Cell Death or Survival Promoted by Alternative Isoforms of ErbB4

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The significance of ErbB4 in tumor biology is poorly understood. The ERBB4 gene is alternatively spliced producing juxtamembrane (JM-a and JM-b) and cytoplasmic (CYT-1 and CYT-2) isoforms. Here, signaling via the two alternative ErbB4 JM isoforms (JM-a CYT-2 and JM-b CYT-2) was compared. Fibroblasts expressing ErbB4 JM-a demonstrated enhanced ErbB4 autophosphorylation, growth, and survival. In contrast, cells overexpressing ErbB4 JM-b underwent starvation-induced death. Both pro- and antisurvival responses to the two ErbB4 isoforms were sensitive to an ErbB kinase inhibitor. Platelet-derived growth factor receptor-alpha (PDGFRA) was identified as an ErbB4 target gene that was differentially regulated by the two ErbB4 isoforms. The soluble intracellular domain of ErbB4, released from the JM-a but not from the JM-b isoform, associated with the transcription factor AP-2 and promoted its potential to enhance PDGFRα transcription. Survival of cells expressing JM-a was suppressed by targeting either PDGFRα or AP-2, whereas cells expressing JM-b were rescued from cell death by the PDGFRα agonist, PDGF-BB. These findings indicate that two alternative ErbB4 isoforms may promote antagonistic cellular responses and suggest that pharmacological inhibition of ErbB4 kinase activity may lead to either suppression or promotion of cellular growth.

INTRODUCTION

ErbB/HER receptors form the epidermal growth factor receptor (EGFR) subfamily of receptor tyrosine kinases including ErbB1 (EGFR, HER1), ErbB2 (c-Neu, HER2), ErbB3 (HER3), and ErbB4 (HER4). ErbB receptors consist of an extracellular ligand-binding ectodomain, a hydrophobic transmembrane domain, and an intracellular cytoplasmic domain with enzymatic tyrosine kinase activity. Several EGF-like growth factors, such as neuregulins (NRG), bind to ErbB receptors, stimulating receptor dimerization, conformational changes, and subsequent autophosphorylation of tyrosine residues. These phosphorylation events trigger activation of downstream signal transduction molecules that couple ErbB4 to cellular responses, such as proliferation, differentiation, apoptosis, and survival. Overexpression and mutations of ErbB4 have been associated with malignant growth. Moreover, drugs that target ErbB1 or ErbB2 have demonstrated clinical effect as cancer therapeutics. These drugs include anti-ErbB antibodies and small-molecular-weight tyrosine kinase inhibitors (Hynes and MacDonald, 2009).

Relatively little is known about the cancer biology of ErbB4. Overexpression of ErbB4 promotes breast cancer cell proliferation and transforms fibroblasts (Cohen et al., 1996; Tang et al., 1999; Maatta et al., 2006). In contrast, ErbB4 activation has also been suggested to induce differentiation of breast cancer cells, confer cell cycle arrest, or stimulate apoptosis (Chen et al., 1996; Jones et al., 1999; Ni et al., 2001; Williams et al., 2004; Vidal et al., 2005; Muraoka-Cook et al., 2006a,b). Interpretation of published results has been complicated by the existence of four structurally and functionally different ErbB4 isoforms. These isoforms are generated from a single ERBB4 gene by tissue-specific alternative splicing (Junttila et al., 2000, 2003). The isoforms are all functional and tyrosine phosphorylated upon treatment with NRG-1 (Maatta et al., 2006). ErbB4 juxtamembrane (JM) isoforms (JM-a and JM-b) differ in their susceptibility to proteolysis at the extracellular JM domains (Elenius et al., 1997). As a consequence, only JM-a isoforms with 23 unique amino acids within the JM domain undergo ectodomain shedding, whereas JM-b isoforms with 13 alternative amino acids at the JM domain do not (Elenius et al., 1997). ErbB4 cytoplasmic (CYT) isoforms differ at cytoplasmic tails by including (CYT-1) or not (CYT-2) a 16-amino acid stretch containing binding sites for phosphoinositide 3-kinase (PI3-K; Elenius et al., 1999; Kainulainen et al., 2000), as well as for WW domain-containing proteins such as Nedd-like ubiquitin ligases (Omerovic et al., 2007; Sundvall et al., 2008b; Feng et al., 2009; Zeng et al., 2009).

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In addition to activating cascadical signaling pathways such as Ras–Raf–MAP/ERK kinase (Mek)–mitogen-activated protein kinase (MAPK) and PI3K/Akt (Kainulainen et al., 2000), the intracellular domains (ICD) of protelytically processed ErbB4 isoforms have been shown to directly translocate into the nucleus and regulate transcription (Ni et al., 2001; Lee et al., 2002; Komuro et al., 2003; Williams et al., 2004; Maatta et al., 2006; Sardi et al., 2006). First, ErbB4 JM-a is cleaved by tumor necrosis factor-α converting enzyme (TACE) approximately eight amino acids N-terminal to the transmembrane domain (Elenius et al., 1997; Río et al., 2000; Cheng et al., 2003). Subsequently, the remaining N-terminally truncated receptor undergoes regulated intramembrane proteolysis (RIP) by γ-secretase activity creating a soluble ICD fragment that may function as a transcriptional coregulator for several regulators of transcription, such as STAT5α, estrogen receptor-α, ETC2, and YAP-2 (Jones, 2008).

Previous findings have supported differential roles for different ErbB4 isoforms in cancer biology. CYT isoforms differ in subcellular targeting and stability (Maatta et al., 2006; Sundvall et al., 2007; Sundvall et al., 2008b) and have opposing effects on mouse mammary epithelium in vivo. ICD of CYT-1 type decreases mammary epithelial growth, whereas ICD of CYT-2 type causes epithelial hyperplasia (Muraoaka-Cook et al., 2009). Only cleavable ErbB4 JM-a CYT-2 capable of releasing a soluble ICD promotes survival of myeloid cells and growth of breast cancer cells in vitro (Maatta et al., 2006). In addition, nuclear localization of ErbB4 epitope associates with worse survival than localization of ErbB4 at the cell surface (Junttila et al., 2005).

