Role of exon-16-deleted HER2 in breast carcinomas

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Abstract

A splice variant of the human gene HER2, lacking exon-16 (∆HER2) which encodes a small extracellular region, has been described. This altered receptor forms disulfide bond-stabilized homodimers. We report here that the ∆HER2 splice variant represents about 9% of the HER2 mRNA obtained from most of the 46 breast carcinoma samples with HER2 expression levels ranging from 3+ to 0 by HercepTest. Analysis of human cells transfected with ∆HER2 or wild-type (WT) cDNA revealed no growth of WT cells in nude mice, whereas clones expressing 10-fold less ∆HER2 were tumorigenic. Unlike WT transfectants, ∆HER2-expressing cells showed low sensitivity to two new therapeutic drugs targeting receptors of the HER family (ZD1839 and Trastuzumab), whereas an inhibitor of the HER2 tyrosine kinase domain (Emodin) blocked activation of both ∆HER2 and WT transfectants. Taken together, our findings indicate that the ∆HER2 transcript encodes the transforming form of the oncoprotein. It is plausible that malignant transformation arises when a critical threshold of ∆HER2 is reached in HER2-overexpressing tumors. Specific inhibitors of HER2 catalytic activity represent a promising approach to therapy of HER2-overexpressing tumors.

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Introduction

Amplification of the HER2 oncogene is one of the genetic abnormalities in breast tissue responsible for the progression from normal breast epithelia to invasive cancer cells. Recent data (Perou et al. 2000, Ménard et al. 2002, Van’T Veer et al. 2002) have shown that HER2-positive breast carcinomas represent a particularly aggressive tumor subset with increased proliferation and metastatic potential. However, HER2 overexpression is relevant to but not sufficient to induce transformation, as clearly established in mice transgenically expressing the rat proto-oncogene HER2/neu. In these transgenic mice, tumors arose only when the oncoprotein carried mutations, in particular, small deletions in the extracellular domain that promote HER2/neu transforming activity of this protein through formation of intermolecular disulfide bonds (Siegel et al. 1999). Interestingly, an alternative splice form of the human homologous HER2 gene, containing an in-frame deletion in the same region that is mutated in neu protooncogene transgenic mice, has been detected in human breast carcinomas (Kwong & Hung 1998, Siegel et al. 1999). This splice variant (∆HER2) encodes a receptor lacking exon 16 (according to Ensembl database-ENSE00001121079), which immediately precedes the transmembrane domain containing two cysteine residues. The loss of these cysteine residues might induce a change in the conformation of the HER2 receptor extracellular domain that promotes intermolecular disulfide bonding and, in turn, homodimers capable of transforming cells. Recent studies have revealed that alternative splicing, resulting in deletions within the extracellular domain of growth factor receptors such as Met (Baek et al. 2004), Ron (Collesi et al. 1996) and fibroblast growth factor receptor 2 (FGFR2) (Li et al. 1995, Meyers et al. 1996), provides a unique mechanism for the generation of novel transcripts encoding constitutively activated molecules.

Studies in mammary carcinoma cells have demonstrated that binding of ligands of the epidermal growth factor (EGF) family to their receptors induces formation of homo- and heterodimers of receptors
belonging to the same family, with a marked preference for HER2 as a dimer partner (Graus-Porta et al. 1997, Tzahar et al. 1997), and that signals induced by HER2-containing heterodimers have the highest biologic activity among the other possible complexes (reviewed in Yarden & Sliwkowski 2001). Accordingly, a recent phase II trial has shown that ZD1839, a tyrosine kinase inhibitor which specifically blocks the phosphorylation and function of the epidermal growth factor receptor (EGFR), is active in patients with advanced or metastatic breast cancer (Normanno et al. 2003). Encouraging clinical data have also been obtained with the humanized anti-HER2 antibody (Trastuzumab) in treating HER2-overexpressing breast tumors (Slamon et al. 2001, Burstein et al. 2003, Gennari et al. 2004). However, for reasons that remain unclear, not all patients with HER2-positive tumors respond to these new therapies. Thus, a better understanding of the involvement of the HER2 splice variant in conditioning the response to new therapeutic approaches targeting this receptor might provide an avenue to improving response rates in patients with HER2-overexpressing carcinomas.

In the present study, we analyzed expression levels of the HER2 splice variant in human breast carcinomas and examined the role of this variant in HER2-related tumorigenicity and sensitivity to new therapeutic options that target the HER family receptors.

