EGFR Protein Expression in Non–Small Cell Lung Cancer Predicts Response to an EGFR Tyrosine Kinase Inhibitor—A Novel Antibody for Immunohistochemistry or AQUA Technology

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Abstract

Introduction: Epidermal growth factor receptor (EGFR) protein expression in non–small cell lung cancer (NSCLC) is not recommended for predicting response to EGFR tyrosine kinase inhibitors (TKI) due to conflicting results, all using antibodies detecting EGFR external domain (ED). We tested the predictive value of EGFR protein expression for response to an EGFR TKI with an antibody that detects the intracellular domain (ID) and compared fluorescence-based Automated QUantitative Analysis (AQUA) technology to immunohistochemistry (IHC).

Methods: Specimens from 98 gefitinib-treated NSCLC Japanese patients were evaluated by IHC (n = 98 of 98) and AQUA technology (n = 70 of 98). EGFRID (5B7)- and ED-specific antibodies (3C6 and 31G7) were compared.

Results: EGFR expression evaluated with 5B7 was significantly higher in responders versus nonresponders to gefitinib both with IHC and with AQUA. ED-specific antibodies did not significantly predict response. Using AQUA and ID-specific antibody resulted in the best prediction performance with a positive and negative predictive value (PPV/NPV) for responders of 50% and 87%, respectively. EGFR expression with ID-specific antibody and AQUA also predicted responders in EGFR-mutated patients. Increased EGFR expression with the ID antibody is associated with increased median progression free survival (PFS; 11.7 months vs. 5.0, log rank, P = 0.034) and overall survival (OS; 38.6 vs. 14.9, P = 0.040) from gefitinib therapy.

Conclusions: EGFR protein expression using an ID-specific antibody specifically predicts response to gefitinib in NSCLC patients, including in EGFR-mutated patients, and increased PFS/OS from gefitinib. These data suggest that the choice of diagnostic antibody and methodology matters to predict response and outcome to specific therapies. The potential clinical application needs further validation.

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Introduction

Personalized therapy with individualized biomarker analysis has come to lung cancer treatment. In patients with advanced non–small cell lung cancer (NSCLC), response to epidermal growth factor receptor (EGFR) tyrosine kinase inhibitors (TKI) is significantly higher in females, never-smokers, patients with Asian ethnicity, adenocarcinoma histology, and tumors harboring activating EGFR mutations (1). EGFR TKIs are shown to be superior to chemotherapy in first-line therapy of advanced NSCLC patients with EGFR mutations (2–5). Thus, it is important to evaluate EGFR mutation status before choosing treatment of advanced NSCLC. However, EGFR mutation status alone may be insufficient to predict outcome as 17% to 38% of patients with mutations do not respond to EGFR TKIs in first-line therapy (2, 6–9) and 58% to 84% in second/third-line therapy (10–12). Furthermore, 1% to 7% of patients without mutations respond to EGFR TKIs in first-line therapy (2, 6–9) and 3% to 7% in second/third-line therapy (10–12). Several other biomarkers are being evaluated in NSCLC patients to predict response or resistance to EGFR TKIs. Current sensitive biomarkers

Note: Supplementary data for this article are available at Clinical Cancer Research Online (http://clincancerres.aacrjournals.org/).

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include EGFR-activating mutations, gene copy number, and protein expression, and resistant biomarkers include EGFR T790M and KRAS mutations, c-Met, and IGF1R expression.

Currently, EGFR protein expression is not recommended for predicting outcome to EGFR TKIs due to conflicting published results. Some studies showed a better outcome after EGFR TKIs treatment for tumors overexpressing the EGFR protein (10, 13, 14) whereas other studies did not (7, 11, 15). Inconsistent results from these studies could be due to insufficient sensitive methodology, lack of stringency in the assessments, cohort differences, or confounded by the concomitant administration of chemotherapy (15).

The mutations that predict response to EGFR TKIs are localized within the kinase domain, resulting in constitutive signaling of EGFR, which can therefore be inactivated by TKIs. The EGFR external domain (ED)–specific antibodies bind to receptors containing the ED and do not discriminate between active or inactive receptors, and may not even detect some truncated forms of the receptor that are constitutively active and potentially valid targets for EGFR TKIs. This may explain why assessment of protein expression using ED-specific antibodies is not a consistent predictor of response to EGFR TKIs.