Here, we compared the transforming potential of two ErbB4 isoforms in stably transfected mouse NR6 fibroblasts, a well-characterized model of ErbB-induced transformation (Chazin et al., 1992; Carey et al., 2006). Consistent with earlier analyses with other models (Junttila et al., 2005; Maatta et al., 2006), the JM-a CYT-2 isoform promoted proliferation, survival, and anchorage-independent growth. However, cells expressing ErbB4 JM-b CYT-2 with an alternative JM domain stimulated, rather than suppressed, apoptosis. Both responses were sensitive to an ErbB kinase inhibitor, indicating that ErbB4 inhibition can either promote or suppress growth, depending on the isoform expressed by the target cell. Further analyses on the mechanisms underlying the responses demonstrated a role for differential regulation of the PDGFRA gene at the transcriptional level. These findings suggest that the two ErbB4 isoforms may stimulate opposite cellular responses and underline the importance of using isoform-specific reagents when analyzing the potential of ErbB4 as a cancer drug target.

MATERIALS AND METHODS

Stable Transfectants

NR6 mouse fibroblasts (Press and Herschman, 1977) were maintained in DMEM (Invitrogen, Carlsbad, CA) supplied with 10% fetal calf serum (FCS; PromoCell GmbH, Heidelberg, Germany). Cells were transfected with pcDNA3.1ErbB4JM-a/CYT-2 or pcDNA3.1ErbB4JM-b/CYT-2 expression constructs (Maatta et al., 2006) using Lipofectamine plus transfection reagent (Invitrogen) according to manufacturer’s instructions. Stable clones were selected and cultured in the presence of 500 μg/ml G418 (geneticin; Calbiochem, La Jolla, CA). ErbB4 protein expression was analyzed as described below.

Chemical Inhibitors and RNA Interference

Inhibitors for ErbB receptors (AG 1478) and PDGFR (AG 1296) were purchased from Calbiochem. siRNAs targeting AP-2α (Hs_TIFAP2A_5), Mek1 (Hs_MAP2K1_6), Erk1/2 (Hs_MAPK1_10), Sp1 (Hs_SP1_5), Oct-1 (Hs_POU2F1_2), or a nonsilencing control siRNA were purchased from Qiagen (Chatsworth, CA). siRNA sequences are listed in Supplemental Table 1. siRNA specific for ErbB4 JM-a and control siRNA specific for the JM-b isoform (not expressed in MCF-7 cells), have been previously described (Maatta et al., 2006). siRNAs were transfected to cells using Lipofectamine 2000 (Invitrogen) according to the manufacturer’s instructions. The knockdown efficiency of RNA interference was determined by real-time RT-PCR as described below.

Western Blotting and Protein Phosphorylation Analyses

For ErbB4 and PDGFR-α protein expression analysis, NR6 transfectants were lysed, and samples equivalent to 75 μg of total protein were separated in 8% SDS-PAGE gels followed by Western blotting with anti-ErbB4 antibody (sc-283; Santa Cruz Technology, Santa Cruz, CA) or polyclonal anti-PDGFR-α antibody (Cell Signaling Technology, Beverly, MA) as previously described (Kainulainen et al., 2000).

For analysis of protein phosphorylation status, cells were starved overnight in DMEM containing no FCS and stimulated for 10–40 min with or without recombinant human NRG-1β1 (50 ng/ml; R&D Systems, Minneapolis, MN). For analysis of ErbB4 and PDGFR-α tyrosine phosphorylation, 1 μg of total protein lysate was immunoprecipitated with an anti-ErbB4 antibody (sc-283) or anti-PDGFR-α antibody (Cell Signaling Technology) and analyzed by Western blotting using an anti-phosphotyrosine antibody (4G10; Upstate Biotechnology, Lake Placid, NY), as previously described (Maatta et al., 2006). Filters were rebotted with anti-ErbB4 (sc-283) or anti-PDGFR-α (Cell Signaling Technology) to control loading. For analysis of Erk, Akt, and p38 phosphorylation, samples equivalent to 75 μg of total protein were separated in 8 or 10% SDS-PAGE gels followed by Western blotting with anti-phospho-p44/42 MAPK (Thr202/Tyr204; Cell Signaling Technology), anti-phospho-Akt (Cell Signaling Technology), and anti-phospho-p38 MAPK (Thr180/Tyr182; Zymed Laboratories, South San Francisco, CA) antibodies. To control loading, membranes were stripped and rebotted with anti-p44/42 (Cell Signaling Technology), anti-Akt (sc-1618; Santa Cruz), anti-phospho MAPK (Zymed Laboratories), or anti-actin (sc-13920) antibodies.

Kinase activity of ErbB4 JM-a CYT-2 and JM-b CYT-2 in NR6 cells was analyzed using in vitro kinase assays as previously described (Maatta et al., 2006).

Proliferation Analyses

For cell-counting experiments, NR6 transfectants were plated on 24-well plates at a density of 50,000 cells/well in DMEM containing 10% FCS. The following day, the media were replaced by DMEM containing 0–5% FCS supplemented with or without NRG-1 (50 ng/ml) or PDGF-BB (50 ng/ml; Peprotech, Rocky Hill, NJ). At days 2–5 after initial plating, cells were visualized and photographed under a phase-contrast microscope, washed with PBS, removed with trypsin, and counted under a microscope with hemocytometer. Analyses were carried out in triplicates. When inhibitors were used, they were added 24 h after plating in serum-free culture medium.

Data were statistically analyzed using Student’s t test.

For MITT proliferation assays, NR6 transfectants expressing ErbB4 JM-a CYT-2 or JM-b CYT-2 were plated onto 96-well plates in triplicates in DMEM containing 10% FCS. The next day, 150 nM siRNA targeting AP-2α or a nonsilencing control siRNA were transfected to cells. The number of viable cells was estimated 1, 2, or 3 d after initiation of the starvation using a CellTiter 96 nonradioactive cell proliferation assay kit (MTT; Promega, Madison, WI). Data were statistically analyzed using Student’s t test.

Soft Agar Colony Formation Assay

Bottom layers (2 ml) composed of DMEM containing 0.5% agar (Bacto-agar; Difco, Detroit, MI), 10% FCS, and 1% l-glutamine-penicillin-streptomycin (GIPS) solution were prepared into six-well plate wells. Top layers (1.2 ml) consisting of 30,000 NR6 transfectants and DMEM containing 0.33% agar, 10% FCS, 1% GIPS, and 0 or 100 ng/ml NRG-1 were added onto the solidified bottom layers. After 3 d of incubation, 200 μl per well of fresh DMEM supplemented with 10% FCS and 1% GIPS was added on wells to maintain humidty. Cells were incubated at 37°C for up to 7 wk and photographed under a phase-contrast microscope. Data were statistically analyzed using ANOVA (Dunnnett T3 posthoc t tests).

