

Epidermal Growth Factor Receptor Mutations in Patients with Non–Small Cell Lung Cancer

Bruce E. Johnson and Pasi A. Jänne

Lowe Center for Thoracic Oncology, Department of Medical Oncology, Dana-Farber Cancer Institute and Department of Medicine, Brigham and Women's Hospital, and Harvard Medical School, Boston, Massachusetts

Abstract

A year has passed since mutations of the tyrosine kinase domain of the epidermal growth factor receptor (EGFR) were discovered in patients with non–small cell lung cancer (NSCLC) who had dramatic clinical responses to treatment with gefitinib. Additional laboratory and clinical studies have provided further insight into the biological impact of EGFR mutations in cell culture experiments and in patients with NSCLC. *In vitro* characterizations of NSCLC cell lines and host cell lines transfected with these mutant and wild-type EGFR show that most cell lines with mutated EGFR are growth-inhibited by 10- to 100-fold lower concentrations of gefitinib and erlotinib compared with wild-type EGFR. NSCLC lines with mutations of the EGFR treated with concentrations of gefitinib and erlotinib that are achievable in the plasma undergo apoptosis rather than growth arrest. Retrospective studies of patients with NSCLC-treated gefitinib have reported a close association between EGFR mutations, increased chance of clinical response and longer survival. This review will provide information on the impact of EGFR mutations on gefitinib and erlotinib treatment by *in vitro* experiments, the outcome of NSCLC patients with these mutations when treated with gefitinib and erlotinib, and the subsets of patients with NSCLC in whom these mutations arise. (Cancer Res 2005; 65(17): 7525-9)

Background

The epidermal growth factor receptor (EGFR) is detected by immunohistochemistry on 40% to 80% of non–small cell lung cancers (NSCLC; ref. 1, 2). This prompted multiple pharmaceutical companies to develop small molecule inhibitors of the tyrosine kinase domain of the wild-type EGFR during the 1990s (3, 4). Two therapeutic agents, gefitinib and erlotinib, have been extensively studied in patients with NSCLC and are approved by the Food and Drug Administration for treatment of patients with relapsed NSCLC in the U.S. (4). The initial testing of gefitinib and erlotinib in phase II trials showed that ~10% of patients of European background and 30% of patients from Japan had clinical responses when treated with the EGFR inhibitors, gefitinib and erlotinib (5–7). The clinical characteristics that are associated with responses to gefitinib and erlotinib were defined in these studies (5–7). Clinical responses to these agents were more common in women than men, in patients from Japan than from Europe and the

U.S., patients with adenocarcinoma than other histologic subtypes, and patients who had never smoked cigarettes.

Studies of another solid tumor, gastrointestinal stromal tumor, showed that activating mutations of the *C-KIT* gene were associated with clinical responses to the small molecule inhibitor of the tyrosine kinase domain of the *C-KIT* gene, imatinib (8). This led multiple groups to identify patients with NSCLC and dramatic clinical responses following treatment with gefitinib and erlotinib for sequencing of the tyrosine kinase domain of *EGFR* in their tumor.

Therapeutic Impact of EGFR Mutations

The association between somatic mutations of *EGFR* and dramatic clinical response to gefitinib was reported online in April of 2004, with the two articles being published in May and June of 2004, respectively (1, 9). Thirteen of the 14 patients with a clinical response to gefitinib therapy had somatic mutations of the *EGFR* identified, whereas all 11 patients whose tumors did not respond to gefitinib treatment had a somatic wild-type *EGFR* sequence. These mutations were all in the tyrosine kinase domain of the *EGFR*. Research in the past year has shown that these mutations in NSCLC are associated with *in vitro* sensitivity to treatment with gefitinib and erlotinib, transfection of the mutant epidermal growth factor gene into host cell lines confers sensitivity to gefitinib and erlotinib, and mutations of the *EGFR* gene are common in patients with dramatic clinical responses to gefitinib and erlotinib. Research from other groups has identified candidate factors other than *EGFR* mutations that may be involved in determining response to gefitinib and erlotinib, including increased *EGFR* copy number and *K-ras* mutations (10, 11). However, the published information on these two genomic markers is limited at the current time, so we are going to restrict our comments to *EGFR* mutations in this review.

