Human Breast Cancer Cells Harboring a Gatekeeper T798M Mutation in HER2 Overexpress EGFR Ligands and Are Sensitive to Dual Inhibition of EGFR and HER2

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Abstract

Purpose: Mutations in receptor tyrosine kinase (RTK) genes can confer resistance to receptor-targeted therapies. A T798M mutation in the HER2 oncogene has been shown to confer resistance to the tyrosine kinase inhibitor (TKI) lapatinib. We studied the mechanisms of HER2-T798M–induced resistance to identify potential strategies to overcome that resistance.

Experimental Design: HER2-T798M was stably expressed in BT474 and MCF10A cells. Mutant cells and xenografts were evaluated for effects of the mutation on proliferation, signaling, and tumor growth after treatment with combinations of inhibitors targeting the EGFR/HER2/HER3/PI3K axis.

Results: A low 3% allelic frequency of the T798M mutant shifted 10-fold the IC50 of lapatinib. In mutant-expressing cells, lapatinib did not block basal phosphorylation of HER2, HER3, AKT, and ERK1/2. In vitro kinase assays showed increased autocatalytic activity of HER2-T798M. HER3 association with PI3K p85 was increased in mutant-expressing cells. BT474-T798M cells were also resistant to the HER2 antibody trastuzumab. These cells were sensitive to the pan-PI3K inhibitors BKM120 and XL147 and the irreversible HER2/EGFR TKI afatinib but not the MEK1/2 inhibitor CI-1040, suggesting continued dependence of the mutant cells on ErbB receptors and downstream PI3K signaling. BT474-T798M cells showed increased expression of the EGFR ligands EGF, TGF-a, amphiregulin, and HB-EGF. Addition of the EGFR neutralizing antibody cetuximab or lapatinib restored trastuzumab sensitivity of BT474-T798M cells and xenografts, suggesting that increased EGFR ligand production was causally associated with drug resistance.

Conclusions: Simultaneous blockade of HER2 and EGFR should be an effective treatment strategy against HER2 gene–amplified breast cancer cells harboring T798M mutant alleles. Clin Cancer Res; 19(19); 5390–401. ©2013 AACR.
Her2T798M cells expressed higher levels of the EGFR ligands EGF, TGFα, amphiregulin, and HB-EGF. Consistent with a causal role of these ligands, the addition of the neutralizing EGFR antibody cetuximab restored sensitivity to trastuzumab in cells and xenografts expressing HER2T798M. Furthermore, inhibition of EGFR with lapatinib also synergized with trastuzumab against xenografts expressing HER2T798M, suggesting simultaneous inhibition of EGFR and HER2 abrogates the resistance induced by the gatekeeper mutation.

Materials and Methods

Generation of cells stably expressing HER2T798M

An HER2T798M expression vector was generated by subcloning the mutant sequence in the SalI/HindIII site of DNR Dual (BD Biosciences) and then recombined using Cre into the JPT1520 retroviral vector. Retroviruses expressing HER2T798M were produced by transfecting Phoenix-Ampho cells using published methods (20) and then used to transduce BT474 and MCF10A cells. Stably transfected cells were selected in 1 mg/mL G418.