A novel antibody, 5B7, specific for the intracellular domain (ID) of EGFR and directed against the epitope located at the suppressor of cytokine signaling 3 (SOCS3) protein binding site has been developed (16). An ID-specific antibody would also detect truncated forms of the receptor that are constitutively active. Therefore, using this antibody to quantify EGFR expression may more accurately predict response to EGFR TKIs. We have previously reported that EGFR expression evaluated by 5B7 does not predict survival in surgical NSCLC patients not treated with EGFR TKIs (17).

A concern about immunohistochemistry (IHC) analyses is the lack of standardization in procedures and assessment. IHC scoring is semiquantitative, subjective, and highly dependent on poorly controlled variables, for example, intensity of staining or percentage of stained cells is highly dependent on the evaluator (18). For applicability in the clinical setting, new NSCLC testing paradigms must produce objective and reproducible results. The Automated QUantitative Analysis (AQUA) technology is an immunofluorescence-based technique allowing automated and quantitative analysis of protein expression providing objective and reproducible scores (19). Analysis of protein expression with AQUA scoring for other biomarkers in NSCLC has been shown to be a compelling methodology for predicting prognosis and response to therapy in patients with NSCLC (20, 21).

This study is the first to report the predictive value of a novel antibody, detecting the ID of EGFR for response to gefitinib in patients with NSCLC. We compared the predictive values of EGFR protein expression with this novel antibody versus 2 ED-specific antibodies, using IHC and AQUA technology.

Patients and Methods

Patients

This study included 98 Japanese patients treated with gefitinib as monotherapy (250 mg/d) for their recurrent disease after having undergone curative pulmonary resection at the Tokyo Medical University Hospital between May 1995 and March 2008. Clinical characteristics are described in Supplementary Table S1. There were 46 (47%) males and 50 (51%) smokers. NSCLC was histologically confirmed on hematoxylin and eosin–stained sections according to the World Health Organization criteria (22) and consisted of 80 adenocarcinomas, 9 squamous cell carcinomas, 5 large cell carcinomas, and 4 other NSCLC. Pathologic staging at the time of surgery using the tumor—node—metastasis classification of malignant tumors seventh edition (23) showed 14, 17, 10, 9, 36, 7, and 5 patients at stages IA, IB, IIA, IIB, IIIA, IIIB, and IV, respectively.

Tumor response to gefitinib therapy was measured according to response evaluation criteria in solid tumors (RECIST; ref. 24) as complete response (CR), partial response (PR), stable disease (SD), and progressive disease (PD) using computed tomographic scanning. A confirmatory evaluation was repeated at least 4 weeks after the initial determination of response. During treatment with gefitinib, assessments were carried out every 4 weeks for the first 4 months and then every 8 weeks until disease progression. Disease control rate (DCR = CR + PR + SD) was evaluated at 12 weeks, as the RECIST (24) recommends that the duration of SD should specify the minimal time interval required between 2 measurements for determination of SD. In the 98 patients, 10 (10%) received gefitinib as their first
systemic anticancer therapy after recurrence, 43 (44%) received gefitinib as a second-, and 45 (46%) as third- or higher line therapy. The objective response rate (ORR) was considered only for patients treated with gefitinib for at least 4 weeks. ORRs were available for 94 of 98 patients. Overall survival (OS) and progression free survival (PFS) were defined as the time from start of gefitinib therapy to death or progression/death, respectively.

**Tissue microarrays**

Tissue microarray (TMA) construction has been described previously (25–27). Seventy tumors (N = 70 patients) were included in the TMA. The specimens were fixed with 10% formalin and embedded them in paraffin, then stored at room temperature.

Three replicate core samples (1.2 mm) from the most representative tumor areas from the formalin-fixed, paraffin-embedded resected tumors were collected, and the TMA was assembled using a tissue-arraying instrument (J.M and T.N, Department of Anatomic Pathology, Tokyo Medical University Hospital, Tokyo, Japan). Normal liver tissues were used for slide orientation purposes. After sectioning, the slides were stored at 4°C.

**EGFR IHC staining**

IHC was carried out on the 98 patients. Serial 4-μm thick tissue sections were cut from the TMA (N = 70 patients) and from whole tumor section (N = 28 patients). The slides were baked at 60°C overnight, then deparaffinized in xylene (Surgipath) and rehydrated through a graded ethanol (Surgipath) series. Unstained slides were barcoded for a standardized antibody-specific protocol and loaded into a Benchmark XT automated stainer (Ventana Medical Systems, Inc.). Antigen retrieval for EGFR 3C6 and EGFR 5B7 was carried out with Cell Conditioning 1 for 60 minutes at room temperature.

