A Novel ALK Secondary Mutation and EGFR Signaling Cause Resistance to ALK Kinase Inhibitors

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Abstract
Anaplastic lymphoma kinase (ALK) tyrosine kinase inhibitors (TKI), including crizotinib, are effective treatments in preclinical models and in cancer patients with ALK-translocated cancers. However, their efficacy will ultimately be limited by the development of acquired drug resistance. Here we report two mechanisms of ALK TKI resistance identified from a crizotinib-treated non–small cell lung cancer (NSCLC) patient and in a cell line generated from the resistant tumor (DFCI076) as well as from studying a resistant version of the ALK TKI (TAE684)–sensitive H3122 cell line. The crizotinib-resistant DFCI076 cell line harbored a unique L1152R ALK secondary mutation and was also resistant to the structurally unrelated ALK TKI TAE684. Although the DFCI076 cell line was still partially dependent on ALK for survival, it also contained concurrent coactivation of epidermal growth factor receptor (EGFR) signaling. In contrast, the TAE684-resistant (TR3) H3122 cell line did not contain an ALK secondary mutation but instead harbored coactivation of EGFR signaling. Dual inhibition of both ALK and EGFR was the most effective therapeutic strategy for the DFCI076 and H3122 TR3 cell lines. We further identified a subset (3/50; 6%) of treatment naive NSCLC patients with ALK rearrangements that also had concurrent EGFR activating mutations. Our studies identify resistance mechanisms to ALK TKIs mediated by both ALK and by a bypass signaling pathway mediated by EGFR. These mechanisms can occur independently, or in the same cancer, suggesting that the combination of both ALK and EGFR inhibitors may represent an effective therapy for these subsets of NSCLC patients. Cancer Res; 71(18); 1. ©2011 AACR.

Introduction
The emerging impact of targeted therapies as cancer treatments has led to a therapeutic paradigm shift in the field of oncology. Several kinase inhibitors have been identified as effective clinical therapies for a broad range of cancers and, specifically, in those in which the target of the kinase inhibitor has undergone a gain of function genomic alteration (1, 2). However, the clinical success of treatment with kinase inhibitors is uniformly limited by the development of acquired drug resistance. Two common mechanisms of acquired drug resistance have been identified. These include secondary mutations in the target of the kinase itself, which abrogate the inhibitory activity of the drug, and activation of alternative signaling pathways that bypass the continued requirement for inhibition of the original target (3–5). The understanding of the mechanistic bases for drug resistance will continue to inform the development of strategies to overcome or prevent clinical drug resistance, thereby providing a greater therapeutic benefit for cancer patients (6, 7).

Chromosomal rearrangements in the anaplastic lymphoma kinase (ALK) gene have been detected in anaplastic large cell lymphoma (ALCL), inflammatory myofibroblastic tumor (IMT), and in non–small cell lung cancer (NSCLC; refs. 8–10). In NSCLC, ALK rearrangements have been detected in 3% to 13% of patients, are more common in never-smokers and in those with adenocarcinoma (11). In addition, they are often mutually exclusive with other oncogenic alterations detected in NSCLC, including epidermal growth factor receptor (EGFR) mutations. ALK kinase inhibitors are effective therapies in both preclinical in vitro and in vivo models and in NSCLC patients harboring ALK rearrangements (2, 12, 13). In the phase I clinical trial of crizotinib, a radiographic tumor...
response rate of 55% was observed in ALK rearranged NSCLC patients (2). This agent is currently in phase III clinical development in this genomically defined patient population.

Recent studies have also identified and studied crizotinib resistance mechanisms. To date 3 secondary mutations, all identified from crizotinib-treated NSCLC or IMT patients, have been reported (14, 15). These mutations either involve the ‘gatekeeper’ residue (L1196) or sites away from crizotinib binding (F1174L and C1156Y; refs. 14, 15). The mechanistic basis for how the different mutations lead to crizotinib resistance is not fully understood. The L1196 mutation may create a steric hindrance for crizotinib binding, whereas the F1174L mutation likely promotes the active conformation of ALK, thus disfavoring crizotinib binding which preferentially binds the inactive conformation of ALK (14). Continued studies of these and other resistance mechanisms will be critical to the design of subsequent treatments for NSCLC patients with ALK rearrangements.

