance. The irreversible EGFR kinase inhibitor WZ4002 is effective against the most common mechanism of drug resistance mediated by the EGFR T790M mutation. Here, we show, in multiple complementary models, that resistance to WZ4002 develops through aberrant activation of extracellular signal-regulated kinase (ERK) signaling caused by either an amplification of mitogen-activated protein kinase 1 (MAPK1) or by downregulation of negative regulators of ERK signaling. Inhibition of MAP–ERK kinase (MEK) or ERK restores sensitivity to WZ4002 and prevents the emergence of drug resistance. We further identify MAPK1 amplification in an erlotinib-resistant EGFR-mutant non–small cell lung carcinoma patient. In addition, the WZ4002-resistant MAPK1-amplified cells also show an increase both in EGFR internalization and a decrease in sensitivity to cytotoxic chemotherapy. Our findings provide insights into mechanisms of drug resistance to EGFR kinase inhibitors and highlight rational combination therapies that should be evaluated in clinical trials.

SIGNIFICANCE: Our study identifies activated ERK signaling as a mediator of resistance to irreversible pyrimidine EGFR inhibitors in EGFR T790M-bearing cancers. We further provide a therapeutic strategy to both treat and prevent the emergence of this resistance mechanism. Cancer Discov; 2(10); 1–14. ©2012 AACR.

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INTRODUCTION

Epidermal growth factor receptor (EGFR) kinase inhibitors gefitinib and erlotinib are effective clinical therapies for non–small cell lung cancer (NSCLC) patients harboring EGFR-mutant cancers. Several phase III clinical trials have showed improved clinical efficacy compared with systemic chemotherapy (1–3). However, despite these benefits, all patients ultimately develop acquired resistance to gefitinib and erlotinib (4). The most common mechanism of acquired resistance, detected in 50% to 60% of patients, is mediated by the secondary EGFR T790M mutation, and results in an increase in ATP affinity (5–8). In preclinical models, irreversible quinazoline-based EGFR inhibitors, including afatinib (BIBW2992) and dacomitinib (PF299804), effectively inhibit the growth of EGFR T790M-containing cell line models in vitro (9, 10). The covalent binding allows these inhibitors to achieve greater occupancy of the ATP site relative to gefitinib or erlotinib, thus providing the ability to inhibit EGFR T790M (8). However, in clinical studies, afatinib did not prolong survival compared with placebo in patients with NSCLC that had developed acquired resistance to gefitinib or erlotinib (11). Furthermore, in preclinical studies, resistance of EGFR T790M tumor cells to dacomitinib develops rapidly and is caused by amplification of the T790M-containing allele (12).

In an effort to overcome the therapeutic limitations of irreversible quinazoline EGFR inhibitors, we previously identified a novel class of irreversible pyrimidine-based EGFR kinase inhibitors (13). These agents, including WZ4002, are more potent than irreversible quinazoline EGFR inhibitors in EGFR T790M-bearing models, but are less potent inhibitors of wild-type (WT) EGFR (13). Coupled with the increased potency, the mutant selective property of this class of agents may provide the ability to achieve clinical concentrations sufficient to inhibit EGFR T790M.

In the current study, we modeled acquired resistance to WZ4002 in EGFR T790M-containing models in vitro and in vivo. We undertook these studies in an effort to identify potential strategies that can be used to enhance the efficacy of this class of EGFR inhibitors. Our studies identify a novel mechanism of resistance to EGFR inhibitors and inform the development of a novel combination therapeutic strategy that can be used to effectively treat EGFR T790M-containing cancers.

RESULTS

WZ4002-Resistant Cells Contain an Amplification in MAPK1

In our prior studies, we generated a gefitinib-resistant (GR) version of the EGFR-mutant PC9 (Del E746_A750) cell line (13). These cells contain the EGFR T790M resistance mutation and are sensitive to WZ4002 (13). When we exposed the PC9 GR cells to dacomitinib (PF299804), a clinical irreversible quinazoline EGFR inhibitor and generated resistant cells, they contained a focal amplification in EGFR T790M tumor cells to dacomitinib develops rapidly and is caused by amplification of the T790M-containing allele (12).

