

## EGFR Mutations in Lung Cancer: Correlation with Clinical Response to Gefitinib Therapy

J. Guillermo Paez,<sup>1,2\*</sup> Pasi A. Jänne,<sup>1,2\*</sup> Jeffrey C. Lee,<sup>1,3\*</sup> Sean Tracy,<sup>1</sup> Heidi Greulich,<sup>1,2</sup> Stacey Gabriel,<sup>4</sup> Paula Herman,<sup>1</sup> Frederic J. Kaye,<sup>5</sup> Neal Lindeman,<sup>6</sup> Titus J. Boggon,<sup>1,3</sup> Katsuhiko Naoki,<sup>1</sup> Hidefumi Sasaki,<sup>7</sup> Yoshitaka Fujii,<sup>7</sup> Michael J. Eck,<sup>1,3</sup> William R. Sellers,<sup>1,2,4†</sup> Bruce E. Johnson,<sup>1,2,†</sup> Matthew Meyerson<sup>1,3,4,†</sup>

<sup>1</sup>Departments of Medical Oncology and Cancer Biology, Dana-Farber Cancer Institute, Boston, MA 02115 USA. <sup>2</sup>Department of Medicine, Brigham and Women's Hospital and Harvard Medical School, Boston, MA 02115, USA. <sup>3</sup>Departments of Pathology and Biological Chemistry and Molecular Pharmacology, Harvard Medical School, Boston, MA 02115, USA. <sup>4</sup>The Broad Institute at MIT and Harvard, Cambridge, MA 02142, USA. <sup>5</sup>Genetics Branch, National Cancer Institute, National Naval Medical Center, Bethesda, MD 20889, USA. <sup>6</sup>Department of Pathology, Brigham and Women's Hospital, Boston MA 02115, USA. <sup>7</sup>Department of Surgery 2, Nagoya City University Medical School, Nagoya 467-8601, Japan.

\*These authors contributed equally to this work.

†To whom correspondence should be addressed. E-mail: William\_Sellers@dfci.harvard.edu; Bruce\_Johnson@dfci.harvard.edu; Matthew\_Meyerson@dfci.harvard.edu

**Receptor tyrosine kinase genes were sequenced in non-small cell lung cancer (NSCLC) and matched normal tissue. Somatic mutations of the epidermal growth factor receptor gene *EGFR* were found in 15 of 58 unselected tumors from Japan and 1 of 61 from the United States. Treatment with the EGFR kinase inhibitor gefitinib (Iressa) causes tumor regression in some patients with NSCLC, more frequently in Japan. *EGFR* mutations were found in additional lung cancer samples from U.S. patients who responded to gefitinib therapy and in a lung adenocarcinoma cell line that was hypersensitive to growth inhibition by gefitinib, but not in gefitinib-insensitive tumors or cell lines. These results suggest that *EGFR* mutations may predict sensitivity to gefitinib.**

Protein kinase activation by somatic mutation or chromosomal alteration is a common mechanism of tumorigenesis (1). Inhibition of activated protein kinases using targeted small molecule drugs or antibody-based strategies has emerged as an effective approach to cancer therapy (2–4). Recently, systematic analysis of kinase genes has identified mutations of the protein serine-threonine kinase gene *BRAF* in melanoma and other human cancers (5) and of multiple tyrosine kinase genes and the phosphatidylinositol 3-kinase p110 $\alpha$  catalytic subunit gene *PIK3CA* in human colorectal carcinoma (6, 7).

Lung carcinoma is the leading cause of cancer deaths in the United States and worldwide for both men and women (8). Chemotherapy for non-small cell lung carcinoma (NSCLC), which accounts for approximately 85% of lung cancer cases, remains marginally effective (9).

Recently, the epidermal growth factor receptor (EGFR) tyrosine kinase inhibitor, gefitinib (Iressa), was approved in Japan and the United States for the treatment of NSCLC. The original rationale for its use was the observation that EGFR is more abundantly expressed in lung carcinoma tissue than in adjacent normal lung (10). However, EGFR expression as detected by immunohistochemistry is not an effective predictor of response to gefitinib (11).

