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Analysis of Tumor Specimens at the Time of Acquired Resistance to EGFR TKI therapy in 155 patients with *EGFR* mutant Lung Cancers

Helena A. Yu^{*1}, Maria E. Arcila^{*1}, Natasha Rekhtman¹, Camelia S. Sima¹, Maureen F. Zakowski¹, William Pao², Mark G. Kris¹, Vincent A. Miller¹, Marc Ladanyi¹, and Gregory J. Riely¹

¹Thoracic Oncology Service, Division of Solid Tumor Oncology, Department of Medicine Department of Pathology Department of Epidemiology and Biostatistics Memorial Sloan-Kettering Cancer Center, Weill Cornell Medical College, New York, NY

²Vanderbilt Ingram Cancer Center

Abstract

Purpose—All patients with *EGFR* mutant lung cancers eventually develop acquired resistance to EGFR tyrosine kinase inhibitors (TKIs). Smaller series have identified various mechanisms of resistance, but systematic evaluation of a large number of patients to definitively establish the frequency of various mechanisms has not been performed.

Experimental Design—Patients with lung adenocarcinomas and acquired resistance to erlotinib or gefitinib enrolled onto a prospective biopsy protocol and underwent a re-biopsy after the development of acquired resistance. Histology was reviewed. Samples underwent genotyping for mutations in *EGFR*, *AKT1*, *BRAF*, *ERBB2*, *KRAS*, *MEK1*, *NRAS* and *PIK3CA*, and FISH for *MET* and *HER2*.

Results—Adequate tumor samples for molecular analysis were obtained in 155 patients. Ninety-eight had second-site *EGFR* T790M mutations (63%, 95% CI 55-70%) and four had small cell transformation (3%, 95% CI 0-6%). *MET* amplification was seen in 4/75 (5%, 95% CI 1-13%). *HER2* amplification was seen in 3/24 (13%, 95% CI 3-32%). We did not detect any acquired mutations in *PIK3CA*, *AKT1*, *BRAF*, *ERBB2*, *KRAS*, *MEK1*, or *NRAS*. (0/88, 0%, 95% CI 0-4%). Overlap among mechanisms of acquired resistance was seen in 4%.

Conclusions—This is the largest series reporting mechanisms of acquired resistance to EGFR TKI therapy. We identified *EGFR* T790M as the most common mechanism of acquired resistance, while *MET* amplification, *HER2* amplification, and small cell histologic transformation occur less frequently. More comprehensive methods to characterize molecular alterations in this setting are needed to improve our understanding of acquired resistance to EGFR TKIs.

Address Correspondence: Gregory J. Riely Memorial Sloan-Kettering Cancer Center 300 East 66th St. New York, NY 10065

rielyg@mskcc.org.

*Contributed equally

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Keywords

EGFR mutant lung cancer; lung adenocarcinoma; targeted therapy; acquired resistance; tyrosine kinase inhibitor therapy

Introduction

In patients with lung cancer whose tumors harbor activating *EGFR* mutations, treatment with EGFR TKIs induces initial tumor shrinkage, with progression of cancer after a median of 8-16 months¹⁻⁴. Various mechanisms of resistance to erlotinib and gefitinib have been identified, and understanding these mechanisms is critical to developing treatment strategies in the acquired resistance setting. The most frequently reported mechanism of acquired resistance is the *EGFR* T790M point mutation within exon 20^{5,6}. Small cell histologic transformation has also been associated with the development of acquired resistance^{7,8}. *MET* amplification and *HER2* amplification are also seen and illustrate the upregulation of parallel signaling pathways⁹⁻¹¹. Rare secondary *BRAF* mutations¹² have also been implicated. The frequency and overlap of these mechanisms of resistance is not well-characterized, as all reports have been in relatively small series of patients⁸.