Cell culture and proliferation assays

BT474 cells were maintained in IMEM medium/10% FBS (Gibco). MCF10A cells were maintained in DMEM/F-12 supplemented with EGF (20 ng/mL, Invitrogen/Gibco), cholera toxin (100 ng/mL, Sigma), hydrocortisone (500 ng/mL, Sigma), insulin (10 μg/mL, Invitrogen), and 5% horse serum (HyClone). Cell proliferation was measured either by fixing and staining cells with crystal violet (29) or by using MIT (Sigma) or premixed WST-1 reagent (Roche) according to the manufacturer’s protocol. The following inhibitors were used for various proliferation assays: 1 μmol/L lapatinib; 1 μmol/L CI-1040; 1 μmol/L BIBW2992 (all from LC Laboratories); 20 μg/mL trastuzumab; 20 μg/mL cetuximab (both from the Vanderbilt University Pharmacy); 1 μmol/L BKM120 (Active Biochem); and 6 μmol/L XL-147 (provided by Exelixis). For MTI/WST-1 assays, 1 × 10^4 cells/well were seeded in 96-well plates. Twenty-four hours after plating, cells were treated with dimethyl sulfoxide (DMSO) or inhibitors. After 5 days of treatment, MTI/WST-1 assays were conducted according to the manufacturer’s protocol. For growth assays following HER3 knockdown, pooled HER3 and control siRNA (Dharmacon) were reverse-transfected into cells using Lipofectamine RNAiMax (Invitrogen) according to the manufacturer’s protocol. Briefly, cells were plated in triplicate in 24-well plates and transfected with HER3 or control siRNA (50 μmol/L). Seven days posttransfection, cells were trypsinized and counted using a Coulter counter. Alternatively, cells were treated with the LNA oligonucleotides directed against HER3 (EZN3920) or control (EZN4455) at a final concentration of 5 μmol/L (30) provided by Enzon Pharmaceuticals for 7 days.

Three-dimensional Matrigel culture

Cells (5 × 10^3/well) were seeded in 8-well chamber slides. Before seeding, BT474 and MCF10A cells were suspended in their respective medium on growth factor–reduced Matrigel.
(BD Biosciences) as described (31). Inhibitors were added at the time of cell seeding and replenished with fresh medium every 3 days. After 12 to 14 days, images were captured from at least 3 different fields. To quantify cell number, Matrigel was dissolved by treatment with dispase for 2 hours at 37°C and acini were dissociated by pipetting. Dissociated cells were treated with trypsin and pelleted by centrifugation before being resuspended in growth medium and counted using a hemocytometer.

**Immunoprecipitation and immunoblotting**

Immunoprecipitations were conducted with a p85 antibody (Millipore) or a HER2 antibody (Neomarkers) followed by Protein A beads (Sigma) as described (32). Immune complexes and whole-cell lysates were subjected to SDS-PAGE and transferred onto nitrocellulose membranes. For immunoblot analysis, cells were lysed in 1% NP-40 buffer containing protease and phosphatase inhibitors. Samples were sonicated for 10 seconds and centrifuged at 14,000 rpm for 5 minutes at 4°C; protein concentrations were quantitated using the BCA assay (Pierce). Primary antibodies included Y1248 P-HER2, Y1068 P-EGFR, total EGFR, Y1197 P-HER3, total AKT, S473 P-Akt, P-Erk1/2, Erk1/2, (Cell Signaling); HER3, EGFR (Santa Cruz Biotechnology); HER2 (Neomarkers); Actin (Sigma); and the 4G10 phosphorysine antibody (Millipore).

**Cell surface biotinylation**

The Cell Surface Protein Isolation Kit (Pierce) was used for biotinylation studies according to the manufacturer’s protocol. After treatment with 20 μg/mL trastuzumab for 16 hours at 37°C, cells were incubated with cold acid wash buffer (0.5 mol/L NaCl, 0.2 mol/L Na acetate, pH 3.0) for 6 minutes to remove bound trastuzumab. The cell monolayers were washed 3× with ice-cold PBS (pH 8.0) before the addition of freshly prepared Sulfo-NHS-Biotin reagent (200 μg/mL; Pierce) for 30 minutes at 4°C. The reaction was quenched with 100 mmol/L glycine in PBS and cells were harvested in lysis buffer (plus protease and phosphatase inhibitors) included in the kit. After sonication for 10 seconds and centrifugation at 14,000 rpm, protein concentration in the supernatants was measured using the BCA assay (Pierce). Equal amounts of protein extracts (500 μg) were subjected to precipitation using immobilized Neutravidin gel (Pierce); eluates were next subjected to SDS-PAGE and HER2 immunoblot analysis.