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Figure 1. WZR EGFR-mutant Del E746_A750/T790M cells contain an amplification in MAPK1. A, PC9 GR4 (Del E746_A750/T790M) and DR1 (Del E746_A750/T790M amplification) cells were treated with WZ4002 at the indicated concentrations, and viable cells were measured after 72 hours of treatment and plotted relative to untreated controls. B, WZR10 and WZR12 cells are resistant to WZ4002. Cells were treated with WZ4002 as in A. C, PC9 GR4 and WZR12 cells were treated with WZ4002 at indicated concentrations for 6 hours. Cell extracts were immunoblotted to detect the indicated proteins. D, WZR cells contain an amplification in MAPK1. The PC9 WZR clones (right) were compared with the PC9 GR4 cells (first column). The blue curve on the right indicates degree of amplification of each SNP from 0 (left) to 8 (right). Left, genome-wide view; right, detailed view of chromosome 22. The genomic location of MAPK1 is indicated by an asterisk. E, metaphase FISH of PC9 GR4 and WZR10 cells using MAPK1 (red) and reference probe (green; RP11-768L22). Amplification of MAPK1 is observed in WZR10 cells (arrow).

identifed and confirmed to be drug resistant (Fig. 1B). The resistant cells still harbored the EGFR Del E746_A750/T790M double mutation but contained no additional EGFR mutations (data not shown) and were also cross resistant to dacomitinib and afatinib (data not shown). WZ4002 still inhibited EGFR phosphorylation in the resistant cells, although slightly less potently in the GR4 cells, but more noticeably, this inhibition was decoupled from inhibition of downstream signaling most notably extracellular signal-regulated kinase 2 (ERK2) phosphorylation (Fig. 1C). The WZR12 cells contain higher levels of both total and phosphorylated ERK2 than the PC9 GR cells (Fig. 1C). To determine whether there was a genomic basis for the increase in ERK2 protein, we conducted a genome-wide copy number analysis of the WZR cells and compared them to the parental PC9 GR4 cells (Fig. 1D). The WZR cells contain an amplification in chromosome 22 that is not present in the parental drug-sensitive cell line. This region contains the gene mitogen-activated protein kinase 1 (MAPK1), which encodes ERK2 (Fig. 1D). We confirmed the MAPK1 amplification using both FISH (Fig. 1E) and quantitative real-time PCR [qRT-PCR (Supplementary Fig. S1)]. The amplification also led to increased MAPK1 gene expression (Supplementary Fig. S2A).
ERK Signaling and EGFR Resistance

Figure 2. Inhibition of ERK1/2 signaling restores sensitivity to WZ4002 in PC9 WZR cells. A, PC9 GR4 or WZR10 cells were treated with the indicated concentrations of CI-1040 for 6 hours. Cell extracts were immunoblotted to detect the indicated proteins. B, PC9 GR4 or WZR10 cells were treated with WZ4002 alone at the indicated concentrations or in combination with CI-1040 (3 μmol/L). Viable cells were measured after 72 hours of treatment and plotted relative to untreated controls. C, PC9 GR4 or WZR10 cells were treated with WZ4002 alone at indicated concentrations or with CI-1040 (3 μmol/L) for 6 or 48 hours (PARP lane only). Cell extracts were immunoblotted to detect the indicated proteins. D, cells were treated with WZ4002 at the indicated concentrations or in combination with Compound (Cmp) 11E (WZR10 only). Viable cells were measured after 72 hours of treatment and plotted relative to untreated controls. E, WZ4002 (6 hours) inhibits p90RSK phosphorylation in PC9 GR4 but not WZR10 cells. F, Cmp 11E (6 hours) inhibits p90RSK phosphorylation in both PC9 GR4 and WZR10 cells. G, WZ4002 treatment (6 hours) leads to BIM upregulation in PC9 GR4 but not WZR10 cells.

Inhibition of MAPK Signaling Restores Sensitivity to WZ4002

We next evaluated whether inhibition of MAPK signaling would restore sensitivity to WZ4002 in the PC9 WZR cells. We first determined the concentration of the MAP-ERK kinase (MEK) inhibitor CI-1040 necessary to downregulate ERK1/2 phosphorylation to similar levels as in the parental cell lines (Fig. 2A). When used in combination with WZ4002, the MEK inhibitors CI-1040 (Fig. 2B) or GSK-1120212 (Supplementary Fig. S3) completely restored the sensitivity to WZ4002 in the WZR cells similar to that of the parental PC9 GR4 cells. Similarly, the combination led to complete inhibition of ERK1/2 phosphorylation and restored WZ4002-mediated apoptosis analogous to that observed in the parental PC9 GR cells (Figs. 2C and Supplementary Fig. S4). WZ4002 sensitivity was also restored following downregulation of MAPK1 using a MAPK1-specific short hairpin (sh)-RNA (Supplementary Fig. S5 and Fig. 2D), or when WZ4002 was combined with an ERK1/2 kinase inhibitor (compound 11e; Fig. 2D; ref. 15). Inhibition of ERK1/2 using compound 11e also restored WZ4002-mediated apoptosis in the PC9 WZR cells (Supplementary Fig. S4). As a pharmacodynamic measure of compound 11e, we evaluated p90RSK phosphorylation, a known ERK substrate (16). In the PC9 GR cells, but not in the WZR cells, WZ4002 treatment inhibited p90RSK phosphorylation (Fig. 2E). However, in both GR4 and WR10 cells, compound 11e was able to inhibit p90RSK phosphorylation (Fig. 2F). The addition of a dual phosphoinositide 3-kinase (PI3K) and mTOR inhibitor, PI103, or the AKT inhibitor MK-2206, did not restore sensitivity to WZ4002, nor did it result in WZ4002-mediated apoptosis (Supplementary Figs. S6A–C; refs. 17, 18).