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**AQUA technology staining**

AQUA technology staining was only applied to the subset of 70 tumors on the TMA due to tissue unavailability for the other 28 tumors. Unstained slides were baked at 60°C for 1 hour and then deparaffinized. Antigen retrieval for EGFR 31G7 (Zymed; #28–0005) was carried out by incubating samples in pepsin solution Digest-All 3 (Invitrogen; #00–3009) at 37°C for 10 minutes. Antigen retrieval for EGFR 5B7 was done in a pressure cooker at 105°C for 20 minutes while using a 1:10 dilution of Tris-EDTA solution, pH 9.0 (Dako; #S2367). Using an automated stainer (Dako), EGFR protein expression was detected with the Aquantiplex EGFR Quantification Assay Kit (HistoRx Inc.; #AQ-EMT1–0001). The slides were blocked with Aquantiplex blocking buffer 1 for 5 minutes at room temperature and then rinsed with working buffer (1:10 diluted Tris-buffered saline containing 0.05% Tween 20, pH 7.6; Dako; #S3006) for 5 minutes. Slides were blocked with a second blocking buffer, Aquantiplex blocking buffer 2, for 10 minutes at room temperature and rinsed with working buffer for 5 minutes. Aquantiplex Primary Antibody Cocktail, EGFR 31G7 (prediluted and included in kit) or EGFR 5B7 (0.1 μg/mL), in addition to anti-pan cytokeratin antibodies, were incubated on slides at room temperature for 1 hour. Slides were washed 3 times with working buffer for 5 minutes each and incubated in Aquantiplex Epithelial Mask Visualization Solution, containing Dako Envision and Alexa Fluor 555 goat anti-rabbit immunoglobulin (H+L), for 30 minutes in the dark at room temperature. For fluorescence amplification, slides were exposed, 10 minutes at room temperature, to Cy5-tyramide and a 1:50 solution of Aquantiplex EGFR Visualization Solution in Aquantiplex EGFR Signal Amplification Diluent, for. Slides were mounted in the Prolong Gold antifade reagent with 4',6-diamidino-2-phenylindole (DAPI) solution (Invitrogen). To assess reproducibility between runs and batches, a control TMA slide was included in each run. The Pearson correlation coefficient was 0.936 with a slope at 0.9899, showing an excellent reproducibility between runs for the control tissue.

**AQUA scoring**

Automated image acquisition and analysis using AQUA technology has been described previously (19, 31). The finalized TMA slides were scanned with a PM-2000 microcopy system (HistoRx), and image data were analyzed with AQUA analysis software (HistoRx). AQUA technology allows measurement of protein concentration within subcellular
DNA sequencing of EGFR mutations

The methodology has been described in a previous publication (25).

Statistical analysis

Groups were compared by t tests choosing specific test and reported results were reported based on parallel testing for equality of variances. The optimal cut points were determined by receiver operating characteristic (ROC) curves by selecting the highest percentage of correct classification when both sensitivity and specificity are 50% or more. Sensitivity, specificity, likelihood ratios, and area under the curves (AUC) were also calculated. Correlations between continuous variables were carried out by Pearson correlation. Standard descriptive statistics and Kaplan–Meier survival curves were used. Differences in PFS were determined by the log-rank test. Association between the continuous scores and PFS were assessed with univariate analysis of variance. All of the above-discussed correlations were statistically significant (P < 0.001).

As illustrated by the histograms (Fig. 1), the expression level of EGFR was lower with ED-specific antibodies. Regardless of the antibody or technology used, both ED with IHC (3C6 antibody) and ED with AQUA technology (31G7 antibody), had lower EGFR scores than the ID-specific antibody 5B7. The lower levels of expression when using ED antibodies as compared with the ID antibody are illustrated in Fig. 2, which displays representative samples by IHC and AQUA staining.

Prediction of response to gefitinib by EGFR expression

We analyzed the predictive value for response of EGFR expression by IHC based on the 94 patients evaluable for response. The level of EGFR expression with ED-specific antibodies and IHC was not significantly different between nonresponders and responders to gefitinib whether evaluating membranous staining (mean H-score 31 versus 61, P = 0.73) or the ID-specific antibodies (5B7 for both methods; P = 0.83). The weakest correlation was between the EGFR expression scores when comparing antibodies detecting the ED versus the ID whether by IHC (3C6 versus 31G7; r = 0.55) or when using AQUA technology (31G7 versus 5B7; r = 0.63). All of the above-discussed correlations were statistically significant (P < 0.001).

