Low-Dose Gefitinib Treatment for Patients with Advanced Non-small Cell Lung Cancer Harboring Sensitive Epidermal Growth Factor Receptor Mutations

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Introduction: Although standard schedule of gefitinib was the administration of 250 mg tablet every day, many patients need dose reduction because of toxicities. However, the efficacy of such low-dose gefitinib for patients with epidermal growth factor receptor-mutated non-small cell lung cancer has rarely been evaluated.

Methods: A post hoc comparison of the efficacy (response rate and survival) in patients treated with gefitinib with or without any dose reduction in NEJ002 study was performed.

Results: Among 114 patients treated with first-line gefitinib in NEJ002, 61 (54%) continued gefitinib without any dose reduction until their diseases progressed, and 53 (46%) reduced their dose of gefitinib because of some toxicities. There was no significant difference of patient characteristics between the two groups. The progression-free survival of low-dose group tended to be better than that of standard-dose group (median progression-free survival, 11.8 versus 9.9 months; $p = 0.144$), and the overall survival of low-dose group was also better than that of standard-dose group (median survival time, 32.7 versus 25.3 months; $p = 0.049$).

Conclusions: The results suggest that low-dose gefitinib may be clinically not inferior to standard-dose gefitinib for non-small cell lung cancer with sensitive epidermal growth factor receptor mutations. Prospective study of low-dose gefitinib is warranted especially for frail patients who need less toxic treatment.

Key Words: Gefitinib, EGFR mutation, Low-dose, Post hoc analysis.

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Cytotoxic chemotherapy such as carboplatin (CBDCA) plus paclitaxel (PTX) had been the standard first-line treatment for advanced non-small cell lung cancer (NSCLC) patients for a long time; however, its efficacy had already reached a plateau in early 2000s, and better treatment strategies have been eagerly anticipated.[1,2] Gefitinib is the first molecular-targeted agent for NSCLC and is classified as a tyrosine kinase inhibitor of the epidermal growth factor receptor (EGFR-TKI).[3] Although gefitinib was initially approved for the entire NSCLC population, pivotal studies published in 2004 had revealed that the presence of somatic mutations in the kinase domain of EGFR strongly correlates with an increased responsiveness to EGFR-TKI.[4,5] Biomarker analysis performed in Iressa Pan-Asia Study, in which efficacy of gefitinib and CBDCA/PTX was compared as the first-line treatment for NSCLC patients with favorable clinical characteristics including adenocarcinoma and nonsmoking history, showed a significant superiority of gefitinib in progression-free survival (PFS) in the subset analysis for NSCLC with mutated EGFR.[6] Recently, we prospectively demonstrated in NEJ002 phase 3 study that the first-line gefitinib exhibited a significantly longer PFS than CBDCA/PTX in patients with advanced NSCLC with mutated EGFR.[7] According to these results, EGFR-TKI has become one of the

standard treatments for advanced NSCLC with mutated EGFR.

A standard dosage of gefitinib is 250 mg, which is administered every day. Nevertheless, not a few patients need a dose reduction of gefitinib due to toxicities including rash, diarrhea, or liver dysfunction. Because the tablet of gefitinib cannot be divided in half, the dose reduction is usually achieved by changing the interval of taking the tablet from every day to every 2 days. However, clinical evidence of such reduced dose of gefitinib is scanty. According to some preclinical data, lung cancer cell harboring sensitive EGFR mutation are much more sensitive to EGFR-TKI than those with wild-type EGFR.[4] Therefore, we hypothesized that selected patients on the basis of EGFR mutations might sufficiently and safely benefit from such "low-dose" gefitinib. The aim of this post hoc analysis from NEJ002 is to examine the efficacy of low-dose gefitinib compared with that of standard-dose gefitinib in EGFR-mutated NSCLC patients.

METHODS

Patient Population

We retrospectively analyzed the 114 patients treated with gefitinib in NEJ002 study, which is a multicenter, randomized, phase 3 trial that compared gefitinib with CBDCA/TXL as the first-line treatment for advanced NSCLC harboring sensitive EGFR mutations. Eligibility criteria of NEJ002 included the presence of advanced NSCLC harboring sensitive EGFR mutations without the resistant EGFR mutation T790M examined by PNA-LNA polymerase chain reaction clamp method,[8] no history of chemotherapy, an age of 75 years or younger, performance status 0 to 1, appropriate organ functions, and written informed consent.

Treatment with Gefitinib

All the patients initially received 250 mg of gefitinib everyday according to the protocol of NEJ002. In NEJ002, a temporary cessation of the drug administration was recommended by the protocol when an intolerable toxicity such as grade 3 or worse adverse event was observed during the treatment with the standard dose, and a dose reduction of gefitinib by changing the everyday schedule to every 2 days schedule was permitted when grade 2 toxicity was observed.

In this analysis, we categorized patients into two groups according to their treatment status as follows: standard-dose group, in which gefitinib was administered without any dose reductions until disease progression was observed, and low-dose group, in which gefitinib was administered with a reduced dose at least once during the treatment period before disease progression (Figure 1).

Clinical Assessments

According to the protocol of NEJ002, the assessment of antitumor response to gefitinib was performed by computed tomography every 2 months until disease progression was observed. Unidirectional measurements were adopted on the basis of the Response Evaluation Criteria in Solid Tumor (RECIST, version 1.0).[9] The PFS was defined as the period from the date of randomization to the date when disease progression was first observed or death occurred. The response and PFS were determined by an external review of the computed tomography films by experts who were not aware of the treatment assignment. Overall survival (OS) was defined as the period from the date of randomization to the date of death.

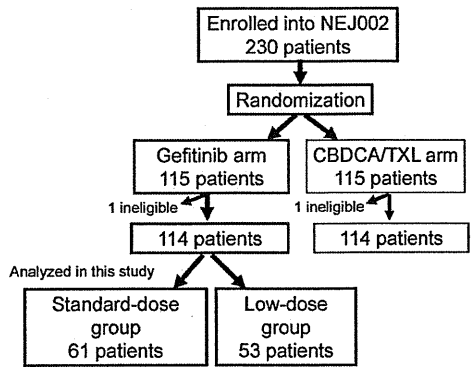

FIGURE 1. Flowchart of the patients analyzed in this study.

Kaplan-Meier survival curves were drawn for PFS and OS, and differences between the groups were compared by log-rank test. The difference in response rate was compared by Fisher's exact test. Each analysis was two-sided, with a 5% significance level and a 95% confidence interval, and was performed using SAS for Windows software (release 9.1, SAS Institute, Cary, NC).

RESULTS

Treatment

The demographics of patients in each group are listed in Table 1. Around half of the patients in NEJ002 were categorized as low-dose group. There was no significant difference in each clinical factor and the type of EGFR mutation between the two groups. Standard-dose group received 250 mg gefitinib for 261 days (median) (Table 2). Nine patients temporarily suspended their treatment (median, 6 days; range, 1–32 days) due to some toxicities but restarted the treatment with standard dose. Low-dose group received 250 mg gefitinib every day for 74 days (median) and then every 2 days for 125 days (median). Before restarting the treatment using a reduced dose, 38 patients needed a break in their treatment (median, 19 days; range, 2–79 days) to recover from adverse events.

At the data cutoff point (early December 2009), 37 patients (61%) in the standard-dose group and 26 patients (49%) in the low-dose group had stopped the first-line gefitinib treatment due to disease progression, while 7 patients (11%) in the standard-dose group and 5 patients (9%) in the low-dose group had terminated the treatment because of treatment-related toxicities such as interstitial lung disease and liver dysfunction.

Efficacy

Low-dose group showed at least not-inferior efficacy (response and survival) compared with standard-dose group.

TABLE 1. Patient Characteristics

	Standard Dose	Low Dose	*p*
No. of patients	61	53	
Sex			
Male	27	15	0.084
Female	34	38	
Mean age (range)	64 (43–75)	64 (47–75)	0.742
Mean body weight (range)	56.2 (41.1–81.6)	54.2 (34.7–93.0)	0.443
Smoking status			
Never smoker	37	38	0.876
Smoker	24	15	
Performance status			
0/1/2	28/33/0	26/26/1	0.824
Histology			
Adenocarcinoma	53	50	0.483
Others	8	3	
Clinical stage			
IIIB	8	7	0.805
IV	46	42	
Postoperative	7	4	
Type of EGFR mutation			
Exon 19 deletion	27	31	
L858R	27	22	
Others	7	0	

TABLE 2. Treatment Pattern with Gefitinib in Each Group

	Standard Dose	Low Dose
Given continuously	*n* = 61	*n* = 53
Mean (SD)	287 d (211)	160 d (197)
Median (range)	261 d (14–790)	74 d (19–1153)
Given intermittently		*n* = 53
Mean (SD)	—	205 d (200)
Median (range)	—	125 d (7–897)
Treatment break period	*n* = 9	*n* = 38
Mean (SD)	13 d (11)	23 d (18)
Median (range)	6 d (1–32)	19 d (2–79)

The response rate and disease control rate were 83% and 98% in the low-dose group and 66% and 82% in standard-dose group, respectively.

PFS for low-dose group tended to be superior to that of standard group, although a statistical significance was not detected. Median PFS and 1-year PFS rate were 11.8 months and 50% in low-dose group and 9.9 months and 36% in standard-dose group, respectively (Figure 2*A*). As some patients in low-dose group had switched to the low dose after a long-term treatment with standard-dose gefitinib, we additionally investigated the efficacy of more "refined" low-dose group (n = 25) who had been treated with gefitinib at standard dose during less than 60 days. The response rate, median PFS, and 1-year PFS rate of the group were 83%, 7.1 months, and 27%, respectively, which was not statistically different from those results of standard-dose group (Figure 2*B*). The OS was significantly longer in low-dose group than standard-dose group (median: 32.7 versus 25.3 months; $p = 0.049$) (Figure 2*C*, Table 3).

DISCUSSION

Recent phase 3 studies including NEJ002 have suggested that EGFR-TKIs are more effective than cytotoxic chemotherapy in the first-line treatment against advanced NSCLC with mutated EGFR.[6,7,10] However, many patients could not continuously receive standard dose of gefitinib because of some adverse effects. In fact, about half of the patients treated with gefitinib in NEJ002 required a dose reduction. Therefore, treatment strategy with less toxicity is required especially for patients with a poor condition or for elderly patients. In this report, we demonstrated that low-dose gefitinib may not be inferior to standard-dose gefitinib for NSCLC patients with EGFR mutations.