To further show the role of activated MAPK signaling in mediating WZ4002 resistance, we introduced an activated MEK1 (MEK1 K57N) allele into the PC9 GR or H1975 cells (Supplementary Fig. S7; ref. 19). This led to WZ4002 resistance, and in the resistant cells WZ4002 treatment no longer resulted in complete inhibition of ERK1/2 phosphorylation or induction of apoptosis (Supplementary Fig. S7A and B). In addition, MEK1 K57N was sufficient to cause resistance to both WZ4002 (data not shown) and gefitinib (Supplementary Fig. S7C) when introduced into the drug-sensitive
PC9 (Del E746_A750) cells. Collectively, our findings suggest that activation of MAPK signaling causes WZ4002 resistance.

We further evaluated how MAPK1 amplification may prevent WZ4002-mediated apoptosis. Prior studies have shown that upregulation of the proapoptotic protein BIM was necessary for EGFR-mediated apoptosis in EGFR-mutant cancers (20–22). BIM upregulation is mediated by ERK signaling (20–22). In the PC9 GR4 cells, WZ4002 treatment led to a dose-dependent upregulation of BIM (Fig. 2G). In contrast, in the PC9 WZR cells, BIM upregulation was blunted consistent with the inability for WZ4002 to fully downregulate ERK1/2 phosphorylation in these cells (Figs. 1C and 2G).

**H1975 WZ4002-Resistant Cells Retain ERK1/2 Signaling But Do Not Contain an Amplification of MAPK1**

We also generated resistant versions of the WZ4002-sensitive H1975 (EGFR L858R/T790M) cell line (Fig. 3A). Similar to the PC9 WZR cells, WZ4002 was still able to inhibit EGFR phosphorylation in the H1975 WZR cells but ERK1/2 phosphorylation was not completely inhibited (Fig. 3B). The H1975 WZR cells did not contain additional EGFR mutations, did not contain an amplification or overexpression of MAPK1 (Supplementary Fig. S2B), and did not harbor other regions of genomic gain when compared with the parental cells (data not shown). The MEK inhibitor CI-1040, but not the PI3K/mTOR inhibitor PI-103 (Supplementary Fig. 5ED), restored sensitivity to WZ4002 in the H1975 WZR cells (Fig. 3C). Furthermore, in the presence of CI-1040, WZ4002 treatment led to complete inhibition of ERK1/2 phosphorylation as in the parental cells (Fig. 3D). To understand the mechanism behind sustained ERK1/2 activation in the H1975 WZR cells, we compared genome-wide mRNA expression between H1975 WZR6 and H1975 cells (Fig. 3E). One of the most downregulated genes in H1975 WZR cells compared with H1975 cells was DUSP6, a dual specificity phosphatase that negatively regulates ERK1/2 phosphorylation (23). We confirmed these findings using qRT-PCR and also observed downregulation of DUSP5, SPRED1, and SPRED2, all of which negatively regulate components of MAPK signaling (refs. 24–26; Fig. 3F). We did not observe downregulation of these genes in the PC9 WZR cells (Supplementary Fig. S8A). Downregulation of DUSP6 using an siRNA was sufficient to cause resistance to WZ4002 in PC9 GR4 cells (Fig. 3G) and to both gefitinib and WZ4002 in PC9 cells (Supplementary Fig. S8B). Our findings suggest that downregulation of negative regulators of MAPK signaling and subsequent activation of ERK1/2 signaling is an alternative mechanism that mediates WZ4002 resistance. Furthermore, activation of ERK1/2 signaling through introduction of MEK1 K57N into H1975 cells was also sufficient to cause WZ4002 resistance (Supplementary Fig. S7D).

