A novel ALK secondary mutation and EGFR signaling cause resistance to ALK kinase inhibitors

Takaaki Sasaki1,2, Jussi Koivunen1,2, Atsuko Ogino1,2, Masahiko Yanagita1,2, Sarah Nikiforow1,2,3, Wei Zheng4,5, Christopher Lathan7,2,3, J. Paul Marcoux1,2,8, Jinyan Du6, Katsuhiro Okuda1,2, Marzia Capelletti1,2, Takeshi Shimamura1,2,3, Dalia Ercan1,2, Magda Stumpfova1,2, Yun Xiao7, Stanislawa Weremowicz7, Mohit Butaney1,2, Stephanie Heon1,2,3, Keith Wilner8, James G. Christensen8, Michel J. Eck4,5, Kwok-Kin Wong1,2,3, Neal Lindeman7, Nathanael S. Gray4,5, Scott J. Rodig7, and Pasi A. Jänne1,2,3,8

Running Title: Resistance mechanisms in ALK kinase inhibitors

Key words: Non-small cell lung carcinoma, translocation, kinase inhibitor, drug resistance, mutation

1Lowe Center for Thoracic Oncology, 2Department of Medical Oncology, 4Department of Cancer Biology, 5Department of Biological Chemistry and Molecular Pharmacology, Dana-Farber Cancer Institute, Boston, MA; 7Departments of Pathology and 3Medicine, Brigham and Women’s Hospital, Boston, MA; 8The Broad Institute, Cambridge, MA; 6The Broad Institute, Cambridge, MA; 8Pfizer Global Research and Development, Department of Research Pharmacology, La Jolla, CA

#Address Correspondence to:

Pasi A. Jänne, M.D., Ph.D.
Lowe Center for Thoracic Oncology
Dana-Farber Cancer Institute, D820
450 Brookline Avenue, Boston, MA 02215
Phone: (617) 632-6076
Fax: (617) 582-7683
E-mail: pjanne@partners.org

Word count: 4993 Figures: 4 Tables: 2
Abstract

Anaplastic lymphoma kinase (ALK) tyrosine kinase inhibitors (TKIs), 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), and from studying a resistant version of the ALK TKI (TAE684) sensitive H3122 cell line. The crizotinib resistant DFCI076 cell line, harboured 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 co-activation of epidermal growth factor receptor (EGFR) signalling. In contrast, the TAE684 resistant (TR3) H3122 cell line did not contain an ALK secondary mutation but instead harboured co-activation of EGFR signalling. 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 naïve 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 signalling 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.
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 where 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 signalling 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) (8-10). In NSCLC, ALK rearrangements have been detected in 3-13% 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 harbouring 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) (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 while the F1174L mutation likely promotes the active conformation of ALK thus
disfavouring 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 the current 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 were treated in a clinical trial (NCT00932893) with crizotinib that was sponsored by Pfizer, Inc (n = 1). Tumor biopsies were obtained under an IRB 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 fluorescence in situ hybridization (FISH) was performed using the break apart probe (Vysis LSI ALK Dual Color, Abbott Molecular, Des Plaines, IL) as previously described (14, 16). EGFR mutation detection was performed in a CLIA certified laboratory using previously described methods(17).

Cell lines and expression constructs

The NSCLC cell lines H3122 (EML4-ALK variant 1 E13;A20) and DFCI-032 (EML4-ALK variant 1 E13:A20), A549, HCC827 (EGFR del E746_A750) have been previously published (13). The H3122 cells were obtained from the NIH and confirmed by fingerprinting using the Power Plex 1.2 system (Promega, Madison, WI)) in October 2010. The DFCI076 (EML4-ALK variant 3 (E6;A20) cell was established at Dana-Farber Cancer Institute from pleural effusion from a patient who had developed acquired resistance to crizotinib. The DFCI076 cells were cultured in RPMI 1640 (GIBCO)
supplemented with 10% fetal bovine serum (FBS), 100 units/mL penicillin and 100 mg/mL streptomycin and 1 mmol/L sodium pyruvate (RPMI 10% medium).

The EML4-ALK (Variant 1) cDNA from the H3122 cell line and the EGFR-del (EGFR delE746_A750) cDNA were cloned into pDNR-Dual (BD Biosciences) as described previously (14). To generate EML4-ALK mutants, L1152R, L1196M, C1156Y or F1174L mutations were introduced using site-directed mutagenesis (Agilent) with mutant specific primers according to the manufacturer’s instructions and as previously described (14). All constructs were confirmed by DNA sequencing. Retroviral infection and culture of Ba/F3 cell were performed using previously described methods (18). Polyclonal cell lines were established by puromycin selection and subsequently cultured in the absence of interleukin-3 (IL-3). Uninfected Ba/F3 cells or cell lines expressing green fluorescent protein (GFP) were used as controls.