Cell Cycle Analysis

NR6 transfectants were starved without serum for 72 h. Subsequently, both adherent and floating cells were harvested, washed with PBS, and fixed with 70% ethanol at ~20°C for 20 min. Fixed samples were washed with PBS, and treated with RNAsin A (0.15 mg/ml; Sigma, St. Louis, MO), and DNA was stained with propidium iodide (PI; 40 μg/ml; Sigma). DNA content per particle was determined with FACS Caliber (BD Biosciences, San Jose, CA). Data were analyzed using CellQuest Pro software (BD).

TUNEL and DAPI Staining

NR6 transfectants were plated onto 13-mm coverslips at a density of 70,000 cells per milliliter. Cells were washed with DMEM, and the media were replaced by DMEM containing no serum. Cells were starved without serum for 2 d, washed with PBS, and fixed with methanol. DNA strand breaks were stained with TUNEL (TdT-mediated...
dUTP nick end labeling) staining reagent according to manufacturer’s instruc-
tions (In Situ Cell Death Detection Kit, TMR red; Roche, Indianapolis, IN). To
analyze nuclear morphology, nuclei were stained with 0.5 μg/ml DAPI
(4′,6-diamidino-2-phenylindole; Sigma) in PBS containing 3% bovine serum albumin
and 0.1% Triton X-100 at room temperature. After staining, coverslips were
washed with PBS and H2O and mounted with Vectashield mounting medium
(Vector Laboratories, Burlingame, CA). Cells were photographed and
counted under a fluorescence microscope. The percentage of condensed nu-
clei to all nuclei was determined from at least five arbitrary fields. Experi-
ments were repeated at least three times.

cDNA Microarrays

For cDNA microarray analyses, NR6 transfectants were starved without
serum for 8 h and treated with or without NRG-1 (50 ng/ml) for 2 h. Vector
control cells without NRG-1 treatment were used as a reference sample. RNA
was extracted with TRZol (Invitrogen) and purified with RNeasy MinElute
Cleanup Kit (Qiagen). The quality of the RNA samples was determined by
spectrophotometry (NanoDrop ND-1000; NanoDrop Technologies, Wilming-
ton, DE), gel electrophoresis, and by analyzing β-actin expression by real-time
RT-PCR (Livinainen et al., 2003; Junttila et al., 2003). Only samples of uniform
quality were chosen for cDNA microarray experiments. The samples were
amplified with Ribon Amp RNA Amplification Kit (Arcturus Bioscience,
Mountain View, CA).

Twenty micrograms of each RNA sample was labeled, and hybridization
was carried out as previously described (Nikula et al., 2005), with the excep-
tion that hybridization chambers were purchased from TeleChem Interna-
tional (Supplemental Table 1). The arrays contained cDNA fragments from
the National Institute on Aging NH mouse library spotted in duplicate on
poly-l-lysine coated glass slides (Finnish DNA Microarray Centre, Turku,
Finland). Microarray data were extracted and normalized using Scan-Array
Express software (v.2.1.8; Perkin-Elmer, Waltham, MA), as described (Nikula
et al., 2005). The sample expression level at each spot on the array was
compared with the expression level of the reference sample, and qualita-
tively poor spots were discarded. A gene was considered as differentially
expressed if its fold-change in expression level was at least a 2.0-fold change in
the average expression level. The results were analyzed with Kensingon
Discovery Edition software (v.2.0.4; InforSense Cambridge, MA) and DAVID
(Database for Activation, Visualition, and Integrated Discover). Functional
Annotation Bioinformatics Microarray Analysis; http://david.abcc.ncifcrf.gov/).

RT-PCR
cDNA microarray data were confirmed by RT-PCR. RNA was isolated and
reverse-transcribed as described before (Junttila et al., 2003). PDGFR trans-
scripts were analyzed with primers listed in Supplemental Table 1. To control
for mRNA quality, primers specific for β-actin (Livinainen et al., 2003) were
used. PCR reactions were carried out in a total volume of 30 μl, containing
0.67 μM primers, 3 μl of 10X Mg2+-free DnAZyme buffer (Finnzymes,
Espoo, Finland), 1 μM of each dNTP (Finnzymes), 1 U of DnAZyme II EXT
DNA Polymerase (Finnzymes), and 1 μl of template cDNA or water
(negative control). PCR samples were denatured at 94°C for 3 min and
subsequently cycled 25 times (β-actin) or 35 times (PDGFR) through 1-min
steps of denaturing (94°C), extension at 72°C, and denaturation at 94°C.
PcR products were separated by electrophoresis using 2% agarose gels, stained
with ethidium bromide, and visualized with UV light.

Real-time RT-PCR analysis of ErbB4 expression was carried out as de-
scribed before (Iivanainen et al., 2003, 2005), except that ABI Prism 7500 or 7900HT
Sequence Detectors (Applied Biosystems. Foster City, CA) were used. For
amplification of other transcripts, primers and probes listed in Supplemental
Table 1 were used.

PDGFR Promoter Assay

The effect of ErbB4 signaling on PDGFR promoter activity was analyzed in
MCF-7 cells, which endogenously express ErB4-JM-a CYT-1 and JM-a CYT-2
isoforms (Maatta et al., 2006). The cells were plated on 24-well plates and
cotransfected with pEGFP-C3 (polymeric enhanced green fluorescent
protein [pEGFP]; Clontech, Palo Alto, CA) and constructs expressing
luciferase reporter driven by PDGFR promoter fragments of different
sizes (pSLA4PDGF_Raluc–444+/118, pSLA4PDGF_Raluc–944/+118, and
pSLA4PDGF_Raluc–1253/+118; Afink et al., 1995) using Lipofectamine 2000
(Invitrogen). Starting 30 h after transfection, the cells were starved in the
absence of serum for 16 h and stimulated with 2 h for 80 ng/ml NRG-1 or for
18 h with 10 μM retinoic acid (RA). The fluorescence signal of EGFP was used
to normalize the luminescence signal generated by the luciferase reporters as
previously reported (Sundvall et al., 2007). To assess the effect of AP-2 and
ErbB4 ICD overexpression on PDGFR promoter, vector control, pCMVHA-
AP2e, pCMVHA-AP2y (Aquilan et al., 2004a), and/or pCDNA3.1ERB4ICD2
(Sundvall et al., 2007), constructs were expressed with pSLA4PDGF_Raluc–
1253/+118 reporter system. pC8 or pRl luciferase (Stratagene, La Jolla, CA) reporter
constructs in human embryonic kidney (HEK)-293T cells. Dual Luciferase
Reporter Assay (Promega) were used to measure luciferase activities. For RNA
interference analyses, siRNAs were transfected to cells as above 4 h after
transfecting the luciferase and EGFP constructs. A minimum of six indepen-
dent experiments was carried out for all promoter assays, and the statistical
significance was determined with one-way ANOVA (Dunnett two-sided or
Dunnett T3 posthoc t tests).