Previous reports of EGFR mutations had suggested that NSCLC cell with mutated EGFR was highly sensitive to EGFR-TKI than those without mutations.[5] Recently, Yeo et al.[11] also showed that both erlotinib and gefitinib suppressed the proliferation of EGFR-mutated NSCLC cell lines even at a very low concentration. Moreover, they reported a retrospective observation that patients treated with 25 mg of erlotinib which was equivalent to 250 mg of gefitinib where 5 out of examined 7 patients respond to the "low-dose" erlotinib and median PFS of those patients was 17 months. The current study employed a larger number of patients and supported their results that NSCLC patients with mutated EGFR received a similar level of efficacy from low-dose gefitinib as standard-dose gefitinib. Although low-dose gefitinib in this study are considered to be much less than 25 mg of erlotinib, twice longer half life in plasma and much higher tumor/plasma concentration ratio of gefitinib compared with erlotinib may favor gefitinib.[12–14]

There are some limitations in the current study. Because the study was a retrospective analysis, biases in patient characteristics or undetectable factors may exist and affected the results. From a pharmacokinetics point of view, as mean body weight tended to be lighter in the low-dose group, relatively higher drug concentration might be obtained in those patients even from the low-dose gefitinib. Considering that the OS for low-dose group was significantly longer than that for standard-dose group, the low-dose group might include more patients with slow-growing tumor than standard-dose group incidentally. More importantly, even for the patients in low-dose gefitinib group, the treatment was not initiated with low dose but with standard dose, thus the period with standard-dose gefitinib might affect the efficacy. Although the refined low-dose group still showed a similar efficacy to standard-dose group, its small sample size cannot draw a definite conclusion. To examine the efficacy and safety, and appropriate treatment schedule of low-dose gefitinib (e.g., initial standard dose followed by low dose versus thoroughly low dose), prospective comparative trials should be conducted.

In conclusion, our retrospective analysis suggests that low-dose gefitinib may be clinically equivalent to standard treatment with gefitinib for NSCLC with sensitive

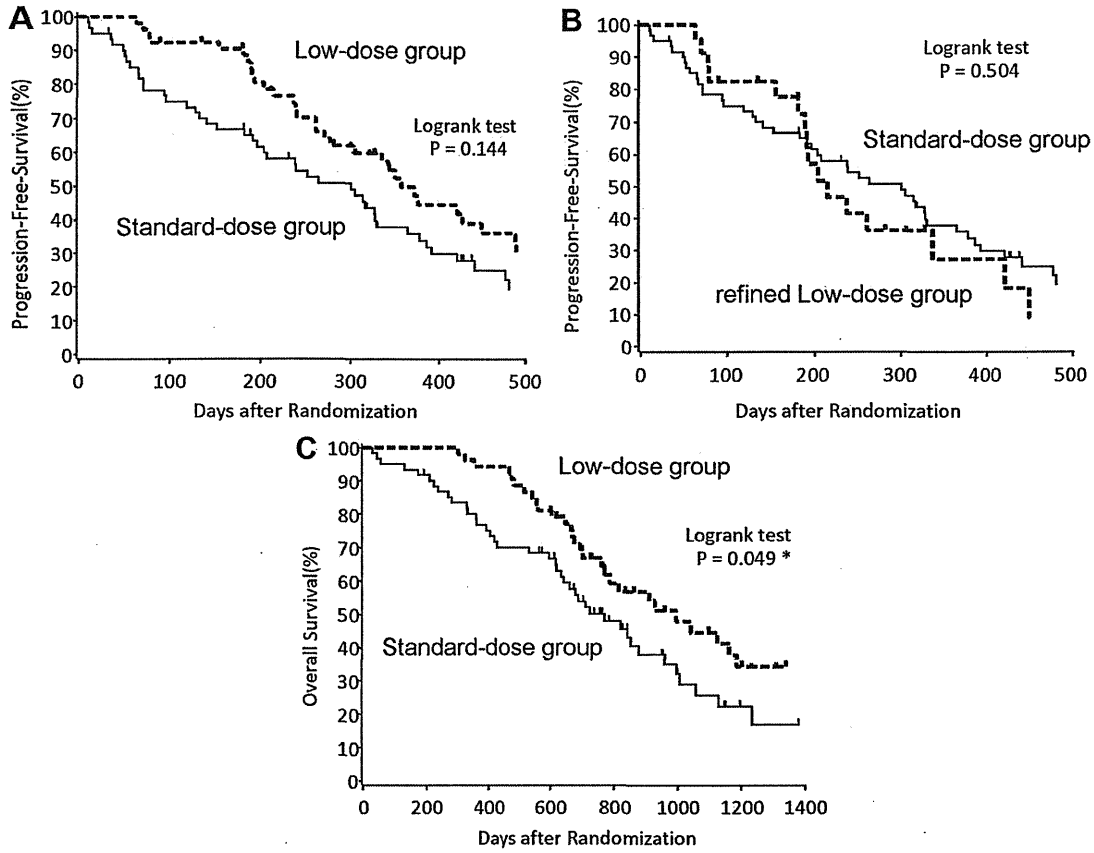

FIGURE 2. Progression-free survival curve of standard-dose group (solid line) and low-dose group (dotted line) with entire population (*A*) and another comparison of progression-free survival between standard-dose group and refined low-dose group (*B*). Overall survival curve of each group (*C*).

TABLE 3. Response and Survival

	Standard Dose	Low Dose	*p*
Overall response rate	66%	83%	0.005
95% CI	52–77	70–92	
Progression-free survival			
Median	9.9 mo	11.8 mo	0.144
1-yr PFS rate	36%	50%	
Overall survival			
Median	25.3 mo	32.7 mo	0.049
2-yr survival rate	50%	67%	

CI, confidence interval; PFS, progression-free survival.

EGFR mutations. Considering the merit of low-dose gefitinib in terms of risk-benefit balance, prospective studies using low-dose gefitinib is warranted targeting NSCLC patients with mutated EGFR, especially elderly or those with poor PS.

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Phase II Study of Gefitinib Readministration in Patients with Advanced Non-Small Cell Lung Cancer and Previous Response to Gefitinib

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Key Words
Epidermal growth factor receptor · Epidermal growth factor receptor-tyrosine kinase inhibitor · Gefitinib · Non-small cell lung cancer · Chemotherapy

Abstract
Objective: Salvage treatment for acquired resistance to gefitinib has yet to be developed. We conducted the first prospective phase II study of gefitinib readministration in previous gefitinib responders. ***Methods:*** Gefitinib (250 mg/day) was readministered to patients with advanced/metastatic non-small cell lung cancer who had achieved objective response to initial gefitinib and subsequently received cytotoxic chemotherapy after disease progression with initial gefitinib. The primary endpoint was the objective response rate with gefitinib readministration. Secondary endpoints were disease control rate, progression-free survival (PFS), overall survival (OS), quality of life, and toxicity. Changes in lung cancer-related symptoms were evaluated using the seven-item lung cancer subscale of the questionnaire. ***Results:*** Sixteen patients were enrolled between February 2005 and January 2008. Most had received ≥3 regimens of chemotherapy. Response and disease-control rates for all patients were 0 and 44%. Median PFS and OS were 2.5 and 14.7 months, respectively. Four of 7 patients with stable disease experienced a long duration (≥6 months) of disease control without severe toxicity. Symptom improvement was observed in 2 of 12 patients (17%) for whom quality of life was evaluable. ***Conclusion:*** Gefitinib represents a useful therapeutic option for selected previous gefitinib responders.

Introduction

Gefitinib is the first commercially available epidermal growth factor receptor (EGFR)-tyrosine kinase inhibitor (TKI) and is widely used for the treatment of advanced or recurrent non-small cell lung cancer (NSCLC). The Iressa Pan-Asia Study (IPASS) demonstrated superior

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progression-free survival (PFS) in the gefitinib arm than in the carboplatin and paclitaxel arm for chemotherapy-naive patients with never-smoker or light-smoking status [1]. For EGFR mutation-positive patients, gefitinib monotherapy can produce superior PFS than carboplatin and paclitaxel or cisplatin and docetaxel combinations in the first-line setting [2, 3]. As a second-line therapy, gefitinib showed significantly better overall survival (OS) than placebo for never-smokers and patients of Asian origin in the Iressa Survival Evaluation in Lung Cancer (ISEL) trial and noninferiority of OS compared to docetaxel in the Iressa NSCLC Trial Evaluating Response and Survival versus Taxotere (INTEREST) study [4, 5].

Despite the initial efficacy of gefitinib monotherapy, acquired resistance appears almost inevitable and median PFS does not exceed 12 months [6]. Approximately 60–70% of cases with acquired resistance to EGFR-TKI can be explained by the secondary resistance T790M mutation [7, 8], acquired amplification of the MET oncogene [9, 10], or a small number of other secondary mutations, such as L858R-D761Y [11], L858R-L747S [12] and L858R-T854A [13]. Details of resistance have yet to be completely clarified, but establishment of salvage treatment is an urgent issue.

Several case reports have described successful readministration of gefitinib to NSCLC patients who achieved objective response with the initial administration of gefitinib before eventual progression [14, 15]. The present study represents the first prospective phase II study to evaluate gefitinib readministration as a therapeutic option for heavily pretreated patients with NSCLC who responded to initial gefitinib treatment and received subsequent cytotoxic chemotherapy.

Patients and Methods

Patient Eligibility

Subjects were patients with recurrent or metastatic NSCLC with documented progressive disease (PD) according to Response Evaluation Criteria in Solid Tumors (RECIST) [16] after achieving objective response with initial gefitinib and then receiving at least one subsequent cytotoxic chemotherapy regimen. Other eligibility criteria included an Eastern Cooperative Oncology Group performance status (PS) of 0–2, at least one unidimensionally measurable lesion, and adequate organ functions. Patients were excluded if they displayed unresolved chronic toxicity of prior therapy, other active malignancies, uncontrolled brain metastasis, or severe comorbidities. The institutional review board at each participating hospital approved all study protocols and the genetic analysis of tumors, and written informed consent was obtained from all patients prior to enrolment.

Treatment Plan

Patients received gefitinib at 250 mg/day. In the event of unacceptable toxicity defined as grade 3 or more, gefitinib was stopped until the toxicity resolved and improved to below grade 3 within 2 weeks. No dose reduction was permitted. Treatment was continued until disease progression, intolerable toxicity, or withdrawal of consent.

Evaluation of Response and Adverse Events

Evaluations of treatment response by computed tomography were repeated every 4 weeks according to RECIST. The minimum interval to qualify for stable disease (SD) was defined as 8 weeks. Responses were evaluated by the physician in charge and confirmed by extramural review. In addition, changes in lung cancer-related symptoms were evaluated using the seven-item lung cancer subscale (LCS) of the questionnaire [17]. The LCS is an independently validated tool that measures disease-related symptoms of lung cancer on a scale of 0 (most symptomatic) to 28 (asymptomatic). A change of ≥ 2 points in LCS score reportedly reflects a minimally important difference associated with PS, weight loss, objective tumor response, and time to progression [17]. Toxicity was graded according to the National Cancer Institute Common Terminology Criteria for Adverse Events v3.0 (CTCAE v3.0).