Rebiopsy of growing tumors at clinical progression has become increasingly important as the results may better predict prognosis^{13,14} or direct a change in therapy⁷. Understanding why acquired resistance occurs is essential as new therapies focus on alternative means of EGFR inhibition and inhibition of parallel signaling pathways to prevent or circumvent resistance. To characterize the frequency of the various mechanisms of acquired resistance in a single population, we report the updated results of a prospective clinical trial initiated in 2004 to determine mechanisms of acquired resistance in patients with *EGFR*-mutant lung cancers who had an initial response to erlotinib or gefitinib¹³.

Methods

Patients

Patients had lung adenocarcinoma with a documented *EGFR* mutation, received treatment with single agent erlotinib or gefitinib, had either prolonged stable disease (>3 months) or a partial response to therapy, and developed radiographic progression while on EGFR TKI. The primary objective of the study was to characterize mechanisms of acquired resistance to EGFR TKI therapy. Biopsies were obtained in the least invasive manner possible, and typically consisted of either a fine needle aspiration or core biopsy done with image guidance, or rarely excisional biopsies. Fluid from malignant effusions was collected to create cell blocks. If a surgical procedure was clinically indicated, tissue from the procedure was obtained for analysis. Protocol #04-103 was approved by the Institutional Review Board of Memorial Sloan-Kettering Cancer Center, and all patients signed informed consent. Partial data from a subset of patients on this protocol have been reported previously^{11,13,15}.

Tissue Analysis

All samples underwent histologic review. If required, additional diagnostic immunohistochemical stains were performed at the discretion of the pathologist. For molecular analysis, genomic DNA was extracted from the tumor samples which included fresh, frozen, and formalin fixed paraffin embedded (FFPE) tissue specimens. Cytologic samples were used to create cell blocks from which DNA was extracted. The initially identified sensitizing *EGFR* mutation was confirmed using previously described methods¹⁶⁻¹⁸.

Standard sequencing and/or fragment analysis were used to identify EGFR T790M using techniques previously described^{15,18}. In July 2009, we began locked nucleic acid based PCR sequencing to improve the sensitivity of EGFR T790M detection¹⁹. Beginning in January 2009, a mass spectrometry-based mutation profiling assay (Sequenom), was used on all samples. This assay identifies 92 specific point mutations in 8 genes: *EGFR*, *BRAF*, *PIK3CA*, *AKT1*, *ERBB2*, *MEK1*, *NRAS* and *KRAS*. If additional material was available on samples prior to 2009, locked nucleic acid -based sequencing and Sequenom analysis were performed. For a subset of patients with available tissue, direct sequencing of *EGFR* exons 18-21 was also available. Available unstained FFPE tumor tissue was analyzed by a dual-color FISH assay using a MET/CEP7 probe cocktail^{15,20}. A MET/CEP7 ratio was established based on a count of at least 200 cells. Samples with a MET:CEP7 ratio greater than 2 were considered to have *MET* amplification (low amplification ≤ 3 , high amplification >3). Assessment of *HER2* gene copy number was also performed on available unstained FFPE tumor tissue using the Vysis PathVysion *HER2* DNA Probe Kit (Abbott Laboratories, Abbott Park, IL) and scored according to previously published criteria^{21,22}. Tumors were classified as amplified if the HER2/CEP17 ratio per cell was >2 or homogeneously staining regions with >15 copies in $>10\%$ of cells were present. At least 40 cells were analyzed for each case.

Statistical Methods

Medical records were reviewed to obtain clinical information. Overall survival from the time of advanced cancer diagnosis and post-progression survival following the development of acquired resistance were calculated using Kaplan-Meier methodology, with patients censored if they were alive at the time of last follow-up, February 2012. Univariate comparisons between groups were performed using the log-rank test.

To evaluate whether patients enrolled on the protocol were representative of patients with advanced NSCLCs, we assembled a reference cohort of all patients diagnosed with advanced NSCLC at our institution during a similar time period (2004-2009), whose tumors harbored *EGFR* mutations, and were not enrolled in this acquired resistance protocol. The two groups were compared with respect to clinical characteristics using the chi-square test.