Materials and methods

Human tumor samples and HER2 expression analysis

Primary breast carcinoma tissues were collected within 5 min of surgical resection, snap-frozen in liquid nitrogen and stored at −80°C. Samples containing at least 50% tumor cells, as determined by histologic examination, were selected according to overexpression (25 cases) or no overexpression (21 cases) of HER2 protein. Immunohistochemical staining for HER2 protein was performed by the pathology unit of our institute, using the DAKO HercepTest immunocytochemical assay (DAKO, Glostrup, Denmark), according to the manufacturer’s instructions, on 4-μm-thick sections of formalin-fixed, paraffin-embedded material. This staining was scored as follows:

- 0 or 1+: no staining or membrane staining in <10% of tumor cells or barely perceptible, incomplete membrane staining in >10% of the tumor cells
- 2+: weak to moderate complete membrane staining in >10% of tumor cells
- 3+: intense complete membrane staining in >10% of tumor cells

On this basis, tumors were classified as 0 (15 cases), 1+ (6 cases), 2+ (5 cases) and 3+ (20 cases). All patients were enrolled at the National Cancer Institute of Milan in 2001 and underwent breast surgery. Tumor characteristics were as follows: mean tumor size at pathologic examination, 33.7 mm (range 15–80 mm); positive lymph-node status, 65% (76% and 52% in HER2-positive and -negative patients respectively); grade III, 52% (55% and 50% in HER2-positive and negative patients respectively).

Total RNA was isolated from each tumor sample with TRIzol Reagent (Invitrogen) according to the manufacturer’s instructions. RNA was quantitated spectrophotometrically. Reverse transcription was carried out at 42°C for 60 min, using 1 μg total RNA, 50 pmol specific primer for HER2 (5'-CAGATGCCCAAGGCGGGAG-3'), 0.5 mM deoxynucleotide triphosphate and 25 U MultiScribe reverse transcriptase (Applied Biosystems, Foster City, CA, USA). To confirm the quality of reverse transcription, PCR analysis was performed in a total volume of 50 μl using primer pairs of the HER2 receptor (+) primer, 5'-GGCTCAGTGACCTGTGGG-3' and (−) primer, 5'-TGATGAGGATCCCAAGACC-3' with an expected amplicon length of 312 bp for the wild-type (WT) receptor and 264 bp for the splice variant receptor. After an initial denaturation step at 95°C for 5 min, 30 cycles at 95°C for 1 min, 55°C for 30 s and 72°C for 1 min, all products were electrophoresed in 8% polyacrylamide gel, stained with ethidium bromide and visualized under UV lamp.

Real-time PCR

Primers and TaqMan probes were designed with Primer Express 1.5 software (Applied Biosystems) and purchased from Applied Biosystems. Amplification reactions were performed in a volume of 25 μl with 1× TaqMan Universal PCR Master Mix (Applied Biosystems), 100 nM of each primer and 200 nM probe. The thermal cycling conditions were 95°C for 10 min, 45 cycles of 95°C for 15 s and 61°C for 30 s. In all experiments, 50 ng cDNA was amplified in single-measurement fluorescence, and all data were collected by a 5700 SDS thermal cycler (Applied Biosystems). Each sample was tested in triplicate, and all PCR runs were performed three times. For WT HER2 amplifications, the TaqMan probe and forward primer were located in exon 16, whereas the reverse primer
annealed in exon 17; for exon 16-deleted HER2 receptor, the probe and reverse primer were located in exon 17, whereas the forward primer encompassed the boundary spanning 15–17 exons.

Real-time PCR probes used were as follows:

- 6-FAM 5′-AAGGGCTGCCCGCGGA-3′ TAMRA for WT
- 6-FAM 5′-ACGTCCATCATCTCTGGTGGG-3′ TAMRA for ΔHER2.

Real-time PCR forward primers used were as follows:

- 5′-TCCTGTGTGACCTGGATGA-3′ for WT
- 5′-CAAACGCACCCCCTCCTCCC-3′ for ΔHER2.

Real-time PCR reverse primers used were as follows:

- 5′-ACCACGAGATGCCCAACCA-3′ for WT
- 5′-CTTGATGAGGATCCCAAAGACC-3′ for ΔHER2.