**In vitro kinase assays**

Five hundred micrograms of total protein from cells was precipitated with an HER2 antibody overnight at 4°C. Precipitates were subjected to an in vitro kinase assay as described (33). Briefly, precipitates were washed twice with NP-40 lysis buffer followed by 1 washes with kinase buffer (20 mmol/L HEPES, pH 7.5, 10 mmol/L MgCl2, 10 mmol/L MnCl2, 1 mmol/L dithiothreitol, 0.1 mmol/L Na3VO4). The immune complexes were next divided on ice into 2 equal aliquots and ATP (final concentration, 0.1 mmol/L) was added to one of the kinase reactions, which were carried out for 5 minutes at 30°C and terminated by adding 5× loading buffer followed by boiling for 3 minutes. Kinase reaction products were then separated on a 7.5% SDS-PAGE gel and subjected to immunoblot analysis.

**Real-time quantitative PCR**

RNA isolation and real-time quantitative PCR (RT-PCR) were carried out as described (34, 35). Primer sequences for ErbB ligands are as follows: Heregulin (HRG): forward 5′-TGGCTGACAGCAAGCAGTAAC-3′, reverse 5′-CTGGCCCTGGATTCTCTC-3′; EGF: forward 5′-AGCTAACCATGATGCAACA-3′, reverse 5′-AGITTTTCATGCTAGCCTCAT-3′; TGFα: forward 5′-GGACACGACTGCCAGAAGA-3′, reverse 5′-CAGGTGATTACAGGCCAATGAG-3′; amphiregulin (AREG): forward 5′-ATAATCAATGAGCTATCTCCCAGCACA-3′, reverse 5′-GGCCCAATTCTGTTTATGATCCAC-3′; HH-EGF: forward 5′-GAAAGACTTCCATGTCATACAAAGA-3′, reverse 5′-ATCTTAAGGTACACAATTATCAAAGCTGA-3′; and betacellulin (BTC): forward 5′-TGCCCCAAAGAAATACCAAGGCACTCA-3′, reverse 5′-CGTCTGCTGGCCGACCC-3′.

**HER2T798M sequencing**

Exons 19-20 of HER2 were amplified from reverse-transcribed RNA isolated from BT474 (37) using the primer pair forward 5′-TGTTGGATCGCTGCTGCTG-3′ and reverse 5′-CAACACTGCTGCTCCACAGC-3′. The RT-PCR product was cloned into the pCR Blunt vector (Invitrogen). A total of 96 colonies were picked to inoculate individual cultures in 96-well blocks, which were then pooled into 12 groups of 8 individual clones. These 12 pools were screened for the presence of HER2T798M by direct (Sanger) sequencing. Individual plasmids from positive pools were resequenced to determine the allelic frequency of HER2T798M.

**Xenograft studies**

Mouse experiments were approved by the Vanderbilt Institutional Animal Care and Use Committee. Mice were housed in the Vanderbilt Animal Care Facility. A 17β-estradiol pellet (Innovative Research of America) was included before tumor cell injection. BT474 cells (5 × 10⁶) mixed 1:1 with Matrigel (BD Biosciences) were injected s.c. in the right flank of each mouse. Tumor diameters were measured with calipers twice per week and volume in mm³ calculated by the formula volume = width² × length/2. When tumors reached a volume ≥200 mm³, mice were treated for 4 to 5 weeks with the following, either alone or in combination: trastuzumab 30 mg/kg twice per week intraperitoneally (i.p.), lapatinib 100 mg/kg daily via orogastric gavage, and cetuximab 1 mg twice per week i.p.

