Mechanisms responsible for ERBB2 gene overexpression in human breast and non-breast cancer cells. The role of AP-2 transcription factors

Review Article

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Key words: the ERBB network, ERBB2 overexpression, transcriptional elements, Molecular mechanisms, breast cancers, rodent Neu promoter, Distant regulatory regions, endogenous ERBB2 gene expression, Transgenic overexpression of AP-2, mice mammary gland

Abbreviations: AP-2 binding sites, (AP2BS); chromatin immunoprecipitation, (ChIP); ductal carcinoma in situ, (DCIS); ETS binding site, (EBS); immunohistochemistry, (IHC); initiator like region, (Inr); invasive carcinoma, (IC)

Received: 21 June 2005; Accepted: 28 June 2005; electronically published: July 2005

Summary

The ERBB2 gene codes for p185erbB2, a transmembrane protein with intrinsic tyrosine kinase activity. P185erbB2 is a member of the EGFR family of growth factor receptors. The gene is expressed in embryonic and adult cells and its function is necessary throughout the entire life. ERBB2 is overexpressed in a significant proportion of human breast cancers where it is correlated to poor prognosis for the patient. The gene is also overexpressed in non-breast cancers but researchers disagree on the prognostic significance of the overexpression in these cancers. Gene amplification and increased transcription rates account for the very high levels of p185erbB2 accumulated in breast cancer cells. In a proportion of breast cancer cells a moderate increase in p185erbB2 level is due to transcriptional deregulation alone. The mechanisms responsible for ERBB2 gene overexpression in non-breast cancer cells is not well understood. The molecular mechanisms responsible for ERBB2 gene overexpression have been investigated mostly in breast cancers. In this paper we review the data from the literature and our own results on the involvement of AP-2 transcription factors family in ERBB2 gene overexpression in breast cancer cells. We conclude that AP-2 family of transcription factors contribute to the ERBB2 overexpression in a fraction of breast cancers. In contrast, AP-2 factors are not responsible for increased ERBB2 expression in the non-breast cancer cells we have analyzed.

I. Introduction: the ERBB network

The ERBB2 gene (also known as HER2 or Neu) encodes a 185 kDa transmembrane protein, p185erbB2, with intrinsic tyrosine kinase activity. P185erbB2 belongs to the EGF receptor (ErbB1) family of tyrosine kinase receptors, along with the products of EGFR, ERBB3 and ERBB4 genes. ErbB -1, -3 and -4 are recognized by more than 20 growth factors belonging to the EGF family. Ligand bound receptors form homodimers and/or heterodimers composed of two different receptors of the EGF family. No soluble growth factor recognizing p185erbB2 with high affinity has been identified so far and p185erbB2 is thus considered as an “orphan receptor”. The enzymatic activity of the ERBB3 gene product is impaired by mutation in the tyrosine kinase domain. P185erbB2 and the ERBB3 gene product are activated by hetero-dimerisation with another active ligand-bound receptor (reviewed in Brennan et al, 2000; Harari and Yarden, 2000; Olayioye et al, 2000; Yarden and Sliwkowski, 2001; Citri et al, 2003; Casalini et al, 2004).

The ErbB receptors together with the EGF family of ligands form the ErbB signaling network. In the healthy tissues the ligands are secreted by stromal cells and bind
receptors present on the surface of epithelial cells (Burden and Yarden, 1997).

Once activated, tyrosine residues at the carboxyl-end of the receptors are phosphorylated, creating docking sites for cytoplasmic signalling molecules. This triggers several signalling cascades, resulting in differentiation, survival, migration, depending on the growth factor, the composition of the dimer and the signalling molecules present in the cell.

P185<sub>erbB2</sub> is the preferred dimerisation partner for the three other receptors of the ErbB family. The dimers containing p185<sub>erbB2</sub> last longer and are more active than all the other dimers. High levels of p185<sub>erbB2</sub>, such as those measured in cancerous cells overexpressing the gene stimulate proliferation, inhibit apoptosis, induce migration and modify the response to chemo- and hormone-therapy (Harari and Yarden, 2000; Olayioye et al, 2000; Yarden and Slwikowski, 2001).

Here we summarise first some data on the normal ERBB2 gene expression and functions. The following section presents an overview of ERBB2 gene overexpression in breast and non-breast cancers. The molecular mechanisms leading to ERBB2 overexpression are the main topic of this paper. We present our data on ERBB2 overexpression in breast cancer cells. We discuss our results and the data from the literature concerning the role of AP-2 transcription factors on ERBB2 gene overexpression. Our results on the overexpression in non-breast cancers are summarised in the last section of this paper.