The *in vitro* studies of NSCLC cell lines and host cell lines transfected with different mutations of the *EGFR* have provided important insights into how the mutations activate the tyrosine kinase domain of *EGFR* and the dramatic impact gefitinib and erlotinib have on EGFR signaling (1, 2, 9, 12, 13). EGFR is constitutively activated as assessed by phosphorylation of the different tyrosine residues on EGFR, the downstream pathways are activated, and gefitinib and erlotinib inhibit both this signaling and the growth of the NSCLC cells (Fig. 1). Investigators have identified six cell lines with deletions and mutations of *EGFR* that are sensitive to treatment with gefitinib and erlotinib (2, 12–15). These include PC-9, HCC-827, NCI-H1650, NCI-H1975, NCI-H3255, and DFCILU-011. Four NSCLC cell lines have deletions of exon 19 (PC-9, H1650, HCC827, and DFCILU-011) and two have point mutations of exon 21 (NCI-H1975 and NCI-H3255). The IC₅₀ of these six NSCLC lines range from 20 to 200 nmol/L of gefitinib when assessed in dye conversion assays.

Requests for reprints: Bruce E. Johnson, Department of Medical Oncology, Dana-Farber Cancer Institute, 44 Binney Street, Boston, MA 02115. Phone: 617-632-4790; Fax: 617-632-5786; E-mail: BEJohnson@Partners.org.

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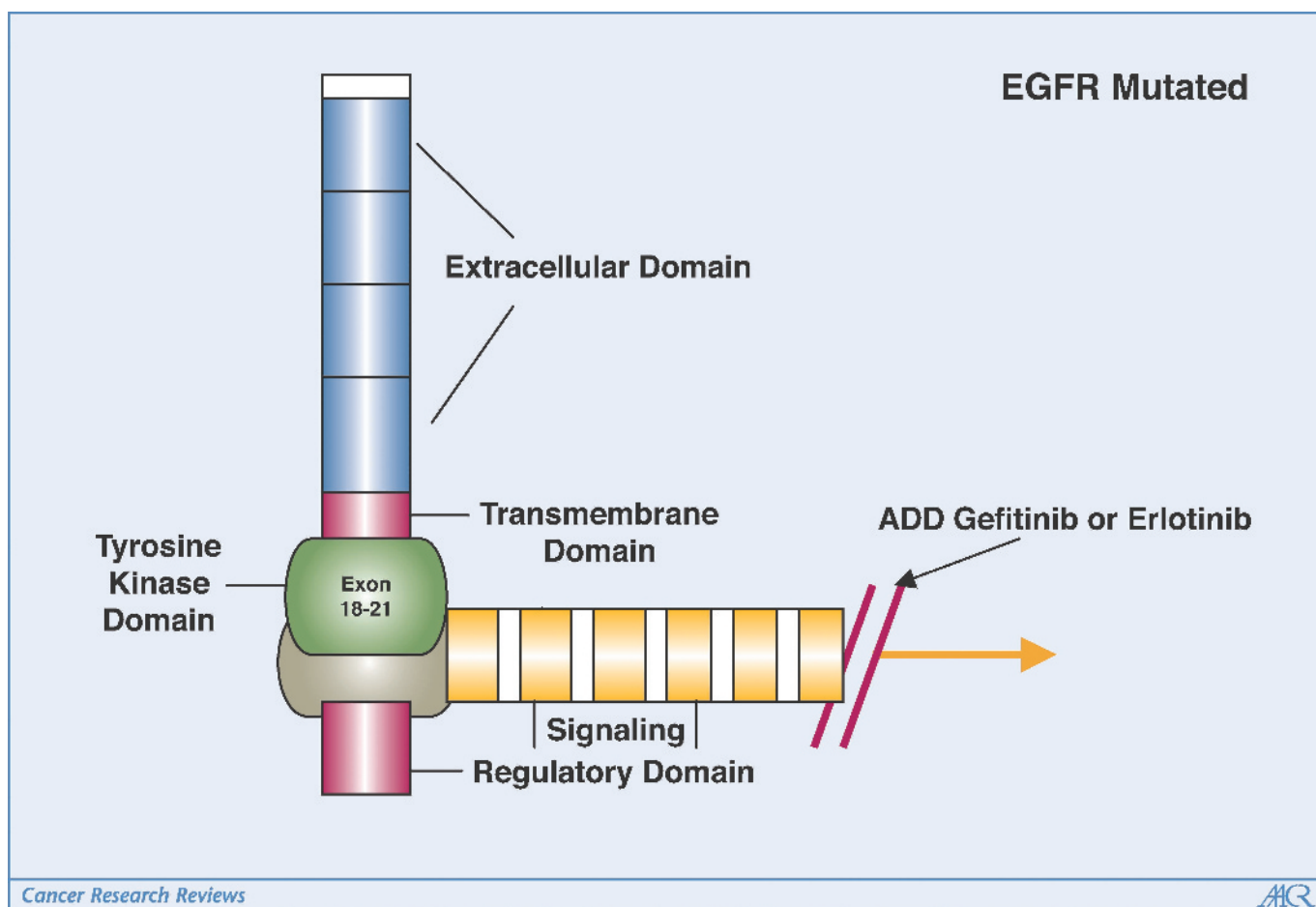