**Immunohistochemistry**

Tumors were harvested at the end of treatment (after 4 to 5 weeks), fixed in formalin, and paraffin embedded. Tumor sections (5 μm) were stained with a S473 P-Akt antibody
Figure 1. Cells expressing HER2 T798M are resistant to lapatinib and trastuzumab. A, BT474 GFP and BT474 T798M cells were treated with increasing concentrations of lapatinib for 5 days. MTT assay was conducted at the end of treatment and dose inhibition curves were produced by Graphpad Prism software. IC₅₀ values were calculated according to the formula Y = 100([1 + 10^X logIC₅₀]) – B. BT474 GFP and BT474 T798M cells were treated with increasing concentrations of lapatinib for 3 hours. Protein extracts were prepared and subjected to immunoblot analyses with the antibodies indicated on the left. C, cells were treated with lapatinib for 3 hours, and protein extracts were subjected to immunoprecipitation with a p85 antibody. Immune complexes associated with p85 were separated by SDS-PAGE followed by immunoblot with the indicated antibodies. D, cells were treated with either 1 µmol/L lapatinib or 20 µg/mL trastuzumab for 9 hours. Crystal violet assays were conducted on days 6 and 9, and images captured using the Li-Cor Odyssey System. E, cells were treated with 1 µmol/L lapatinib or 20 µg/mL trastuzumab for 3 hours. Protein extracts were prepared and subjected to immunoblot analyses with antibodies indicated on the left. F, cells were treated with 20 µg/mL trastuzumab overnight and then cell surface proteins were biotinylated as described in Methods. Biotinylated proteins were captured with Neutravidin gel and analyzed by immunoblot with a HER2 antibody. Bottom, HER2 and actin immunoblots of whole-cell lysates to control for gel loading.

(Cell Signaling) and staining intensity was scored by an expert pathologist (M.V. Estrada) blinded to treatment groups. Intensity of cytoplasmic staining was scored from 0 to 3++, in 5 different fields at ×400 magnification for each section. The average score from those 5 fields was then used to calculate an H score by the following formula: 3 × (% of 3+ cells) + 2 × (% of 2+ cells) + 1 × (% of 1+ cells). The mean H scores ± SEM for each treatment group were compared by ANOVA.

Results

T798M mutation in HER2 confers resistance to HER2 antagonists in HER2-amplified breast cancer cells

BT474 cells were stably transduced with a retroviral vector encoding either HER2 T798M or GFP. Expression of the T798M mutant isoform increased the IC₅₀ to lapatinib by 10-fold compared with GFP-expressing cells (Fig. 1A). Treatment with 1 µmol/L lapatinib blocked phosphorylation of HER2, HER3, Akt, and Erk1/2 in BT474 GFP but not in BT474 T798M cells (Fig. 1B). Presence of the mutation also resulted in continued association of HER3 with the p85 regulatory subunit of PI3K in the presence of lapatinib (Fig. 1C). Lapatinib or trastuzumab inhibited growth of BT474 GFP cells, but BT474 T798M cells were resistant to both inhibitors (Fig. 1D). Treatment with trastuzumab inhibited Akt phosphorylation in BT474 GFP but not in BT474 T798M cells (Fig. 1E). Trastuzumab binds to domain IV of HER2 (36) and induces receptor internalization and downregulation from the cell surface, thus attenuating downstream signal transduction (37). As trastuzumab did not inhibit downstream signaling in cells expressing T798M (Fig. 1E), we...
investigated whether this mutation would impair trastuzumab-induced receptor internalization. Cell surface biotinylation followed by precipitation of labeled proteins with neutravidin showed that trastuzumab marked downregulated cell surface HER2 in both BT474GFP and BT474T798M cells (Fig. 1F).

We next examined whether the T798M mutant allele was required for growth and survival of mutant-expressing cells by using the covalent irreversible HER2/EGFR small molecule inhibitor BIBW2992 (afatinib). Afatinib has been shown to bind to and inhibit the EGFR T790M gatekeeper mutant (38). Treatment with BIBW2992 but not with lapatinib eliminated phosphorylation of HER2 and EGFR as measured with site-specific receptor antibodies (Fig. 2A) and potently inhibited growth of both BT474GFP and BT474T798M cells (Fig. 2B). BIBW2992 also disrupted the association of p85 with HER2 and inhibited P-AKT levels in both cell lines (Fig. 2C). Similar results were observed with treatment with the pan-ErbB irreversible inhibitor CI-1033 (39), which inhibited HER2 phosphorylation and growth of both BT474GFP and BT474T798M cells (Supplementary Fig. S1). These results suggest that HER2T798M-expressing cells rely on the mutant allele for activation of the PI3K/AKT pathway and their survival.