Confocal Microscopy

NR6 cells were transiently transfected with constructs encoding hemagglu-
tinin (HA)-tagged ErB4 JM-b CYT-2 or the sole intracellular domain of
the CYT-2-type, fixed 24 h after transfection, and stained with rat anti-HA anti-
body (epitope 12CA5; Zymed) and mouse monoclonal anti-AP-2α antibody
(sc-25343; Santa Cruz Biotechnology), as previously described (Sundvall et
al., 2008b).

Coimmunoprecipitation of ErbB4 with AP-2

Interaction between full-length or ICD of ErbB4 and AP-2 was determined by
coimmunoprecipitation analysis performed in transiently transfected NR6
transfectants, as previously described (Sundvall et al., 2008b). Constructs encoding
HA-tagged ErB4 JM-b CYT-2 or the sole intracellular domain of the CYT-2-type
(Sundvall et al., 2007) and Myc-tagged AP-2α or AP-2γ (Aquilan et al., 2004a) were used.

Glutathione S-transferase Pulldown Assay

To generate glutathione S-transferase (GST) fusion constructs encoding either
ICD of the CYT-2-type (ICD2), N-terminally truncated ICD2 (ICD-ΔN, includ-
ing amino acids 997-1292) or C-terminally truncated ICD2 (ICD-ΔC; amino acids
676-996), pCDNA3.1ERB4ICD2 (Sundvall et al., 2007) was amplified with primer
pairs and extended in Table 1) including sites for restriction enzymes.
The PCR products were ligated into a pGEX-6p-1 vector (GE Healthcare-
Waukesha, WI) using Sall and NotI restriction sites. For GST pulldown
assays, Myc-tagged AP-2γ (Aquilan et al., 2004a) or Myc-tagged Wwox
(Aqeilan et al., 2008b) were used as bait proteins. AP-2α and AP-2γ
were expressed as crystalline GST fusion proteins and the interaction between
AP-2γ and Wwox and the GST fusion proteins was analy-
yzed as previously described (Sundvall et al., 2008b).

RESULTS

NR6 Transfectants Expressing ErbB4 JM-a CYT-2 and
ErbB4 JM-b CYT-2

NR6 cells are a population of Swiss 3T3 fibroblasts that was
originally selected for a lack of EGF response and are devoid of
EGFR (Pruss and Hershman, 1977). NR6 cells also lack
endogenous ErB3 and ErB4 and express only ErB2 (data not
shown). Moreover, NR6 cells have successfully been used
to analyze transforming potential of ErBs (Chazin
et al., 1992; Carey et al., 2006). Because only nonadherent
hematopoietic cells totally lack ErB2 (Maatta et al., 2006), NR6
cells represent a model to analyze transforming activity of
ErbB4 isoforms in a cell background with minimal endoge-
 nous ErB expression.

NR6 cells were stably transfected to overexpress two ErbB4 isoforms with the same CYT-2 domain but different
JM domains (JM-a CYT-2 and JM-b CYT-2). The JM-a CYT-2
isoform was chosen as it has previously been shown to be
the most potent ErB4 isoform in stimulating ligand-inde-
pendent survival of myeloid 32D cells (Maatta et al., 2006)
and growth of MCF-7 breast cancer cells (Junttila et al.,
2005; Maatta et al., 2006). As the ligand-independent responses to
a CYT-2 expression have been shown to be partially
dependent on cleavage of a soluble ICD by RIP (Maatta et
al., 2006), the noncleavable JM-b CYT-2 was included in the
experiments for comparison. Several independent transfect-
ance clones were established and screened for ErbB4 expres-
sion by Western blotting (Figure 1A; Supplemental Figure
1). In all ErbB4 transfectants a 180-kDa band representing the
full-length ErbB4 was visible. An 80-kDa fragment represent-
ing the carboxy-terminal cleavage product of ErbB4 was con-
stitutively generated in cells expressing ErB4 JM-a CYT-2, but
not in cells expressing ErB4 JM-b CYT-2. Both ErbB4 isoforms
were tyrosine-phosphorylated upon NRG-1 stimulation, but
only JM-a CYT-2 demonstrated efficient constitutive phosphor-
ylation in the absence of ligand stimulation (Figures 1B and
5B). Furthermore, the 80-kDa fragment of ErbB4 JM-a CYT-2
demonstrated high basal tyrosine phosphorylation (Figures 1B
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and 5B). These findings are consistent with our previous observations in other cell backgrounds (Maatta et al., 2006) and demonstrate that JM-a CYT-2 but not JM-b CYT-2 is constitutively processed to generate an 80-kDa phosphorylated carboxy-terminal fragment in NR6 cells.

**ErbB4 JM-a CYT-2 Has Efficient Autokinase Activity**

Differential tyrosine phosphorylation of the two isoforms could result from differences in intrinsic kinase activities between the two proteins. To address the relative kinase activities, both isoforms were immunoprecipitated from NR6 cells and subjected to in vitro kinase assay in the presence of ATP. Both isoforms demonstrated basal autokinase activity (Figure 1C). However, the activity of the 180-kDa JM-a CYT-2 was on average twice the activity observed for 180-kDa JM-b CYT-2, after normalizing for ErbB4 protein expression. In addition, enhanced autokinase-stimulated phosphotyrosine content of the 80-kDa JM-a CYT-2 fragment was observed. However, chemical inhibition of ErbB4 cleavage by blocking either TACE or γ-secretase activity did not reduce the basal 180-kDa JM-a CYT-2 tyrosine phosphorylation, suggesting that proteolytic production of an active 80-kDa fragment was not necessary for phosphorylation of the full-length receptor (data not shown). These findings demonstrate a difference between kinase activities of the two ErbB4 isoforms.