Clinical trials have revealed significant variability in the response to gefitinib, with higher responses seen in Japanese patients than in a predominantly European-derived population (27.5% vs. 10.4%, in a multi-institutional phase II trial) (12). In the U.S., partial clinical responses to gefitinib have been observed most frequently in women, in non-smokers, and in patients with adenocarcinomas (13–15).

To determine whether mutation of receptor tyrosine kinases plays a causal role in NSCLC, we searched for somatic genetic alterations in a set of 119 primary NSCLC tumors, consisting of 58 samples from Nagoya City University Hospital in Japan and 61 from the Brigham and Women's Hospital in Boston, Massachusetts. The tumors included 70 lung adenocarcinomas and 49 other NSCLC tumors from 74 male and 45 female patients, none of whom had documented treatment with gefitinib.

As an initial screen, we amplified and sequenced the exons encoding the activation loops of 47 of the 58 human receptor tyrosine kinase genes (16) (table S1) from genomic DNA from a subset of 58 NSCLC samples including 41 lung adenocarcinomas. Three of the tumors, all lung adenocarcinomas, showed heterozygous missense mutations

in *EGFR* not present in the DNA from normal lung tissue from the same patients (table S2; S0361, S0388, S0389). No mutations were detected in amplicons from other receptor tyrosine kinase genes. All three tumors had the same *EGFR* mutation, predicted to change leucine 858 to arginine (Fig. 1A; CTG→CGG; L858R).

We next examined exons 2 through 25 of *EGFR* in the complete collection of 119 NSCLC tumors. Exon sequencing of genomic DNA revealed missense and deletion mutations of *EGFR* in a total of 16 tumors, all within exons 18 through 21 of the kinase domain. All sequence alterations in this group were heterozygous in the tumor DNA; in each case, paired normal lung tissue from the same patient showed wild-type sequence, confirming that the mutations are somatic in origin. The distribution of nucleotide and protein sequence alterations, and the patient characteristics associated with these abnormalities, are summarized in table S2. Substitution mutations G719S and L858R were detected in two and three tumors, respectively. These mutations are located in the GXGXXG motif of the nucleotide triphosphate binding domain or P-loop and adjacent to the highly conserved DFG motif in the activation loop (17), respectively. The mutated residues are nearly invariant in all protein kinases and the analogous residues (G463 and L596) in the B-Raf protein serine-threonine kinase are somatically mutated in colorectal, ovarian and lung carcinomas (5, 18) (Fig. 1A, B).

We also detected multiple deletion mutations clustered in the region spanning codons 746 to 759 within the kinase domain of EGFR. Ten tumors carried one of two overlapping 15-nucleotide deletions eliminating *EGFR* codons 746 to 750, starting at either nucleotide 2235 or 2236 (Del-1; Fig. 1C; table S2). *EGFR* DNA from another tumor displayed a heterozygous 24-nucleotide gap leading to the deletion of codons 752 to 759 (Del-2; Fig. 1C). Representative chromatograms are shown in fig. S1.

The positions of the substitution mutations and the Del-1 deletion in the three-dimensional structure of the active form of the EGFR kinase domain (19) are shown in Fig. 2. Note that the sequence alterations cluster around the active site of the kinase, and that the substitution mutations lie in the activation loop and glycine-rich P-loop, structural elements known to be important for autoregulation in many protein kinases (17).

The *EGFR* mutations show a striking correlation with patient characteristics. Mutations were more frequent in adenocarcinomas (15/70 or 21%) than in other NSCLCs (1/49 or 2%); more frequent in women (9/45 or 20%) than in men (7/74 or 9%), and more frequent in the patients from Japan (15/58 or 26%, and 14/41 adenocarcinomas or 32%) than in those from the U.S. (1/61 or 2%, and 1/29 adenocarcinomas or 3%). The highest fraction of *EGFR* mutations was

observed in Japanese women with adenocarcinoma (8/14 or 57%). Notably, the patient characteristics that correlate with the presence of *EGFR* mutations are those that correlate with clinical response to gefitinib treatment.

To investigate whether *EGFR* mutations might be a determinant of gefitinib sensitivity, pre-treatment NSCLC samples were obtained from 5 patients who responded and 4 patients who progressed during treatment with gefitinib out of more than 125 patients treated at the Dana Farber Cancer Institute either on an expanded access program or after regulatory approval of gefitinib (13). Four of the patients had partial radiographic responses ( $\geq 50\%$  tumor regression in a CT scan after 2 months of treatment) while the fifth patient experienced dramatic symptomatic improvement in less than two months. All of the patients were from the United States and were Caucasian.