HER2T798M has increased autocatalytic activity compared to wild-type HER2

Expression of T798M resulted in increased HER3 phosphorylation and its association with the p85 subunit of PI3K (Supplementary Fig. S2), suggesting that the mutant HER2 might be catalytically more active than wild-type HER2. To examine this possible gain of function, we stably expressed HER2WT or HER2T798M in MCF10A human mammary epithelial cells that normally express low levels of HER2. Expression of both HER2WT and HER2T798M resulted in increased phosphorylation of HER2, HER3, AKT and ERK1/2 compared to controls (Fig. 3A). Treatment with lapatinib inhibited pHER2 and pHER3 as well as growth in 3-dimensional (3D) Matrigel of MCF10AWT but not MCF10AT798M cells (Fig. 3B and C). In addition, MCF10AT798M acini were larger and more invasive than MCF10AWT acini and proliferated faster than MCF10AWT cells (Fig. 3D) in both full-serum and serum-free conditions, further supporting a gain of HER2 function conferred by the mutant allele. Finally, to test HER2 kinase activity, HER2WT and HER2T798M were immunoprecipitated from both cell types and the pull-downs were tested in an in vitro kinase reaction (Fig. 3E). Immunoprecipitates from parental MCF10A were used as controls. HER2T798M showed markedly higher tyrosine phosphorylation than HER2WT, suggesting that the mutant allele has higher catalytic activity (Fig. 3E).

HER2T798M expressed at low frequency is sufficient to confer resistance

It has been shown that a very low allele frequency of the EGFRT790M gatekeeper mutation is enough to confer resistance to the EGFR-TKI gefitinib (40). Using dilutional cloning, we found that approximately 3.1% of HER2 alleles contain T798M in lapatinib-resistant BT474T798M cells (Supplementary Fig. S3). This is consistent with earlier reports which showed that T790M mutation in EGFR can render cells resistant to gefitinib with an allele frequency of

![Image](attachment://Figure_2.png)

Figure 2. Cells expressing HER2T798M remain dependent on the ErbB pathway to activate PI3K/AKT. A, cells were treated with 1 μmol/L lapatinib or 1 μmol/L BIBW2992 for 3 hours. Protein extracts were then prepared and subjected to immunoblot analysis with the indicated antibodies. B, cells were treated with 1 μmol/L BIBW2992. Monolayers were fixed and stained with crystal violet when DMSO-treated cells reached confluence (day 6). C, cells were treated with 1 μmol/L lapatinib or 1 μmol/L BIBW2992 for 3 hours; protein extracts were precipitated with a p85 antibody. Antibody pull-downs were next washed, separated by SDS-PAGE, and subjected to immunoblot analysis as described in Methods using the indicated antibodies (top 2 panels). Immunoblot analyses on whole-cell extracts were conducted using the antibodies indicated on the left (bottom 2 panels).
3.3% (40). To support further that this low frequency of expression was sufficient to confer resistance, we carried out co-culture experiments wherein varying proportions of BT474GFP (green) and BT474 T798M cells (unlabeled) were mixed and then subjected to selection with lapatinib. We found that lapatinib-resistant acini emerge when as low as 5% of the total cell population is BT474 T798M (Supplementary Fig. S4). In this experiment, expansion of the mutant population of cells was indicated by loss of the GFP fluorescence from the resistant acini.