**ERK1/2 Signaling Mediates Resistance to WZ4002 in a Murine Model of EGFR T790M Lung Cancer**

We previously showed that WZ4002 is effective *in vivo* using murine models of EGFR T790M (L858R/T790M and Del E746_A750/T790M) NSCLC over a 2-week treatment course (13). With prolonged treatment, although we observed increased survival compared with erlotinib in both EGFR T790M-bearing models (Fig. 4A), we also observed the development of acquired resistance (Figs. 4B and C and Supplementary Figs. S9A and B). At the time of resistance, we examined the tumors from the treated mice and noted that although EGFR phosphorylation was still inhibited by WZ4002, we were able to detect the emergence of robust expression of ERK1/2 phosphorylation (Figs. 4D and E and Supplementary Fig. S10). In contrast, short-term (24-hour) treatment with WZ4002 effectively inhibits both EGFR and ERK1/2 phosphorylation in the mouse tumors (Fig. 4E). We did not detect evidence of *Mapk1* amplification by FISH in the resistant tumors (Supplementary Fig. S11A), evidence of *Kras* mutations (data not shown), or loss of NFI, a negative regulator of MAPK signaling, at either the protein (Supplementary Fig. S11B) or RNA (Supplementary Fig. S11C) level (27). However, some of the resistant tumors had evidence of decreased *Dusp6* expression compared with their drug-sensitive counterparts (Supplementary Fig. S12). Given the persistent ERK1/2 signaling in the WZR tumors, we investigated whether a clinical MEK inhibitor, GSK-1120212, could restore the sensitivity to WZ4002 *in vivo*. Following the development of acquired resistance to WZ4002 (after 19, 20, and 28 weeks of therapy), we switched treatment to the combination of WZ4002 and GSK-1120212 (Fig. 4F). In 3/3 mice, GSK-1120212-restored sensitivity to WZ4002 (Figs. 4G and H).

An alternative strategy to treating drug resistance is to delay or prevent it from occurring. To determine whether this strategy may be applicable to the current model, we evaluated this using an *in vitro* model. We exposed the WZ4002-sensitive PC9 GR (Fig. 4I) or H1975 (Fig. 4J) cells to either WZ4002 alone, CI-1040 alone, or the combination of both agents for 3 months and quantified resistant clones. CI-1040 was ineffective in both models whereas WZ4002 alone led to a decreased number of resistant clones only in the PC9 GR4 cells (Fig. 4I). However, the combination of WZ4002/CI-1040 was significantly more effective at preventing the emergence of drug-resistant clones in both models (Figs. 4I and J).

**MAPK1 Amplification Is Present in an Erlotinib-Resistant NSCLC Patient**

Our preclinical studies suggest that reactivation of ERK1/2 signaling not only can mediate resistance to WZ4002 but also to gefitinib in drug-sensitive EGFR-mutant NSCLC cell lines (Supplementary Fig. S7C). We thus evaluated tumor specimens from erlotinib-treated NSCLC patients that had developed drug resistance (Supplementary Table S1) for the presence of MAPK1 amplification. In 1 of 21 patients (4.8%) examined, we identified a MAPK1 amplification that was not present in the pretreatment drug-sensitive tumor specimen (Fig. 5). The resistant tumor also lacked the more common drug-resistance mechanisms EGFR T790M or MET amplification (data not shown).

**MAPK1 Amplification Leads to an Increase in EGFR Internalization**

We initially noticed that despite the absence of EGFR secondary mutations in the PC9 WZR cells, 10 times greater concentrations of WZ4002 were required to inhibit EGFR phosphorylation (Fig. 1C and 6A). This observation could be because of the presence of mutant or WT phosphorylated EGFR [the PC9 GR and WZR cells are both heterozygous for
ERK Signaling and EGFR Resistance