In this study, using cell line models of ALK inhibitor resistance, either derived from a crizotinib-resistant patient or generated in vitro, we uncover additional mechanisms of ALK kinase inhibitor resistance. Our findings underscore the complexity of drug resistance mechanisms and the therapeutic challenges of treating multiple concurrent resistance mechanisms.

Materials and Methods

Patients

Patients were either identified from the Thoracic Oncology Program at DFCI (n = 3) or treated in a clinical trial (NCT00932893) with crizotinib that was sponsored by Pfizer, Inc (n = 1). Tumor biopsies were obtained under an Institutional Review Board approved protocol. All patients provided written informed consent.

ALK and EGFR genomic analyses

The ALK kinase domain was sequenced from all of the available specimens. The PCR primers and conditions are available upon request. ALK FISH was carried out using the break apart probe (Vysis LSI ALK Dual Color; Abbott Molecular) as previously described (14, 15). FISH was carried out using the Vysis LSI ALK Dual Color probe (Abbott Molecular) as previously described (14, 15). The mechanistic basis for how the different mutations lead to crizotinib resistance is not fully understood. The L1196 mutation may create a steric hindrance for crizotinib binding, whereas the F1174L mutation likely promotes the active conformation of ALK, thus disfavoring crizotinib binding which preferentially binds the inactive conformation of ALK (14). Continued studies of these and other resistance mechanisms will be critical to the design of subsequent treatments for NSCLC patients with ALK rearrangements.

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purchased from R&D Systems and used according to the manufacturer’s recommended conditions. ALK immunohistochemistry (IHC) was done using the mouse monoclonal anti-human ALK (clone: 5A4; Abcam) as previously described (16). EGFR IHC was done as previously described (22).

**Phosphotyrosine profiling**

Phosphotyrosine profiling was done using a bead based assay using previously described methods (23). Parental and drug-resistant cells were treated with either vehicle or drug for 6 hours followed by cell lysis prior to analysis.

**Detection of EGFR ligands**

EGF, amphiregulin, TGF-α, HB-EGF, and epiregulin were measured in cell culture medium using an ELISA, were done according to the manufacturer’s recommended procedures (Quantikine; R&D Systems) and as described previously (24).

**Cell-cycle analysis and apoptosis assays**

A total of $1 \times 10^6$ cells treated with each of the compound at indicated concentration or dimethyl sulfoxide were washed in PBS, fixed in 70% ethanol, incubated with RNase in PBS, and resuspended in 500 μL, propidium iodide. The percentage of cells in G1, S-phase, and G2-M phases were analyzed by flow cytometry. Apoptosis was analyzed by terminal deoxynucleotidyl transferase–mediated dUTP nick end labeling (TUNEL) assay using the APO-BRDU Kit (BD Biosciences) according to the manufacturer’s instructions.

**Results**

**The novel somatic ALK L1152R mutation results in drug resistance to ALK inhibitors**

To identify additional mechanisms of resistance to crizotinib, we first studied a NSCLC patient with an ALK rearrangement [EML4-ALK variant 3 (E6;A20)] who had developed clinical acquired resistance to crizotinib, following a brief radiographic response after 3 months of treatment. Sequencing of the ALK gene from the clinically progressing tumor
(pleural effusion) revealed the presence of a novel mutation (Fig. 1A). This mutation resulted in a change from a leucine to an arginine at position 1152 (L1152R). The recurrent tumor was wild-type for EGFR and KRAS (data not shown). This mutation was not detected in the tumor of the patient obtained prior to crizotinib treatment (data not shown).

We evaluated the biological impact of the L1152R mutation by introducing it into EML4-ALK and generating Ba/F3 cells. Both EML4-ALK and EML4-ALK.L1152R led to IL-3 independent growth of Ba/F3 cells (Supplementary Fig. S1A). The EML4-ALK.L1152R cells were significantly more resistant than the parental cells to both crizotinib (Fig. 1B) and ALK inhibitor TAE684 (Supplementary Fig. S1B). The L1152R mutation diminished crizotinib-mediated inhibition of downstream AKT and ERK 1/2 phosphorylation (Supplementary Fig. S1C). Consistent with these findings on growth, greater concentrations of crizotinib were required to inhibit ALK phosphorylation in the EML4-ALK.L1152R cells compared with those with EML4-ALK alone (Fig. 1C). Furthermore, to compare the impact of resistance in endogenous EML4-ALK NSCLC cells, the L1152R and previously identified resistance mutations (C1156Y, L1196M, and F1174L) were stably expressed in H3122 cells and the cells were examined for crizotinib resistance (14, 15). All of the resistance mutations, C1156Y, L1196M, L1152R, and F1174L, resulted in the significant elevation of IC50 compared with the control cells (GFP or EML4-ALK wild-type), but there were no significant difference among the C1156Y, L1196M, and L1152R mutations (Supplementary Fig. S1D and Table 1). Analogous to the known resistance mutation C1152Y, examination of the published crystal structure of ALK in an inactive conformation reveals that the L1152R mutation is not in direct contact with the ATP-binding pocket, where both crizotinib and TAE684 are expected to bind (Fig. 1D, ref. 25). The currently available structures do not reveal a clear mechanistic basis as to how L1152R may mediate ALK inhibitor resistance.