**Cell proliferation and growth assays**

Crizotinib and the pan-ERBB inhibitor PF299804 were provided by Pfizer. TAE684 and BMS-536,924 were synthesized as previously described (19, 20). Recombinant human EGF (PHG0314) was purchased from Invitrogen (Camarillo, CA). Growth and inhibition of growth was assessed by MTS assay according to previously established methods (18). All experimental points were set up in six to twelve wells and all experiments were repeated at least three times. For clonogenic assays, cells were plated in triplicate on the 6-well plates and subject to drug exposure for 14 days, the colonies were fixed and stained with 0.5% crystal violet in 25% methanol, and the numbers of colonies were counted.
**ALK and EGFR shRNA constructs and lentiviral infection**

ALK and EGFR shRNA constructs cloned into the pLKO.1 puro vector as previously described (21). A vector containing a non-targeting (NT) shRNA and GFP shRNA was used as a control. Lentivirus production, titrations and infections were performed as in (21). The specific shRNA sequences are available upon request.

**Generation of In Vitro Drug-Resistant H3122 Cells**

In order to generate drug resistant cells, the H3122 cells were exposed to increasing concentrations of TAE684, similar to our previously described methods (3, 21). TAE684 concentrations were increased stepwise from 1 nM to 100 nM when the cells resumed growth kinetics, similar to untreated parental cells. To confirm the emergence of a resistant clone, MTS assays were performed following growth at each concentration. The in vitro drug-resistant cells were subcloned by single cell isolation.

**Antibodies and Western blotting**

Cell lysis, Western blotting and immunoblotting was performed as previously described (18). Anti-ALK (DF53), anti-phospho-EGFR, anti-total-EGFR, anti-EGFR L858R, anti-EGFR delE746_A750, anti-PARP, anti-α tubulin, anti-phospho-Akt (Ser-473) and anti-total-Akt, were obtained from Cell Signaling Technology. Total ERK1/2 and phospho-ERK1/2 (pT185/pY187) antibodies were from Invitrogen (Carlsbad, CA). Immunoprecipitations were performed using anti-Flag-M2 agarose (Sigma-Aldrich Co.; St. Louis, MO). The receptor tyrosine kinase (RTK) array was purchased from R&D.
Systems and used according to the manufacturer's recommended conditions. ALK immunohistochemistry (IHC) was performed using the mouse monoclonal anti-human ALK (clone: 5A4, Abcam; Cambridge, MA) as previously described (16). EGFR IHC was performed as previously described (22).

*Phosphotyrosine profiling*

Phosphotyrosine profiling was performed 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, and 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). All samples were run in triplicate. Color intensity was measured at 450 nm using a spectrophotometric plate reader. Growth factor concentrations were determined by comparison with standard curves.

*Cell cycle analysis and apoptosis assays*

1 x 10⁶ cells treated with each of the compound at indicated concentration or DMSO 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 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

In order 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 patient’s tumor obtained prior to crizotinib treatment (data not shown).

We evaluated the biologic 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 (Fig. S1A). The EML4-ALK L1152R cells were significantly more resistant than the parental cells to both crizotinib (Figure 1B) and ALK inhibitor TAE684 (Fig. S1B). The L1152R mutation diminished crizotinib mediated inhibition of downstream AKT and ERK 1/2 phosphorylation (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 to those with EML4-ALK alone (Figure 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 to the control cells (GFP or EML4-ALK wild-type), but there were no significant difference among the C1156Y, L1196M and L1152R mutations (Fig. S1D and Table1). 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 (Figure 1D) (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 (Figs. 2A and S2A). However, these cells were still dependent on ALK for their growth as downregulation of ALK using an ALK specific short hairpin (sh) RNA resulted in significant growth inhibition compared to either a non-targeting (NT) or an EGFR specific shRNA (Figs 2B, S2B and S2C). Similarly, the ALK shRNA but not the EGFR 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 to 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 receptor tyrosine kinases (RTKs) using the human phospho-receptor tyrosine kinase (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 (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 (Figs. S2E and S2F).

**ALK inhibitor resistant H3122 cells contain activation of EGFR signaling**

In order 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 nM of TAE684. In our prior studies, we demonstrated that 100 nM of TAE684 inhibited ALK signalling and significantly decreased cell viability in H3122 cells but this concentration was not generally toxic in non-ALK rearranged NSCLC cell lines (13). We sub-cloned the TAE resistant (TR) cells from single cells (H3122 TR3) and these cells were resistant to both TAE684 and crizotinib (Fig. 3A, 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 fluorescence in situ hybridization (FISH). While all of the H3122 cells contained the EML4-ALK inversion, this was only detected in a small fraction (5%) of the H3122 TR3 (Fig S3B and S3C). The cells that retained the inversion also harboured a concurrent amplification in the ALK locus (Fig. S3C). Together, these findings suggest that the H3122 TR3 cells have evolved to lose their ALK dependence for growth.