II. ERBB2 expression in healthy tissues

Low levels of membranous p185<sub>erbB2</sub> were detected in epithelial cells of a variety of normal human tissues such as those of the gastro-intestinal, respiratory, reproductive and urinary tract, as well as in skin, breast and placenta (Press et al, 1990; King et al, 1992; Camp et al, 2003).

An intact ErbB signalling network is required during embryonic development and throughout the entire life of an animal. Mice embryos carrying knocked-out ErbB2 gene died as a consequence of defects in the development of the heart and the nervous system. Animals where the ErbB2 gene was inactivated specifically in the heart after birth developed dilated cardiomyopathy. Formation of neuromuscular synapses, development of muscle spindles, Schwann cell function and survival of motor neurons were impaired in ErbB2 deficient mice (reviewed by Garratt et al, 2003; Holbro and Hynes, 2004). ErbB2 gene expressed in mice colon epithelial cells ensured the survival of enteric neurons and glia (Crone et al, 2003). In the inner ear, ErbB2 expressed by supporting cells ensured the survival of spiral ganglion neurons (Stankovic et al, 2004). The differentiating virgin mouse mammary glands express and activate ErbB2. The receptor drives the alveolar differentiation during pregnancy (reviewed by Troyer and Lee, 2001; Stern, 2003).

P185<sub>erbB2</sub> levels are physiologically modulated in healthy tissues and in non-cancerous pathologies. Erbb2 expression was increased in the regenerating mice intestine after small bowel resection (Falcone et al, 1999). During the maturation of the mice (Schroeder and Lee, 1998) and rat (Darcy et al, 2000) mammary gland changes in cell types expressing p185<sub>erbB2</sub> and expression levels were observed. Variations in p185<sub>erbB2</sub> levels during the menstrual cycle in the adult human breast were described. The protein was more abundant during the luteal than during the follicular phase of the cycle (Gompel et al, 1996).

III. ERBB2 overexpression in cancers

Not surprisingly given the importance of the cellular processes it regulates, the ErbB signalling network plays a central role in the development of numerous human cancers. Indeed, shortly after the discovery of the ErbB2 gene (Neu) as an oncogene in chemically induced rat brain cancers, Slamon and co-workers described the amplification and overexpression of the corresponding human gene in breast and ovary cancers. Moreover, the overexpression was associated with a poor prognosis (reviewed by DiGiovanna, 1999). This initial observation has been confirmed since by numerous studies and lead to the development of p185<sub>erbB2</sub> targeted therapies for breast cancer (Ross et al, 2003). Interestingly, ErbB2 overexpression was reported recently in spontaneous canine (de la Mulas et al, 2003) and feline (De Maria et al, 2005) mammary cancers. In both species this was a poor prognostic factor.

ErbB2 gene overexpression was also observed in non-breast human cancers, such as Wilms’ tumours, bladder, pancreas, colon, lung and prostate cancers. The prognostic significance of ErbB2 gene overexpression in non-breast tumours is debated (Klapper et al, 2000; Menard et al, 2001).

Twenty to forty percent of ovary cancers were reported to overexpress ERBB2 (Kupryjanczyk et al, 2004). The overexpression was most frequent in metastatic ovary carcinoma specimen and cancer cell lines (Hellsström et al, 2001). In a subset of ovarian cancers the gene was amplified but not overexpressed (Wu et al, 2004). ERBB2 overexpression was shown to be necessary for the growth of the ovarian cancer cells (Juhl et al, 1997; Hsieh et al, 2000) and might condition the response to chemotherapy (Abuhabirde et al, 2004).

ERBB2 status in other types of human cancer is controversial, mostly because of methodological problems. Maurer et al. (1998) reported co-expression of ERBB2 and ERBB3 genes in a high proportion of primary colorectal cancers. This was interesting since in breast cancers the erbB2/erbB3 dimer was shown to be the most tumorigenic (Harari and Yarden, 2000). Vadamudi and co-workers (1999) further showed that these receptors were constitutively phosphorylated in colon cancer cells. However, other investigators detected ERBB2 gene amplification and overexpression only in a small proportion of primary human colon cancers (Nathanson et al., 2003; Half et al, 2004).