Results

Enrollment and rebiopsy

From August, 2004 to January, 2012, 175 patients were enrolled and 162 underwent rebiopsy at the time of acquired resistance (see Table 1). Seven patients had biopsy samples with either insufficient tumor content for molecular analysis (n=5) or no evidence of the previously present *EGFR* sensitizing mutation upon rebiopsy (n=2). One lung core biopsy had insufficient tumor cells. One patient's core bone biopsy was inadequate for DNA analyses due to decalcification. Two patients had core biopsies of the lung with tumor evident where the sensitizing mutation could not be identified. Two samples, a brain resection and a pneumonectomy specimen, had no viable tumor cells due to tumor necrosis. Finally, one patient had a core biopsy of the adrenal gland that failed to sample the tumor, whereas the corresponding FNA revealed small cell transformation, but there was insufficient material for molecular testing. A total of 155 patients had biopsy samples that were sufficient for molecular analysis, including fine needle aspirations, core biopsies, surgical samples and cytology from malignant effusions. There was only one serious adverse event, a pneumothorax requiring pigtail catheter placement.

Baseline clinical and molecular characteristics

Pre-treatment clinical and molecular characteristics of the 155 patients are described in Table 2. Compared with a reference group of patients with *EGFR* mutant lung cancers diagnosed in the same time period (data not shown), patients enrolled on the protocol were significantly younger, were more likely to be never smokers, had significantly fewer pack years, and were more likely to have *EGFR* exon 19 deletions.

Pre-biopsy course

The 155 patients began EGFR TKI therapy from February 1999 to January 2011. One hundred ten patients (71%) were started on EGFR TKI as first line therapy. Twenty four patients (15%) received EGFR TKI as second line therapy, and 9 patients (6%) as third or fourth line therapy. Twelve patients (8%) received EGFR TKI as adjuvant or maintenance therapy after surgery and/or chemotherapy. The majority of patients (78%, 121/155) received single agent EGFR TKI therapy, while 22% (34/155) were initially treated concurrently with EGFR TKI and cytotoxic chemotherapy. The patients on this protocol had documented clinical progression on EGFR TKI between March, 2004 and December, 2011. The median time from start of EGFR TKI to clinical progression was 13 months with a range of 2 to 73 months. The time to progression on EGFR TKI was similar for patients with EGFR exon 19 deletions versus EGFR L858R mutations, 15 and 17 months respectively ($p=0.99$). One patient with EGFR exon 19 deletion and EGFR T790M at baseline had a time to progression on EGFR TKI of 2 months. Another patient with EGFR exon 19 deletion and a *PIK3CA* mutation had a time to progression of 5 months. No other patients had either EGFR T790M or *PIK3CA* mutations in their pre-TKI specimens. There was no difference in time to progression on EGFR TKI for patients with secondary EGFR T790M mutations and patients with other mechanisms of resistance, 16 and 17 months respectively ($p=0.37$). Ninety one percent (141/155) of patients continued their EGFR TKI after evidence of clinical progression.

Findings at the time of acquired resistance

All 155 samples were tested for known mechanisms of acquired resistance. Not all analyses were conducted on all specimens due to the limited amount of tissue available. Figure 1 illustrates the prioritization of analyses conducted. All specimens underwent pathologic review by a thoracic pathologist. Four of 155 had evidence of small cell histologic transformation (3%, 95% CI 0 to 6%). Samples with small cell histology had further immunostains performed including synaptophysin, chromogranin, and CD56 to confirm the diagnosis (Figure 2). There was no evidence of small cell lung cancer in any of the pretreatment biopsy specimens. Morphologic changes consistent with epithelial-to-mesenchymal transition were not seen, although no immunohistochemical stains for vimentin or E-cadherin were performed.