While sequencing of the kinase domain (exons 18 through 24) revealed no mutations in tumors from the four patients who progressed on gefitinib, all five tumors from gefitinib-responsive patients harbored *EGFR* kinase domain mutations. The chi-squared test revealed the difference in *EGFR* mutation frequency between gefitinib responders (5/5) and non-responders (0/4) to be statistically significant with  $p = 0.0027$ , while the difference between the gefitinib-responders and unselected U.S. NSCLC patients (5/5 vs. 1/61) was also significant with  $p < 10^{-12}$  (20). The *EGFR* L858R mutation, previously observed in the unselected tumors, was identified in one gefitinib-sensitive lung adenocarcinoma (Fig. 1A; table S3, IR3T). Three gefitinib-sensitive tumors contained heterozygous in-frame deletions (Fig. 1C and table S3, Del-3 in two cases and Del-4 in one) and one contained a homozygous in-frame deletion (Fig. 1C and table S3, Del-5). Each of these deletions was found within codons 746 to 753 of *EGFR* where deletions were also found in unselected tumors. Each of these three deletions is also associated with an amino acid substitution (table S3). In all four samples where matched normal tissue was available, these mutations were confirmed as somatic.

To determine whether mutations in *EGFR* confer gefitinib sensitivity in vitro, the mutation status and response to gefitinib were determined in four lung adenocarcinoma and bronchioloalveolar carcinoma cell lines. The H3255 cell line was originally derived from a malignant pleural effusion from a Caucasian female non-smoker with lung adenocarcinoma (21). This cell line was 50-fold more sensitive to gefitinib than the other lines with an IC<sub>50</sub> of 40 nM for cell survival in a 72-hour assay (Fig. 3A).

Treatment with 100 nM gefitinib completely inhibited EGFR autophosphorylation in H3255 (Fig. 3B). Such treatment also inhibited the phosphorylation of known downstream targets of EGFR such as the extracellular signal-regulated kinase 1/2 (ERK1/2) and the v-akt murine thymoma

viral oncogene homolog (AKT kinase) (Fig. 3B), a correlation that has been noted by others (22). In contrast, the other three cell lines showed comparable levels of inhibition of target protein phosphorylation only when gefitinib was present at roughly 100-fold higher concentrations (Fig. 3B).

The sequence analysis of *EGFR* cDNA in these four cell lines showed the L858R mutations in H3255 (table S3), while the other three cell lines did not contain *EGFR* mutations. We also confirmed the presence of the L858R mutation in the primary tumor from which H3255 was derived (table S3, IRG), though no matched normal tissue was available. The results suggest that L858R mutant EGFR is particularly sensitive to inhibition by gefitinib compared to the wild-type enzyme and that this likely accounts for the extraordinary drug sensitivity of the H3255 cell line.

The identification of *EGFR* mutations in a subset of human lung carcinomas and the association between *EGFR* mutation and gefitinib sensitivity extend the emerging paradigm whereby genetic alterations in specific kinases, and not simply kinase expression, render tumors sensitive to selective inhibitors as is the case for imatinib treatment of *c-kit* mutant gastrointestinal stromal tumors (23). Thus although randomized trials of cytotoxic therapy with or without gefitinib revealed no survival benefit for the gefitinib-treated NSCLC patients (24, 25), our current data suggest that gefitinib may be particularly effective for treating lung cancers with somatic *EGFR* mutations and that prospective clinical trials of EGFR inhibition in patients with *EGFR* mutations might reveal increased patient survival. Identification of *EGFR* mutations in other malignancies, perhaps including glioblastomas in which *EGFR* alterations are already known (26), may identify other patients who could similarly benefit from treatment with EGFR inhibitors. Important questions remain to be answered including whether these alterations result in activated and transforming alleles of *EGFR*, whether receptors harboring such mutations will show differential sensitivity to any of the multiple EGFR small molecule inhibitors, and whether EGFR receptors harboring such mutations are inhibited by antibodies directed against the extracellular domain. Furthermore, it will be of interest to determine whether resistance to EGFR inhibition emerges through secondary mutation as is the case in imatinib-treated chronic myelogenous leukemia (27). These results should stimulate further in vitro studies regarding these questions. Finally, the striking differences in the frequency of *EGFR* mutation and response to gefitinib between Japanese and U.S. patients raise general questions regarding variation in the molecular pathogenesis of cancer in different ethnic, cultural and geographic groups and argue for the benefit of population diversity in cancer clinical trials.