**Signal Transduction Pathways Activated by JM-a CYT-2 and JM-b CYT-2**

Differences in the activation patterns and kinetics of signaling pathways, such as Mek/Erk pathway associate with different cellular responses, such as proliferation versus differentiation (Marshall, 1995). To test whether isoform-specific characteristics associated with differential intracellular signaling, NR6 transfectants were stimulated with NRG-1 and analyzed by Western blotting using phospho-specific antibodies for the MAPKs Erk1/2, and p38, as well as Akt (Figure 1D). Both isoforms were capable of activating Erk1/2, although the phosphorylation stimulated by JM-a CYT-2 seemed to be sustained somewhat longer. Neither of the isoforms activated p38. In line with earlier findings (Kainulainen et al., 2000), activation of Akt, a downstream target of PI3-K, was relatively weak by both of the CYT-2 isoforms lacking the direct PI3-K docking site (Elenius et al., 1999). These findings suggest that, with the exception of differences in the kinetics of Erk activation, the two ErbB4s did not significantly differ in stimulating some of the major signal transduction pathways involved in ErbB-regulated proliferation and survival.

**ErbB4 JM-a CYT-2 Promotes Proliferation and Anchorage-independent Growth**

To test whether JM-a CYT-2 and JM-b CYT-2 expression affected proliferation, growth curves were generated for transfectants maintained in DMEM containing 5% FCS. An increase in proliferation was evident in cells expressing JM-a CYT-2 when compared with vector transfectants (Figure 2A). JM-b CYT-2 expression had no effect on cell numbers in the presence of 5% FCS (Figure 2A). To analyze the potential of the isoforms to induce anchorage-independent growth, transfectants were seeded in soft agar. Cells expressing JM-a...
All transfectants displayed normal fibroblast morphology when cultured in 10% FCS. The next day the medium was replaced with medium containing 5% FCS with or without 50 ng/ml NRG-1. Adherent cells were counted at indicated time points with hemocytometer. *p < 0.05 for a difference between ErbB4 overexpression versus vector in the presence of NRG-1. (B and C) Cells were cultured in soft agar for 7 wk. Representative images (B) and quantitation of colonies (C) are shown.

Figure 2. Growth of NR6 cells expressing ErbB4 isoforms. (A) NR6 transfectants were plated onto 24-well plates in the presence of 10% FCS. The next day the medium was replaced with medium containing 5% FCS with or without 50 ng/ml NRG-1. Adherent cells were counted at indicated time points with hemocytometer. *p < 0.05 for a difference between ErbB4 overexpression versus vector in the presence of NRG-1. (B and C) Cells were cultured in soft agar for 7 wk. Representative images (B) and quantitation of colonies (C) are shown.

CYT-2 formed significantly more colonies than cells expressing JM-b CYT-2 or vector control cells (Figure 2, B and C). These data suggest that ErbB4 JM-a CYT-2, but not JM-b CYT-2, promotes growth of NR6 cells in soft agar.

ErbB4 JM-b CYT-2 Promotes Starvation-induced Cell Death

To compare the effect of ErbB4 isoform expression on cells progressing in cell cycle or induced into quiescence, NR6 transfectants were grown in the presence or absence of serum. All transfectants displayed normal fibroblast morphology when cultured in 10% FCS (Figure 3A). However, cells expressing JM-a CYT-2 preserved their normal morphology longer than vector control cells under serum-free conditions. Interestingly, cells expressing JM-b CYT-2 seemed to lose their spindle-shaped morphology and detach from the culture plates clearly before the vector control cells (Figure 3A). Consistent with the morphological differences, JM-a CYT-2 expression stimulated resistance to starvation-induced decline in cell numbers (Figure 3B). In contrast, expression of JM-b CYT-2 induced a rapid loss of all adherent cells when grown in medium containing 1% or 0% FCS (Figure 3B). Similar results were obtained with independent clones and when the cells were treated with different concentrations of the ErbB4 ligand NRG-1 (Supplemental Figure 2). Taken together, these data suggest that ErbB4 JM isoforms confer opposite cellular responses to serum deprivation: JM-a CYT-2 promotes resistance but JM-b CYT-2 sensitivity to cell death.

Cells Expressing ErbB4 JM-b CYT-2 Have Characteristics of Apoptosis

To characterize the mechanism leading to facilitated death of cells expressing ErbB4 JM-b CYT-2 under serum deprivation, DNA content of transfectants was analyzed by fluorescent-activated cell sorting (FACS). After 3 d of starvation, the subG1 population with small DNA content was considerably greater in cells expressing JM-b CYT-2 when compared with other transfectants (Figure 4A), consistent with apoptosis. Within 2 d after serum deprivation the nuclei in 43% of the vector control cells gained morphological characteristics of apoptosis (Figure 4, B and C). The percentage of cells with apoptotic changes was more than doubled to 91% in cells expressing JM-b CYT-2, but was only 13% in cells expressing JM-a CYT-2 (Figure 4, B and C). Condensed nuclei demonstrated by bright DAPI staining were also almost exclusively TUNEL positive (Figure 4B). These data indicate that cells expressing ErbB4 JM-b CYT-2 die because of apoptosis-like mechanisms in response to serum deprivation.

Chemical ErbB Kinase Inhibitor Reverses Both ErbB4 Isoform-specific Responses to Serum Deprivation

To test whether ErbB4 kinase activity was necessary for the two opposite cellular responses stimulated by the two ErbB4 isoforms upon starvation, NR6 transfectants were cultured under serum-free conditions in the presence and absence of a chemical ErbB kinase inhibitor AG 1478. Addition of AG 1478 significantly inhibited the growth of cells expressing JM-a CYT-2 (Figure 5A). No significant effect on growth was observed in vector control cells (data not shown). Significantly, adding AG 1478 into cells expressing JM-b CYT-2 partially rescued them from apoptosis (Figure 5A). The effect of AG 1478 on blocking both basal and ligand-induced tyrosine phosphorylation of both ErbB4 isoforms was demonstrated by Western analysis (Figure 5B). These findings suggest that both the pro- and antisurvival responses were at least partially dependent on ErbB4 kinase activity. The observation also indicates that inhibition of ErbB4 kinase activity may result in either promotion or suppression of apoptosis, depending on the isoforms present on the targeted cell. Similar findings with AG 1478 were also made in analyses of MCF-7 breast cancer cell transfectants expressing either JM-a CYT-2 or JM-b CYT-2 isoforms (data not shown).