Statistical Analysis

Objective response rate (RR) with gefitinib readministration was taken as the primary endpoint. Secondary endpoints were disease control rate (DCR), PFS, OS, symptom improvement rate, time to symptom improvement, and toxicity. DCR was defined as the sum of the RR plus the rate of SD. Simon's two-stage minimax design was used to determine the sample size and decision criteria for this phase II study. With a target activity level of 25% (P1) and the minimum RR of interest set at 5% (P0), 14 evaluable patients were needed to accept the hypothesis and a 5% significance level to reject the hypothesis with 80% power. Assuming an inevaluability rate of $\leq 15\%$, we projected an accrual of 16 patients. All patients who were enrolled and treated with gefitinib were included in both efficacy and toxicity analyses. OS was defined as the interval between enrolment in this study and death from any cause. PFS was defined as the interval between enrolment in this study and the date of documented PD or death from any cause. If a patient was lost to follow-up, that patient was censored at the last date of contact. Median OS and PFS were estimated using the Kaplan-Meier analysis. Factors potentially associated with long SD were assessed as follows. Categorical variables were compared using Fisher's exact test or the χ^2 test, while continuous variables were assessed using the Mann-Whitney nonparametric test. Relevant parameters for influence on long SD were studied by univariate analysis using the log-rank test. Differences were considered to be significant at the level of $p < 0.05$. Statistical analysis was performed using JMP 8 software (SAS Institute, Cary, N.C., USA).

Results

Patient Characteristics

Between February 2005 and January 2008, a total of 16 patients were enrolled in this study. Patient characteristics are described in table 1. The major tumor histological

Table 1. Patient characteristics (n = 16)

Characteristics	n (%)
Age, years	
Median	66.5
Range	53–79
Sex	
Male	3 (19)
Female	13 (81)
ECOG PS	
0	5 (31)
1	9 (56)
2	2 (13)
Histology	
Adenocarcinoma	14 (88)
Squamous cell carcinoma	1 (6)
Large-cell carcinoma	1 (6)
Smoking history	
Current or ex-smoker	5 (31)
Never-smoker	11 (69)
Stage	
IIIB	1 (6)
IV	10 (63)
Recurrence	5 (31)
EGFR mutation	
Positive	3 (19)
Negative	3 (19)
Unknown	10 (63)

ECOG = Eastern Cooperative Oncology Group.

Table 2. Summary of prior therapy for NSCLC (n = 16)

Characteristics	n (%)
Number of prior chemotherapy regimens	
2	2 (13)
3	9 (56)
4	2 (13)
5	2 (13)
6	1 (6)
Best response to prior cytotoxic chemotherapy	
Partial response	6 (38)
SD	7 (44)
PD	3 (19)
Time from first-line treatment to readministration of gefitinib	
≤12 months	2 (13)
12–24 months	4 (26)
≥12 months	10 (63)
Period of initial gefitinib administration	
≤6 months	1 (6)
6–12 months	7 (44)
≥12 months	8 (50)
Time from last day of initial gefitinib administration to first day of gefitinib readministration	
≤6 months	8 (50)
6–12 months	6 (38)
≥12 months	2 (13)

type was adenocarcinoma in 14 patients (88%). Eleven patients (69%) were never-smokers. Three patients showed EGFR gene mutations (2 patients with exon 19 deletions; 1 patient with L861Q in exon 21), 3 had the wild-type gene, and the status of the remaining 10 patients was unknown. All mutational analyses were performed using biopsy specimens obtained before initial gefitinib treatment.

All patients had received various therapies before study entry (table 2). Fourteen patients received gefitinib readministration as a fourth-line or later therapy.

Tumor Response and Survival

Responses were evaluable for 15 of the 16 enrolled patients. No patients achieved an objective response, with an overall RR of 0% [95% confidence interval (CI), 0–21%], while 7 patients (44%) showed SD and 8 patients (50%) had PD as the best response. DCR was 44% (95% CI, 20–70%). One patient experienced a transient reduction in diameter of the primary lesion. However, due to regrowth of other metastasis, the best response of this patient was SD (fig. 1). By the time of analysis, all patients had experienced disease progression and 14 patients had died. With a median follow-up of 14.7 months, median PFS and OS were 2.5 months (95% CI, 1.6–3.2 months) and 14.7 months (95% CI, 11.1–15.5 months), respectively (fig. 2). Four of 7 patients with SD experienced a long duration (≥6 months) of disease control. When we compared baseline characteristics between patients with and without long SD (≥6 months), no significant differences were observed in age, sex, PS, histology, smoking history, number of previous treatment regimens, duration of initial gefitinib treatment, or interval between initial and rechallenge of gefitinib (table 3). One of the 3 patients with EGFR gene mutations (L861Q) had SD with 6.7 months of PFS, while the other 2 patients had PD as the best response.

Toxicity Profile

Toxicity was evaluated in all eligible patients. The most common adverse event was fatigue in 13 patients (81%), including 2 patients with grade 3. One patient experienced grade 4 central nervous system cerebrovascu-

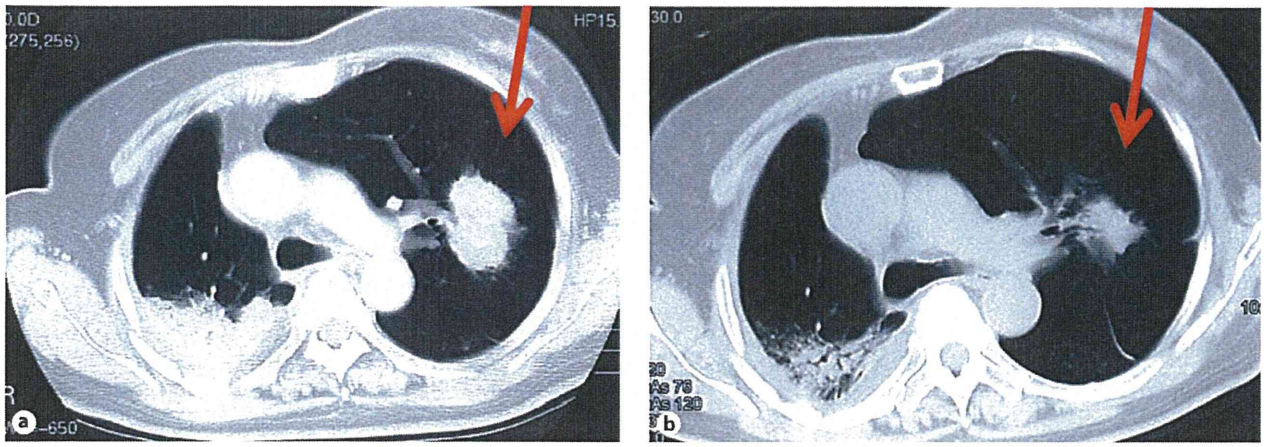

Fig. 1. Primary lesion in patient 5 (arrow) before (**a**) and 45 days after (**b**) gefitinib readministration.

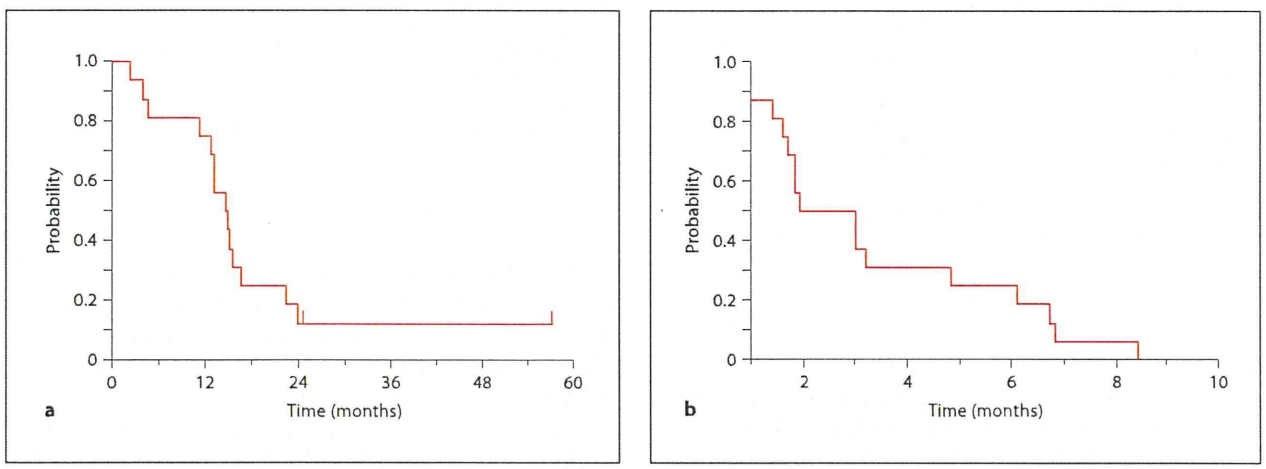

Fig. 2. OS (**a**) and PFS (**b**) for all eligible patients (n = 16) calculated according to the Kaplan-Meier method. Median survival time was 14.7 months (95% CI, 11.1–15.5 months) and median PFS was 2.5 months (95% CI, 1.6–3.2 months).

lar ischemia and terminated gefitinib treatment on day 47. Overall, toxicity appeared to be similar to the previously published trials of gefitinib monotherapy.

Symptom Improvement

LCS was evaluated in 12 of the 16 enrolled patients and compliance rate (ratio of the number of assessable weekly forms to the number of forms expected) was 70%. Median baseline LCS was 22 (range 12–28). Symptom improvement was observed in 2 of 12 patients, providing a symptom improvement rate of 16.7% (95% CI, 2.1–48.4%). Time to symptom improvement in these 2 patients was 1 and 4 weeks [17].

Discussion

To the best of our knowledge, this represents the first prospective phase II study to assess whether gefitinib readministration confers any clinical benefit in patients

Table 3. Comparison between patients with or without long duration (≥6 months) of SD

Characteristics/groups	Patients with long SD (n = 4)	Patients without long SD (n = 12)	p
Mean age ± SD, years	72.5 ± 3.9	64.5 ± 2.3	0.10
Sex (male/female)	3/1	10/2	1.00
ECOG PS (0/1/2)	2/1/1	3/8/1	0.33
Histology (Ad/Sq/La)	4/0/0	10/1/1	0.68
Smoking history (ever/never)	2/2	3/9	0.55
Stage (IIIB/IV/Rec)	0/1/3	1/9/2	0.09
Mean number of previous regimens	3.5	3.4	0.90
Median duration of initial gefitinib treatment, months	19.4	10.6	0.59
Median interval between initial and rechallenge gefitinib administrations, months	8.8	5.5	0.10
MST of gefitinib rechallenge, months	NR	12.8	0.03

Ad = Adenocarcinoma; Sq = squamous cell carcinoma; La = large-cell carcinoma; Rec = recurrence; MST = median survival time; NR = not reached.

with advanced NSCLC who have previously achieved objective response with the initial administration of gefitinib. No patients exhibited objective response, the primary endpoint of this study, suggesting that gefitinib readministration has little effect with respect to tumor shrinkage. However, the fact that 4 patients achieved a long duration (≥6 months) of disease control without severe toxicity is noteworthy.