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20. Note that the frequency of EGFR mutation in the unselected U.S. patients, 1 of 61, appears to be low when compared to the frequency of reported gefitinib response at 10.4%. This difference has a modest statistical significance ( $p = 0.025$  by the chi-squared test). Thus this result could still be due to chance, could be due to a fraction of responders who do not have EGFR mutations, or could be due to failure to detect EGFR mutations experimentally in this tumor collection. If the frequency of EGFR mutation in gefitinib-responsive U.S. patients (5/5) is compared to the expected frequency of gefitinib response (10.4%), the chi-squared probability is again less than 10<sup>-12</sup>.
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### Supporting Online Material

[www.sciencemag.org/cgi/content/full/1099314/DC1](http://www.sciencemag.org/cgi/content/full/1099314/DC1)

Materials and Methods

Fig. S1

Tables S1 to S4

References

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**Fig. 1.** Sequence alignment of selected regions within the EGFR and B-Raf kinase domains. Depiction of each type of EGFR mutation in human NSCLC. EGFR (gb:X00588) mutations in NSCLC tumors are highlighted in yellow. B-Raf (gb:M95712) mutations in multiple tumor types (5) are highlighted in blue. Asterisks denote residues conserved between EGFR and B-Raf. (A) L858R mutations in activation loop. (B) G719S mutant in P-loop. (C) Deletion mutants in EGFR exon 19.

**Fig. 2:** Positions of missense mutations G719S and L858R and the Del-1 deletion in the three-dimensional structure of the EGFR kinase domain. The activation loop is shown in yellow, the P-loop is in blue and the C-lobe and N-lobe are as indicated. The residues targeted by mutation or deletion are highlighted in red. The Del-1 mutation targets the residues ELREA in codons 746 to 750.

**Fig. 3.** A lung adenocarcinoma cell line with EGFR receptor mutation is sensitive to growth and signaling inhibition by gefitinib. (A) Cells were treated with gefitinib at the indicated concentrations and viable cells measured after 72 hours of treatment. Percentage of cell growth is shown relative to untreated controls. H3255 cells have the EGFR L858R mutation while the three remaining cell lines have wild-type EGFR (WT). (B) Inhibition of EGFR phosphorylation and of downstream phosphorylation of Akt and Erk1/2. The cell lines were treated with gefitinib for 24 hours. Cell extracts were immunoblotted to detect the indicated protein species. Akt, v-akt murine thymoma viral oncogene homolog; Erk, extracellular signal-responsive kinase.

A

                                  activation loop  
L858R  KTPQHVKITDFGR**AK**LLGAEKEYH  870  
EGFR   KTPQHVKITDFGLAKLLGAEKEYH  870  
BRAF   H**E**DLTVKIGD**FGLATV**KSRWSGS HQ  608  
                                  \*\*\*  \*\*\*\*\*

B

                                  P-loop  
G719S  E~~TE~~FKKIKVL**SS**GAFGTVYKGLWIP  733  
EGFR   E~~TE~~FKKIKVLGSGAFGTVYKGLWIP  733  
BRAF   DGQITVGQRI**GS**S**F**GTVYK**G**KWHG  477  
                                  \*\*\*  \*\*\*\*\*  \*

C

Del-1  VAIK~~-----~~T-SPKANKEILDEAYV  765  
Del-2  VAIKELREAT-~~-----~~LDEAYV  765  
Del-3  VAIKE~~---~~PT-SPKANKEILDEAYV  765  
Del-4  VAIKE~~-----~~**S**KANKEILDEAYV  765  
Del-5  VAIKV~~-----~~**S**PKANKEILDEAYV  765  
EGFR   VAIKELREAT-SPKANKEILDEAYV  765  
BRAF   VAVKMLNVTAPT**P**QQLQAFKNEVG**V**  503  
                                  \*\*  \*                                  \*  \*