We identified a second-site EGFR T790M mutation in 98 of 155 samples (62%, 95% CI 55-70%). One patient had an acquired T854A mutation [observed incidence <1% (5% CI <1 to 4%)]. In 88 patients, no acquired mutations were identified in *PIK3CA*, *AKT1*, *BRAF*, *ERBB2*, *MEK1*, *NRAS* and *KRAS* (0%, 95% CI 0 to 4%).

Sufficient tissue was available for *MET*FISH analysis for 75 patients. Four of 75 patients tested had *MET* amplification, using the standard *MET*/*CEP7* ratio of greater than 2 (5%, 95% CI 1 to 13%). 24 patients had sufficient tissue available for *HER2* FISH analysis. 2 of 24 patients had evidence of *HER2* amplification using the standard *HER2*/*CEP17* ratio of greater than 2 (13%, 95% CI 3-32%). Baseline samples for the 4 *MET*-amplified and 2 *HER*-amplified cases were not available for FISH analysis. The frequency of the different mechanisms of resistance was similar when comparing patients with baseline EGFR L858R

mutations versus EGFR exon 19 deletions. The relative percentages of the observations are illustrated in Figure 3.

Overlap of Mechanisms of Resistance

4% of samples had more than one mechanism of resistance identified. Tumors from two patients had both small cell histologic transformation and EGFR T790M. One patient had small cell histologic transformation and *MET* amplification. In these patients showing small cell histologic transformation, there was no residual adenocarcinoma component in the biopsies studied, indicating that the aforementioned acquired genetic alterations were present in the small cell carcinoma. Two patients had EGFR T790M and *MET* amplification by FISH; both molecular findings were identified in the same tumor samples. One patient had two acquired resistance samples; one sample was EGFR T790M positive and the other had evidence of *HER2* amplification. The autopsy specimen was EGFR T790M positive, but negative for *HER2* amplification, and the adrenalectomy sample had evidence of *HER2* amplification, but was *EGFR* T790M negative. The time to progression on EGFR TKI for patients with two mechanisms of resistance ranged from 7 to 24 months.

Outcomes

Sixty-four percent (99/155) of patients have died as of February 2012. The median overall survival from diagnosis of stage IV disease was 3.8 years (95% CI 3.1-5.1 years) (Figure 4). The median post-progression survival was 1.7 years (95% CI 1.6-2.0 years) (Figure 4). In patients with EGFR T790M, the median post-progression survival was 1.9 years (95% CI 1.6-2.6 years) and was 1.6 years (95% CI 1.2-1.8 years) for those without EGFR T790M ($p=0.015$) (Figure 5).

Discussion

To provide a more precise understanding of mechanisms of acquired resistance to EGFR TKIs and their overlap in a single cohort, we report this prospective study of 155 patients. While the most commonly observed mechanism of resistance is EGFR T790M, our data demonstrate that tumors biopsied at the time of clinical acquired resistance to EGFR TKIs display a spectrum of mechanisms, with rare overlap among mechanisms.

EGFR T790M is the most common mechanism of acquired resistance, seen in nearly two-thirds of cases. *MET* amplification is uncommon and is less frequent than initially proposed¹⁰. Acquired mutations in *EGFR* other than T790M, including T854A, D761Y and L747S, are infrequent²³⁻²⁵. Except for the one patient with a baseline *PIK3CA* mutation, no additional patients in this large series had a mutation in *PIK3CA*, *AKT1*, *BRAF*, *HER2*, *MEK1*, *NRAS* and *KRAS*, which is consistent with another series that found no mutations in *MEK1*, *NRAS* or *KRAS*, but did identify a secondary *BRAF* mutation in 2 of 195 acquired resistance samples¹². Point mutations in these genes including *PIK3CA* appear to be infrequent, having been occasionally reported in other series^{8,12}. *HER2* amplification may be a more common finding at the time of resistance, seen in 13% of cases in our series. Pretreatment samples were not available for *HER2* FISH testing to confirm that amplification was not present prior to treatment. However, *HER2* testing performed on 99 untreated lung adenocarcinomas has been reported, with only 1 tumor (1%) displaying *HER2* amplification pretreatment¹¹.