**HER2T798M-expressing cells rely on HER3-PI3K for survival**

In HER2 gene–amplified breast cancer cells, HER2 potently activates the PI3K prosurvival pathway mainly by dimerizing with and phosphorylating the HER3 coreceptor (41, 42). To determine whether cells bearing the T798M mutant remain dependent on PI3K/AKT, we treated BT474T798M and BT474T798M cells with the pan-PI3K inhibitor BKM120 (43). Treatment with BKM120 blocked phosphorylation of AKT in S473 (Fig. 4A) and inhibited growth of both BT474T798M and BT474T798M cells (Fig. 4B and C). Amplified HER2 signaling also hyperactivates the RAS/MEK/ERK pathway (44). Treatment with the MEK1/2 inhibitor CI-1040 (45) blocked phosphorylation of ERK1/2 in both cell types (Fig. 4A) but did not inhibit their growth (Fig. 4B and C). These data suggest that expression of HER2T798M does not dispense with the dependence of HER2-overexpressing cells on PI3K. We next examined whether treatment with a second pan-PI3K inhibitor, XL-147 (46), would overcome resistance to trastuzumab of cells expressing HER2T798M. The combination of trastuzumab and XL-147 was more potent than either drug.
alone at inhibiting BT474T798M cell growth (Fig. 4D). Immunoblot analyses confirmed that XL-147 inhibited S473 P-AKT in both BT474 GFP and BT474T798M cells (Fig. 4E). Because HER3 is the major activator of PI3K in HER2-dependent cells, we next tested the effects of HER3 inhibition. RNA interference-induced knockdown of HER3 resulted in growth inhibition of both BT474 GFP and BT474T798M cells (Supplementary Fig. S5A). Furthermore, knockdown of HER3 using an HER3-specific locked nucleic acid (LNA) antisense oligonucleotide (30) markedly reduced S473 P-AKT in BT474T798M cells (Supplementary Fig. S5B). These results suggest BT474T798M cells remain dependent on the HER3-PI3K axis for survival.

**BT474T798M cells overexpress EGFR ligands and combined blockade of EGFR and HER2 inhibits their growth**

We speculated that another explanation for both the increased intracellular signaling generated by HER2T798M (Figs. 1C and 3B; Supplementary Fig. S2) and the acquired resistance to trastuzumab would be enhanced activation of HER2 by ligand-induced ErbB coreceptors. Therefore, we carried out quantitative PCR with mRNA isolated from BT474GFP and BT474 T798M cells using primers specific for the ErbB receptor ligands heregulin, EGF, TGFα, amphiregulin, HB-EGF, epiregulin, and betacellulin. BT474 T798M cells expressed >2-fold higher levels of the EGFR ligands EGF, TGFα, amphiregulin, and HB-EGF compared with BT474GFP cells (Fig. 5A). Consistent with enhanced ErbB ligand production, HER2 antibody pull-downs contained more HER3 and EGFR in BT474 T798M than in BT474GFP cells in the absence of exogenous TGFα (Fig. 5A). If overexpression of EGFR ligands is causal to the resistance to HER2 inhibitors, we proposed that blockade of ligand binding with the EGFR antibody cetuximab should overcome resistance to lapatinib and trastuzumab. However, treatment of BT474T798M cells with cetuximab did not add to the modest growth inhibition by lapatinib, although...
Figure 5. HER2T798M cells express higher levels of EGFR ligands and HER2-containing heterodimers. A, RT-qPCR analysis for ErbB receptor ligand expression was conducted using RNA template from BT474GFP and BT474T798M cells, normalized to expression in GFP cells for each ligand. B, lysates prepared from BT474GFP (+40 ng/mL TGFα) and BT474T798M were immunoprecipitated with a HER2 C-terminal antibody followed by immunoblot analyses with the indicated antibodies. C, lysates prepared from MCF10AT798M and MCF10A were analyzed as in B. D, BT474T798M cells were treated with 20 μg/mL cetuximab and 1 μmol/L lapatinib, either alone or in combination for 5 days. MTT assays were conducted at the end of treatment. E, cells were treated with 20 μg/mL cetuximab and/or 1 μmol/L lapatinib for 3 hours. Lysates were prepared and subjected to immunoblot analyses with the indicated antibodies. F, for 3D Matrigel growth assays, cells were treated with 20 μg/mL trastuzumab, 20 μg/mL cetuximab, or the combination. Cells were plated in duplicates and images captured on day 14. Fresh medium and inhibitors were replenished every 3 days. G, average acinar area was quantified with the ImageJ software. Each bar represents the mean acinar area ± SEM (n = 2). H, cells were treated with 20 μg/mL cetuximab and/or and 20 μg/mL trastuzumab and lysates analyzed as in E. I, BT474T798M xenografts were established in female athymic mice as indicated in Methods. Once tumors reached at least 200 mm3 in volume, mice were treated with trastuzumab (30 mg/kg i.p. twice per week), cetuximab (1 mg i.p. twice per week), or both antibodies. Each data point represents the mean tumor volume ± SEM.