In order to further characterize the H3122 TR3 cells we performed phospho-RTK arrays in both the parental and drug resistant cells with and without TAE684 treatment (Fig. 3C). Compared to 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 three proteins in further detail (23). Consistent with the genomic findings, ALK phosphorylation was greater in the H3122 compared to 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 H3122TR3 clone using this assay (Fig S3D). Of note, the ectopic expression of ALK secondary mutations (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 two different (A3 and D) EGFR shRNAs. Compared to 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 where treatment with PF299804 resulted in a significant decrease (p < 0.001) in H3122 TR3 but not H3122 colonies (Fig. 3F) compared to 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 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 harbouring evidence of IGF1R activation (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 (Fig. S3G) suggesting that the mechanism of EGFR activation in these cells is through a ligand mediated autocrine activation.

**Activation of EGFR signalling induces resistance to crizotinib**

Our studies from the ALK inhibitor resistant DFCI032, DFCI 076 and H3122 TR3 cells suggest a role for EGFR signalling in mediating crizotinib resistance. In order to formally evaluate this hypothesis we activated EGFR signalling 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 Fig. S4A). Analogously *EML4-ALK* promotes gefitinib resistance in the HCC827 *EGFR* mutant NSCLC cell line (Fig. S4B), which was reversed by concurrent treatment with TAE684 (Fig S4C).
A subset of EML4-ALK NSCLC patients harbour concurrent EGFR mutations

Our in vitro studies suggest that EGFR signalling can contribute to ALK kinase inhibitor resistance in EML4-ALK NSCLC. In addition we demonstrate that a cancer cell line that harbours 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 TKI naive patients(26). In our prior study we identified one treatment naive NSCLC patient that harboured 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 harbouring ALK rearrangements at DFCI, all detected in a clinical laboratory, we have now identified 3 (6%) patients that also harbour 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 pre-treatment tumor from patient 1 using the EGFR L858R specific antibody demonstrates EGFR staining (Fig 4E) while no staining was observed with the ALK specific antibody (Fig 4E) despite the presence of the ALK genomic rearrangement (Table 2).
DISCUSSION

ALK tyrosine kinase inhibitors 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 the current 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 thus disfavoring 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 based on the 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 (Fig. S3B), but not the L1196M mutation. Since 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) while the H3122 TR3 cells are more EGFR dependent (Fig. 3D) for their growth. The DFCI032 cells are equally co-dependent with very little effect on growth by only EGFR or ALK inhibition (Fig. S2Fand (13)). These different examples may be representative 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 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 two 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 naïve 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 co-expression 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.
<table>
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<th>Cell line</th>
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<th>TAE684 IC$_{50}$ (nM)</th>
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**Table 1.** Summary of *in vitro* growth assays.
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**Table 2.** Characteristics and outcomes of NSCLC patients harboring concurrent *EGFR* mutations and *ALK* rearrangements. FISH, fluorescence in situ hybridization; IHC, immunohistochemistry; PR, partial response; N.D., not done; N/A, not applicable
Figure Legends

**Figure 1. The ALK mutation L1152R causes the ALK tyrosine kinase inhibitor resistance.**  
A. Sequence tracing from post-treatment tumor specimens. There is a T to G mutation in codon 3455 in exon 23 resulting in the L1152R mutation.  
B. Ba/F3 cells were treated with crizotinib at the indicated concentrations, and viable cells were measured after 72 hours of treatment and plotted relative to untreated controls. There is a significant effect of the L1152R mutation at 300 nM (p < 0.001).  
C. Ba/F3 cells with indicated genotypes were treated with increasing concentrations of crizotinib for 6 hours. Cell extracts were immunoprecipitated with an anti-FLAG antibody followed immunoblotting to detect the indicated proteins.  
D. Ribbon diagram depicting the crystal structure of Alk kinase in complex with crizotinib. The sidechains of residues that are sites of resistance mutations, including the L1152R mutation described here, are shown in green. Note that L1152 and C1156 are not in contact with the ATP-binding cleft, but are adjacent to each other and to the C-helix (pink). Both the L1152R and C1156Y mutations could introduce hydrogen bond interactions with E1161 on the C-helix. All of the resistance mutations identified to date cluster around the conformationally sensitive C-helix and activation loop, suggesting that they may affect kinase activity and inhibitor binding through alterations in the structure or stability of these elements. The activation loop (A-loop, colored orange) is partially disordered in this structure as denoted by the dashed line. Figure is drawn from PDB ID 2XP2.
Figure 2. DFCI076 cells are co-dependent on ALK and EGFR. A. The H3122 or DFCI 076 cells were treated with crizotinib, alone or concurrently with 1 μM PF299804, at the indicated concentrations, and viable cells were measured after 72 hours of treatment and plotted relative to untreated controls. B. Downregulation of ALK or EGFR using shRNAs in H3122 and DFCI076 cells. Further growth inhibition is observed with the addition of 1 μM PF2990804. Cell viability is measured relative to the non-targeting (NT) control shRNA. C. A phospho-RTK array reveals that the DFCI076 cells contain strong phosphorylation of both EGFR and MET. Cells were grown in medium and the cell lysates were hybridized to a phospho-RTK array. Hybridization signals at the corners serve as controls. D. H3122 and DFCI076 cells are treated with indicated concentrations of crizotinib for 6 hours. Immunoblotting was used to detect the indicated proteins.