Small cell histologic transformation was also less frequent than previously reported⁸. Interestingly, 3 of 4 cases of small cell histologic transformation occurred in addition to another mechanism of resistance. It is unclear if small cell transformation is merely associated with the development of resistance or is itself a causal mechanism. Small cell

histologic transformation may be a phenomenon unique to TKI therapy as it has not been reported in patients who are treated and progress on cytotoxic chemotherapy, but re-biopsy data on such patients are limited. The patients with small cell histologic transformation all had a relatively aggressive clinical course as typically seen with small cell lung cancer. Two of the four patients received platinum based doublet therapy and had partial responses after completion of six cycles of therapy. One patient received adjuvant cisplatin and etoposide after metastasectomy and had a 13 month disease free interval prior to developing recurrent disease. One patient had a poor performance status and was treated with single agent etoposide without response. Although the role of small cell histologic transformation in acquired resistance is presently unclear, histologic transformation is important to identify because it significantly alters our treatment recommendations.

MET amplification was seen concurrently with another mechanism of resistance in 3 of 4 cases. Two patients had both EGFR T790M and *MET* amplification and one patient had *MET* amplification and evidence of small cell transformation. This raises the question as to whether *MET* amplification alone is sufficient to induce resistance to EGFR TKI therapy. Previous reports suggest a reciprocal relationship between EGFR T790M and *MET* amplification, with overlap of the two mechanisms becoming less frequent with increasing *MET* amplification (4-fold)²⁶. This reciprocal relationship was not seen in our cohort, but is limited by the small number of patients with *MET* amplification. In two samples with EGFR T790 and *MET*, one had high level *MET* amplification (>10-fold) and one had moderate amplification (4-fold), and the sample with *MET* amplification only was determined by qPCR, and not quantified by FISH. Finally, one patient had different mechanisms of resistance, EGFR T790M and *HER2* amplification, identified in two distinct resistance samples with the same *EGFR* sensitizing mutation. This suggests that either genetic alteration may be sufficient to impart clinical resistance, but different mechanisms of resistance may exist in distinct clones of a patient's cancer. Intratumor heterogeneity is a significant limitation of basing treatment decisions on molecular analysis of a single tumor biopsy in the metastatic setting²⁷.

While many aspects of our findings are similar to other series, there are several differences. The median time to progression on EGFR TKI of 13 months in our cohort is similar to previously published *EGFR* mutant cohorts.¹⁻³ Despite this and other similarities to a similar cohort of patients with advanced *EGFR* mutant lung cancers, these patients were somewhat younger with less tobacco exposure and were more likely to have *EGFR* exon 19 deletion. These factors have been associated with improved survival in previous studies²⁸⁻³⁰ which may explain the patients' ability to enroll in a prospective trial at the time of development of acquired resistance.

The majority of patients (91%) continued EGFR TKI therapy after clinical progression, sometimes in combination with chemotherapy. This treatment approach is consistent with preclinical data that continued EGFR inhibition is indicated due to the presence of a heterogeneous population of tumor cells, with varied sensitivity to EGFR inhibition³¹ as well as clinical data demonstrating rapid clinical progression (flare) after discontinuation of EGFR TKI^{32,33}. Recent retrospective analyses support the clinical observation of improved outcomes with continued EGFR TKI therapy after radiologic progression³⁴⁻³⁶. Prospective evaluation of continued EGFR TKI after clinical progression will be important and will inform future clinical practice.