*P < 0.005 versus trastuzumab; #, P < 0.05 versus cetuximab. The number of mice in each treatment arm is indicated next to each curve.
EGFR phosphorylation was inhibited. In addition, P-HER2, P-HER3, P-AKT, and P-Erk1/2 were maintained following treatment with this combination (Fig. 5D and E). We speculate that this activation reflects EGFR-independent HER2 signaling, which is maintained because of the inability of lapatinib to bind HER2T798M with high affinity and inhibit its kinase activity.

In 3D Matrigel, the HER2 T798M mutant–expressing cells were resistant to single-agent cetuximab or trastuzumab. However, the combination of trastuzumab and cetuximab blocked BT474T798M cell growth (Fig. 5F and G). Consistent with the growth-inhibitory effect of the combination, immunoblot analysis showed that treatment with both antibodies markedly inhibited S473 P-AKT (Fig. 5H). To test the effect of the combination in vivo, we injected BT474T798M cells into athymic nude mice and treated established tumors with trastuzumab, cetuximab, or the combination for 5 weeks. Trastuzumab or cetuximab alone had no effect on tumor growth. However, treatment with both inhibitors resulted in complete response in 3 of 7 (43%) mice (Fig. 5I). Immunohistochemical analysis of tumors after about 5 weeks of treatment showed that cetuximab alone or in combination with trastuzumab resulted in a slight decrease in cytoplasmic P-Akt intensity (Supplementary Fig. S6). These observations suggest that dual inhibition of HER2 and EGFR limits the growth of trastuzumab-resistant cells in tumors bearing HER2T798M.

Finally, we hypothesized that as lapatinib also inhibits the EGFR tyrosine kinase, BT474T798M cells should be sensitive to dual HER2 blockade with trastuzumab and lapatinib. In this combination, trastuzumab should partially downregulate mutant HER2 and lapatinib should inhibit transactivation of HER2 (and HER3) by ligand-induced EGFR. Indeed, the combination of trastuzumab and lapatinib inhibited BT474T798M cell growth in 3D Matrigel even though the cells were resistant to each drug alone (Fig. 6A and B). Treatment with the combination also inhibited Y1068-pEGFR and Y1197-pHER3. Treatment with trastuzumab had no effect, whereas lapatinib modestly inhibited HER2/HER3 heterodimers. However, treatment with both inhibitors markedly reduced HER2/HER3 heterodimers potentially explaining the inhibition of S473 P-AKT (Fig. 6C). Furthermore,
treatment with both inhibitors but not each drug alone induced regression of BT474 T798M xenografts established in athymic mice (Fig. 6D). There was a modest reduction in S473 P-Akt levels as measured by immunohistochemistry (IHC) in tumors in all treatment arms at the end of 4 weeks of therapy (Supplementary Fig. S7). These results suggest that even though HER2 T798M confers resistance to lapatinib or trastuzumab when used as single agents, simultaneous blockade of HER2 and EGFR with both of these inhibitors is effective against HER2-overexpressing breast cancer cells bearing HER2 T798M alleles.

Discussion

In this report, we studied cellular and biochemical effects of the gatekeeper T798M mutation in the HER2 kinase domain in breast cancer cells. Expression of T798M conferred resistance to both lapatinib and trastuzumab. As the T790M gatekeeper mutation in EGFR has increased affinity for ATP (47), we speculate the corresponding T798M mutation in HER2 may similarly stabilize HER2 in an active conformation (26). Consistent with this, we observed that HER2 T798M has increased catalytic activity compared to HER2 WT. In addition, structural modeling of T798M suggests that the methionine substitution at T798 sterically inhibits drug binding and/or further destabilizes the inactive conformation of HER2. As lapatinib binds preferentially the inactive binding and/or further destabilizes the inactive conformation of HER2, this further contributes to drug resistance (24). This may also explain the marked shift in the IC50 of lapatinib against HER2 T798M cells.