Regulation of PDGFRA Expression by ErbB4 Isoforms

To identify molecular mechanisms underlying the different cellular responses promoted by the two ErbB4 isoforms, a cDNA microarray including 15,000 mouse cDNAs was screened for genes regulated in an ErbB4 isoform-specific manner. The cDNA array analysis indicated that ErbB4 JM-a CYT-2 and ErbB4 JM-b CYT-2 indeed regulated different sets of genes (Supplemental Table 2). One of the identified genes, *PDGFRa*, was up-regulated by JM-a CYT-2 but down-regulated by JM-b CYT-2. The finding was confirmed by RT-PCR analysis of *PDGFRa* mRNA (Figure 6A) and Western analysis of PDGFR-a protein (Figure 6C). Consistent with
the regulation taking place at the level of transcription, no differences in the relative degradation rate of the PDGFR-α protein, or the expression of the known PDGFR E3 ubiquitin ligase, Cbl, were observed between the transfectants (data not shown).

Because the antagonistic cellular responses stimulated by the two ErbB4 isoforms were both sensitive to AG 1478, the effect of the kinase inhibitor was also tested on isoform-regulated PDGFRA mRNA expression (Figure 6B). As expected, AG 1478 reduced PDGFRA mRNA expression in cells expressing JM-a CYT-2 but induced PDGFRA expression in cells expressing JM-b CYT-2. Analysis of PDGFR-α protein expression in transfectants cultured overnight in the presence or absence of FCS also demonstrated that starvation alone induced PDGFR-α expression, and expression of JM-a CYT-2 facilitated this induction, whereas expression of JM-b CYT-2 suppressed it (Figure 6C). These data suggest that ErbB4 isoforms regulate different sets of genes and identify PDGFRA as one gene that is regulated in opposite directions by ErbB4 JM-a CYT-2 and JM-b CYT-2.

**PDGFR-α Has a Functional Role on the Pathway Leading to Different Cellular Responses Downstream of the Two ErbB4 Isoforms**

The amount of tyrosine phosphorylated PDGFR-α followed the changes in total PDGFR-α expression in the transfectants (Figure 6D), suggesting functional significance. To further evaluate the functional contribution of PDGFR-α in regul-
ing different cellular responses to the two ErbB4 isoforms, serum-starved NR6 transfectants were treated with the PDGFR kinase inhibitor AG 1296 or with the PDGFR ligand PDGF-BB (Figure 6E). AG 1296 reduced the number of cells expressing JM-a CYT-2, whereas PDGF-BB rescued cells expressing ErbB4 JM-b CYT-2 from starvation-induced death. The effect of AG 1296 on blocking the tyrosine phosphorylation of PDGFR-a but not of ErbB4 JM-a was confirmed by Western analysis (Figure 6F).

Taken together, these findings indicate that ErbB4 isoforms may mediate opposite cellular responses. The data also suggest that differential regulation of PDGFR
ga is a central mechanism involved in isoform-specific regulation of cell behavior in fibroblasts.

**Regulation of PDGFR
ga Promoter Activity by ErbB4**

Targeting ERBB4 by RNA interference (73% knockdown as estimated by real-time RT-PCR from parallel samples) significantly suppressed the expression of PDGFRA mRNA in SK-N-MC neuroblastoma cells that naturally overexpress constitutively active ErbB4 JM-a isoforms (Figure 7A), demonstrating transcriptional regulation of PDGFRA expression also by endogenous ErbB4. To address the mechanism by which stimulation of endogenous ErbB4 JM-a regulates PDGFRA promoter activity, MCF-7 breast cancer cells (that express JM-a CYT-1 and JM-a CYT-2; Maatta et al., 2006) were transfected with luciferase reporter gene constructs encoding PDGFRA promoter fragments of different sizes. NRG-1 stimulation enhanced the promoter activity of the longest construct (1253 base pairs upstream of the transcription start site) by ~50% (Figure 7B). An increase ranging between 45 and 85% was achieved with all the promoter constructs when cells were stimulated with 10 μM retinoic acid, a positive control known to promote PDGFRA expression (Figure 7B; Wang et al., 1990). The NRG-1–induced...
**PDGFRA promoter activity in MCF-7 cells was blocked to the level of nonstimulated control by siRNA targeting endogenous ErbB4 (JM-a isoform-specific siRNA, 63% knockdown) but not by control siRNA (Figure 7C).**

Previous reports have indicated that PDGFRA promoter contains putative binding sites for transcription factors such as Sp-1, AP-2, and Oct-1 (Afink et al., 1995; Kawagishi et al., 1995). To determine factors involved in ErbB4-mediated PDGFRA regulation, the effects of specific siRNAs were tested on NRG-1–stimulated PDGFRA promoter activity in MCF-7 cells (Figure 7D). siRNA targeting Oct-1 did not tested on NRG-1–stimulated PDGFRA promoter activity in MCF-7 cells (Figure 7D), and the cleavable ErbB4 isoform was unique in promoting PDGFRA transcription (Figure 6A), a possible colocalization of AP-2 with the soluble ErbB4 ICD was addressed. Confocal microscopy of COS-7 transfectants demonstrated a partial colocalization of ErbB4 ICD, but not of full-length noncleavable ErbB4 JM-a, with AP-2α in the nuclei (Figure 8A). Furthermore, both AP-2α as well as AP-2γ associated with ErbB4 ICD but not with full-length ErbB4 JM-b in coprecipitation experiments (Figure 8B). GST pull-down experiments confirmed an interaction between AP-2γ and the N-terminal kinase region of ErbB4 ICD (Figure 8C, lanes 1–3). As a control demonstrating a previously characterized interaction (Agelan et al., 2005), Wwox was shown to bind to the C-terminal part of ICD (Figure 8C, lanes 4–6). Consistent with the effects of AP-2–specific RNA interference on PDGFRA promoter activity (Figure 7D), both AP-2α and AP-2γ increased the potential of ErbB4 ICD to stimulate PDGFRA promoter activity in HEK-293T transfectants (Figure 8D). Interestingly, coexpression of AP-2 with nonstimulated full-length ErbB4 did not result in enhanced promoter activity (data not shown).