Several retrospective studies have described the clinical activity of one EGFR-TKI treatment after the failure of another [18–24] or readministration of the same drug [14, 15, 25]. Most such reports have noted favorable results, although Viswanathan et al. [19] and Costa et al. [24] reported no or only a limited response to erlotinib after progression on gefitinib. Two prospective studies by Cho et al. [26] and Lee et al. [27] have shown results similar to our own, namely that RR/DCR were 9.5%/28.6% and 4.3%/8.7% each. In another prospective study, Riely et al. [28] also reported that in patients who develop acquired resistance, stopping gefitinib or erlotinib results in symptomatic progression, worsening of results on FDG-PET, and increased tumor size, while restarting EGFR-TKI results in a median 1% decrease in tumor diameter, 4% decrease in FDG-PET uptake and improvement of symptoms. These results imply that some patients with clinically acquired resistance to EGFR-TKI possess some tumor cells that remain sensitive to EGFR blockade and may benefit from readministration of EGFR-TKI.

Identifying the predictive factors to distinguish those who might benefit from gefitinib readministration is also an important issue. Tomizawa et al. [25] mentioned the importance of the 'EGFR-TKI-free interval'. This retrospective study of gefitinib readministration demonstrated a favorable result, with RR 25% and DCR 65%, accompanying a sufficient EGFR-TKI-free interval (median 217 days) with 1–3 regimens of cytotoxic chemotherapy in all patients [25]. Conversely, Costa et al. [24] reported that erlotinib was ineffective (RR 6%; DCR 22%) in 18 patients with resistance to gefitinib without any interval after resistance to gefitinib. In the present study, due to the lack of a control group (i.e. cohort of patients who did not have any gefitinib readministration), we could only examine the prognostic factors for patients retreated with gefitinib. No significant differences were seen regarding baseline characteristics (including EGFR-TKI-free interval) between patients with long SD (n = 4) and without long SD (n = 12). This may, in part, be attributed to the small sample size.

Some authors have explained the usefulness of EGFR-TKI readministration with the hypothesis that cytotoxic chemotherapy administered after the initial EGFR-TKI might modify the proportion of sensitive or resistant cells or produce some genetic changes in the tumor [14, 15, 25]. We could not perform comparative molecular analysis of tissue specimens between before initial administration and readministration of gefitinib. Further investigations are required regarding this issue.

In conclusion, gefitinib readministration seems to represent a potential therapeutic option for some selected NSCLC patients who respond to the initial gefitinib therapy. New approaches for identifying molecular markers are important to overcome the resistance to EGFR-TKIs seen with progression after initial response.

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Disclosure Statement

The authors have no conflicts of interest to declare.

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CANCER

Optimization of Dosing for EGFR-Mutant Non–Small Cell Lung Cancer with Evolutionary Cancer Modeling

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Non–small cell lung cancers (NSCLCs) that harbor mutations within the epidermal growth factor receptor (*EGFR*) gene are sensitive to the tyrosine kinase inhibitors (TKIs) gefitinib and erlotinib. Unfortunately, all patients treated with these drugs will acquire resistance, most commonly as a result of a secondary mutation within *EGFR* (T790M). Because both drugs were developed to target wild-type EGFR, we hypothesized that current dosing schedules were not optimized for mutant EGFR or to prevent resistance. To investigate this further, we developed isogenic TKI-sensitive and TKI-resistant pairs of cell lines that mimic the behavior of human tumors. We determined that the drug-sensitive and drug-resistant *EGFR*-mutant cells exhibited differential growth kinetics, with the drug-resistant cells showing slower growth. We incorporated these data into evolutionary mathematical cancer models with constraints derived from clinical data sets. This modeling predicted alternative therapeutic strategies that could prolong the clinical benefit of TKIs against EGFR-mutant NSCLCs by delaying the development of resistance.

INTRODUCTION

Gefitinib (Iressa) and erlotinib (Tarceva) are first-generation epidermal growth factor receptor (EGFR) tyrosine kinase inhibitors (TKIs) that were designed as adenosine triphosphate (ATP) mimetics to block wild-type receptor activity. While being developed, these drugs were serendipitously found to be most clinically effective against those non–small cell lung cancers (NSCLCs) that harbor mutations in exons encoding the kinase domain of EGFR (*1*–*3*). Common alterations include small in-frame deletions in exon 19 (19 dels) and a point mutation within exon 21 (L858R), both of which lead to sustained activity of the kinase (*4*–*6*). More than 70% of patients with *EGFR*-mutant tumors treated prospectively with either TKI show tumor volume decreases, with an overall median survival of ~30 months (*7*–*9*).

Unfortunately, lung tumors in all patients eventually develop acquired resistance (*7*, *10*). The most common mechanism of resistance is a second site mutation within exon 20 of *EGFR* (T790M), observed in ~50% of cases (*11*, *12*). This change leads to altered binding of the drug within the ATP pocket (*13*).

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Currently, targeted therapeutic options for T790M-harboring NSCLCs are limited. Second-generation EGFR TKIs [for example, HKI-272 (neratinib) and BIBW-2992 (afatinib)] are more potent than gefitinib and erlotinib against EGFR T790M (*14*, *15*). However, because they inhibit drug-sensitive mutants at lower doses than they inhibit the T790M mutant, they still select for T790M-harboring clones in models of acquired resistance in vitro (*14*). Their antitumor activity in patients with acquired resistance to gefitinib and erlotinib has been disappointing (*16*, *17*).

We hypothesized that, because clinically available EGFR TKIs were developed against wild-type EGFR, current empiric dosing regimens were not optimally designed to inhibit the *EGFR* mutants in NSCLC nor to minimize the development of drug resistance. Here, we have identified differences in the growth kinetics of TKI-sensitive and TKI-resistant (T790M-containing) isogenic NSCLC cells. We incorporated these findings, along with patient data, into evolutionary cancer models (*18*) to generate mathematical models predictive of tumor behavior. This approach identified several strategies to improve the treatment of EGFR-mutant NSCLC before and after the emergence of T790M-mediated acquired resistance.

RESULTS

Derivation of *EGFR*-mutant TKI-resistant lung adenocarcinoma cells

To determine the physical characteristics of TKI-sensitive and TKI-resistant cells, we derived in vitro cellular models of T790M-mediated resistance using EGFR-mutant TKI-sensitive PC-9 cells (19 del), well-established TKI dose-escalation protocols (*14*, *19*, *20*), and either a reversible quinazoline (erlotinib) or an irreversible quinazoline (BIBW-2992) that binds covalently to C797 in EGFR. After 120 days in culture, PC-9 cells resistant to erlotinib and BIBW-2992 emerged that grew in drug concentrations ~100-fold (5 μM) and ~1000-fold (500 nM) the initial IC_{50} (median inhibitory concentration), respectively, of the

parental cells (Fig. 1, A and B). On comparative genomic hybridization arrays, the *EGFR* locus appeared further amplified in erlotinib-resistant (ER) and BIBW-2992–resistant (BR) cells compared to parental cells (fig. S1, A and B). Fluorescence in situ hybridization (FISH) analyses indicated that *EGFR* alleles were not amplified on double-minute chromosomes, as reported in other studies (*21*) (fig. S1C). The resistant cells had no evidence of *MET* amplification, another mechanism of acquired resistance to EGFR TKIs (fig. S1, A and B) (*20*, *22*). No other obvious amplifications or deletions were found.

DNA from polyclonal PC-9/ER and PC-9/BR cells harbored the T790M allele plus the primary drug-sensitizing exon 19 del (Fig. 1C). No other mutations were found within any coding exons of *EGFR*. Analysis of cloned PC-9/BR complementary DNA (cDNA) products generated by reverse transcription–polymerase chain reaction (RT-PCR) showed that the T790M mutation was in cis with the primary drug-sensitive mutation. Signaling within the EGFR pathway was minimally affected by erlotinib in the PC-9/ER cells or by BIBW-2992 in the PC-9/BR cells (Fig. 2C and fig. S1D). Phospho-receptor tyrosine kinase arrays showed grossly similar profiles for PC-9/ER and PC-9/BR cells (fig. S1E).

Restoration of drug sensitivity after EGFR TKI withdrawal

We cultured resistant polyclonal cells in the absence of drug. After eight passages, PC-9/BR cells regained partial sensitivity to BIBW-2992 (Fig. 2A, upper panel). By 16 passages, drug sensitivity was restored to parental levels (Fig. 2A, lower panel). Loss of resistance corresponded with a decrease in the proportion of the T790M allele (Fig. 2B). Consistent with these data, lysates from parental cells and late-passage PC-9/BR–resistant cells treated with BIBW-2992 showed significantly reduced phosphorylation of EGFR and its downstream targets, extracellular signal–regulated kinase (ERK) and AKT, whereas lysates from resistant cells maintained in the presence of TKI and treated with the same concentrations of drug did not (Fig. 2C).

To extend our observations, we examined other *EGFR*-mutant isogenic pairs of drug-sensitive and drug-resistant lung cancer cell lines. Like PC-9 cells, HCC827/ER cells (19 del + T790M) regained TKI sensitivity after multiple passages in the absence of inhibitor and lost the T790M allele (fig. S2, A and B). By contrast, H3255 (L858R) cells, which also acquired T790M in response to continuous TKI exposure, neither regained TKI sensitivity nor lost the T790M after multiple passages in the absence of inhibitor, and they grew at the same rate as the parental line (fig. S3). Thus, two of three lines studied displayed resensitization. We characterized representative PC-9/BR cells in more detail.

Growth of parental cells and EGFR-mutant cells with T790M

To investigate the growth properties of drug-sensitive and drug-resistant cells, we counted the total number of viable cells in culture after plating each cell cohort in the absence of drug. To avoid contact inhibition as a confounding factor, cultures were not allowed to reach confluence. The parental cultures always had more cells (Fig. 2D) and showed more DNA synthesis (Fig. 2E) than did PC-9/BR cells. On average, parental cells doubled ~1.22 times faster than T790M-containing resistant cells. PC-9/BR cells withdrawn from drug for 25 passages (P-25) displayed parental growth kinetics (Fig. 2F). PC-9/ER cells harboring T790M followed the same slower growth pattern as PC-9/BR cells (fig. S2C).