Results

Evaluation of EGFR protein expression

Among the 98 patients, the median H-scores for the membranous EGFR expression were 10 (range 0–400) and 180 (range 0–400) for ED- and ID-specific antibodies, respectively. For the combined membranous + cytoplasmic staining, the median H-scores were 23 (range 0–280) and 200 (range 0–350) for ED- and ID-specific antibodies, respectively. The distribution of EGFR expression in these patients are illustrated in the histograms in Fig. 1.

On the 70 patient cohort on TMA, EGFR protein expression was determined both with IHC (70 of 70 evaluable) and AQUA technology (66 of 70 evaluable) using the 5B7 ID-specific antibody. We also evaluated, on the same cohort, EGFR expression with 2 different ED-specific antibodies (3C6 and 31G7), which detect the same epitope of EGFR, with IHC (using 3C6, 70 of 70) and AQUA (using 31G7, 69 of 70), respectively. When using IHC, the median H-scores for the membranous EGFR expression were 10 (range 0–400) with ED-specific antibody and 205 (range 0–400) with ID-specific antibody, respectively. In the evaluation of the membrane and cytoplasm staining, the median H-scores were 10 (range 0–280) and 200 (range 0–350) for ED and ID, respectively. The median AQUA scores were 8.05 (range 6.80–11.58) and 11.68 (range 6.89–14.30), respectively, when using ED- and ID-specific antibodies.

Pearson correlation tests were carried out between results according to the different antibodies, compartments, and technologies (Supplementary Fig. S1). The correlations were carried out on 98 patients when including IHC evaluations only and on 70 patients when including AQUA technology. A strong correlation was found between IHC scores for the membranous versus membranous + cytoplasmic expression when using the 3C6 ED antibody (r = 0.92) and the 5B7 ID antibody (r = 0.7). There was also a strong correlation between the scores obtained by IHC and AQUA technologies, for ED-specific antibodies even if the antibodies used were different (3C6 versus 31G7; r = 0.73) and for the ID-specific antibodies (5B7 for both methods; r = 0.83). The weakest correlation was between the EGFR expression scores when comparing antibodies detecting the ED versus the ID whether by IHC (3C6 versus 5B7) when evaluating the membrane only (r = 0.55), when evaluating membrane + cytoplasm (r = 0.51) or when using AQUA technology (31G7 versus 5B7; r = 0.63). All of the above-discussed correlations were statistically significant (P < 0.001).
the membranous staining (156 versus 213, \(P = 0.0214\)) and slightly more significantly when assessing membranous + cytoplasmic staining (168 versus 231, \(P = 0.0013\)). EGFR expression assessed with the ID-specific antibody and IHC evaluating membranous + cytoplasmic staining predicted response with a positive predictive value (PPV), negative predictive value (NPV), and accuracy of 42%, 89%, and 72%, respectively. The best cut point was 217 as determined by ROC curve analysis (Fig. 3B).

We further compared the prediction of response of EGFR protein expression by using IHC versus AQUA in 70 patients (Table 1). The level of EGFR expression by IHC using ED-specific antibodies was not significantly different between responders and nonresponders to gefitinib whether...
evaluating membranous staining (mean H-score 34 versus 72, nonresponders versus responders, respectively, $P = 0.27$) or membranous + cytoplasmic staining (43 versus 76, $P = 0.27$). However, by using AQUA, it was borderline (8.2 versus 8.9, $P = 0.0581$). When using the ID-specific antibody, EGFR expression was significantly higher in gefitinib responders versus nonresponders using IHC and scoring membranous staining (185 versus 257, $P = 0.0063$). Results were more significant for IHC when assessing membranous + cytoplasmic staining (179 versus 245, $P = 0.0026$) and even more significant when assessing ID by AQUA analysis (11.2 versus 12.7, $P = 0.0017$; scatter plots shown in Supplementary Fig. S2).

To determine the highest accuracy for predicting response to gefitinib for each type of EGFR expression quantification, we carried out ROC curve analysis (Table 2 and Fig. 3A). When evaluating EGFR expression with ED-specific antibodies, the ROC curves did not significantly discriminate between responders and nonresponders. When using ID-specific antibody, the ROC curves were able to significantly discriminate between responders to gefitinib and nonresponders. Using the ID antibody, the AUC was highest when using the AQUA scoring (0.78, $P = 0.0018$), intermediate when using IHC with evaluation of the membrane + cytoplasm staining (0.73, $P = 0.0078$) and the lowest by IHC with evaluation of membrane-only staining (0.70, $P = 0.0289$). The corresponding PPVs for being responders were 38%, 38.5%, and 50%; the NPVs were 85%, 88%, and 88%; and the accuracies were 70%, 69%, and 80% when evaluating EGFR expression by IHC membrane only (cut point = 235), IHC membrane and cytoplasm (cut point = 215) and AQUA scoring (cut point = 12.72), respectively.