Since this protocol opened, our understanding of the mechanisms of resistance has grown significantly, leading to some limitations in our analysis. Sufficient tissue from re-biopsies was not obtained for all the molecular tests currently performed. Histologic analysis and testing for EGFR T790M was performed on every sample, but FISH for *MET* and *HER2*

and sequenom for other acquired oncogene mutations were performed on only a portion of the samples. This limits the accuracy of the relative frequency of the various mechanisms we present, and potentially underestimates the prevalence of overlap among the different mechanisms of resistance. Our analysis did not encompass alterations in autocrine or paracrine growth pathways that may also confer resistance^{37,38}. Epithelial to mesenchymal transition has been described as a potential mechanism of resistance⁸, although we did not note any evidence of spindle-like mesenchymal morphology on histologic review of our samples. However, we did not perform immunohistochemistry for e-cadherin or vimentin which limits the conclusions that can be made. We confirmed the presence of the *EGFR* sensitizing mutation in the pre-treatment tumor sample of each patient included in this analysis, but we were unable to assess for *HER2* or *MET* amplification, or perform comprehensive genotyping on the majority of pre-treatment specimens. Consequently, we cannot say with certainty that the genetic changes identified were acquired after treatment with an EGFR TKI.

This prospective study confirms that standardized, step-wise molecular testing at the time of acquired resistance is feasible and safe. We plan to perform comprehensive next generation based sequencing based mutation profiling as well as protein and gene expression analysis on specimens where no mechanism of acquired resistance was identified. Other proposed mechanisms of acquired resistance to EGFR TKI therapy including upregulated AXL and HGF expression and *MAPK1* amplification will need to be tested and validated in our larger data set³⁷⁻⁴⁰. While the intent of these studies is to discover additional mechanisms of resistance to EGFR inhibition, the ultimate purpose is to better inform treatment decisions in the acquired resistance setting. Our growing knowledge of oncogenes and the molecular basis of resistance to kinase inhibition will allow for personalized treatment strategies in both the initial and resistance settings.

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Statement of translational relevance

Responses to EGFR tyrosine kinase inhibitors (EGFR TKIs) in *EGFR* mutant lung cancer are limited by acquired resistance. The goal of this prospective study was to characterize the mechanisms of resistance by performing repeat tumor biopsies at clinical disease progression. Previously published reports included small numbers of patients, and do not adequately establish the frequency of the various mechanisms of resistance. This is the largest reported cohort of patients with *EGFR* mutant lung cancer and acquired resistance to EGFR TKI therapies that have had comprehensive mutational analysis on acquired resistance biopsy samples. Our findings indicate that second site *EGFR* T790M mutations are the dominant mechanism of resistance identified. *MET* amplification, small cell histologic transformation, and *HER2* amplification are uncommon. There were no acquired mutations in other oncogenes identified. This protocol illustrates that post-progression tumor biopsies can be done on a large scale with minimal adverse events. Comprehensive tumor analysis at the time of resistance is important to develop new therapeutic strategies and also to inform patient care in the acquired resistance setting.

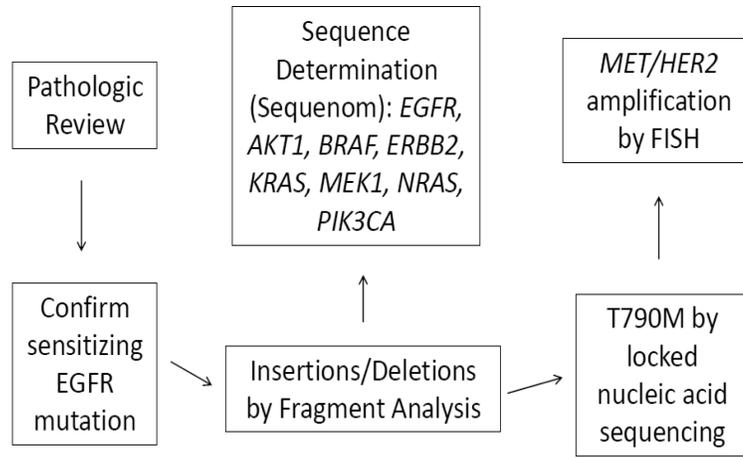


Figure 1.
Assay prioritization.