To address the functional significance of AP-2 on promoting cellular growth downstream of the different ErbB4 isoforms, number of viable serum-starved NR6 transfectants was estimated by MTT assays on 96-well plates in the presence of siRNA targeting AP-2α or nonsilencing siRNA control. The siRNA targeting AP-2α (42% knockdown) suppressed the number of cells expressing JM-a CYT-2 but had no significant effect on cells expressing JM-b CYT-2 (Figure 8E), consistent with the inability to JM-b CYT-2 to partially colocalize (Figure 8A) and associate with (Figure 8B) with AP-2.

These findings indicate that AP-2 promotes PDGFRA transcription downstream of ErbB4 JM-a by directly interacting with the soluble ICD in the nucleus. These data

**AP-2 Solely Interacts with Soluble ICD of ErbB4**

As AP-2 was identified as a transcription factor positively regulating PDGFRA promoter in cells expressing ErbB4 JM-a (Figure 7D), and the cleavable ErbB4 isoform was unique in promoting PDGFRA transcription (Figure 6A), a possible interaction (Aqeilan et al., 2006), consistent with the inability to JM-b CYT-2 to partially colocalize (Figure 8A) and associate with (Figure 8B) with AP-2.
Erbb4 promotes cell death and survival

**Figure 7.** Regulation of PDGFRα transcription by ErbB4 activity. (A) SK-N-MC human neuroblastoma cells were treated for 48 h with or without control or ErbB4-specific siRNAs. Relative PDGFRα and ERBB4 mRNA expression was analyzed by real-time RT-PCR and normalized to the expression of the reference gene β-actin. (B) MCF-7 breast cancer cells were transfected with the PDGFRα promoter luciferase reporter constructs pSLA4PDGFRα–1253/+118 (1253), pSLA4PDGFRα–944/+118 (944), or pSLA4PDGFRα–1253/+118 (1253) together with a plasmid encoding EGFP. Cells starved for 16 h were treated for 2 h with or without 80 ng/ml NRG-1 to activate ErbB4 or for 18 h with 10 μM retinoic acid (RA) as a positive control known to stimulate PDGFRα promoter activity. Columns represent relative luciferase activity of promoter constructs normalized by the EGFP fluorescence signal. (C) MCF-7 cells expressing pSLA4PDGFRα–1253/+118 were treated for 48 h with or without control or ErbB4-specific siRNAs, starved for 16 h, and treated for 2 h with 0 or 80 ng/ml NRG-1. Columns represent relative luciferase activity of promoter constructs normalized by the EGFP fluorescence signal. (D) MCF-7 cells expressing pSLA4PDGFRα–1253/+118 were treated for 48 h with control siRNA or siRNAs targeting the indicated transcription factors (TF), starved for 16 h and treated for 2 h with 0 or 80 ng/ml NRG-1. PDGFRα promoter activity was determined as in C. The values represent the effect of NRG-1 treatment as percentages of the control siRNA sample. The transcription factor mRNA expression levels, as determined by real-time RT-PCR, are shown relative to control siRNA treatment (TF mRNA %).

Also provide a mechanistic explanation for the observation that only the cleavable JM-a CYT-2 isoform promoted PDGFRα transcription.

**DISCUSSION**

ErbB1 and ErbB2 receptors have successfully been used as cancer drug targets in the clinic (Hynes and MacDonald, 2009). However, the biological role of ErbB4 and its potential applicability as a cancer drug target has remained unclear (Sundvall et al., 2008a; Hollmen and Elenius, 2010). Currently, there is no consensus about the cellular responses stimulated via ErbB4. Several lines of evidence suggest that ErbB4 induces differentiation (Chen et al., 1996; Jones et al., 1999) or apoptosis (Arasada and Carpenter, 2005; Naresh et al., 2006). However, ErbB4 has also been documented to promote proliferation and tumor growth (Tang et al., 1999; Alaaoui-Jamali et al., 2003; Hollmen et al., 2009). One possible explanation for the different conclusions is that the ERBB4 gene is spliced into four functionally unique isoforms (Juntila et al., 2003; Maatta et al., 2006; Muraoka-Cook et al., 2009), and most available data has been produced using undefined reagents or analyzing different isoforms.

Here, two of the ErbB4 isoforms, JM-a CYT-2 and JM-b CYT-2, were overexpressed in NR6 cells, and their signaling responses were compared. JM-a CYT-2 has previously been shown to promote survival and proliferation in myeloid and breast cancer cells (Junttila et al., 2005; Maatta et al., 2006). JM-a CYT-2 promoted survival also in NR6 fibroblasts upon serum deprivation, but interestingly, JM-b CYT-2 induced cell death. Consistent with differential roles also in vivo, JM-a isoforms are frequently present in various types of epithelial carcinomas at relatively high quantities, whereas the JM-b isoforms are typically absent (Junttila et al., 2005; Hollmen and Elenius, 2010; data not shown). In addition, there is a selective up-regulation of the JM-a isoforms in pediatric ependymoma when compared with normal brain tissue (Gilbertson et al., 2002). These findings demonstrate that ErbB4 isoforms may have significantly different biological activities and indicate a selection pressure favoring expression of the survival-promoting JM-a isoform in malignant cells.

The known functional difference between the JM-a CYT-2 and JM-b CYT-2 isoforms is that the 23 unique amino acids in the extracellular juxtamembrane region of JM-a provide a protease cleavage site that is missing from the alternative 13 amino acids of JM-b (Elenius et al., 1997). As a consequence, only isoforms of the JM-a type may signal via a mechanism involving a two-step proteolytic cleavage generating a soluble ICD (Ni et al., 2001; Maatta et al., 2006). In accordance, only NR6 transfectants expressing JM-a CYT-2 demonstrated efficient ligand-independent accumulation of a highly tyrosine-phosphorylated and kinase active 80-kDa proteolytic fragment. These observations implicate a role for the release of the soluble ICD solely from the JM-a CYT-2 isoform as a mechanism causally involved in the differential cellular functions promoted by the two isoforms. Addressing the significance of ErbB4 cleaving enzymes on the cellular responses of NR6 transfectants using inhibitors of either TACE or γ-secretase was precluded by the significant background effects of these compounds on the parental NR6 cell line (data not shown). Consistent with the role of JM-a...
isoform cleavage in promoting growth, however, an antibody specifically recognizing the JM-a isoform and preventing its cleavage suppresses the growth of breast cancer cells (Hollmen et al., 2009).