**Association of EGFR protein expression with EGFR mutations analyses**

A statistically significant association was found between EGFR protein expression and mutation status, except when assessing ED by IHC. Tumors with EGFR mutations harbored a significantly higher level of EGFR protein expression when using an ID-specific antibody or an ED-specific antibody by AQUA (Table 3).

We further compared the level of EGFR protein expression of patients with tumors harboring activating mutations and expected to be sensitive to EGFR TKIs (exon 19 and exon 21), versus other patients (EGFR wild-type tumors and those harboring other EGFR mutations, i.e., exon 18 or 20). Activating EGFR mutations in the tumor were associated with a significantly higher level of EGFR protein expression, regardless of the method used. The most significant association was obtained when detecting the ID with mean scores 195 versus 152 for tumors with activating mutations or not, respectively ($P = 0.0412$), 213 versus 156 ($P = 0.0006$), and 12.19 versus 10.99 ($P = 0.0010$) when using IHC membrane only, IHC membrane + cytoplasm, and AQUA technology, respectively. When detecting the ED, the level of EGFR expression was also significantly higher in mutated tumors but only with AQUA and not IHC: 50 versus 25, $P = 0.0912$, 61 versus 40, $P = 0.1533$, and 8.78 versus 8.09, $P = 0.0105$, when using IHC membrane only, IHC membrane + cytoplasm, and AQUA technology, respectively.
The nonresponders within mutated patients, another cut point (11.6), which optimized the NPV and the sensitivity, was chosen. Doing so, resulted in a NPV, PPV, and accuracy of 93%, 50%, and 66%, as 1 of 14 of responders highly expressed EGFR.

**Outcome**

The median OS and PFS are reported in Supplementary Table S1. We evaluated PFS and OS first by Kaplan–Meier curves and log-rank analyses with the best cut points derived from ROC analysis and then by Cox proportional models evaluating EGFR expression as a continuous variable. EGFR protein expression, regardless of the antibody used, compartment analyzed, or technique used, did not significantly associate with PFS in the cohort of 70 patients with the log-rank test. However, with the Cox model, EGFR expression evaluated with the ID-specific antibody and AQUA technology was significantly associated with PFS in univariate \( P = 0.0406 \) and multivariate analyses \( (P = 0.0134) \). In the total cohort of 98 patients, increased EGFR expression determined with the ID antibody and membranous + cytoplasmic evaluation associated with increased median PFS (11.7 months vs. 5.0, log-rank test, \( P = 0.034 \) and OS (38.6 vs. 14.9, \( P = 0.040 \)). The association between increased EGFR expression determined with the ID antibody using membranous + cytoplasmic evaluation and increased PFS was confirmed by Cox proportional models in univariate \( (P = 0.0242) \) and multivariate \( (P = 0.0151) \) analyses, but the association between EGFR expression and OS was not confirmed in the Cox proportional model.

In the subgroup of patients with EGFR mutations, EGFR expression evaluated with the ID-specific antibody and scoring membranous + cytoplasm was also associated significantly with PFS in univariate \( (P = 0.0323) \) and multivariate \( (P = 0.0074) \) analyses and borderline for OS \( (P = 0.0794 \) and 0.0666, respectively) using the Cox proportional hazards model.

PFS and OS Kaplan–Meier curves are shown in Supplementary Figs. 3 and 4, respectively.