The specificity of primers and probes was verified by assaying each in combination with different concentrations of plasmid vector carrying cloned WT or alternatively spliced HER2 cDNA; fluorescence signal was generated during real-time PCR. The efficiency of probe and primer sets was calculated by the formula E = 10^{(-1/slope)} (Pfaffl 2001). For two different breast carcinoma samples (controls), the ratio between the ΔHER2 and WT HER2 transcript levels was calculated by the formula T_{ΔHER2}/T_{WT} = (E_{WT}) C_{WT} / (E_{HER2}) C_{ΔHER2}, where T is the amount of WT or ΔHER2 mRNA in each sample before amplification, E is the reaction efficiency and Ct is the threshold cycle. The WT and ΔHER2 threshold cycles of other breast carcinoma samples were normalized to the two controls by the mathematical model described by Pfaffl (2001).

**PCR and vectors**

Plasmid pcDNA3/HER2-WT was prepared by excising full-length human HER2 cDNA from the LTR-2/erbB-2 expression vector (kindly provided by Dr P P Di Fiore) (Di Fiore et al. 1987) by XhoI digestion (New England BioLabs, Beverly, MA, USA) and subcloning the fragment into the XhoI site of plasmid pcDNA3 (Invitrogen). The pcDNA3/ΔHER2 vector was obtained as previously described (Kwong & Hung 1998).

**Cells and treatments**

The SKBr3 human breast carcinoma, HEK-293 embryonic kidney and NIH3T3 murine fibroblast cell lines were provided by ATCC (Rockville, MD, USA). Cells were maintained in RPMI-1640 medium (Sigma) supplemented with 10% fetal calf serum (FCS), 1-glutamine and antibiotics.

Transfections were performed with cells at 80% confluence in serum-free medium with 10 μg DNA, 30 μg Lipofectamine reagent and 20 μg Plus reagent according to the manufacturer’s instructions (Invitrogen). Cells were kept at 37°C for 4 h, and, after replacement of serum-free with complete medium, they were maintained for an additional 2 h. Transiently transfected cells were treated with different drugs within 48 h of transfection. Sensitivity to 25–50 μM ZD1839 was evaluated after 72 h of treatment; the activity of Emodin was used at 20 and 40 μM and assayed at 24 h after treatment. Concentrations of both drugs corresponded to growth inhibition IC₅₀ (50 μM ZD1839 and 40 μM Emodin) and IC₃₀ (25 μM ZD1839 and 20 μM Emodin) calculated in HEK-293 cells overexpressing WT HER2. Stably transfected cells were selected in the presence of 1 mg/ml G418, and individual G418-resistant colonies were picked, expanded and maintained in the presence of G418. Control cells were transfected with pcDNA3 vector (mock). Individual clones of G418-selected cells were tested for p185HER2 surface expression by FACS-calibur analysis.

**Monoclonal antibodies**

The following monoclonal antibodies (mAb) were used: mouse MGR2 (Tagliabue et al. 1991) and humanized Trastuzumab, directed against the extracellular domain of p185HER2; c-neu Ab3, directed against the carboxy-terminal peptide of p185HER2 (Oncogene Science, Manhasset, NY, USA); and 4G10, directed against phosphotyrosine (Upstate Biotechnology, Lake Placid, NY, USA).

**Western blot analysis**

Transfected cells were solubilized with lysis buffer (50 mM Tris–HCl (pH 7.4), 150 mM NaCl, 1% Triton X-100, 2 mM Na-orthovanadate, 1 mM phenylmethyl-sulfonyl-fluoride, 10 μg/ml leupeptin and 10 μg/ml aprotinin), and lysates were centrifuged at 15 500 g for 10 min at 4°C. Total cell lysates (50 μg/lane) were
subjected to 3–10% gradient SDS-PAGE with a low-concentration stacking gel (4%). Proteins were blotted to nitrocellulose membranes (Amersham), nonspecific binding was blocked with Blotto solution (5% low-fat dry milk in PBS), and membranes were probed with antibodies. Proteins were visualized with peroxidase-coupled secondary antibody by the ECL detection system (Amersham).

Flow cytometric analysis
Indirect immunofluorescence assay was performed on live cells with MGR2 purified mAb (10 μg/ml) or Trastuzumab (10 μg/ml). Cells were incubated with 100 μg/ml antibody for 30 min at 37°C, washed twice, and incubated with FITC-labeled goat antimouse IgG or FITC-labeled goat antihuman IgG (1:100) (Kirkegaard & Perry Laboratories, Gaithersburg, MD, USA) for 30 min at 0°C. After a final wash, cells were suspended in PBS. Fluorescence was evaluated by FACScalibur with CellQuest software (Becton Dickinson, Mountain View, CA, USA).