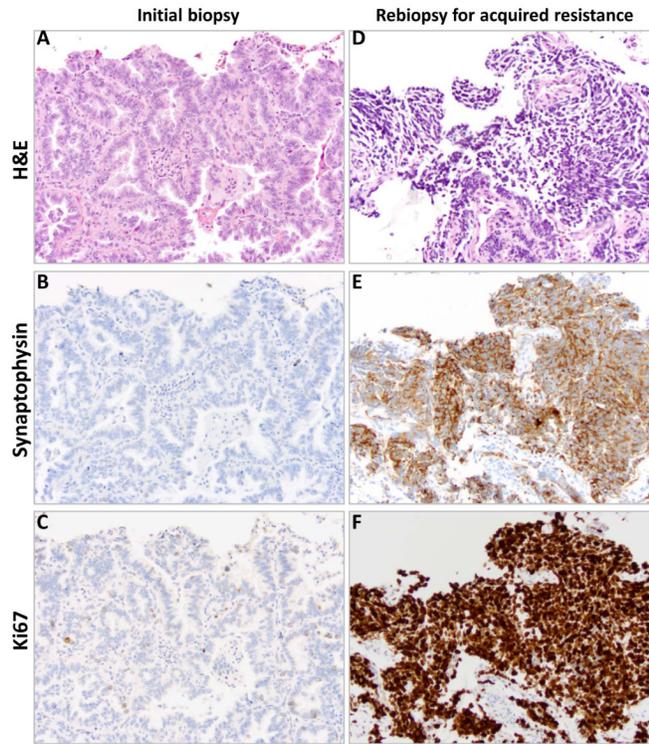


Figure 2.

A patient's tumor tissue at initial lung biopsy (A-C) and biopsy at acquired resistance (D-F) with small cell histologic transformation. Hematoxylin and eosin stained material demonstrating histologic changes from initial biopsy (A) to biopsy at acquired resistance (D) with immunohistochemical staining for CD56 and Ki67 on initial biopsy (B, C) and biopsy at acquired resistance (E, F).

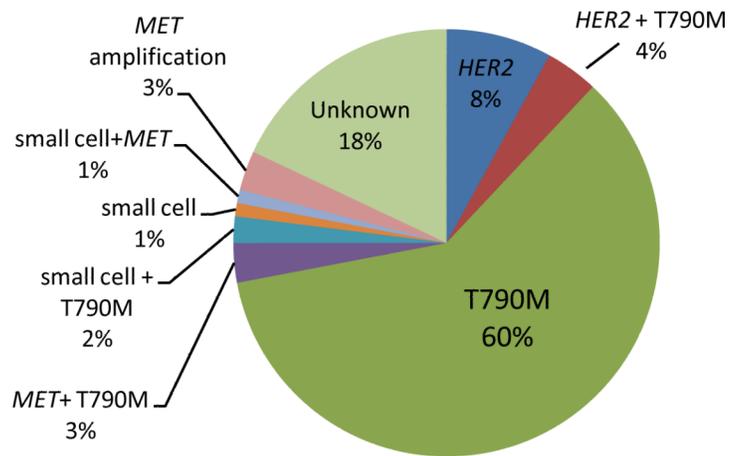


Figure 3. The relative frequencies of the various mechanisms of acquired resistance. Composite pie chart with percentages compiled from tests with varying denominators.