**Discussion**

We assessed and compared the predictive role of the novel antibody, 5B7, which detects the ID of EGFR versus antibodies detecting its ED, using 2 detection methods, namely, IHC (evaluation of the membrane only versus evaluation of both the cytoplasm and the membrane) and the AQUA technology. EGFR expression levels were significantly correlated between the different antibodies/techniques. The level of EGFR expression using ED-specific antibodies was markedly lower as than those detecting the ID. EGFR expression by IHC using the ID-specific antibody was a significant predictor of response to gefitinib in this cohort of Japanese NSCLC patients and assessment of EGFR expression measured by AQUA technology using the ID antibody increased the predictive performance of the assay. In addition, EGFR expression...
using the ID-specific antibody predicted responders in the subgroup of mutated patients. Finally, high EGFR expression evaluated with the ID-specific antibody was associated with increased PFS and OS. Although significantly associated to mutation status, EGFR expression determined by ED-specific antibodies did not significantly predict response to gefitinib. Thus, we found EGFR expression being predictive of response to gefitinib as using a novel ID-specific antibody. The importance of epitope variability has been shown previously (33). The 5B7 antibody for EGFR, which was predictive of response to gefitinib in our cohort of Japanese NSCLC patients, detects the SOCS3 binding epitope of the ID. When SOCS3 is bound to EGFR, it is thought to inhibit the downstream signaling cascade of the receptor (16). Therefore, it is hypothesized that when SOCS3 is present, EGFR is inactive and 5B7 will not bind due to steric hindrance. When the 5B7 antibody binds the receptor on this particular epitope, it only does so when SOCS3 is not present and cannot inhibit the EGFR cascade. This may explain the enhanced ability of 5B7-mediated detection of EGFR to predict response to EGFR TKIs.

Another point is that previously published studies were using cutoff as low as 10% (10–14) of positive cells to define EGFR IHC-positive tumor. When we carried out the ROC analyses to determine the best cutoff to discriminate between responders and nonresponders, the cutoff values were much higher than 10% of cells. The measured levels of expression of EGFR was globally lower when assessing the ED versus the ID, many cases even being negative for the former and positive for the latter. The level of expression of EGFR using ED-specific antibodies in our study (median H-score of 10) was a little bit lower than observed in the BR21 study (median H-score 40 using Dako PharmDX kit; ref. 34) and much lower than in the ISEL study (median H-score of 300 using 31G7 and median of 45% using Dako PharmDX kit; ref. 28). The variable results strongly indicate the need for standardization of IHC procedure. However, the lower level of EGFR expression using ED-specific antibody compared with ID-specific antibody is consistent whether using IHC with 3C6 or AQUA technology with 31G7 to detect the ED. Thus, this is not antibody or technology related but more likely to the detection of ED versus ID. One hypothesis to explain this difference in EGFR expression level when detecting the receptor by ED or ID could be a cleavage of the ED. Truncated forms of the HER2 receptor with a basal cleavage of the ED has been largely reported and shown to keep and even increase the tyrosine kinase activity of the receptor (35–38). An amino-terminal truncation of EGFR

### Table 1. Association of EGFR expression with response status to gefitinib

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<th>Methods of evaluation of EGFR expression</th>
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NOTE: To compare the performance of the techniques/antibodies to discriminate between responders and nonresponders, this table displays the results with the 70 patients on which the 6 different evaluations were carried out.

<sup>a</sup>Independent, 2-sample t test for difference in mean score between responders and nonresponders. Equivalence of variance was tested.

<sup>b</sup>In case of inequality of variance, a t test not assuming equality of variances was used.
extracellular domain has been reported (39, 40). This hypothesis requires further experimentation. Due to the fact that the ED-truncated form is constitutively activated, EGFR TKIs are supposed to be an efficient treatment for tumors harboring these forms of EGFR. Therefore, using an ID-specific antibody able to detect these ED-truncated EGFR proteins is worthy of predicting response to EGFR TKIs. Conversely, as monoclonal therapeutic antibodies target the ED, the use of a diagnostic antibody detecting the expression of the ligand domain is required to predict any potential response to these therapeutic antibodies. Therefore, using an antibody detecting the ED might be a better choice to predict response to therapeutic monoclonal antibodies against EGFR, and using an ID-specific antibody could be more accurate to predict response to EGFR TKIs, but this conclusion requires further validation and evidentiary support.

Previous publications on EGFR IHC were based on the evaluation of membrane staining exclusively (10, 13, 14, 30). We assessed membranous staining, membranous + cytoplasmic staining by IHC and compared it with membrane + cytoplasmic staining by AQUA technology. The evaluation of 5B7 by IHC was more significantly predictive of response to EGFR TKIs once cytoplasmic staining was integrated in the evaluation. This could reflect that the presence of a high turnover of the receptor in the cytoplasm indicating a higher activity of EGFR in the cell and a higher sensitivity to EGFR TKIs.

Finally, using AQUA technology to evaluate EGFR expression further improved the predictive performance as compared with IHC, even with the use ED-specific antibodies. However, we must be cautious in interpreting these last results because the ED-specific antibodies used to compare IHC and AQUA scoring were different (3C6 versus 31G1), but this bias is very likely minimal as the 2 antibodies detect the same epitope on the ED of the receptor. Using 5B7, AQUA technology improved PPV and accuracy by 10% and specificity by 17% as compared with IHC.