Figure 1. The mutated EGFR is constitutively activated and sends augmented intracellular signals stimulating the growth rate of the NSCLC cells. The augmented growth signal is dramatically inhibited by the addition of gefitinib and erlotinib represented by the broad band emerging from the receptor. The dramatic decrease in the growth signal caused by gefitinib and erlotinib is represented by the marked decrease in the width of the band.

Three cell lines with wild-type EGFR have intermediate sensitivities (NCI-1819, NCI-H1666, and Calu-3) with IC_{50} 's between 1 and 5 $\mu\text{mol/L}$ (2, 13, 15). Most other NSCLC cell lines with wild-type EGFR require concentrations of gefitinib >10 $\mu\text{mol/L}$ to inhibit their growth, >10-fold the achievable plasma concentrations in patients (2, 4, 13).

The cell lines with mutant EGFR are more likely to have activated EGFR as assessed by phosphospecific antibodies of the intracellular phosphorylated kinase domains. The phosphorylation of EGFR in these cell lines with mutant EGFR is inhibited by low concentrations of gefitinib and erlotinib (10-100 nmol/L). The signaling pathways downstream from EGFR, pERK and pAKT, are inhibited by these same low concentrations of 10 to 100 nmol/L of gefitinib as well (2, 9, 12, 13). Treatment of cell lines with an EGFR point mutation in exon 21 (NCI-H3255) and a deletion mutant in exon 19 (HCC-827) with 100 nmol/L to 1 $\mu\text{mol/L}$ gefitinib or erlotinib leads to apoptosis as assessed by the sub- G_1 fractions on flow cytometry studies and by activation of the caspase pathway (2, 13).

The ability of the mutant EGFR to mediate changes in growth and signaling have been verified by transfection experiments into multiple cell systems. The mutant and wild-type EGFR have been transfected into different host cells including NMuMg, COS-7, Chinese hamster ovary cells, and HEK293 cells to determine

differences in biochemical signaling and growth (1, 2, 12, 14, 15). The growth and downstream signaling inhibition of the host cell lines transfected with mutant EGFR are consistently more sensitive to treatment with gefitinib and erlotinib than cells with wild-type receptors. The wild-type EGFR receptor typically sends a downstream signal that ultimately stimulates the growth of the NSCLC cells that are dependent on the receptor and gefitinib or erlotinib can modestly inhibit this relatively weak signal (Fig. 2). The mutated EGFR receptor is constitutively activated with a prominent downstream signal that can be dramatically inhibited by gefitinib and erlotinib.