A NSCLC cell line harboring the L1152R mutation is ALK and EGFR dependent

We successfully established a cell line, DFCI076, from the pleural effusion of the patient harboring the ALK L1152R mutation. Similar to the Ba/F3 cells harboring the L1152R mutation, the DFCI076 cells were resistant to both crizotinib and TAE684 (Fig. 2A and Supplementary Fig. S2A). However, these cells were still dependent on ALK for their growth as downregulation of ALK using an ALK-specific shRNA resulted in significant growth inhibition compared with either a NT- or an EGFR-specific shRNA, was effective in the crizotinib and TAE684-sensitive H3122 cell line (Fig. 2B). However, the degree of growth inhibition by the ALK shRNA was not as dramatic in the DFCI076 cells compared with the H3122 cells. This prompted us to evaluate whether the DFCI076 cells might contain other concurrent resistance mechanisms. We assessed the activation status of multiple RTKs using the human phospho-RTK arrays as in our prior study (3). Using this approach, we observed strong EGFR and MET phosphorylation in the DFCI076 cells (Fig. 2C). The DFCI076 cells did not contain an EGFR mutation or an EGFR amplification (data not shown) but secreted the EGFR ligand amphiregulin (Supplementary Fig. S2D). Although crizotinib is a potent MET inhibitor and successfully inhibited phospho-MET, it does not inhibit EGFR activity and, even at high concentrations, did not lead to downregulation of pAKT and pERK1/2 to the extent observed in H3122 cells (Fig. 2D). Combined inhibition of ALK (using a shRNA) and EGFR, using the pan-ERBB inhibitor PF299804, was significantly more effective (P < 0.001) than either strategy alone in the DFCI076 cells (Fig. 2B). In addition, the growth curve of DFCI076 cells treated with both PF299804 and crizotinib was similar to the H3122 cells engineered to express the L1152R mutation and subjected to crizotinib treatment (Fig. 2A). Collectively, these findings suggest that although the DFCI076 cells remain largely ALK dependent for their growth, concurrent EGFR inhibition may provide additive growth inhibition. These findings are similar to our prior studies of the DFCI032 cell line generated from a NSCLC patient with EML4-ALK who was never treated with an ALK inhibitor (13). We further confirmed that the DFCI032 cells were sensitive to the combination of the ALK shRNA and PF299804 (Supplementary Fig. S2E and F).

<table>
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<th>Cell line</th>
<th>Vector</th>
<th>Crizotinib IC50 (nmol/L)</th>
<th>TAE684 IC50 (nmol/L)</th>
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<tr>
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<td>3 ± 1</td>
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<tr>
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<td>66 ± 6</td>
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Table 1. Summary of in vitro growth assays

This content is from the provided text and has been reformatted into a table and includes some mathematical expressions and tables for better clarity.
ALK inhibitor–resistant H3122 cells contain activation of EGFR signaling