The need to standardize biomarker testing for clinical use led us to assess and compare AQUA technology to classical IHC. IHC provides information on protein expression and localization and has been the standard protein in situ assay. However, IHC scoring is semiquantitative and subjective (41). TMAs provide a high-throughput method to analyze potential biomarkers on multiple samples but are limited by the pathologist’s ability to reproduce scores on a continuous scale, discriminate between subtle low-level staining differences, and accurately score expression within subcellular components. AQUA analysis is an immunofluorescence-based technique with automated and quantitative analysis of proteins, thus reducing the human variability occurring with IHC scoring. AQUA technology automatically measures protein expression in subcellular compartments (i.e., nuclear versus cytoplasmic), providing a continuous score in an accurate, reliable, and

### Table 2. Accuracy to predict response to gefitinib according to the method used to evaluate EGFR expression

<table>
<thead>
<tr>
<th>Methods of evaluation</th>
<th>Best cutoff</th>
<th>Sensitivity</th>
<th>Specificity</th>
<th>Accuracy</th>
<th>PPV</th>
<th>NPV</th>
<th>LR</th>
<th>AUC</th>
<th>P</th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>Subset of 70 patients</strong></td>
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<tr>
<td>Specific antibodies for the ED of EGFR</td>
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<tr>
<td>ED IHC membrane</td>
<td>NA</td>
<td>NA (%)</td>
<td>NA (%)</td>
<td>NA (%)</td>
<td>25.8</td>
<td>80.6</td>
<td>1.21</td>
<td>0.54</td>
<td>0.6197</td>
</tr>
<tr>
<td>ED IHC membrane and cytoplasm</td>
<td>8.48</td>
<td>53.3</td>
<td>55.2</td>
<td>65.2</td>
<td>36.4</td>
<td>83.3</td>
<td>1.70</td>
<td>0.66</td>
<td>0.0653</td>
</tr>
<tr>
<td>Specific antibody for the internal domain of EGFR</td>
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<tr>
<td>ID IHC membrane</td>
<td>235</td>
<td>53.3</td>
<td>75</td>
<td>70.1</td>
<td>38.1</td>
<td>84.8</td>
<td>2.13</td>
<td>0.70</td>
<td>0.0289</td>
</tr>
<tr>
<td>ID IHC membrane and cytoplasm</td>
<td>215</td>
<td>66.7</td>
<td>68.7</td>
<td>79.4</td>
<td>50</td>
<td>87.8</td>
<td>3.85</td>
<td>0.78</td>
<td>0.0018</td>
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<tr>
<td><strong>Whole cohort of 98 patients</strong></td>
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<td>Specific antibodies for the ED of EGFR</td>
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<tr>
<td>ED IHC membrane</td>
<td>NA</td>
<td>NA</td>
<td>NA</td>
<td>NA</td>
<td>NA</td>
<td>NA</td>
<td>NA</td>
<td>0.58</td>
<td>0.2643</td>
</tr>
<tr>
<td>ED IHC membrane and cytoplasm</td>
<td>37.5</td>
<td>52.4</td>
<td>64.4</td>
<td>61.7</td>
<td>29.7</td>
<td>82.5</td>
<td>1.47</td>
<td>0.59</td>
<td>0.1763</td>
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<tr>
<td>Specific antibody for the internal domain of EGFR</td>
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<tr>
<td>ID IHC membrane</td>
<td>205</td>
<td>52.4</td>
<td>69.9</td>
<td>65.9</td>
<td>33.3</td>
<td>83.6</td>
<td>1.74</td>
<td>0.64</td>
<td>0.0484</td>
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<tr>
<td>ID IHC membrane and cytoplasm</td>
<td>217</td>
<td>66.7</td>
<td>74.0</td>
<td>72.3</td>
<td>42.4</td>
<td>88.5</td>
<td>2.56</td>
<td>0.72</td>
<td>0.0016</td>
</tr>
</tbody>
</table>

**NOTE:** To compare the performance of the techniques/antibodies to discriminate responders versus nonresponders, this table displays the results with the 70 patients on which the 6 different evaluations have been carried out. In addition, data on the total cohort are reported for IHC.