The *in vitro* sensitivity of EGFR mutant NSCLC cell lines also has a clinical correlate because the association between EGFR mutations and clinical response to gefitinib and erlotinib has subsequently been documented around the world. Reports from other institutions in the U.S., Japan, Taiwan, and Korea have confirmed that 70 of the 91 of patients (77%) with clinical responses to gefitinib and erlotinib have detectable mutations of the EGFR (1, 9, 11, 16-19). In contrast, only 10 of 133 patients (8%) with stable or progressive disease after treatment with gefitinib or erlotinib have a somatic EGFR mutation (1, 9, 11, 16-19). In addition to the differences observed in the response rates, the patients who have somatic mutations of EGFR are likely to live longer than patients with wild-type EGFR when treated with

gefitinib. Three different studies of 170 patients from Japan and Korea have provided Kaplan-Meier survival curves of patients treated with gefitinib whose tumors have undergone EGFR sequencing (16, 18, 19). The 59 patients with NSCLC with somatic mutations of *EGFR* treated with gefitinib had median survivals in excess of 2 years compared with median survivals of 7 to 14 months for the 111 patients with wild-type *EGFR*.

The types of *EGFR* mutations in patients treated with gefitinib and erlotinib have been similar around the world (1, 9, 11, 16–19). The mutations involve multiple overlapping deletion mutations of exon 19 in 45% of patients, missense mutations in exon 21 in 40% of patients (predominately L858R), and missense or insertion mutations in exons 18 to 21 in the other 15% of patients. There is no clear difference in the mutational pattern in the tumors from patients of European background versus those from East Asia. There is not yet enough information to make firm conclusions about the efficacy of gefitinib and erlotinib treatment in patients with NSCLC as a function of their different types of mutations of *EGFR*.

The *EGFR* sequence has been characterized in large numbers of patients with early stage NSCLC that have not been treated with gefitinib or erlotinib. There have been three large studies sequencing >1,600 resected NSCLCs from patients in the U.S., Europe, and East Asia that provide potential explanations about

differences between the response rates of 5% to 10% in patients from the U.S. and Europe versus the response rates of 20% to 30% in patients from East Asia (20–22). The mutations involve deletion mutations of exon 19 in ~50% of patients, missense mutations in exon 21 in 40%, and mutations in exons 18 and 20 in the other 10%. The clinical characteristics of patients with mutations of *EGFR* closely parallel the subsets of patients who are more likely to respond to treatment with gefitinib and erlotinib. The patients with NSCLC from the U.S., Europe, and Australia have an *EGFR* somatic mutation frequency of ~10% compared with a mutation rate of 30% in patients from Japan and Taiwan. There is also a close association between adenocarcinoma and mutations in the *EGFR*. The three studies showed that 263 of 888 patients with adenocarcinomas (30%) had mutations detected, whereas 7 of 764 patients with other types of NSCLC (1%) had a somatic mutation of *EGFR* (20–22). The somatic mutations of *EGFR* were also two to three times more likely in women than men and three to five times more likely in nonsmokers than those who were current or former smokers. The findings clearly mirror the increased response rates in these same patient populations when treated with gefitinib and erlotinib.

Despite the observation that patients with NSCLC and somatic mutations of *EGFR* treated with gefitinib live longer than patients whose NSCLC have wild-type *EGFR* with similar