To confirm these observations, we established single-cell clones from both PC-9/BR and PC-9/ER cell lines. Six T790M-containing clones were derived in the presence of BIBW-2992 from the PC-9/BR cells. All clones displayed slower growth kinetics compared to parental cells or polyclonal resistant cells that had been passaged 25 times without drug. PC-9/BR clones also grew more slowly than the resistant polyclonal population maintained under selective pressure (Fig. 2F). Four T790M-harboring clones were derived in the presence of erlotinib from PC-9/ER cells and showed analogous characteristics (fig. S2, D and F). The growth properties of parental cells and PC-9/BR–resistant clones were also maintained in vivo (Fig. 2G). We saw no differences in cell cycle profiles, rates of apoptosis, or rates of senescence between parental and resistant cells. Notably, the T790M-harboring cells described here are distinct from the recently described subpopulation of *EGFR*-mutant cancer cells lacking T790M that transiently exhibit a distinct phenotype characterized by the engagement of insulin-like growth factor 1 receptor (IGF-1R) activity, hypersensitivity to histone deacetylase (HDAC) inhibition, altered chromatin, and an intrinsic ability to tolerate drug exposure (*23*).

Collectively, these results can be explained by two scenarios (Fig. 2H). First, tumor cell populations with acquired resistance are composed of a heterogeneous mixture of cells, some of which harbor the T790M allele. After drug withdrawal, previously growth-arrested but faster-growing TKI-sensitive cells repopulate the tumor, and the population of cells displays resensitization. In the second possibility, tumor cell populations with acquired resistance are composed of a homogeneous group of resistant cells; after drug withdrawal, every cell loses the T790M allele and the population becomes resensitized. Several lines of evidence support the former possibility. Polyclonal populations of resistant cells "lose" the T790M allele after passages in vitro in the absence of inhibitor. By contrast, single-cell clones harboring T790M retain the allele even after multiple passages in the absence of drug in vitro (fig. S2, E and F) and as xenografts (up to 78 days) (Fig. 2G and fig. S2G). Retention of the T790M allele in the single-cell clones, both in vitro and in vivo, suggests that acquisition of that allele is not reversible within individual cells, making the second scenario less likely.

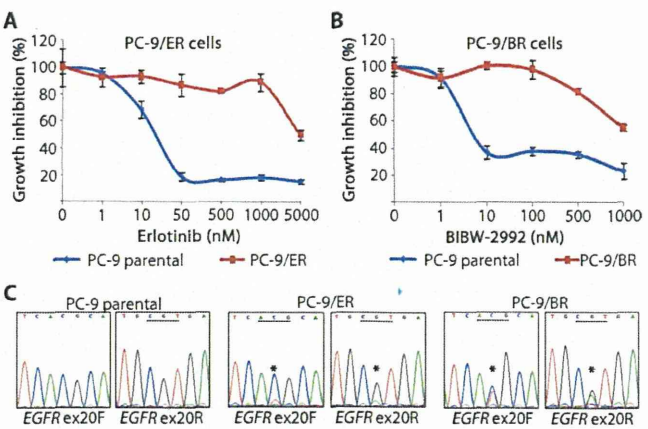

Fig. 1. Derivation and characterization of TKI-resistant cells. (**A** and **B**) PC-9 erlotinib-resistant cells (PC-9/ER) (panel A) and PC-9 BIBW-2992–resistant cells (PC-9/BR) (panel B) were derived after ~120 days of culture with increasing concentrations of drug. Growth inhibition assays show that these cells are resistant to respective TKIs compared to the parental cells. (**C**) Direct dideoxynucleotide sequencing chromatograms from *EGFR* exon 20 (ex20) show the presence of the T790M mutation (*ACG→ATG) in the PC-9/ER and PC-9/BR cells but not in parental cells. F, forward; R, reverse directions.

Effect of the percentage of T790M clones on the sensitivity and growth of a population of mixed tumor cells

Biopsies of growing lesions in patients do not provide information on whether a tumor consists of a heterogeneous mix of sensitive and resistant cells or a homogeneous mass of only resistant cells (Fig. 2H), because which cells harbor the T790M mutation cannot be ascertained directly. To estimate the proportion of T790M-containing cells within a population necessary for the entire population to display resistance, we performed reconstitution experiments. T790M-harboring clonal cells (PC-9/BR clone 1) were mixed with TKI-sensitive parental cells at known percentages (Fig. 3A), and cell mixture drug sensitivity was measured by growth inhibition assays. Populations with small percentages of resistant cells (1 and 10%) displayed similar sensitivity to erlotinib as parental cells (0%), whereas sensitivity was reduced when T790M clones made up >25% of the population (Fig. 3B). These data can explain why patients whose tumors harbor low levels of T790M can still undergo an objective radiographic response to EGFR TKI treatment (*24*, *25*).

We next estimated the percent of resistant cells needed in a population of cells to display tumor growth. Cell mixtures were treated with dimethyl sulfoxide (DMSO) or 1 μM erlotinib for 72 hours (Fig. 3C). The addition of erlotinib did not alter the growth of cell populations with low proportions of resistant cells (1%). However, compared to DMSO-treated cells, populations containing greater than 10% T790M-positive cells proliferated faster than parental cells (0%) in the presence of drug. These findings are further consistent with the notion that tumor cell populations with acquired resistance to EGFR TKIs can be composed of heterogeneous tumor cell mixtures.

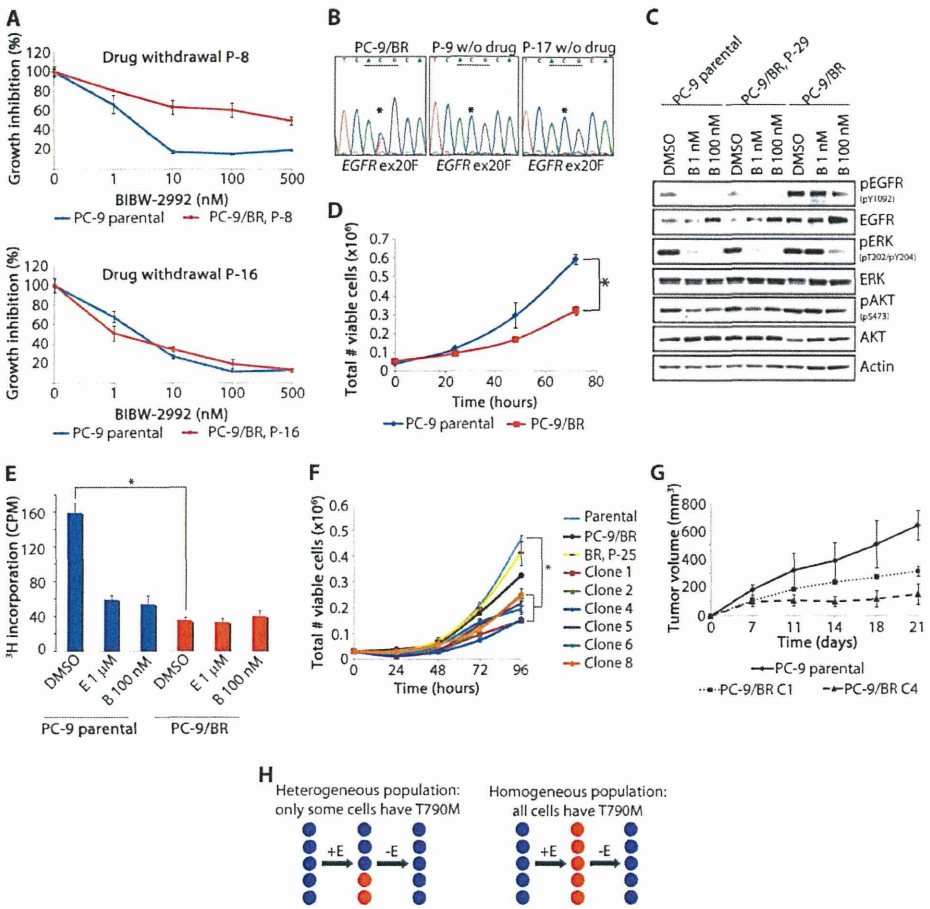

Fig. 2. Growth characteristics of TKI-sensitive and TKI-resistant cells. (**A**) Polyclonal PC-9/BR cells cultured without BIBW-2992 for 8 and 16 passages (P-8 and P-16, respectively) regained intermediate and complete sensitivity to BIBW-2992, respectively. (**B**) Sequencing of *EGFR* exon 20 (ex20) showed a decrease in the T790M allele that correlates with restored TKI sensitivity. Genomic DNA was extracted from cells after 9 and 17 passages (P-9 and P-17, respectively) without drug (*ACG→ATG). (**C**) Parental and late-passage resistant cells (P-29) show decreased phosphorylation of EGFR and its downstream targets in the presence of BIBW-2992, whereas signaling in the PC-9/BR cells remained intact. Cells were treated with vehicle (DMSO) or BIBW-2992 (B) for 3 hours. (**D**) T790M-containing PC-9/BR cells proliferated more slowly than parental cells over 72 hours in the absence of inhibitor. Graphs represent the average of triplicate wells ± SD. *$P < 0.01$. (**E**) [^{3}H]Thymidine incorporation confirms the slower proliferation rate of the PC-9/BR cells compared to parental cells. Cells were treated with DMSO, erlotinib (E), or BIBW-2992 (B) for 24 hours. Data are expressed as counts per million (CPM) relative to each other. (**F**) Cell counts for PC-9 parental cells, BR (polyclonal), BR late-passage (P-25), and T790M-containing BR clones (1, 2, 4, 5, 6, 8) show that the clones grow more slowly than parental and P-25 cells. (**G**) PC-9 parental and PC-9/BR cells (clones 1 and 4) were injected subcutaneously into nude mice, and tumor growth in the absence of drug was monitored over time. The slower growth pattern of T790M-harboring PC-9/BR clones 1 and 4 is maintained in vivo. Data are average tumor volumes ($n = 3$ per group) ± SEM. (**H**) At the onset of acquired resistance, an *EGFR*-mutant tumor (blue) develops T790M in a small proportion of cells (red) after exposure to erlotinib (E; left). Upon withdrawal of drug, previously growth-arrested TKI-sensitive cells repopulate the tumor. Alternatively (right), all cells contain some level of T790M at progression. Upon discontinuation of the inhibitor, all cells revert back to parental genotype.

Biological properties of sensitive and resistant cells compared to EGFR-mutant NSCLC in human patients

The T790M substitution confers synergistic kinase activity and transformation potential when combined with drug-sensitive EGFR mutations (*5*, *14*). We had therefore expected that resistant clones harboring the T790M allele would display a growth advantage compared to parental drug-sensitive cells. Our results to the contrary prompted us to examine the clinical course of patients with EGFR-mutant NSCLC to verify that our preclinical findings reflected the human disease.

First, we asked what percentage of patients with EGFR-mutant tumors could remain on long-term EGFR TKI therapy. We analyzed unpublished data from patients enrolled in NEJ002, a prospective trial for patients with untreated metastatic

EGFR-mutant tumors (*7*), to evaluate the range of time on TKI therapy. Although the median duration on gefitinib was 0.83 years, the range was as high as 3.3 years (Fig. 4A). Patients (32, 4, and 1%) were on drug for 1, 2, and 3 years, respectively. These data are consistent with the notion that some *EGFR*-mutant tumors display indolent progression.