Apoptosis assay
Cells grown to 60% confluency in 10 mm² dishes were examined by indirect immunofluorescence assay with the annexin V-FITC Kit (Bender MedSystem, Vienna, Austria) according to the manufacturer’s protocol. For qualitative analysis of cytoplasmic DNA fragmentation, adherent and floating cells were harvested, washed once, centrifuged, resuspended in 200 μl lysis buffer (10 mM Tris–HCl (pH 8.0), 10 mM EDTA and 0.5% Triton X-100) and kept on ice for 5 min. After centrifugation at 15,500 g, the supernatant was collected and treated overnight at 37°C with 100 μg/ml RNase A (Boehringer, Mannheim, Germany) before addition of SDS and proteinase K (Sigma) at 0.5% and 200 μg/ml respectively. Extracts were incubated at 50°C for 2 h, and low-molecular-weight DNA was extracted twice in phenol and once in phenol–chloroform. Resuspended DNA was loaded on a 1.5% ethidium bromide-stained agarose gel.

Proliferation assay
Transfected NIH3T3 (1 × 10⁵) or HEK-293 (1 × 10⁴) cells were seeded in 96-well plates and maintained in 10% FCS with the appropriate G418 concentration. After each day of growth, cells were fixed with cold 10% trichloroacetic acid for 1 h at 4°C, washed with PBS and incubated for 30 min with 0.4% sulforodamine B (SRB) in 1% acetic acid (100 μl/well). After three washes in 1% acetic acid, the dye was dissolved in 10 mM Tris (pH 10.5) (100 μl/well) and evaluated spectrophotometrically at 550 nm. Growth index was calculated as the ratio of optical density (OD) of a sample after each day of treatment/OD of the sample at the beginning of the experiment.

In vivo cellular tumorigenesis
Eight-week-old BALB/c athymic mice were purchased from Charles River (Calco, Italy). Care and use of the animals was in accordance with institutional guidelines. Mice were injected subcutaneously in the right flank with 8 × 10⁵ WT- or ΔHER2-transfected cells, and tumors were calibrated twice weekly. Tumor volume was calculated as 0.5 × d₁² × d₂, where d₁ and d₂ are the larger and smaller diameters respectively.

Statistics
Tumor growth was evaluated by Fisher’s and chi-square tests. Differences were considered significant at *P < 0.05.

Results
Expression of alternatively spliced and wild-type HER2 mRNA in human breast carcinomas
Total RNA obtained from 46 samples of breast carcinoma tissue was retrotranscribed, and this was followed by real-time PCR using two 5′-FAM-modified probes and different primers designed to detect and amplify only WT or splice variant HER2 mRNA. Specificity of the primer pairs was controlled with WT or ΔHER2 cDNA cloned in the pcDNA3 vector as template, and confirmed by PAGE separation of real-time PCR products, resulting in the respective single band with the expected length. Based on the efficiencies of amplification reactions and threshold cycles of two tumor samples (controls) classified as HercepTest 3+ and 1+, the ratio between the expression level of splice variant and WT receptor in controls was calculated as 9% (see Materials and methods). The ratio between the normalized WT and splice variant expression level was then determined for each tumor sample by the following formula:

\[ R = R1 / R2 = \left( \frac{E_{\Delta Ct(\text{control-sample})}}{E_{\Delta Ct(\text{control-sample})}} \right)^{\Delta Ct(\text{WT-HER2})} \]

A direct correlation between sample R1 and R2 values was found (r=0.99) that revealed in most cases a relative abundance of splice variant mRNA compared with the WT of 9% (Fig. 1). In eight tumors, the ratio
of ΔHER2 mRNA compared with the WT exceeded the 95% confidence interval (8.6–9.9%), ranging from 19.7% to 1.1%. Three samples, scored 0 (two cases) and 3+ (one case) by HercepTest, expressed more than 9% of ΔHER2, and five samples, scored 0 (two cases) and 3+ (three cases), expressed less than 9% of ΔHER2. While determination of ΔHER2 ratios in global tumor samples instead of microdissected carcinomas did not exclude the possibility that the splice variant derives from cellular types other than carcinoma, the presence of at least 50% tumor cells in the samples tested makes it highly unlikely that transcript of nontumor cells was prevalently examined. Indeed, in normal mammary cells, which have never been found to overexpress HER2, the low levels of ΔHER2 mRNA (9% of the WT) would not affect quantitation of ΔHER2.