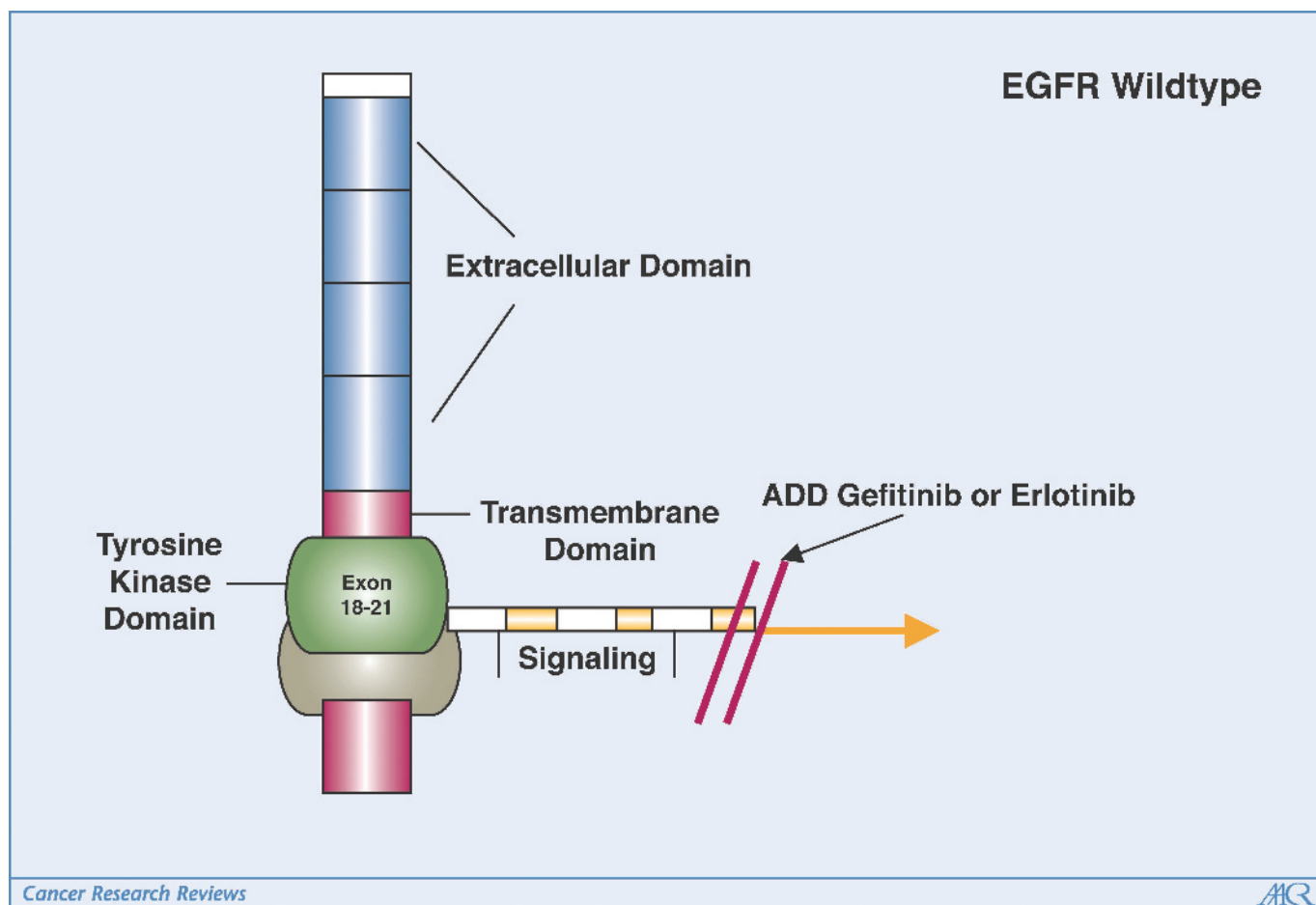


Figure 2. The wild-type EGFR is activated by an agonist, undergoes dimerization, and sends intracellular signals to increase the growth rate of the NSCLC cells. The modest growth signal is inhibited by the addition of gefitinib and erlotinib represented by the band emerging from the receptor. The diminution in the growth signal caused by gefitinib and erlotinib is represented by the modest decrease in the width of the band before and after addition of these drugs.

Table 1. The current state of knowledge of *EGFR* mutations in patients with NSCLC

Known	Unknown
<i>EGFR</i> mutations are associated with responses to gefitinib and erlotinib	The etiology of the <i>EGFR</i> mutations
<i>EGFR</i> mutations are somatic	The relative oncogenic properties of the different <i>EGFR</i> mutations
<i>EGFR</i> mutations are more common in women, nonsmokers, in adenocarcinomas, and East Asians	The outcome of patients with different <i>EGFR</i> mutation treated with different EGFR-TKIs
Secondary <i>EGFR</i> mutations are associated with resistance to gefitinib and erlotinib in patients and <i>in vitro</i>	The mechanisms of resistance to gefitinib and erlotinib in the patients who do not have the identified T790M secondary <i>EGFR</i> mutation

treatment, the *EGFR* status does not seem to have a dramatic impact on the outcome of early stage patients. The patients with early stage lung cancer who undergo surgical resection of their NSCLC with somatic mutations of the *EGFR* have a similar survival compared with those with wild-type receptor (22). The Kaplan-Meier survival curves of the patients with resected NSCLC showed that >80% of the patients with somatic mutations of *EGFR* (91) and those with wild-type *EGFR* (145) were alive at 3 years.