Figure 3. H3122 TR3 cells contain are ALK inhibitor resistant and contain co-activation of EGFR signaling. A. H3122 and TR3 cells were treated with indicated concentrations of TAE684. Viable cells were measured after 72 hours of treatment and plotted relative to untreated controls. B. ALK shRNA has minimal effect on H3122 TR3 cell viability. Cell viability is measured relative to non-targeting (NT) control. H3122 and A549 cells serve as positive and negative controls, respectively. Successful ALK knockdown in H3122 TR3 cells is confirmed by Western blotting. C. Summary of RTK array from H3122 and H3122 TR3 cells with and without TAE684 (100 nM; 6 hrs) treatment. The protein lysates were exposed to the RTK array (R&D). Each spot of membrane were calculated as signal intensity and shown in the bar graph. D. ALK and EGFR phosphorylation in H3122 and H3122 TR3 cells with and with TAE684 and
gefitinib treatment. Phosphorylation was measured using a bead based assay (methods).

E. Proliferation of H3122 TR3 but not H3122 cells is effected following EGFR knockdown using two different shRNAs. NT; non-targeting. F. Results of colony formation assay after 14 days treatment with indicated compounds with both H3122 and H3122TR3. The combination of crizotinib (1 μM) and PF299804 (1 μM) effectively inhibited colony formation in H3122 TR3 cells. G. H3122 and H3122TR3 cells were treated with indicated compounds for 6 hours, and immunoblotting was used to detect the indicated proteins. For the PARP blot, cells were treated for 24 hours.

Figure 4. Concurrent ALK and EGFR signaling leads to drug resistance. A. H3122 cells were treated with crizotinib at the indicated concentrations in the presence or absence of EGF (10 ng/ml) and PF299804 (1 μM). Viable cells were measured after 72 hours of treatment and plotted relative to untreated controls. B. H3122 cells were treated with crizotinib for 6 hrs at indicated concentrations in the absence or presence of EGF (10 ng/ml). Immunoblotting was used to detect the indicated proteins. C. H3122 cells stably expressing GFP or EGFR E746_A750 were treated with crizotinib in the absence or presence of gefitinib (1 μM). Viable cells were measured after 72 hours of treatment and plotted relative to untreated controls. D. Results of colony formation assay after 14 days treatment with indicated compounds using H3122 and H3122 EGFR E746_A750. The combination of crizotinib and PF299804 effectively inhibited colony formation. E. EGFR sequence tracing (left) and ALK FISH analysis (right) from patient 1. Asterix, T to G mutation resulting in L858R; arrows, split red and green FISH signals. F. Immunohistochemistry for EGFR L858R (left) and ALK (right) from patient 1.
Acknowledgements

This study was supported by NIH R01CA136851 (N.S.G. and P.A.J.), R01CA135257 (P.A.J.) and by the NCI Lung SPORE P50CA090578 (P.A.J.). The authors would like to also acknowledge the clinical trial support from Pfizer, Inc.
References


A. CTG to CGG

L1152R mutation

B. EML4-ALK WT
   EML4-ALK L1152R

\[
\text{Crizotinib Concentration (μM)}
\]

\[
\% \text{ of control}
\]

C.

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pALK

ALK

Flag

D. N-lobe
   C-lobe
   C-helix
   L1152
   C1156
   E1161
   F1174
   F1245
   R1275
   A-loop

Sasaki et al., Figure 1
**A.**

Phospho-RTK Array

- **PF**: PF0299804
- **EGFR c-MET**

**B.**

- **H3122**
- **DFCI076**

% of NT

- **NT**
- **ALK**
- **EGFR(A3)**

**D.**

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- **pALK**
- **ALK**
- **pEGFR**
- **EGFR**
- **pAKT**
- **AKT**
- **pERK1/2**
- **ERK1/2**
- **α-tubulin**

Sasaki et al., Figure 2
Sasaki et al., Figure 3
A. 

B. 

C. 

D. 

E. 

F. 

Sasaki et al., Figure 4
A novel ALK secondary mutation and EGFR signaling cause resistance to ALK kinase inhibitors

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Cancer Res  Published OnlineFirst July 26, 2011.