Figure 3. WZR H1975 cells exhibit persistent ERK activation and MEK inhibition restores WZ4002 sensitivity. A, WZR H1975 clones. Cells were treated with WZ4002 at the indicated concentrations, and viable cells were measured after 72 hours of treatment and plotted relative to untreated controls. B, WZ4002 treatment does not fully inhibit ERK1/2 phosphorylation in WZR6 cells. H1975 and H1975 WZR6 cells were treated with increasing concentrations of WZ4002. Cell extracts were immunoblotted to detect the indicated proteins. C, CI-1040 (1 µmol/L) restores sensitivity to WZ4002 in the WZR6 cells. D, CI-1040 (1 µmol/L) restores the ability of WZ4002 to fully inhibit ERK1/2 phosphorylation in the WZR6 cells. E, comparison of expression profiles of H1975 and WZR6 cells (left). Hierarchical clustering of the differentially expressed genes [P < 0.0025, fold change (FC) > 3.9] was conducted using GENE-E. DUSP6 (asterisk) ranks among the top differentially expressed genes (right). F, qRT-PCR of genes in MEK/ERK transcriptional output in H1.975 and H1975 WZR cells. The data are normalized to the H1.975 cells. Error bars denote standard deviation. G, PC9 GR4 cells were treated with gefitinib (1 µmol/L) or WZ4002 (100 nmol/L) following transfection with control (NT) or DUSP6 siRNA and viable cells were measured after 48 hours of treatment and plotted (mean ± SD) relative to untreated controls. *P < 0.05 DUSP6 versus NT.
Development of in vivo resistance to WZ4002 in genetically engineered mouse models of EGFR T790M. A, Kaplan-Meier survival curves of L858R/T790M or Del E746_A750/T790M mice treated with erlotinib, vehicle, or WZ4002. Treatment with WZ4002 significantly prolongs survival compared with erlotinib [P = 0.0015 (L858R/T790M) and P = 0.0064 (Del E746_A750/T790M); both log-rank test]. B, change in tumor volume over time in EGFR L858R/T790M mice (n = 5) treated with WZ4002. Each curve represents an individual mouse. C, MRI images from mouse 7907 from B. T, tumor. D, immunohistochemical analyses using indicated antibodies of tumors from EGFR L858R/T790M untreated and WZ4002 treated (10 weeks) mice. EGFR phosphorylation but not ERK1/2 phosphorylation is inhibited. H&E, hematoxylin and eosin. E, immunohistochemical analyses using indicated antibodies of tumors from EGFR Del E746_A750/T790M untreated and WZ4002 treated (24 hours and 26 weeks) mice. WZ4002 treatment inhibits both EGFR and ERK1/2 phosphorylation at 24 hours but ERK1/2 phosphorylation returns following 26 weeks of therapy. (continued)

Del E746_A750 (data not shown). We immunoprecipitated the mutant EGFR from the PC9 GR4 and WZR cells using a mutant-specific (EGFR Del E746_A750M) EGFR antibody (Fig. 6A) following WZ4002 treatment. Compared with the PC9 GR4 cells, greater concentrations of WZ4002 were required to inhibit Del E746_A750/T790M consistent with the observations in whole cell lysates (Fig. 6A). One potential explanation for these differences is an alteration in EGFR internalization. An alteration in EGFR internalization could lead to changes in cellular localization of EGFR that may impact drug access and hence the need for an increased drug concentration required to inhibit EGFR phosphorylation. We evaluated EGFR internalization using 125I labeled EGF. In both the WZR10 and 12 cells, we observed a significantly larger internalization rate constant ($k_e$) than in the GR4 cells (Fig. 6B). There was no difference between the PC9 GR4 and the PC9 cells (Fig. 6B). Inhibition of MEK using CI-1040 did not alter $k_e$ in GR4 cells, but significantly, although not completely, reduced both EGFR phosphorylation and $k_e$ in the WZR cells to levels similar to that observed in the parental PC9 GR4 cells (Figs. 6C and D). Prior studies have implicated Thr-669 of EGFR as an ERK phosphorylation site and associated with EGFR turnover possibly through internalization (28–30). This site is highly phosphorylated in the PC9 WZR
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Figure 4. (Continued) F, serial MRI images of an EGFR L858R/T790M mouse treated with WZ4002 alone or with the combination of WZ4002 and GSK-1120212. T, tumor. G, tumor volume measurements from mouse in F. Blue arrow, treatment with WZ4002; red arrow, treatment with both WZ4002 and GSK-1120212. Numbers indicate weeks of treatment. H, waterfall plot of tumor volume from 3 L858R/T790M mice following treatment with WZ4002 and GSK-1120212. I, Long-term treatment of PC9 GR4 cells with CI-1040 alone, WZ4002 alone, or the combination of both drugs. The percentages of resistant colonies relative to control are plotted from 2 independent experiments. J, long-term treatment of H1975 cells with CI-1040 alone, WZ4002 alone, or the combination of both drugs. The percentages of resistant colonies relative to control are plotted from 2 independent experiments.