Increased p185<sub>erbB2</sub> levels were detected by IHC in ductal pancreatic adenocarcinoma (Apple et al, 1999; work cited by Hruban et al, 2000). In contrast, Koeppen et al. (2001) did not observe a significant increase in p185<sub>erbB2</sub> levels in pancreatic cancers.
According to Craft et al. (1999) and to Signoretti et al. (2000) ERBB2 expression was increased in prostate cancer cells after androgen ablation and in hormone independent cancers. Some authors confirmed these observations (Osman et al., 2001; Shi et al., 2001). P185<sup>erbB2</sup> overexpression might thus contribute to progression toward androgen independence. The high p185<sup>erbB2</sup> levels detected in a significant proportion of circulating prostate cancer cells supported a role for the oncogene in prostate cancer progression (Ady et al., 2004; Carles et al., 2004). However, no consensus has been reached yet as to the role of ERBB2 in the progression of hormone independent prostate cancers, since other investigators did not observe a correlation between ERBB2 expression and hormone sensitivity (Reese et al., 2001; Savinainen et al. 2002; Calvo et al. 2003). The discrepancy between the results is probably due to methodological problems (Sanchez et al., 2002).

In summary, the involvement of ERBB2 gene overexpression in breast and ovary cancers progression is generally accepted. Breast cancer cells contain very high amounts of p185<sup>erbB2</sup> as a consequence of gene amplification combined with increased transcription rates. P185<sup>erbB2</sup> targeted therapies are developed for the treatment of breast cancer patients with ERBB2 overexpression. Whether ERBB2 gene overexpression is significantly involved in non-breast tumours progression is less clear. When present, the increase in p185<sup>erbB2</sup> levels in most of these tumours was moderate and the methodological problems concerning the detection of ERBB2 gene overexpression are not solved.

IV. Molecular mechanisms leading to ERBB2 overexpression in breast cancers

The mechanisms responsible for ERBB2 gene overexpression were investigated almost exclusively in breast cancers. Gene amplification and increased transcription rates lead to the very high increase in erbB2 transcript and protein levels in breast cancers. Moderate overexpression was often the consequence of transcriptional deregulation alone (Jimenez et al., 2000; Pauletli et al., 2000; Ménard et al., 2001; Hammock et al., 2003; Merkelbach-Bruse et al., 2003; Owens et al., 2004). We did show by run-on experiments, increased transcription rates in breast cancer cells overexpressing ERBB2 (Pasaleu et al., 1993).

Several teams, including our own, are interested in unravelling the mechanisms of deregulated ERBB2 transcription in breast cancer cells.

Briefly, transcription rates are controlled by binding of transcription factors to specific enhancer sequences on the promoter. Transcription factors bound to regulatory sequences (enhancers or silencers) interact directly or indirectly with general transcription factors which recruit RNA polymerase II to the core promoter.

Transcription rates can be increased by different mechanisms: increased levels or activity of transcription factors; mutations in the promoter creating binding sequences for a new activator or disrupting the binding site for a repressor. Recently, epigenetic mechanisms – DNA and histone methylation, histone acetylation – were involved in gene expression levels modulations.

To the best of our knowledge no mutations of the ERBB2 promoter have been reported in the cancerous cells overexpressing the gene. In contrast, overexpression and activation of transcription factors have been involved in ERBB2 overexpression in breast cancer cells.

We have analyzed the transcriptional activity of a 6kb fragment of the ERBB2 promoter. After describing the general transcriptional elements on the promoter, we focus on our data and the results from the literature concerning the role of increased levels of AP-2 transcription factors on ERBB2 overexpression.

A. General transcriptional elements on the human ERBB2 promoter

Three independent transcription start sites have been mapped on the ERBB2 gene promoter (Figure 1A). First, a TATA (-22 to -26) and a CAAT (-71 to -75) box direct transcription initiation at the site marked +1. This site will be referred to as the main transcription start site. An initiator like region (Inr), consisting of six GGA polypurine / polypyrimidine repeats, located from -65 to -45 base pairs upstream of the major transcription start site directs a second set of transcription start sites. The TATA box and the Inr independently govern the initiation of transcription (Mizuguchi et al. 1994). A third set of transcription initiation sites has been identified recently 12kb upstream from the main transcription start site. The mRNA initiated at this upstream site was present in low amounts in all the tested cells. It has an original 5’ untranslanted region and encodes a protein that is identical to the one translated from the major transcripts (Nezu et al., 1999).

The polypurine (GGA)-polypyrimidine (TTC) rich region forms an internal triplex structure (H-DNA) that represses ERBB2 gene transcription (Scott et al., 2000).

An approximately 500bp sequence at the 5’ end of the 6kb fragment contains multiple AA, TA and CA dinucleotide repeats. These features are characteristic of DNA sequences associated with the nuclear matrix and mediate the attachment of chromatin loops to the nuclear matrix (Laemmli et al., 1992). These Matrix Attachment Regions (MAR) have been involved in important cellular processes such as transcription activation (Bode et al., 2000) or insulation of genes from position effects (Allen et al., 2000).