To identify additional mechanisms of resistance to ALK kinase inhibitors, we generated a TAE684-resistant version of the EML4-ALK H3122 NSCLC cell line. We have used a similar approach to identify known and previously unknown EGFR kinase inhibitor resistance mechanisms (3, 21). After 6 months of gradually increasing TAE684, we were able to isolate cells that proliferated in 100 nmol/L of TAE684. In our prior studies, we showed that 100 nmol/L of TAE684 inhibited ALK signaling and significantly decreased cell viability in H3122 cells, but this concentration was not generally toxic in non-ALK rearranged NSCLC cell lines (13). We subcloned the TAE-resistant (TR) cells from single cells (H3122 TR3) and these cells were resistant to both TAE684 and crizotinib (Fig. 3A, Supplementary Fig. S3A). DNA fingerprinting confirmed that the H3122 TR3 cells were derived from the H3122 parental cells (data not shown). We sequenced the entire ALK kinase domain from the H3122 TR3 cells and did not detect any secondary ALK mutations (data not shown). To determine whether the H3122 TR3 cells were still ALK dependent for their growth, we downregulated ALK using an ALK-specific shRNA (Fig. 3B). However, unlike the parental H3122 cells, the H3122 TR3 cells were only minimally growth inhibited by ALK downregulation (Fig. 3B). We further evaluated the ALK locus using FISH. Although all of the H3122 cells contained the EML4-ALK inversion, this was only detected in a small fraction (5%) of the H3122 TR3 (Supplementary Fig. S3B and C). The cells that retained the inversion also harbored a concurrent amplification in the ALK locus (Supplementary Fig. S3C).

Together, these findings suggest that the H3122 TR3 cells have evolved to lose their ALK dependence for growth.

To further characterize the H3122 TR3 cells, we carried out phospho-RTK arrays in both the parental and drug-resistant cells with and without TAE684 treatment (Fig. 3C). Compared with the parental cells, the H3122 TR cells contained greater EGFR, IGF1R, and MET phosphorylation and these proteins remained persistently phosphorylated despite TAE684 treatment (Fig. 3C). We also used a previously described quantitative bead based phospho-tyrosine assay to specifically study these 3 proteins in further detail (23). Consistent with the genomic findings, ALK phosphorylation was greater in the H3122 compared with the H3122 TR3 cells (Fig. 3D). TAE684 still effectively inhibited ALK phosphorylation in both cell lines. In contrast and consistent with the RTK array, EGFR phosphorylation was markedly elevated in the H3122 TR3 cells (Fig. 3D). This was inhibited by the EGFR kinase inhibitor gefitinib but not TAE684 (Fig. 3D). We also observed phosphorylated ERBB2 and IGF1R in H3122 TR3 clone using this assay (Supplementary Fig. S3D). Of note, the ectopic expression of ALK secondary mutations (Supplementary Fig. S1D) did not lead to an increase in EGFR expression in the H3122 cells (data not shown).

Next, we examined whether activated EGFR had a functional role in the H3122 TR3 cells. We first downregulated EGFR using 2 different (A3 and D) EGFR shRNAs. Compared with a control shRNA, EGFR knockdown led to significant (P < 0.05) decrease in cell proliferation by day 6 in the H3122 TR3 but not the parental cell line (Fig. 3E). This observation was mirrored in a colony formation assay in which treatment with PF299804 resulted in a significant
decrease ($P < 0.001$) in H3122 TR3 but not H3122 colonies (Fig. 3F) compared with untreated cells. The combination of the pan-ERBB inhibitor PF299804 and crizotinib was most effective in the H3122 TR3 cells leading to complete inhibition of colony formation. However, the effects of PF299804 and crizotinib were mostly cytostatic as judged by only minimal changes in cleaved PARP and by using a TUNEL assay (Fig. 3G and Supplementary Fig. S3E). There was no effect on growth using the combination of an IGF1R kinase inhibitor BMS-536,924 and crizotinib in the H3122 TR3 cells despite harboring evidence of IGF1R activation (Supplementary Fig. S3F).

We further determined how EGFR was activated in the H3122 TR3 cells. We did not identify evidence of an EGFR mutation or amplification as detected by FISH (data not shown). However, the supernatant of the H3122 TR3 cells contained significantly ($P < 0.05$) greater amounts of known EGFR ligands including amphiregulin and EGF (Supplementary Fig. S3G), suggesting that the mechanism of EGFR activation in these cells is through a ligand-mediated autocrine activation.
Activation of EGFR signaling induces resistance to crizotinib

Our studies from the ALK inhibitor-resistant DFCI032, DFCI 076, and H3122 TR3 cells suggest a role for EGFR signaling in mediating crizotinib resistance. To formally evaluate this hypothesis, we activated EGFR signaling in H3122 cells using EGFR ligands and by oncogenic forms of EGFR and determined the effects on crizotinib sensitivity. We observed that exogenous EGF was indeed sufficient to promote resistance to ALK inhibition, and resistance could be reversed using a combination of ALK and EGFR inhibitors (Fig. 4A). In the presence of EGF, crizotinib was still able to inhibit ALK phosphorylation but not AKT, S6, and ERK 1/2 phosphorylation (Fig. 4B). Similarly, introduction of EGFR E746_A750 into H3122 cells promoted crizotinib resistance (Fig. 4C) which is reversed by the concurrent administration of the EGFR inhibitor gefitinib or PF299804 (Fig. 4D and Supplementary Fig. S4A). Analogously EML4-ALK promotes gefitinib resistance in the HCC827 EGFR mutant NSCLC cell line (Supplementary Fig. S4B), which was reversed by concurrent treatment with TAE684 (Supplementary Fig. S4C).