Successive Tyrosine Kinase Inhibitor Resistance Also Leads to Chemotherapy Resistance

Following the development of clinical resistance to EGFR kinase inhibitors, NSCLC patients are often treated with systemic chemotherapy. Our successive cell line models (PC9, gefitinib and WZ4002 sensitive; PC9 GR, gefitinib resistant but WZ4002 sensitive; and PC9 WZR, gefitinib and WZR) provide a system in which to evaluate whether kinase inhibitor resistance impacts chemotherapy sensitivity. We treated the cells with staurosporine, paclitaxel, and etoposide. As can be seen in Fig. 7A, these agents induce the greatest degree of cell death in the parental PC9 cells and the least in the PC9 WZR cells. All 3 of these agents, as well as EGFR inhibitors, are known to kill via the mitochondrial pathway of apoptosis, suggesting that cells may select for resistance to apoptosis more generally when they select for resistance to tyrosine kinase inhibition (21). MEK inhibition in PC9 WZR cells did not reverse resistance to chemotherapy (data not shown). It has recently been shown that...
one can measure pretreatment proximity of the mitochondria to the apoptotic threshold, known as mitochondrial priming, using BH3 profiling (31). Proximity to the threshold, indicated by increased mitochondrial depolarization in response to BH3 peptides, was shown to correlate to chemosensitivity across a broad range of cancers (31). We found that the successive generations of kinase inhibitor–resistant PC9 cells were indeed less primed (Fig. 7B). This result suggests that a more broad resistance to apoptotic signaling may be selected for when cells select for tyrosine kinase inhibitor (TKI) resistance.

DISCUSSION

Despite the dramatic clinical efficacy of EGFR kinase inhibitors in EGFR-mutant NSCLC, single-agent EGFR inhibitors will not cure advanced NSCLC. Studies of drug resistance mechanisms provide insights into how cancers develop resistance and the findings from these studies can be used to design rational combination therapeutic strategies (14). EGFR T790M is the most common mechanism of acquired drug resistance to erlotinib and gefitinib and, to date, has been the most difficult to treat clinically (5–7, 11). This is mirrored by our prior preclinical studies using a clinical irreversible quinazoline EGFR inhibitor (PF299804 or dacomitinib; ref. 12). Although the PC9 GR cells are transiently sensitive to PF299804, resistant cells harboring EGFR T790M amplification rapidly emerge (12). These EGFR T790M-amplified cells retain sensitivity to the mutant-selective EGFR inhibitor WZ4002 (Fig. 1A) and remarkably, EGFR T790M amplification never emerges as a resistance mechanism when PC9 GR4 cells are exposed to WZ4002. These findings not only highlight the potential clinical efficacy of a more potent EGFR inhibitor but also the rapid ability of cancer cells to adapt to such an inhibitor as we are still able to select WZR clones from the PC9 GR cells.

We further show that our findings have clinical relevance as MAPK1 amplification can also emerge in erlotinib-resistant EGFR-mutant NSCLC patients (Fig. 5). The frequency at which this occurs is low (Supplementary Table S1) but not unexpected, given the high prevalence of EGFR T790M as an erlotinib resistance mechanism (7). These observations may be because of the preexistence of EGFR T790M in some treatment-naïve cancers coupled with the current lack of effective clinical therapies against EGFR T790M (11, 36). This hypothesis is supported by preclinical studies of the PC9 cells in which multiple studies show the emergence of EGFR T790M following exposure to first- or second-generation EGFR TKIs.
Figure 6. MAPK1 amplification alters EGFR internalization. A, PC9 GR4 or WZR10 cells are treated with increasing concentrations of WZ4002 for 6 hours. Cell extracts from whole lysates (top) or following immunoprecipitation with an EGFR Del E746_A750 antibody (bottom) were immunoblotted to detect the indicated proteins. B, internalization rate constants (k_e) for 125I-labeled EGF in different cell lines. The k_e is significantly greater for the WZR cells compared with the PC9 GR4 cells. C, PC9 GR4 and WZR10 cells treated with WZ4002 alone or in combination with CI-1040 for 6 hours. Cell extracts following immunoprecipitation with an EGFR Del E746_A750 antibody were immunoblotted to detect the indicated proteins. D, internalization rate constants (k_e) for 125I-labeled EGF in following treatment with CI-1040 (3 µmol/L) for 24 hours. There is a significant reduction in k_e in the WZR10 cells with CI-1040 treatment. E, EGFR phosphorylation at Thr-669 is markedly increased in WZR10 compared with GR4 cells. CI-1040 alone inhibits phosphorylation at Thr-669 but not Tyr-1068.