**Cellular expression of splice variant HER2**

ΔHER2 cDNA was obtained from total RNA of the HER2-overexpressing breast carcinoma cell line SKBr3 by recombinant PCR and cloned into the pcDNA3 expression vector (see Materials and methods). To determine whether receptors encoded by the splice variant were activated by the formation of disulfide bond-stabilized dimers, proteins from NIH3T3 cells transfected with WT and ΔHER2 cDNA constructs were examined by immunoblot analysis of individual clones obtained after selection in G418 medium and indirect immunofluorescence assay. Elevated levels of disulfide bond-stabilized dimers in each established cell line expressing the HER2 splice variant were detected when soluble extracts were resolved under nonreducing electrophoresis conditions, but not when 2-mercaptoethanol was present (Fig. 2A, lanes 3 and 4). By contrast, NIH3T3 cells expressing WT HER2 revealed monomeric HER2 oncoprotein in both reducing and nonreducing conditions (Fig. 2A, lanes 1 and 2). Moreover, individual ΔHER2 clones showed a significantly higher growth capacity both in vitro \( (P = 0.0004) \) (Fig. 2B) and in vivo \( (P < 0.001) \) (Fig. 2C) compared with WT transfectants.

To establish the role of the ΔHER2 receptor in transformation, human embryonic kidney cells (HEK-293), which have been used as normal human cells to study the oncogenic potential of genes (Graham *et al.* 1977, Kamei *et al.* 2003), were transfected with either ΔHER2 or WT cDNA cloned in the pcDNA3 vector.
HEK-293 cells have a high transfection rate facilitating biochemical analysis of $\Delta$HER2 in transient transfectants, unlike human normal breast cell lines which generally present low transfection rates. Immunoblot analysis of cell extracts obtained 48 h after transfection revealed the presence of HER2 disulfide dimers in the lysates of splice variant transfectants resolved under nonreducing conditions, but not in the presence of 2-mercaptoethanol (Fig. 3A). Two clones overexpressing the WT HER2 at the same level as in SKBr3, and two clones expressing about 10-fold less $\Delta$HER2 as determined by FACS analysis were selected (Fig. 3B). The two splice variant clones presented an in vitro growth index comparable to that of the two WT HER2-expressing clones and of the mock-transfected cells (data not shown). These transfectants and two empty, vector-transfected clones were injected in nude mice (six animals/clone). Both $\Delta$HER2 clones formed tumors with similar growth patterns in 2/6 injected mice (Fig. 3C), whereas cells transfected with WT HER2 or empty vector did not form tumors ($\Delta$HER2 vs WT HER2; $P = 0.04$). On the other hand, in vitro growth analysis of HEK-293 clones expressing HER2 splice variant at levels comparable with those in

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**Figure 2** (A) Biochemical analysis of homodimer expression in NIH3T3 transfected clones. Proteins were separated on 3–10% gradient SDS–PAGE under nonreducing (left) or reducing conditions (right) and probed with monoclonal antibody Ab3 directed against the HER2 receptor. 'D' indicates the $\Delta$HER2 dimers and 'M' indicates the monomers. (B) In vitro growth of selected NIH3T3 clones overexpressing WT (●,▲) or $\Delta$HER2 (●,▲) or mock (■) NIH3T3. Cells were cultured for 5 days in 96-well plates, fixed and stained with SRB. Growth index was calculated as the ratio between OD on a given day and the starting OD. (C) In vivo growth capability of selected WT (●,▲) or $\Delta$HER2 (●,▲) clones or mock (■) NIH3T3. Tumors in mice injected with $8 \times 10^5$ cells were measured twice weekly, and tumor volume was calculated (mean ± s.d.).
WT HER2-overexpressing clones (Fig. 4A) revealed a lower growth index in the HER2 splice variant-overexpressing clones than mock or WT-expressing HEK-293 clones (Fig. 4B). Analysis of phosphatidylserine expression in immunofluorescence assays indicated apoptotic death in about 40% of the cells in the ΔHER2-overexpressing clones compared with only about 10% of WT HER2-expressing cells (Fig. 4C). Activation of apoptotic pathways was confirmed by the presence of cytoplasmic DNA fragmentation in the splice variant transfectants (data not shown).