A subset of EML4-ALK NSCLC patients harbor concurrent EGFR mutations

Our in vitro studies suggest that EGFR signaling can contribute to ALK kinase inhibitor resistance in EML4-ALK NSCLC. In addition, we show that a cancer cell line that harbors a concurrent ALK rearrangement and an EGFR mutation would be expected to be resistant to both single-agent ALK and EGFR inhibitors. Acquired drug resistance
mechanisms can sometimes also occur de novo and both EGFR T790M and MET amplification have been described in cancers from EGFR tyrosine kinase inhibitor (TKI) naive patients (26). In our prior study, we identified one treatment naive NSCLC patient that harbored a concurrent EGFR mutation and EML4-ALK (13). However, this tumor was obtained from a patient that had undergone surgery and thus never received systemic therapy. Subsequently, in 50 crizotinib treatment naive NSCLC patients harboring ALK rearrangements at DFCI, all detected in a clinical laboratory, we have now identified 3 (6%) patients that also harbor concurrent EGFR mutations (Table 2). Two of the three patients have undergone therapy with erlotinib and both have achieved partial responses (Table 2). Evaluation of the pretreatment tumor from patient 1 using the EGFR L858R–specific antibody shows EGFR staining (Fig 4E), whereas no staining was observed with the ALK-specific antibody (Fig 4E) despite the presence of the ALK genomic rearrangement (Table 2).

Discussion

ALK TKIs are emerging as effective clinical therapies for cancers containing genetic rearrangements in ALK including NSCLC, IMT, and ALCL (8, 10, 27). However, the clinical success of this therapeutic approach is uniformly limited by the development of drug resistance. The mechanistic understanding of drug resistance may help to develop effective subsequent clinical treatments and/or rational combination therapeutic strategies.

In this study, by studying patient-derived tumors and cell lines, we uncover novel ALK TKI resistance mechanisms. These include both a secondary mutation (L1152R) in ALK and activation of EGFR signaling. Importantly, these can occur together in the same tumor (i.e., the DFCI 076 cell line) highlighting both the complexity of drug resistance mechanisms and the therapeutic challenges in developing strategies to overcome clinical drug resistance.

Secondary mutations in kinases are a common mechanism of drug resistance to kinase inhibitors (4, 5, 28, 29). A few distinct categories of mutations have so far been identified. These include secondary mutations that alter drug contact residues, thus creating a steric hindrance for drug binding (30). Alternatively, secondary mutations can promote conformational changes in the kinase and thus favoring the binding of a kinase inhibitor (30). The L1152R mutation is not located in the kinase domain. The currently available crystal structures of ALK do not provide a clear explanation of the mechanistic basis of drug resistance imparted by this mutation. Furthermore, despite different EML4-ALK variants that have been described to date, there is no evidence to suggest that the mechanisms of acquired resistance will vary on the basis of specific EML4-ALK variant (11). Notably the L1152R mutation, unlike the F1174L mutation, is also resistant to TAE684 (14). Thus structurally distinct ALK inhibitors are needed to overcome this mutation and several are under preclinical development. Additional studies, including solving the crystal structure for the ALK L1152R, will be necessary to obtain further insight into how this mutation causes drug resistance.

Prior studies have generated crizotinib-resistant H3122 cells and detected both evidence of an ALK amplification and the presence of the L1196M gatekeeper mutation (31). We also identify ALK amplification in a subset of the H3122 TR3 cells (Supplementary Fig. S3B) but not the L1196M mutation. Because TAE684, unlike crizotinib, can effectively inhibit the growth of H3122 EML4-ALK L1196M cells, our findings are consistent with the prior studies (31). In fact, they suggest that a more potent ALK inhibitor may be able to prevent the emergence of this specific drug resistance mechanism. Whether this will ultimately translate into a clinical benefit (such as a prolongation if progression-free survival) for NSCLC patients can only be determined from clinical trials.