Although this difference may at first glance seem subtle, in cancer patients receiving therapy with a kinase inhibitor, this change in drug concentration required for target inhibition could be the difference between a clinically sensitive and resistant tumor. Previous studies have shown a reduced rate of ligand-mediated EGFR internalization in drug-sensitive EGFR-mutant NSCLC cell lines (40). The decreased rate of EGFR endocytosis was found to be associated with an impaired ability of EGFR to fully use SHP2 for complete activation of ERK signaling (40). In contrast, enhanced ERK signaling, as observed in the PC9 WZR cells, plays a causal role in increased EGFR endocytosis. This observation may be because of the ability of ERK to phosphorylate EGFR at Thr-669, as observed in the WZR cells (Fig. 6E), leading to...
altered EGFR trafficking (28–30). Although clinically relevant, it will remain a challenge to study changes in receptor internalization from clinical diagnostic specimens unless they are because of a genomic alteration, as in the current study. Our findings also reveal that sequential resistance to kinase inhibitors (gefitinib and WZ4002) renders EGFR-mutant NSCLC cells less susceptible to chemotherapeutic agents (Fig. 7B). These observations are potentially clinically significant as EGFR kinase inhibitors are currently being used as initial therapy for EGFR-mutant NSCLC and may ultimately impact the sensitivity to a broad range of subsequent therapies (2, 3). These findings also serve to highlight that drug resistance may not simply be an alteration in one signaling pathway but rather a more complex process that more broadly impacts apoptotic signaling.

Findings from our study show that the combination of WZ4002 and an allosteric MEK inhibitor may be an effective strategy not only to treat drug-resistant cancers (Figs. 2B, 3C, and 4G and H) but also to prevent the emergence of drug-resistant clones (Fig. 4I and J). Coupled with our prior studies showing that WZ4002 alone can prevent the emergence of EGFR T790M in model systems, the combination of WZ4002 and a MEK inhibitor may be a particularly effective therapeutic strategy for EGFR-mutant NSCLC and should be tested in a clinical trial (13).

METHODS

Cell Culture and Reagents
The EGFR-mutant NSCLC cell lines PC9 (Del E746_A750), PC9 GR4 (Del E746_A750/T790M), and H1975 (L858R/T790M) have been previously characterized (12, 13, 41). The PC9 and H1975 cells were confirmed by fingerprinting using the PowerPlex 1.2 system (Promega) most recently in March 2012. Gefitinib, CI-1040, and MK-2206 were obtained from Selleck Chemicals. 1.2 system (Promega) most recently in March 2012. Gefitinib, CI-1040, and MK-2206 were obtained from Selleck Chemicals.

Antibodies and Western Blotting
Cells grown under the previously specified conditions were lysed in NP-40 buffer. Western blot analyses were conducted after separation by SDS-PAGE electrophoresis and transfer to poly(vinylidene difluoride)-P immobilized membranes (Millipore). Immunoblotting was conducted according to the antibody manufacturers’ recommendations. Anti- phospho-AKT (Ser-473), anti-total-AKT, EGFR Del E746_A750 specific, phospho (Thr-669) EGFR, pRSK, total-RSK, DUSP6, and BIM antibodies were obtained from Cell Signaling Technology. The phospho-EGFR (pY1068), total-ERK1/2, and phospho-ERK1/2 (pT185/pY187) antibodies were purchased from Biosource International Inc. Total EGFR antibody was used as previously described (45).

Generation of Drug-Resistant Cell Lines
To generate drug-resistant cell lines, NSCLC cells were exposed to increasing concentrations of WZ4002 similar to previously described methods (12, 14, 32). Individual clones were isolated and confirmed to be drug resistant.

EGFR Mutational Analyses
Total RNA was isolated from cell lines or tumors using TRIzol (Invitrogen) and purified using RNeasy MinElute Cleanup Kit (Qiagen). cDNA was transcribed with Superscript II Reverse Transcriptase (Invitrogen Life Technologies) and used as template for subsequent...
qRT-PCR-based studies (14, 32). The qRT-PCR products were also cloned into a TOPO TA vector (Invitrogen), transformed into bacteria, and the inserts from individual clones sequenced. The qRT-PCR primers and conditions are available upon request.

**SNP Analyses**

SNP analyses were conducted as previously described (14). Samples were processed for the Human Mapping 250K Sty single-nucleotide polymorphism (SNP) array according to the manufacturer's instructions. Comparison of gene copy number differences was conducted using the dChip software according to previously established methods (14, 46). The SNP data have been deposited to GEO (accession number GSE37700).

**MAPK1 Copy Number Analysis**

The absolute copy number for MAPK1 was determined using qRT-PCR as previously described (14). Quantification was based on standard curves from a serial dilution of normal human genomic DNA. All specimens were analyzed in triplicate. The qRT-PCR primers are available upon request.