We analyzed the sequence of a 20kb fragment of the human ERBB2 promoter with the MAR-finder program (Singh et al., 1997) to find out if the region containing the repeats has indeed the characteristics of a MAR. A maximal MAR potential was revealed in the region located between the positions -6/-5.6kb upstream from the main transcription start site (Figure 1B). This region of the ERBB2 promoter could thus be implicated in the regulation of ERBB2 transcription by organizing the chromatin domain containing the gene. Interestingly, a DNase hypersensitive site has been previously localized around position -5.5kb, indicating that this chromatin region is accessible to DNA binding factors (Vernimmen, unpublished). The accessibility is essential for MAR
sequences that often co-localize with DNaseI hypersensitive sites (Bode et al, 2000).

**B. Regulated transcriptional elements of the ERBB2 promoter**

1. The proximal promoter

The transcriptional activity of the proximal 500bp of the ERBB2 promoter was in good agreement with the level of expression of the endogenous gene in different breast cancer cell lines (Scott et al, 1994; Hollywood and Hurst, 1993; Grootecaes et al, 1994).

Three binding sites for transcription factors implicated in the overexpression of the gene have been localized on the proximal promoter. An ETS binding site (EBS) was located immediately upstream the TATA box (Scott et al, 2000) and two AP-2 binding sites (AP2BS) were located 213 (Bosch et al, 1996) and 495bp upstream from the transcription start site (Grootecaes et al, 1994; 1999; Vermimmen et al, 2003a) (Figure 1C).

![Diagram A](image1)

![Diagram B](image2)

![Diagram C](image3)

**Figure 1. A.** General transcriptional elements on 12kb of the human ERBB2 promoter. The broken arrows indicate the transcription start sites. The start site at position +1 is considered as the main transcription start site of the human gene. GGA: region containing the GGA repeats corresponding to the Initiator element (Inr). The gray box indicates the region containing the dinucleotide repeats. B. MAR potential analysis of the ERBB2 promoter. Positions are given relative to the major transcription start site. The sequence of an 18kb fragment of the human ERBB2 promoter was reconstituted from Z13970 (Hudson et al, 1990), X56495 (Grootecaes et al, 1994) and AB025285 (Nezu et al, 1999) sequences. C. Regulated transcriptional elements of the ERBB2 promoter. Broken arrows indicate the transcription start sites. Positions of the EBS and AP2BS associated with ERBB2 overexpression are indicated. The arrows point to the extremities of the promoter fragments which have been tested for activity. The plus signs indicate the promoter fragments active in the breast cancer cells which overexpress ERBB2. The minus signs indicate the repressing fragments. ± indicates a fragment which has different transcriptional activity according to the cell line.
The identity of the Ets transcription factor responsible for ERBB2 overexpression is not precisely yet. Several members of this vast family of transcription factors, such as ESX, are overexpressed and/or activated in breast cancer cells which overexpress ERBB2 (Chang et al, 1997). The AP-2 family of transcription factors includes five members: AP-2 -α, -β, -γ (Bosher et al, 1996), -δ (Cheng et al, 2002) and -ε (Tummala et al, 2003). Breast cancer cell lines overexpressing ERBB2 contain high amounts of AP-2-α and -γ factors (Bosher et al, 1995; 1996; Grootelaes et al, 1999).

We assessed the contribution of the -495 AP2BS to the promoter activity. For this purpose, we used a reporter vector containing the luciferase cDNA under the control of the proximal 750bp of the ERBB2 promoter. New vectors were derived from the initial one where each one or both AP2BS were inactivated by site-directed mutagenesis. Mutating the AP-2 sites, either individually or in combination, reduced the activity of the promoter to one-fifth the activity of the wild type promoter. Thus, both AP-2 sites must be present for full promoter activity (Vermimmen et al, 2003a).

2. Distant regulatory regions

We have investigated the transcriptional activity of promoter regions located upstream the proximal promoter (Figure 1C). The 3.5kb fragment preceding the proximal promoter repressed its activity in most cells. The mechanism of repression remains to be precised. The further upstream 2.2kb fragment repressed the repression specifically in breast cancer cells overexpressing ERBB2 (Grootelaes et al, 1994; Delacroix et al, in press).

The distal promoter region contains two AP-2 binding sites (Figure 1C). Binding of the factors to these sites contributed to the activity of the fragment. Indeed, the region of the distal activating fragment containing the two distal AP2BS was able to stimulate transcription from a heterologous TK promoter (Delacroix et al, in press).