**Splice variant sensitivity to new therapies against HER2**

To investigate the responsiveness to new therapeutic tools targeting receptors of the HER family, HER2 activation was analyzed in cells transiently transfected with splice variant or WT HER2 cDNAs and treated with ZD1839, a specific inhibitor of the EGFR tyrosine-kinase domain. Western blot analysis revealed an inhibition of phosphorylation of monomeric HER2 receptor expressed by the splice variant (Fig. 5A), indicating the expected involvement of monomeric HER2 receptors in EGFR-driven heterodimers. By contrast, ZD1839 at the same concentrations did not detectably inhibit phosphorylation of the high-molecular-weight species corresponding to disulfide-bond dimeric HER2 present only in splice variant-transfected cells (Fig. 5A). In transiently transfected HEK-293 cells treated with Emodin, a tyrosine-kinase inhibitor affecting the HER2 catalytic domain (Jayasuriya et al. 1992, Zhang et al. 1999), neither HER2 monomeric nor disulfide-bond HER2 was found to be phosphorylated (Fig. 5B), indicating that the constitutive phosphorylation of disulfide-bond HER2 homodimers is sensitive to this tyrosine kinase inhibitor. Complete inhibition of HER2 monomeric phosphorylation was observed at an Emodin concentration that inhibits proliferation by only 30%, suggesting that other proliferation pathways were active. The humanized antibody Trastuzumab recognizes a conformational epitope in the juxtamembrane region of HER2, which might be altered in the ΔHER2 variant. Indirect immunofluorescence assay of Trastuzumab binding with transfected HEK-293 cells revealed a mean fluorescence intensity in WT HER2-expressing clones similar to that obtained with MGR2, an anti-HER2 mAb that does not cross-react with Trastuzumab. By contrast, the splice variant HER2-expressing cells were completely negative with Trastuzumab but positive with MGR2 antibody. However, human antibody reactivity with the splice variant-expressing cells was restored when cells were cultured in the presence of increasing concentrations of 2-mercaptoethanol (Table 1).

**Discussion**

The present study demonstrates that the HER2 splice variant lacking exon 16 is expressed in breast carcinoma samples as a proportion (about 9%) of the WT amount of encoded HER2. Moreover, the splice variant, at 10-fold lower concentrations than the WT receptor-overexpressing clones, induces transformation of human cells, suggesting that transformation associated with HER2 overexpression might reflect the increase in absolute levels of the splice variant to a critical threshold for constitutive activation of HER2. Consistent with this assumption, the formation of tumors in mice transgenically overexpressing the rat neu protooncogene has been associated with mutations of the transgene, including small deletions in the extracellular domain that promote formation of intermolecular disulfide bonds (Slamon et al. 1989, Lemoine et al. 1990, Siegel et al. 1999).

Although our analysis of the HER2 splice variant used more sensitive and quantitative methods than those in the previous study by Siegel et al. (1999), we also found that ΔHER2 mRNA represents about 9% of the WT HER2 transcript in breast carcinomas, and that consequently the absolute levels of the spliced transcript are higher in HER2-overexpressing tumor samples. The consistent direct linear correlation between the abundance of the two HER2 transcript forms indicates the efficiency of splicing machinery even in breast tumors with HER2 gene amplification. Indeed, tumors classified 3+ presented the same splice variant level found in those scored 2+, 1+ or 0 by HercepTest. Furthermore, eight cases in which the relationship between the two HER2 forms was found at the 95% confidence interval, the three samples (one case classified as 3+ and two cases as 0) expressing more than 9% of ΔHER2 and five samples (three cases classified as 3+ and five cases classified 0) expressing less suggested that, in some breast tumors, the regulation of basal splicing machinery might be disturbed.