**FISH Probes and Hybridization**

The human MAPK1 probe consisted of a mixture of 3 fosmids (W12-1114H9, W12-1468D5, and W12-3011D5) and spanned the entire gene locus. A bacterial artificial chromosome (BAC, RP11-768L22) located on 22q13.33 was used as a reference probe. A BAC (RP23-122A24) located on chromosome 16q11 was used as a reference probe. All fosmids and BACS were purchased from Children’s Hospital Oakland Research Institute. DNA was extracted using a Qia gen kit (Qiagen Inc.) and labeled with Spectrum Green- or Spectrum Orange-conjugated dUTP by nick translation (Vysis/Abbott Molecular). The CEP7 probe (Vysis/Abbott Molecular) was used according to the manufacturer’s instructions. Chromosomal mapping and hybridization efficiency for each probe set were verified in normal metaphase spreads (data not shown). Three-color FISH assays were conducted as previously described (12, 14). Tumor cells were classified as containing a MAPK1 amplification if the ratio of MAPK1/reference was 2 or more or if there were 1 or less reference signals and 3 or more MAPK1 signals.

**Generation of Mouse Cohorts and Treatment with WZ4002**

Doxycycline inducible EGFR-TL (L858R/T790M) and EGFR-TD (Del E746_A750/T790M) transgenic mice were generated as previously described (13, 47). All mice were housed in a pathogen-free environment at the Harvard School of Public Health and were handled in strict accordance with Good Animal Practice as defined by the Office of Laboratory Animal Welfare, and all animal work was done with Dana-Farber Cancer Institute IACUC approval. Offi ce of Laboratory Animal Welfare, and all animal work was done

**RNA Expression Profiling and qRT-PCR**

Total RNA was prepared from drug-sensitive and drug-resistant cells as described above. Synthesis of cRNA and hybridization to Human Expression Array U133A2.0 chips were conducted following Affymetrix protocols (Affymetrix, Inc.). Probe-level intensity data files in the .CEL format were preprocessed using Robust Multichip Average program using the GenePattern software (Broad Institute). Probes representing the same genes were collapsed into a single value, and standardized by taking the median value for each gene across sample set in the GenePattern software. Comparative marker selection module was used to select differentially expressed genes that met defined criteria [P < 0.0025, fold change (FC) > 3.9]. Hierarchical clustering of the differentially expressed genes that met the criteria was conducted using GENE-E (Broad Institute). The expression data have been deposited to GEO (accession number GSE37700). To evaluate expression of genes associated with MEK/ERK-dependent transcriptional output, qRT-PCR was conducted in triplicate as described previously (24). NF1 expression was conducted using the NF1-TaqMan Gene Expression Assay (Mm00812424_m1; Applied Biosystems).

**RNA Expression Profiling**

Hierarchical clustering of the differentially expressed genes that met the criteria was conducted using GENE-E (Broad Institute). The expression data have been deposited to GEO (accession number GSE37700). To evaluate expression of genes associated with MEK/ERK-dependent transcriptional output, qRT-PCR was conducted in triplicate as described previously (24). NF1 expression was conducted using the NF1-TaqMan Gene Expression Assay (Mm00812424_m1; Applied Biosystems).

**BH3 Profiling**

BH3 profiling was conducted as previously described (31).
FACS Analyses

Cell viability experiments were conducted using drug-sensitive and drug-resistant cell lines exposed following drug exposure for 24 to 72 hours. Cells were stained with fluorescent conjugates of annexin-V (BioVision) and/or propidium iodide (PI) and analyzed on a FACS-Canto machine (Becton Dickinson). Viable cells are annexin-V and PI negative, and cell death is expressed as a percent of viable cells.

Patients

NSCLC patients treated with erlotinib were identified from the Thoracic Oncology Program at the Dana-Farber Cancer Institute. Tumor biopsies at the time of relapse were obtained under an IRB-approved protocol. Analyses for EGFR T790M and MET amplification were conducted as previously described (14). All patients provided written informed consent.

Disclosure of Potential Conflicts of Interest

P.A. Jänne is a consultant/advisory board member of AstraZeneca, Boehringer Ingelheim, Pfizer, Roche, Genentech, and Sanofi, has post-marketing royalties from Dana-Farber Cancer Institute–owned intellectual property on EGFR mutations licensed to Lab Corp, and is an inventor on a Dana-Farber Cancer Institute–owned patent on WZ4002. A. Letai is a consultant/advisory board member of Eutropics Pharmaceuticals.

C.A. Pratilas is a consultant/advisory board member and has a commercial research grant from Novartis Pharmaceuticals. L. Garraway also has ownership interest in Foundation Medicine.

N.S. Gray is an inventor on Dana-Farber Cancer Institute–owned patent on WZ4002 and has ownership interest (including patents) in Gatekeeper, Inc.

Neal Rosen has commercial research grants from AstraZeneca, Merck, and Chugai and is a consultant/advisory board member of Chugai, Astra-Zeneca, GSK, Novartis, and Millennium.

No potential conflicts of interest were disclosed by the other authors.

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