To further characterize the molecular mechanisms underlying the functional differences between the cleavable and noncleavable ErbB4 isoforms, gene expression patterns of NR6 transfectants were compared using cDNA microarrays.

Figure 8. Selective and functional association of soluble ErbB4 ICD with AP-2. (A) COS-7 cells were transfected with pcDNA3.1ICD2-HA or pcDNA3.1ErbB4JM-bCYT-2-HA, stained with anti-HA (green) and anti-AP-2α (red) antibodies. The nuclei were stained with DAPI (blue). The cells were visualized by confocal microscopy. Bar, 10 μm. (B) COS-7 cells were transiently transfected with constructs encoding HA-tagged ErbB4 JM-b CYT-2 or ErbB4 ICD2 and Myc-tagged AP-2α or AP-2-γ. Lysates were immunoprecipitated with anti-Myc antibody and anti-HA antibody was used in Western blotting. Expression levels were controlled by Western analysis with anti-HA and anti-Myc antibodies. (C) GST fusion proteins including the whole intracellular domain of the CYT-2-type (ICD), N-terminally truncated ICD (ICD-N), or C-terminally truncated ICD (ICD-C) were incubated with lysates of COS-7 cells transiently expressing Myc-tagged AP-2-γ or Wwox. Material precipitating with glutathione Sepharose beads was analyzed by Western blotting with anti-Myc antibody. Membranes were reblotted with anti-GST antibody. (D) HEK-293T cells were cotransfected with the PDGFRA promoter-luciferase construct pSLA4PDGFRα-1253/+118 and a construct encoding Renilla luciferase together with an empty vector, constructs encoding the ErbB4 ICD of CYT-2-type (ICD), AP-2α, or AP-2-γ, or a combination of constructs encoding ICD and AP-2. Columns represent relative luciferase activity of the PDGFRA promoter construct normalized by fluorescence signal from the Renilla luciferase. (E) NR6 cells stably expressing JM-a CYT-2 or JM-b CYT-2 were transfected with siRNA targeting AP-2α or with a nonsilencing control siRNA. After siRNA transfection the cells were starved for 3 d, and the number of viable cells was determined with MTT assay. *p < 0.05.
The analysis indicated PDGFRα as one of the target genes that was differentially regulated by JM-a CYT-2 and JM-b CYT-2. Experiments with a chemical inhibitor of the PDGFRα kinase that suppressed the survival effect of JM-a CYT-2 further suggested a functional link between PDGFRα up-regulation and ErbB4 JM-a CYT-2 expression. In addition, PDGF-BB, an agonist of PDGFRα, rescued cells from JM-b CYT-2-induced death. Interestingly, FCS used to supplement cell culture media is known to be a rich source of PDGF ligands (Ross et al., 1974). This may indicate that the survival effects of ErbB4 isoforms were only observed after serum starvation as the lack of medium-derived PDGF sensitized cells to regulated PDGFR expression. Serum starvation alone also up-regulated PDGFRα expression in the vector control NR6 cells, putatively as an adaptation to low extracellular ligand concentration (Lih et al., 1996), and this up-regulation was further enhanced by the presence of ErbB4 JM-a CYT-2, but was reversed by JM-b CYT-2. Previously NRG-1 has been shown to inhibit PDGF-BB-stimulated vascular smooth muscle cell functions (Clement et al., 2007), but a direct role of ErbB4 in regulation of PDGFR has not been described. Our data indicate PDGFRα as one of the target molecules differentially regulated by ErbB4 isoforms and suggest a major role for it in ErbB4 isoform specific signaling responses leading to distinct behavior of the NR6 transfectants.

PDGFRα promoter assays in the presence and absence of siRNAs targeting transcription factors with suggested interactions with the PDGFRα promoter (Afink et al., 1995; Kawagishi et al., 1995) identified AP-2 as a factor positively regulating PDGFRα transcription. The specific association of AP-2 with the cleaved ICD derived from ErbB4 JM-a was indicated as the soluble ICD but not full-length ErbB4 1) partially colocalized with AP-2 in the nucleus, 2) interacted with AP-2 in coprecipitation and GST pull-down assays, and 3) had a synergistic effect with AP-2 on enhancing PDGFRα promoter activity. Moreover, 4) siRNA targeting AP-2 efficiently blocked the survival of cells expressing the cleavable JM-a CYT-2 but not of cells expressing JM-b CYT-2. Both AP-2α and AP-2γ associated with ErbB4 ICD, although the transcriptional synergism between the ICD and AP-2γ seemed to be stronger compared with AP-2α. In contrast, full-length ErbB4 JM-b not capable of releasing a soluble ICD fragment, did not demonstrate colocalization or association with AP-2, and the viability of cells expressing the JM-b isoform was not significantly affected by siRNA targeting AP-2. These findings support a model in which the survival-promoting effect of the JM-a CYT-2 isoform involves up-regulation of PDGFRα transcription via a unique and direct interaction of the released ICD fragment in the nucleus with AP-2. The observations also imply that the survival-promoting activity of the soluble ICD may, in the case of cleavable ErbB4 JM-a, counterbalance death-promoting signaling pathways, such as the Mek/Erk pathway, stimulated by all full-length ErbB4 forms at the cell surface. Indeed, our unpublished observations indicate that targeting of Mek significantly rescues cells expressing ErbB4 JM-b from starvation-induced death.

In conclusion, we provide evidence of opposite cellular functions promoted by alternatively spliced JM isoforms of ErbB4. Recently, similar observations of dramatically different cellular responses were reported for another pair of ErbB4 isoforms, the CYT isoforms, which promote either proliferation or differentiation in the mouse mammary gland (Muraoka-Cook et al., 2009). Our findings with the AG 1478 compound indicated that a wide-spectrum ErbB kinase inhibitor could promote either cell death or survival depending on the type of ErbB4 isoform present. These data underline the importance of investigating the basic biology of ErbB4 isoforms. Moreover, the findings indicate that differential consequences of blocking different ErbB4 isoforms should be taken into consideration when developing novel diagnostic tests and therapeutics for targeting ErbB receptors.

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