Trastuzumab is unable to block transactivation of HER2 by ligand-induced ErbB coreceptors (48). Exogenous and endogenous ligands of EGFR and HER3 have been shown to rescue from the growth-inhibitory effect of the antibody (9, 35, 49). Furthermore, HER2+ xenografts selected in vivo for acquired resistance to trastuzumab exhibit higher levels of P-EGFR and EGFR/HER2 heterodimers as well as overexpression of EGFR, TGFα, HB-EGF, and heregulin RNAs compared with parental trastuzumab-sensitive tumors (50). Finally, expression of drug-resistant mutants of EGFR (38) and HER2 (33, 51) also results in overproduction of ErbB receptor ligands. Thus, we examined expression of ErbB receptor ligands in cells expressing the HER2 mutant. BT474 T798M cells overexpressed EGF, TGFα, amphiregulin, and HB-EGF mRNAs and exhibited higher levels of HER2-containing heterodimers compared to BT474 GFP cells. Addition of cetuximab, an antibody that blocks ligand binding to EGFR, overcame the resistance to trastuzumab (Fig. 5), suggesting that ligand overexpression was causal to this resistance. These data suggest that although HER2 T798M is intrinsically sensitive to trastuzumab-induced downregulation similar to HER2 WT (Fig. 1F), its expression increases ligand-induced HER2-containing heterodimers (Fig. 5B and C), potentially explaining how T798M contributes to trastuzumab resistance. Further studies are required to determine the mechanisms by which amplification of HER2 signaling results in enhanced production of ErbB receptor ligands.

The HER2 T798M kinase was exquisitely sensitive to submicromolar concentrations of BIBW2992 (afatinib). This is an irreversible small-molecule inhibitor that covalently binds Cys805 and Cys773 in the ATP pocket of HER2 and EGFR, respectively, and potently inhibits the receptors’ kinase activity (52). Afatinib is also effective against the analogous drug-resistant T790M mutation in EGFR and has shown clinical activity in lung cancers harboring this mutation (53). Cells expressing HER2 T798M were also sensitive to HER3 knockdown and to 2 pan-PI3K inhibitors currently in clinical development. These results suggest that cells expressing the mutant continue to rely on the HER2/HER3/PI3K axis for growth and survival. Therefore, afatinib and other irreversible HER2 TKIs, HER3 antibodies, PI3K inhibitors, and drugs that disrupt ligand-induced HER2-HER3 dimers (i.e., pertuzumab) represent clinical approaches and combinations currently used in patients with HER2-overexpressing cancers that may prevent the acquisition or the effects of HER2 T798M.

Mutations in HER2 are present in breast tumors, but, to our knowledge, with very few exceptions, they have all been reported in breast cancers without HER2 gene amplification (23, 27, 52). One possibility is that allelic dilution may render it difficult to identify this drug resistant mutant by conventional direct sequencing in cancers with HER2 gene amplification. It is also possible that this mutant may require enrichment after treatment of a clinically sensitive tumor with lapatinib, analogous to the enrichment of imatinib-resistant gatekeeper mutants in BCR-ABL in patients with CML (14). To detect low-frequency mutations, direct sequencing will need to be combined with methodologies which are more sensitive to detect rare mutations, especially in highly amplified genes such as HER2. This has been observed in lung cancer, where use of SURVEYOR but not Sanger sequencing (40) detected the EGFR T790M mutation in gefitinib-resistant primary lung tumors. This suggests next-generation massively parallel sequencing that can provide deep gene coverage may be required to detect HER2 mutations in patients with HER2 gene–amplified breast cancer. This is also consistent with our findings that a low frequency of expression of the mutant allele (~3%) was sufficient to confer drug resistance. Finally, sequencing efforts to date have focused on pretreatment samples. We speculate that many resistance-associated mutations are acquired (or enriched from a small and undetectable pre-existing population). As such, they may only be detected following treatment and progression of clinically resistant disease.

Disclosure of Potential Conflicts of Interest

J.A. Engelman has a commercial research grant from Novartis, Sanofi, and is a consultant/advisory board member of Novartis, Genentech, and GSK. No potential conflicts of interest were disclosed by the other authors.

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