Second, we examined the prospective clinical course of patients with *EGFR*-mutant tumors and T790M-mediated acquired resistance. We extracted unpublished data from a clinical trial in which a cohort of 14 patients was treated prospectively with erlotinib (*26*). There were four patients whose tumors had a documented T790M mutation at the time of disease progression, two of whom had measurable disease amenable to analysis. Both patients displayed slow growth of the T790M-harboring lesion (Fig. 4, B and C, and fig. S4). In the first case, the patient was biopsied when she was deemed to have progression of disease after 25 months (*11*). Analysis of previous computed tomography (CT) scans indicated that the tumor began to grow at least 6 months before the biopsy and that it grew slowly from the time of maximal response (Fig. 4C). The second patient showed similar findings (fig. S4A). By comparison, a similar analysis of two patients with *EGFR* wild-type tumors that progressed after receiving benefit from first-line chemotherapy (*27*) showed that both displayed rapid tumor growth from the time of maximal response to the time when criteria for progressive disease were met (fig. S4B). Notably, the median time to progression on chemotherapy is ~4 months in unselected NSCLC but more than 9 months on erlotinib for *EGFR*-mutant tumors (*10*, *28*).

Third, using unpublished data from the same prospective erlotinib study that was used for image analysis (*26*), we asked what proportion of patients displayed progression of disease on erlotinib but continued a TKI as a result of indolent tumor growth (Fig. 4, B and C, and fig. S4A). Among 14 patients, 4 patients continued on single-agent TKI for at least 6 months beyond disease progression, because they were relatively asymptomatic (Fig. 4D). Three of the four patients had biopsies within 2 months of coming off study, and all three (patients B, C, and D) harbored the T790M mutation. T790M was also detected in the re-biopsy specimen from one patient despite the addition of chemotherapy to continuous erlotinib treatment.

Fourth, we examined the frequency of the T790M allele by using 454 sequencing of DNA extracted from 16 untreated early-stage resected *EGFR*-mutant NSCLCs (Table 1). From mutant allele dilution experiments, the limit of detection of the 454 method was ~0.2%. We did not detect the T790M allele in any of the resected specimens or in parental PC-9 cell DNA. These data are consistent with our evolutionary modeling results (see below) and demonstrate that in the absence of TKI selection, the T790M allele is either absent or highly infrequent (less than 1 in 500).

Finally, numerous published reports support our preclinical data: (i) EGFR-mutant tumors can "flare" after patients stop EGFR TKI treatment (*29*); (ii) serial biopsies over the course of treatment demonstrate a decrease in prevalence of the T790M allele during the period off therapy (*30*); (iii) EGFR-mutant cancers that recur after stopping adjuvant TKI do not harbor the T790M mutation, suggesting a growth disadvantage to these clones (*31*); (iv) EGFR-mutant tumors with documented progression can re-respond to an EGFR TKI after a hiatus off TKI therapy (*30*, *31*); (v) patients with EGFR-mutant tumors and T790M-mediated acquired resistance paradoxically have a better survival than those with acquired resistance and no T790M (*32*, *33*); and (vi) ultrasensitive locked nucleic acid technology (LNA-PCR; limit of detection ~0.1%) was unable to detect T790M in TKI-naïve samples, half of which harbored the mutation upon progression (*33*). Collectively, these data

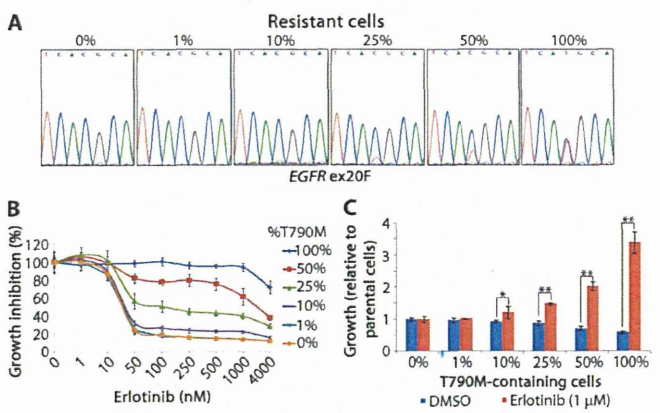

Fig. 3. Reconstitution experiments to study T790M-mediated resistance. (**A**) T790M-containing PC-9 cells (BR, clone 1) were spiked into parental PC-9 cells at various proportions. The increased proportion of the T790M allele (*ACG→ATG) is evident from representative direct sequencing chromatograms of *EGFR* exon 20. (**B**) Mixed populations of cells were treated with increasing concentrations of erlotinib for 72 hours, at which point growth inhibition was measured. (**C**) Cell populations with varying proportions of T790M-containing cells were grown in the presence of DMSO or erlotinib (1 μM) to mimic various states of a TKI-resistant heterogeneous solid tumor. Total cell number was determined after 72 hours and graphed as the percent growth compared to parental cells (0%) ± SD. *$P < 0.05$; **$P < 0.01$.

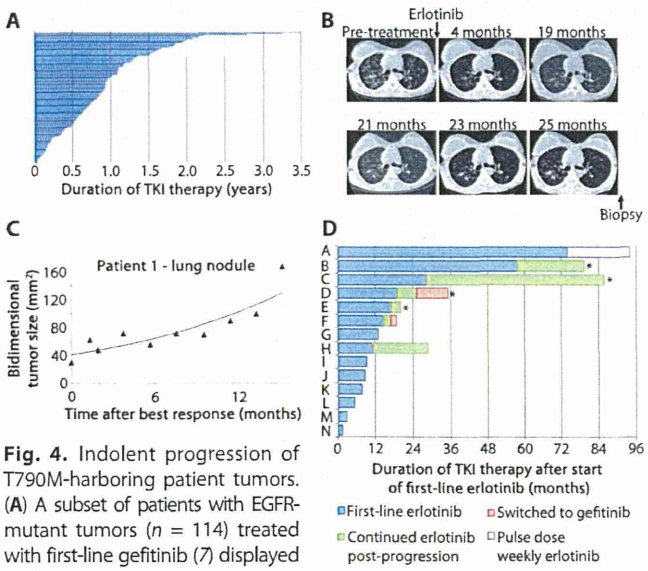

Fig. 4. Indolent progression of T790M-harboring patient tumors. (**A**) A subset of patients with EGFR-mutant tumors (n = 114) treated with first-line gefitinib (*7*) displayed prolonged responses to treatment. The average time on gefitinib before progression was 0.9 years. (**B**) Serial computed tomography scans from a patient with an *EGFR*-mutant tumor (ex 19 del) [images from (*11*)]. (**C**) Serial bidimensional measurements taken from the time of best response for the patient in panel B illustrate the slow rate of progression in this lesion. (**D**) Patients receiving first-line erlotinib as part of a phase II trial. Four of 14 patients (28%; patients B, C, D, and H) were continued on treatment with single-agent TKI (erlotinib or gefitinib) for >6 months after RECIST progression. Asterisk denotes the presence of T790M.

all support the notion that tumors with acquired resistance to gefitinib or erlotinib may be composed of mixed populations of cells, and continued TKI selection is needed to promote the outgrowth of slower-growing T790M-mutant cells.

Evolutionary cancer modeling applied to *EGFR*-mutant NSCLC

Having established the clinical relevance of our preclinical models, we applied evolutionary cancer modeling, involving detailed mathematical descriptions of our tumor cell populations in vitro, to design optimized dosing strategies for *EGFR*-mutant NSCLC. We incorporated pharmacokinetic data from human clinical trials with erlotinib to ensure that the drug doses proposed were clinically achievable in humans (*34*, *35*).

First, we tested whether this approach could be used to determine the potential frequency of T790M-containing clones within a population of untreated PC-9 cells. We measured the growth and death rates of PC-9 and PC-9/ER cells (see Materials and Methods) cultured in the presence of various doses of erlotinib (fig. S5) and modeled the drug-sensitive and drug-resistant cell populations as a multitype binary branching process (*36*). Application of the experimentally determined estimates of viable cells as well as apoptosis in the presence and absence of drug generated fitted curves describing the birth and death rates of both cell populations as a function of the concentration of erlotinib (Fig. 5, A to D). These curves were used to estimate the number of resistant cells

Table 1. 454 sequencing of *EGFR* exon 20. About 100,000 454 reads per sample were generated from PCR products generated with *EGFR* exon 20 (ex20)–spanning primers. All tumors were from treatment-naïve patients. TKI-R-1 and TKI-R-2 were run as positive control samples. 1°mutn, primary *EGFR* mutation, as assessed by direct sequencing.

Sample	Stage	1°mutn	454 ex20 T790M (%)
Lung TKI-R-1	IV	19 DEL	Y (59%)
Lung TKI-R-2	IV	L858R	Y (1.07%)
H3255	Cell Line	L858R	N
PC-9	Cell Line	19 DEL	N
130T	IA	19 DEL	N
169T	IA	19 DEL	N
230T	IA	19 DEL	N
474T	IA	19 DEL	N
631T	IA	19 DEL	N
20T	IB	19 DEL	N
734T	IB	19 DEL	N
739T	IB	19 DEL	N
388T	IIIA	19 DEL	N
3T	IA	L858R	N
5T	IA	L858R	N
485T	IA	L858R	N
570T	IB	L858R	N
685T	IB	L858R	N
25T	IB	L858R	N
166T	IB	L858R	N