Abbreviations: NA, no accuracy for both a sensitivity and specificity of at least 50%; LR, likelihood ratio; AUC, area under the curve; P, P value for the AUC.
reproducible way. The remaining investigator-based operations in the AQUA score acquisition are the selection of the area to be scanned and, after acquisition of the image, the cropping of artifactual features or exclusion of entire cores. The other steps of AQUA score acquisition are fully automated, therefore reducing the investigator-based variability. Reported results in NSCLC support AQUA technology as a valid methodology for use (20, 21). Few other studies compared IHC versus AQUA scoring. Anagnostou and colleagues (33) found that estrogen receptor evaluation by IHC and AQUA scoring were correlated and in close proportion (Spearman correlation coefficient at 0.69) to what we observed (0.732 and 0.827, respectively, for ED- versus ID-specific antibodies). Analyses of TS expression in small cell lung cancer by IHC versus AQUA scoring showed a much lower, but significant correlation \( r = 0.25; \) ref. 42). An analysis of HER2 expression in breast tumors showed a correlation at 0.704 between manual (4 categories) versus automated acquisition of the score for protein expression (43). The prediction of the categories as determined by IHC or AQUA scoring was different. These results showed clearly the difficulty in manually translating a biological (continuous) marker into a nominal 4-point scale. Even for a trained pathologist, accurate distinction between categories (e.g., histoscore of 2 versus 3) is difficult and potentially arbitrary. The lack of reproducibility of IHC scoring has been reported by many authors (44–46). The AQUA assay is standardized, and the acquisition of the score is automated. Therefore, the value of the cut point will be obtained with a high reproducibility. However, to determine the optimal cut point, further validation studies must be carried out in different cohorts.

Attention must be given to the specific characteristics of the cohort we studied when interpreting our data. The cohort was exclusively Asian (Japanese) and therefore may not translate into a non-Asian population. The treatment lines within the current cohort, 10% having received gefitinib as their first systemic anticancer therapy after relapse, 44% as second, and 45% as third- or higher line therapy were highly variable. Therefore, the interpretation of the outcome data in this cohort is difficult. There is a need for validation of the present study’s results in other cohorts and the applicability to a Caucasian cohort needs to be shown.

In conclusion, this study shows that the evaluation of EGFR protein expression using a novel antibody detecting a specific epitope on the ID, which is only accessible on activated EGFR, can predict response and outcome to gefitinib using traditional IHC or AQUA technology. This data shed a new light on the potential use

<table>
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<tr>
<th>Table 3. Association of EGFR expression with EGFR mutation</th>
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<tr>
<td>Methods of evaluation of EGFR expression</td>
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<tr>
<td>Specific antibodies for the ED of EGFR</td>
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<td>ED IHC membrane</td>
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<td>ED IHC membrane and cytoplasm</td>
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<tr>
<td>ID IHC membrane and cytoplasm</td>
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</table>

\( ^a \)Independent, 2-sample \( t \) test for difference in mean score between responders and nonresponders. Equivalence of variance was tested.

NOTE: The analyses were conducted for on the total population for IHC and on 70 patients for AQUA technology.
of EGFR protein expression as a biomarker for the prediction of response to EGFR TKIs. The current results also emphasize the importance of the choice of the methods to be used (e.g., type of antibody, compartment assessed, and detection technique) for the detection of EGFR protein, and in particular, the choice of the diagnostic antibody to evaluate EGFR expression relative to the therapeutic strategy, that is, an ED-specific antibody may be better predicting response to anti-EGFR monoclonal antibodies, whereas an ID-specific antibody may be better for EGFR TKR responses prediction. This hypothesis needs further validation. Interestingly, EGFR expression using the ID-specific antibody predicted responders in the subgroup of EGFR-mutated patients. This could have a potential clinical application, as EGFR mutation might not be sufficient as stand alone procedure for discriminating responders versus nonresponders to EGFR TKIs.

References


Disclosure of Potential Conflicts of Interest

F.R. Hirsch: commercial research grant, OSI, AstraZeneca, Genentech, Syndax, Ventana; ownership interest, Imclone; co-investigator of University of Colorado patent licensed to Abbott: “EGFR FISH as predictive marker for EGFR inhibitors,” consultant/advisory board, AstraZeneca, Genentech/OSI/Roche, Biotheringer Ingelheim, Syndax. The other authors disclosed no potential conflicts of interest.

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EGFR Protein Expression in Non–Small Cell Lung Cancer Predicts Response to an EGFR Tyrosine Kinase Inhibitor—A Novel Antibody for Immunohistochemistry or AQUA Technology

Celine Mascaux, Murry W. Wynes, Yasufumi Kato, et al.

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