Our studies identify activation of EGFR signaling as a bypass signaling mechanisms that contributes to ALK inhibitor resistance. Concurrent inhibition of both EGFR and ALK is therapeutically effective in all of the resistant models. Intriguingly, different models have differing degrees of apparent EGFR dependence. The DFCI076 cells are mostly ALK dependent (Fig. 2B), whereas the H3122 TR3 cells are more EGFR dependent (Fig. 3D) for their growth. The DFCI032 cells are equally codependent with very little effect on growth by only EGFR or ALK inhibition (Supplementary Fig. S2F and ref. 13). These different examples may be representative of a dynamic process with variable degrees of adaptation to EGFR signaling in the presence of ALK inhibition. However, we cannot completely exclude the possibility that activation of EGFR signaling in these cell lines did not arise in the process of generating the cell lines. Additional evaluation of tumor specimens for changes in EGFR phosphorylation obtained from patients that have developed crizotinib resistance will be necessary. Further investigation is also needed to study

Table 2. Characteristics and outcomes of NSCLC patients harboring concurrent EGFR mutations and ALK rearrangements

<table>
<thead>
<tr>
<th>Pt.</th>
<th>EGFR mutation</th>
<th>ALK FISH</th>
<th>EGFR IHC</th>
<th>ALK IHC</th>
<th>Erlotinib Therapy</th>
<th>Outcome</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>L858R</td>
<td>+</td>
<td>L858R Ab positive</td>
<td>Negative</td>
<td>Yes</td>
<td>PR; 9 mo</td>
</tr>
<tr>
<td>2</td>
<td>Del E746_A750</td>
<td>+</td>
<td>Exon 19 del Ab positive</td>
<td>Negative</td>
<td>Yes</td>
<td>PR; 5 mo</td>
</tr>
<tr>
<td>3</td>
<td>A767_V769dupASV</td>
<td>+</td>
<td>N.D.</td>
<td>Positive</td>
<td>No</td>
<td>N/A</td>
</tr>
</tbody>
</table>

Abbreviations: IHC, immunohistochemistry; PR, partial response; N.D., not done; N/A, not applicable.
changes in EGFR signaling over time to further understand how this adaptive process evolves. Furthermore, whether the process will revert in the absence of ALK inhibition needs to be determined. Such observation may be clinically significant as it would suggest that drug-resistant cancers could regain their sensitivity following a therapeutic holiday from ALK inhibitors. To date we have grown the H3122 TR3 cells 60 passages in the absence of TAE684 and have not observed a reversion to TAE684 sensitivity (data not shown).

It is noteworthy that both in vitro and in NSCLC patients, activated EGFR signaling occurs concurrently with EML4-ALK. Such cancers could still retain sensitivity to single-agent EGFR or ALK inhibitors if the tumor was heterogenous and contained 2 independent populations: one with EML4-ALK and one with an EGFR mutation. Alternatively, a tumor could contain both genetic alterations but only expressed one of the mutant proteins. In both instances, such patients may achieve a transient partial response following therapy with either single agent. Our limited studies of crizotinib naive NSCLC patients, with both genetically confirmed EML4-ALK and EGFR mutations, suggest that ALK is not expressed as both patients treated with erlotinib achieved a clinical response. In contrast, the in vitro studies would predict that coexpression of EML4-ALK and mutant EGFR in the same cells would lead to resistance to both single-agent ALK and EGFR inhibitors. Why some cancers harbor an ALK rearrangement which does not lead to ALK expression remains to be determined. It will also be of interest to determine whether the mechanism of erlotinib resistance in our patients, with both an EGFR mutation and ALK rearrangement, will involve reactivation of ALK expression.

Currently there is an ongoing phase I clinical trial of crizotinib and PF299804 (NCT01121575) originally designed to evaluate the therapeutic benefit of inhibiting MET (crizotinib is a potent MET inhibitor) and EGFR T790M in erlotinib-resistant EGFR mutant NSCLC patients. However, our studies suggest that combination of crizotinib and PF299804 may represent a rational therapeutic strategy for at least a subset of EML4-ALK NSCLC patients that develop acquired crizotinib resistance.

Disclosure of Potential Conflicts of Interest

M.J. Eck: commercial research support. Novartis. P.A. Jänne: consultant/advisory board and clinical trial support, Pfizer. The other authors disclosed no potential conflicts of interest.

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References


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