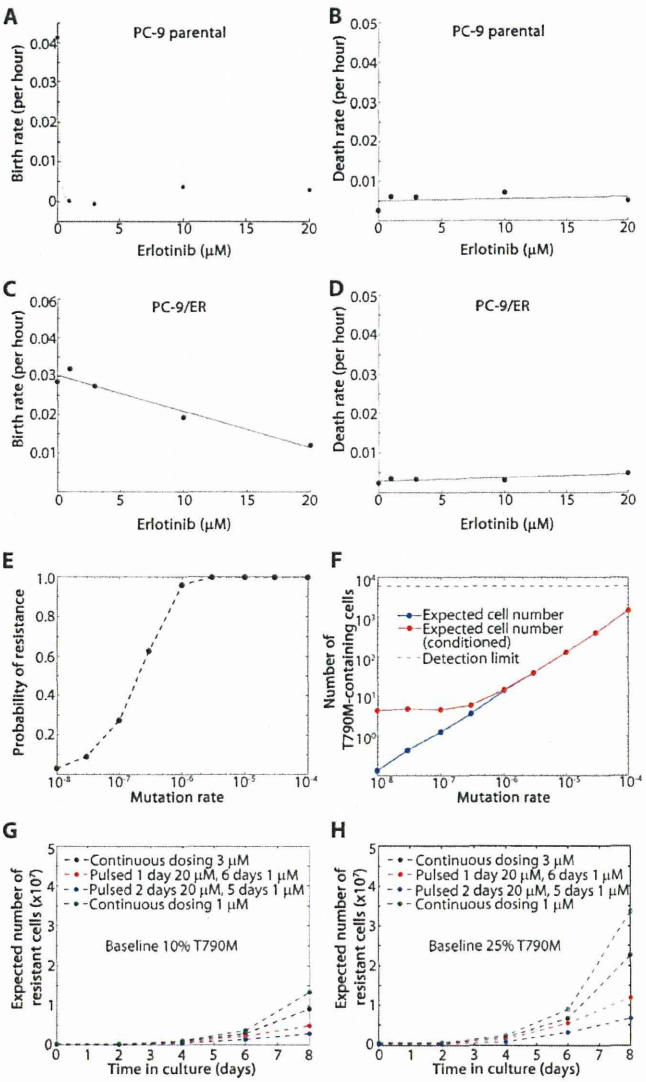

Fig. 5. Evolutionary cancer modeling predictions to delay the development of resistance. (**A**) PC-9 cell birth rate at erlotinib concentrations of 0, 1, 3, 10, and 20 μM. (**B**) PC-9 cell death rate as a function of increasing erlotinib concentration. (**C**) PC-9/ER cell birth rate in the presence of erlotinib (0, 1, 3, 10, and 20 μM). (**D**) PC-9/ER cell death rates as a function of increasing erlotinib concentration. (**E**) Probability of preexisting T790M-harboring cells in a population of 3 million cells initiating from one cell harboring just a drug-sensitive EGFR mutation that grew in the absence of drug for a range of mutation rates (10^{-4} to 10^{-8} per cell division). (**F**) Expected number of resistant cells present in the population, both averaged over all cases and averaged only over the subset of cases, where at least one resistant cell is present. (**G**) An initial population of 750,000 cells, 10% of which harbor T790M, treated with continuous low-dose erlotinib (1 and 3 μM) selects for the emergence of T790M-harboring cells (green and black lines). The addition of one or two high-dose erlotinib "pulses" (20 μM) followed by 1 μM for the remaining days of a 7-day cycle decreases the expected number of resistant cells (red and blue lines). (**H**) Analogous results as in panel (G) starting with an initial population with 25% T790M-harboring cells.

present in a population of 3 million cells [an estimate of the number of cells in a ~1-cm tumor (*37*)] that initiated from a single cell harboring only a drug-sensitive EGFR mutation and that grew in the absence of drug. The probability that at least one resistant cell exists in the 3 million cell population (Fig. 5E) ranged from 3% (for a mutation rate of 10^{-8} per TKI-sensitive cell division) to 100% (for mutation rates above 10^{-6}). We also estimated the number of T790M-containing cells expected when the population reaches 3 million cells for a range of mutation rates (10^{-4} to 10^{-8}) (Fig. 5F); we determined the expected number of cells both averaged over all cases and averaged over the subset of cases in which at least one resistant cell was present. By the standard estimate of mutation rates per base pair per cell division (10^{-8} to 10^{-7}) (*38*, *39*), cells with T790M in the final population would be about 1 cell out of 3 million. These data were consistent with our 454 deep sequencing results (Table 1), which showed that T790M was rare (<0.2%) in untreated early-stage EGFR-mutant tumors.

Second, we used mathematical modeling to predict how long it would take to restore drug sensitivity in the PC-9/BR polyclonal resistant cell population, based on our cell growth and death rates. Using the observed doubling times for sensitive cells and resistant cells of ~19 hours and ~23 to 25 hours, respectively, we estimated that after drug withdrawal, about 35 to 40 days would be needed for a population of cells with 87.5% resistant cells to have only 1% resistant cells. These data fit well with the observation that between 8 and 16 passages (with 1 passage every 3 days) were required to restore full sensitivity after drug withdrawal (Fig. 2). Collectively, these data demonstrate that evolutionary cancer modeling could accurately describe and predict our biologically observed phenomena and were consistent with the presence of a mixed cell population in resistant tumors (Fig. 2H).

Modeling-predicted delay of resistance by high-dose pulses combined with a continuous low dose of TKI

We then used mathematical modeling to predict the relative effects of alternative dosing schedules on the development of resistance. Under the previously mentioned pharmacokinetic constraints, we hypothesized that intermittent high-dose pulses of erlotinib (20 μM) in conjunction with a continuous low-dose administration (1 μM) could be a tolerated dosing schedule to delay the establishment of large resistant cell populations. Using the cell growth and death rates calculated in the presence of 1 and 20 μM erlotinib, we determined the number of PC-9/ER cells expected under various pulsed continuous treatment schedules, starting from an initial population of 750,000 cells with 10 and 25% of the population initially containing T790M (Fig. 5C). Modeling predicted that the use of continuous low-dose treatment with simultaneous high-dose pulsed administration of erlotinib should delay the acquisition of T790M-mediated resistance (Fig. 5, G and H).

To corroborate the mathematical predictions, we applied the calculated dosing schedules to our cell lines. Using T790M-harboring clones mixed with parental cells, we treated cell populations with 0, 25, or 100% resistant cells with erlotinib at the indicated doses for 7 days (one cycle, as modeled in Fig. 5H). As expected, T790M mutations were not selected for in the absence of drug in the population with 25% resistant cells but were enriched for when 1 μM erlotinib was administered daily (Fig. 6A). Addition of one or two high-dose pulses of erlotinib (20 μM) together with daily low-dose erlotinib (1 μM) also selected for T790M-harboring cells in the mixed population. However, the frequency of the mutant allele was lower than with daily dosing (Fig. 6A), consistent with our mathematical predictions (Fig. 5G) and with the notion that this regimen could delay the acquisition of T790M-mediated resistance.

To circumvent the limitations of erlotinib dosing (maximum of 20 μM) and to apply our predictions to a long-term model, we substituted BIBW-2992, which is more potent against the T790M mutant, with an IC_{50} of about 100 nM (*15*). This concentration of drug can be achieved in humans at the standard dose of 40 mg daily (*40*). We used the same continuous dose escalation protocol as we used for erlotinib and BIBW-2992 to select for T790M-mediated resistance in PC-9 cells. Whereas T790M was detectable with low concentrations of BIBW-2992 and erlotinib alone, the combination of high-dose weekly BIBW-2992 plus continuous erlotinib did not select for this mode of resistance

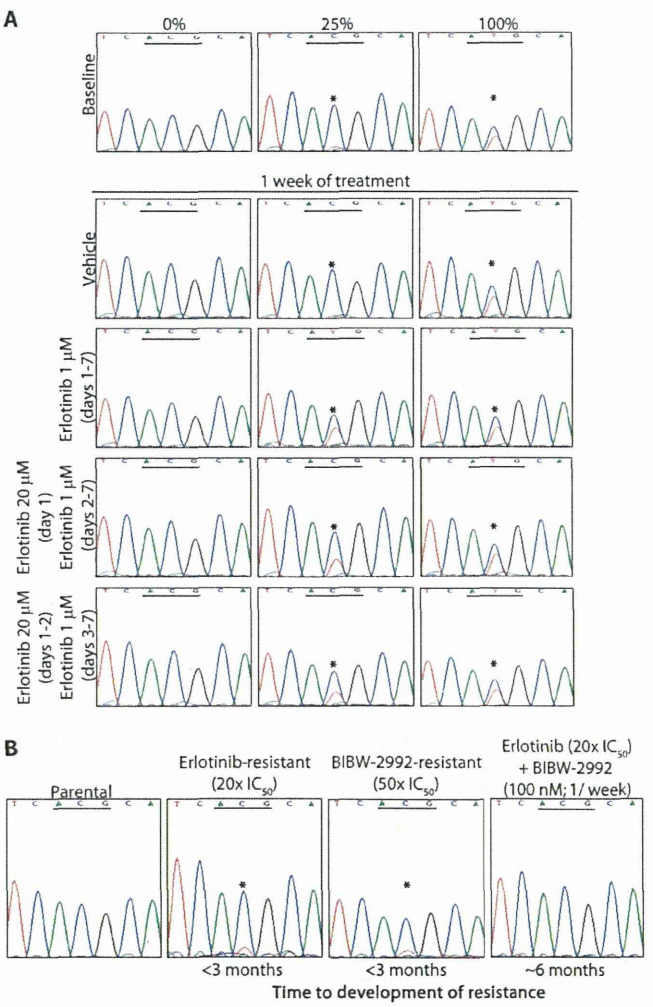

Fig. 6. Effect of pulsed high-dose TKI treatment on the number of T790M-harboring cells. (**A**) Using a T790M-harboring clone (PC-9/BR, c1), we mixed cell populations to have 0, 25, or 100% resistant cells. The baseline panel shows forward sequence tracings from exon 20 of EGFR (the underlined codon encodes T790). Cell populations were then treated with erlotinib at the indicated doses for 7 days. (**B**) Chromatograms display exon 20 forward sequences of *EGFR* from PC-9 cells treated with different drugs (*ACG→ATG).

(Fig. 6B). Furthermore, the total time for the development of complete resistance (100- to 1000-fold the initial IC_{50}) was twice as long for cells treated with the pulsed dosing regimen. The mechanism of resistance in these cells remains under investigation. These data confirm the modeling predictions and show that resistance can be delayed with combination of a pulsed high-dose potent TKI and continuous low doses of erlotinib.

Modeling-predicted tumor cell control after the emergence of *EGFR* T790M by continuation of TKI therapy

We next used our models to predict better treatment strategies for patients whose tumor cell populations have developed T790M-mediated resistance. In standard oncology practice, progression while on a specific therapy leads to cessation of that therapy and initiation of a new treatment. However, our data suggest that resistant tumors may be composed of a heterogeneous mix of TKI-sensitive and TKI-resistant cells (Fig. 3) and that stopping TKI therapy may permit expansion of the faster-growing TKI-sensitive cells. We modeled this scenario in vitro by diluting PC-9 T790M-containing clonal cells in parental cells at various concentrations, as described above. Cell populations were treated with physiologically achievable doses of chemotherapy alone or chemotherapy plus erlotinib, and cell numbers were counted every 48 hours (Fig. 7A). We used two chemotherapeutic agents with activity in lung cancer: a platinum-based drug, cisplatin (*41*), and an antifolate, pralatrexate (*42*). The latter was used rather than the chemically related pemetrexed, because pralatrexate is more stable after reconstitution.

Cells treated with cisplatin (500 nM) (*28*) grew slower in the presence of erlotinib, both in vitro and in vivo (Fig. 7, B and C). Similar in vitro results were obtained with pralatrexate (100 μM) (*43*) (fig. S6). Collectively, these data suggest that patients may benefit from continued treatment with an EGFR TKI, even after developing T790M-mediated progression of disease.