Acquired Resistance to EGFR Inhibitors

Despite the therapeutic success of EGFR-TKIs in NSCLC patients with *EGFR* mutations, the majority of such patients will ultimately develop disease progression. The mechanism of acquired resistance to gefitinib is beginning to be understood. Three recent studies reported nine patients who had a clinical and radiographic response to gefitinib or erlotinib and had EGFR mutations documented in their initial tumor. These nine patients then developed progressive NSCLC on gefitinib or erlotinib therapy underwent repeat biopsy of their tumor, and then sequencing of *EGFR* (23–25). Six of the nine patients had a secondary mutation in addition to the initial *EGFR* mutation, a substitution of a methionine for a threonine at position 790 (T790M). Structural modeling suggests that the bulkier methionine residue creates a steric hindrance preventing gefitinib or erlotinib from binding to the ATP binding pocket of the EGFR. Furthermore, biochemical studies show that in the presence of T790M *EGFR* mutation, gefitinib is no longer able to inhibit the phosphorylation of either wild-type or mutated EGFR. However, other irreversible EGFR inhibitors still retain inhibitory activity, suggesting that a further understanding of the structure/function relationship of mutated *EGFR* and EGFR inhibitors (23, 24). This may ultimately identify second-generation EGFR TKIs that could be used in patients who develop an acquired T790M mutation and lead to sequencing tumors from patients who relapse after successful treatment with an EGFR-TKI.

Meaning and Implications of Mutations of the EGFR

The therapeutic efficacy of conventional combination chemotherapy for previously untreated patients with advanced NSCLC offers a modest 20% response rate, a 2- to 4-month prolongation of survival, and a median survival of 8 to 10 months (26, 27). The identification of a subset of patients with adenocarcinoma with mutations in the *EGFR* has provided a therapeutic alternative to the consistently modest results with chemotherapy. Previous therapeutic studies of patients with advanced NSCLC have not

divided patients by histologic subtypes (adenocarcinoma, squamous cell carcinoma, and others) but have lumped 85% of the lung cancers into NSCLC. The patients with adenocarcinoma of the lung and nonsmokers are more likely to have a response to gefitinib or erlotinib treatment and these responses are associated with the presence of a somatic mutation of *EGFR* in ~80% of the patients. This may provide a rationale for selecting patients with specific histologies (adenocarcinoma) and smoking status as candidates for clinical trials with EGFR inhibitors, a new concept in the treatment of NSCLC. The retrospective collection of information shows that patients with NSCLC and *EGFR* mutations have a clinical response rate of ~80%, can be treated for at least a year, and have at least a 2-year median survival after the start of treatment. Prospective clinical trials for patients with NSCLC are ongoing to prospectively assess the impact of giving gefitinib or erlotinib to previously untreated patients with NSCLC and mutations in the *EGFR*. If these retrospective observations are confirmed in prospective trials, patients with NSCLC who have a mutation identified in their *EGFR* will likely be offered an EGFR inhibitor as their initial therapy for NSCLC. The prospect of being able to treat a subset of patients (10-30% of the population of NSCLC) with gefitinib or erlotinib for a median of a year or more with the expectation of a median survival of ≥ 2 years has the potential to dramatically improve the outcome for this subgroup of patients. Clinical trials will also be needed to determine if patients with NSCLC and mutations of the *EGFR* need to be treated with erlotinib or gefitinib alone or if there is an advantage to adding chemotherapy to their regimen.

The discovery of the association between *EGFR* mutations and the response to gefitinib and erlotinib has transformed NSCLC from one disease treated with conventional combination chemotherapy to subsets of NSCLC identified by genomic studies. Patients with NSCLC and *EGFR* mutations can be effectively treated with gefitinib and erlotinib. Although many aspects of EGFR mutations have been characterized, several unknown questions remain (Table 1). The information on the association between *EGFR* mutations and response to gefitinib and erlotinib has now been available for more than a year. The answers to the remaining important questions will come from additional well-conducted ongoing and planned preclinical and clinical studies of patients and NSCLC cell lines with wild-type and mutated *EGFR* treated with EGFR inhibitors.

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