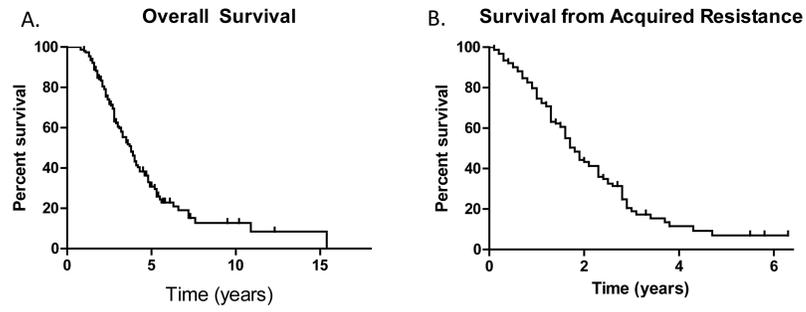


Figure 4. A) Overall survival (from the development of Stage IV disease), and B) post progression survival (from the time of acquired resistance)

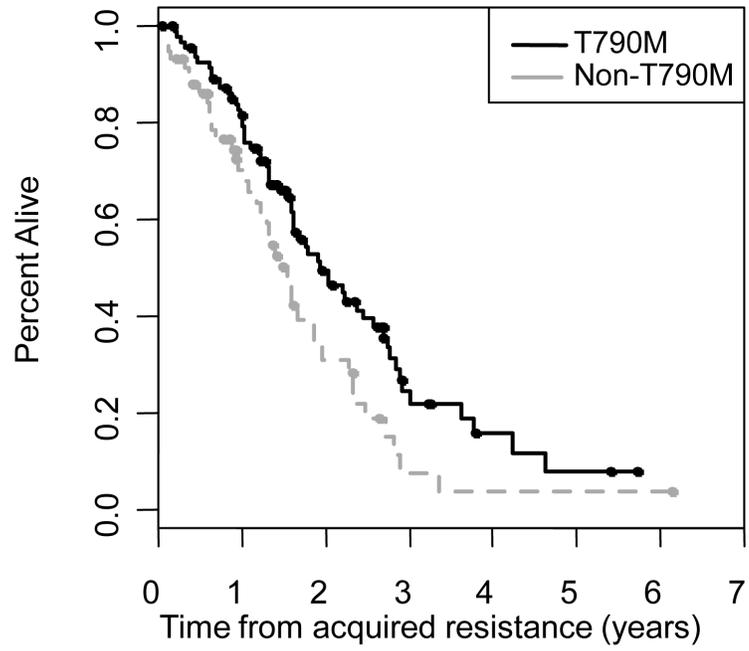


Figure 5. Post progression survival for EGFR T790M+ patients and non-T790M+ patients

Table 1

Procedures performed

Procedures Performed	N=162
Adrenalectomy	3
Brain resection	10
Lung resection	4
Lymph node excision	5
Autopsy	2
Biopsies	
Lung/Chest Wall (Core/FNA)	82 (64/18)
Bone (Core/FNA)	9 (7/2)
Liver (Core/FNA)	13 (10/3)
Lymph node (Core/FNA) *	9 (2/7)
Other (Core/FNA) **	9 (4/5)
Fluid	
Pleural	14
Peritoneal	1
CSF	1

* inguinal, neck (n=6), mediastinal (N=3)

** Other includes biopsy of adrenal (n=2), soft tissue (N=2), omentum, spleen, kidney (N=2), cervix

Table 2

Clinical and Molecular Characteristics

Patient Characteristics	
	N=155
Age	
Median	57
Range	33-81
Sex-n (%)	
Female	100 (66)
Male	55 (35)
Race-n (%)	
White	113 (73)
Asian	30 (19)
Black	11 (7)
Other	1 (1)
Smoking history-n (%)	
Never smoker	107 (69)
Former smoker	48 (31)
Current smoker	0
Median pack yr	10
Range	0-96
Pretreatment <i>EGFR</i> mutation- n (%)	
Exon 19 deletion	103 (66)
Exon 21 L858R	46 (30)
Exon 21 L861Q	1
Other/double mutations	
Exon 19 deletion + T790M	1
Exon 19 deletion + PIK3CA	1
Exon 21 L861Q and Exon 20 R776H	1
Exon 21 L833V and Exon 21 H835L	1
Exon 21 L858R and Exon 20 R776H	1