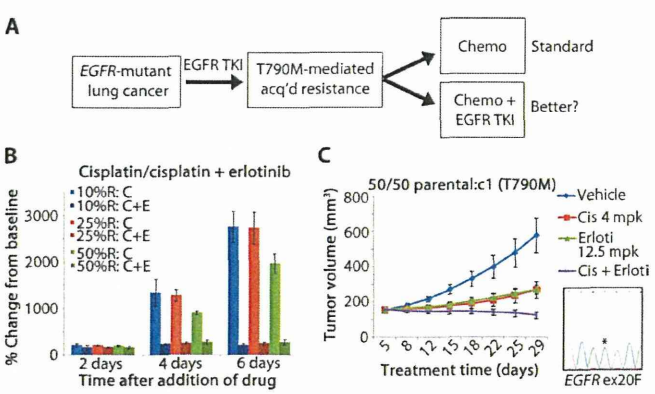

Fig. 7. Effect of continuation of TKI therapy with chemotherapy on heterogeneous TKI-resistant tumors. (**A**) Schematic outline of treatment options for patients with *EGFR*-mutant disease. (**B**) PC-9/BR c1–resistant cells were diluted in parental cells at various concentrations (see Fig. 3) and treated with chemotherapy (cisplatin, 500 nM) or chemotherapy plus erlotinib (3 μM). In all cases, the TKI-chemotherapy combination was more efficacious at inhibiting cell growth. (**C**) Athymic nude mice with established tumors (50:50 mixture of PC-9 parental and BR c1 cells) were administered vehicle, cisplatin (4 mg/kg), erlotinib (12.5 mg/kg), or cisplatin plus erlotinib. At the start of treatment, T790M-containing cells made up ~25% of the population, as measured by direct sequencing (bottom right). Tumor volumes were graphed as averages (n = 5 per group) ± SEM. mpk, mg/kg. * indicates residue of interest.

DISCUSSION

All patients with metastatic EGFR mutant–harboring lung adenocarcinomas will eventually develop acquired resistance if treated with the EGFR TKIs gefitinib and erlotinib. In ~50% of cases, tumor cells harbor a second mutation in the EGFR kinase domain (T790M), which alters a gatekeeper residue within the ATP-binding pocket. Because existing treatment schedules were established empirically with drugs developed against wild-type EGFR, we hypothesized that evolutionary cancer modeling could be used to develop more optimal dosing strategies against the mutant receptors in NSCLC. We combined in vitro cell culture experiments, multiple clinically relevant data sets, and mathematical modeling to describe tumor behavior. We then used the models to predict dosing strategies that were validated in vitro and in vivo. These dosing regimens will need to be further validated in clinical trials with patients with EGFR-mutant lung cancer. We propose the use of high-dose pulsed once-weekly BIBW-2992 with daily low-dose erlotinib to delay the emergence of T790M-mediated resistance. PC-9 cells treated with this regimen required twice as long to develop resistance and did not show selection for T790M mutations. In patients, the combination of two EGFR TKIs could lead to overlapping toxicities involving rash and diarrhea. Thus, in a phase IB dose-safety trial, we would recommend a more tolerable strategy, with lower doses of erlotinib still known to be effective against EGFR-mutant tumors (25 or 50 mg daily, orally) (*44*). For BIBW-2992, we would suggest starting at 40 mg once a week and escalating to the maximum tolerated dose, aiming to achieve as high a concentration of the drug in patients as possible.

We determined that tumors with acquired resistance likely harbor mixed populations of drug-sensitive and drug-resistant cells with differential growth rates. To treat these tumors, we would propose continuing EGFR TKI suppression with chemotherapy beyond T790M-mediated progression for maximal disease control, based on the benefits of this approach in both in vitro and in vivo models. Such practice would be analogous to what is done for HER2-positive breast cancer patients who continue receiving the anti-HER2 antibody trastuzumab even after the development of progressive disease (*45*).

Our findings raise a paradox involving the T790M mutation. Surrogate kinase assays in Sf9 transfectants and transformation assays in fibroblasts showed that the addition of the T790M mutant to a drug-sensitive mutant confers synergistic oncogenic activity (*5*, *46*). Yet, our preclinical data demonstrate that acquisition of the T790M mutation is associated with a growth disadvantage in the absence of TKI selection. One explanation is that the oncogenic activity of double-mutant EGFRs can be toxic to lung adenocarcinoma cells when the protein is expressed at a certain level. This hypothesis is supported by our own observations that transfectants with lower levels of the double-mutant receptor are spontaneously selected for over time (fig. S7A). Other lung cancer cells expressing a different gatekeeper mutation also display a growth disadvantage (fig. S7B). How double-mutant EGFR signaling leads to slower growth rates remains an area of investigation.

Although our preclinical data are supported by many data sets of patients with resectable early-stage to metastatic late-stage EGFR-mutant tumors, the slower growth rate of T790M-harboring cells in

our in vitro models may not be representative of all T790M-positive cells in human patients. Consistent with this, one of the three isogenic pairs of EGFR drug-sensitive/drug-resistant cell lines that we developed did not display resensitization after drug withdrawal. Other factors, such as fibroblast growth factor receptor (FGFR), IGF-1R, and nuclear factor κB (NFκB) signaling, may also modulate responses to EGFR TKIs (*47–49*).

The characteristics of T790M-harboring NSCLC may be broadly applicable to other tumor types. For example, in gastrointestinal stromal tumors (GISTs) harboring imatinib-sensitive activating mutations in KIT, "flares" have been observed after imatinib cessation upon progression (*50*), and a recent clinical study showed that patients with documented imatinib resistance can re-respond to imatinib after a period off TKI therapy (*51*). Furthermore, an analogous *ABL* gatekeeper mutation (T315I) observed in imatinib-resistant chronic myelogenous leukemia (CML) cells decreases in abundance after imatinib therapy is stopped (*52*).

We predict that in patients with acquired resistance whose disease begins to accelerate rapidly, genetic alterations other than just the presence of the EGFR T790M mutation may play a role in tumor progression. That is, a third hit could enable escape from a slower growth phenotype and contribute to accelerated disease progression. Candidate third-hit genetic alterations remain to be identified.

In summary, evolutionary cancer modeling coupled with an understanding of the unique biological properties of TKI-sensitive and TKI-resistant cells has allowed us to propose optimized dosing schedules for the treatment of *EGFR*-mutant lung cancer. This approach could be more generally applied toward the optimization of dosing strategies of other targeted therapies used against oncogene-driven cancers.

MATERIALS AND METHODS

Patient samples and data

Tumor specimens were obtained with patients' consent under Memorial Sloan-Kettering Cancer Center (MSKCC) Institutional Review Board–approved protocols. Samples were frozen and stored at −80°C in institutional tumor banks.

CT scans from four patients treated prospectively with erlotinib (*26*) who then developed T790M-containing tumors were available for analysis (*11*). Two patients had a complete response with no residual measurable disease, leaving two patients evaluable. The presence of T790M was confirmed in rebiopsy samples from the remaining two patients after progression of disease, as determined by Response Evaluation Criteria in Solid Tumors (RECIST) (*53*). These cases were re-reviewed for characteristics of indolent progression. Serial bidimensional measurements of reference lesions were performed by a radiologist (M.S.G.) from the time of best response.

Growth assays

Growth inhibition was measured with CellTiter Blue Reagent (Promega) as per the manufacturer's instructions using cells plated in triplicate at a density of 4000 cells per well. Fluorescence was measured on a SpectraMax fluorometer. Growth inhibition was calculated as percentage of vehicle-treated wells ± SD.

For PC-9 cell counting assays, 20,000 to 40,000 cells per well were plated in six-well plates. Cell counting was performed in triplicate with an automated ViCell counter (Beckman Coulter) or a Coulter Counter. H322M cells were plated at a density of 100,000 per well and counted in quadruplicate with a Z2 Coulter Counter (Beckman Coulter). Cells were not allowed to reach >70% confluence at the final time point. Statistical significance was determined with the Student's two-tailed *t* test. For all assays conducted in the presence of drug, fresh TKI was added every 72 hours.

For reconstitution experiments, PC-9/BR C1 cells were mixed with parental cells at the indicated concentrations before plating. DNA was isolated in parallel from each dilution for PCR-based *EGFR* exon 20 sequencing to confirm mutant peak levels. All experiments were conducted at least two independent times.

Mathematical modeling

PC-9 and PC-9/ER populations were modeled as a two-type stochastic birth and death process. In the context of our model, each PC-9 or PC-9/ER cell waits an exponentially distributed amount of time to divide or die; this waiting time is governed by the cell birth and death rates. During PC-9 cell replication, a cell harboring the T790M mutation arises with a given probability (the mutation rate). Sensitive and resistant cells have distinct growth and death rates that vary depending on the drug concentration; these parameters were experimentally determined. We estimated the net (birth minus death) growth rate by fitting the mathematical model to cell counts at 48, 60, and 72 hours in the presence and absence of drug. Death rates were estimated from annexin V/propidium iodide fluorescence-activated cell sorting (FACS) counts; we considered double-positive cells to make up the dead cell population. We accounted for cell clearance by assuming that 50% of dead cells are cleared every 12 hours; this assumption was made to account for the degradation of dead cells in the cell culture over time. Measurements were performed at drug concentrations of 0, 1, 3, 10, and 20 μM erlotinib (Fig. 5A).

To calculate the expected frequency of T790M alleles in a population of 3 million cells that initiated with a single cell harboring only a drug-sensitive EGFR mutation and growing in the absence of drug, we used the growth and death rates obtained in the absence of drug (0 μM data point). We performed 100,000 Monte Carlo simulations of the model ending when the total population reaches the desired size (3 million cells). We recorded the number of resistant cells present at the final time point. For details, see (*18*, *54*).

To compare the relative effects of various dosing strategies on the development of resistance, we used analytical formulas describing the expected resistant cell population size under time-dependent dosing strategies. These calculations are based on the generating function for an inhomogeneous two-type birth and death process; birth and death rates of the sensitive and resistant cell population at each drug concentration are informed by data shown in Fig. 5A [see (*18*, *55*)].

Xenograft studies

Cells (5×10^6 to 10×10^6) were injected with Matrigel into the hind flanks of 8-week-old athymic (*nu/nu*) female mice (Harlan). When tumors reached ~150 mm^3, animals were randomized to receive vehicle alone, cisplatin (4 mg/kg twice per week, intraperitoneally), erlotinib (12.5 mg/kg daily, orally), or a combination of both erlotinib and cisplatin. Tumor volume was calculated as $L \times W^2 \times \pi/6$ and recorded twice per week. All animals were housed in pathogen-free facilities and provided with abundant food and water under guidelines approved by the MSKCC Institutional Animal Care and Use Committee and Research Animal Resource Center.