Consistent with the enhanced focus-forming ability in vitro described for murine fibroblasts transfected with cDNA encoding the alternative spliced receptor (Siegel et al. 1999), we found that expression of the ΔHER2 receptor in NIH3T3 fibroblast induced transformation, providing a higher proliferation signal than that given by the WT receptor. This enhanced
Figure 3 (A) Biochemical analysis of HEK-293 cells at 48 h from transfection with WT or ΔHER2 cDNA. Proteins were separated on 3–10% gradient SDS–PAGE under nonreducing (left) or reducing conditions (right) and probed with monoclonal antibody.
growth signaling can be attributed to disulfide bond-stabilized homodimers, as detected under nonreducing conditions in soluble extracts of spliced HER2-expressing NIH3T3 cells. Indeed, growth factor receptors that are homodimerized through disulfide bonds are constitutively phosphorylated (Rubin & Yarden 2001), providing a crucial step in cell growth signaling. Furthermore, it is possible that clustering of EGFR on the plasma membrane of NIH3T3 human fibroblasts driven by activated ΔHER2 homodimers contributes to the enhanced oncogenicity of altered HER2 receptors even if none of the selected clones exhibited significant endogenous EGFR expression levels (data not shown).

Note, however, that in human HEK-293 cells, which reportedly have only moderate sensitivity to transformation (Cheng et al. 2002, Graham et al. 1977), ΔHER2 was sufficient by itself to initiate tumorigenesis, whereas WT HER2 did not induce cellular transformation. One explanation for these observations is that disulfide bond-homodimerized HER2 does not require the cooperation of other gene alterations to transform human cells. Furthermore, HEK-293 cells expressing high levels of ΔHER2
showed activation of apoptotic pathways, as indicated by the presence of phosphatidylserine outside the cell membrane and by the presence of fragmented cytoplasmic DNA. These findings are consistent with previous evidence showing that normal cells undergo apoptosis upon a highly aberrant cell growth signal (Hognason et al. 2001, Lehto 2001) such as that provided when high levels of constitutively activated ΔHER2 receptor are expressed. In agreement with this evidence, our findings indicate that alternatively spliced ΔHER2 never exceeded 20% of the WT receptor expressed.

Not all molecules encoded by alternatively spliced ΔHER2 mRNA are dimerized in transfected cells, suggesting that disulfide bond stabilization also depends on the redox conditions of the tumor microenvironment. Thus, the proliferation signal derived from dimerized ΔHER2 receptor may change as a function of cellular metabolism as well as the vascular network present around tumor cells.

Importantly, the ΔHER2 receptor was found to be resistant to two new breast cancer therapeutic approaches targeting receptors of the HER family, that is, the HER1 tyrosine kinase inhibitor ZD1839 and the humanized anti-HER2 mAb Trastuzumab, but its activation was completely blocked by the ΔHER2 tyrosine kinase inhibitor Emodin. Clinical data showing that not all patients with HER2-positive tumors respond to new HER2-targeted therapies might reflect, in part, the inefficient targeting of the splice variant receptor, particularly, the disulfide-bonded ΔHER2 dimers, by these drugs. Indeed, tyrosine phosphorylation of spliced ΔHER2 in the disulfide bond-stabilized

Table 1 MGR2 and Trastuzumab reactivity on ΔHER2-expressing HEK-293 clones cultured in the presence of 2-mercaptoethanol

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Figure 5 Analysis of ΔHER2 activation in HEK-293 cells transfected with ΔHER2 cDNA and treated with (A) ZD1839 at three different concentrations (0, 25 or 50 μM) or (B) Emodin (0, 20 or 40 μM). Total lysates were separated on 3–10% gradient SDS–PAGE under nonreducing (left) or reducing conditions (right). Filters were probed with monoclonal antibody Ab3 (αHER2) or antiphosphotyrosine (αP-Tyr). ‘D’ indicates ΔHER2 dimers while ‘M’ marks the position of monomers.
dimer form is resistant to treatment with a HER1 tyrosine kinase inhibitor, whereas phosphorylation of the same molecule in monomeric form is completely inhibited, indicating that only the splice variant monomers, and not the homodimers, depend on HER1 activation for phosphorylation. Trastuzumab, which binds to the juxtamembrane region of HER2, also demonstrated a lower reactivity with splice variant-transfected HEK-293 cells, reflecting a lack of reactivity with disulfide-bond HER2 homodimers, since culture of these transfectants in the presence of a reducing agent increased the number of Trastuzumab-positive cells. These results also point to the need for a better understanding of the relevance of redox conditions in the tumor microenvironment to activation of growth factor receptors such as HER2 and, consequently, to antitumor activity of anti-HER2 reagents.

Taken together, our findings suggest the potential role of a constitutively activated ΔHER2 splice variant in breast carcinomas, as well as the need for therapeutic approaches that target this variant.

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