Thus, the ERBB2 promoter contains at least four AP-2 binding sites, which contribute to the overexpression of the gene in breast cancer cells (Figure 1C). To evaluate the contribution of AP-2 factors to the transcriptional activity of the entire 6kb fragment of the ERBB2 promoter, we expressed an amino-terminal truncated AP-2 protein with dominant negative activity (DN-AP2). DN-AP2 has conserved the dimerisation and DNA binding domains, but lacks the transactivation domain (Williams and Tjian, 1991). DT-474 and ZR-75-1 breast cancer cells, overexpressing ERBB2 and containing high amounts of endogenous AP-α and -γ, were co-transfected with a constant amount of a reporter vector containing the 6kb promoter fragment and increasing amounts of the DN-AP2 expression vector. We measured a dose dependent decrease in the activity of the ERBB2 promoter, reaching 50% of the activity measured in the absence of the inhibitor. This shows that AP-2 factors contribute significantly to the activity of the ERBB2 promoter (Delacroix et al, in press).

C. The rodent Neu promoter

The promoters of the Neu genes, the rat and mice orthologues of the human ERBB2 gene, have been sequenced and the sequences were compared to those of the human promoter. The sequences of proximal promoters, extending 200bp upstream from the human main transcription start site are well conserved in the three promoters (White et al, 1992). However, there are some important differences between these sequences, indicating that the regulation of the human and the rodent genes expression might differ. For instance, the Neu promoters lack the TATA box and there is no initiation of transcription at the sites marked +1 on the human promoter. Moreover, some regulatory sites mapped on the rodent proximal promoters have not been found to regulate the activity of the human promoter (reviewed by Barnes and Hurst, 1997). Interestingly, as shown in Figure 2A, the two proximal AP-2 binding sites are not conserved in the rodent promoters.

A multalin alignment of the regions extending upstream the proximal 200bp revealed very limited sequence identity between the human, mouse and rat ERBB2 promoters (not shown). We also analyzed the mouse and rat Neu gene promoter sequences with the MAR-finder program. Indeed, several experimentally identified MARs are present at similar positions in the promoters of orthologous genes (Avramova et al, 1998; Greally et al, 1999). Despite limited sequence conservation, the potential of MAR occurrence on Neu promoters was very high for a region overlapping the position located 6kb upstream from the transcription start sites (Figure 2B and C). This conserved putative MAR sequence of ERBB2 distal promoter might thus a general regulator of ERBB2 gene expression. Noteworthy, the effect of such a MAR cannot be detected in reporter vectors experiments, since they are believed to act by chromatin remodeling. Transgenic animal models or stable transfection experiments have to be used to further study the contribution of the distal MAR to the expression of ERBB2 gene.

V. AP-2 transcription factors and ERBB2 expression in breast cancer cells

AP-2 factors activate the ERBB2 promoter in reporter vectors. These results initiated new research to find out if these transcription factors do indeed play a role in the overexpression of the endogenous ERBB2 gene in breast cancer cells. Three methodologies were used to address this question. First, AP-2 binding to the endogenous ERBB2 promoter and the consequences of AP-2 down-regulation on ERBB2 expression were analyzed in cultured cells. Second, AP-2 and p185HER2 levels, visualized by immunohistochemistry (IHC) on primary breast cancer sections, were compared. Third, Neu expression levels were investigated in transgenic mice overexpressing AP-2 in the mammary gland.
Figure 2. A. Alignment of the human ERBB2 (-590/+183bp relative to the main transcription start site), the mouse (-652/+6bp relative to the ATG translation initiation codon) and rat Neu (-683/+15bp relative to the ATG translation initiation codon) proximal promoters. The black nucleotides are conserved, whereas the grey nucleotides are not conserved between the three species. The broken line indicates the main transcription start site on the human promoter. The sequences corresponding to the human EBS and AP2BS are boxed. B. The mouse Neu promoter sequence from -13/+2.9kb (relative to translation start site) isolated from mouse BAC clone AL591390 was analyzed for the presence of MAR. Classically, the ATG, which is conserved in the human sequence, is designated as position +1 of the mouse promoter and the transcriptional start site lies 211bp upstream. C. The rat Neu promoter sequence comprised between positions -9.3 and +3kb, extracted from the rat supercontig NW-47339.1 (Rat genome resource, NCBI), was subjected to MAR analysis. In the rat promoter the ATG is located 9bp upstream the human and mouse ATG and defines classically the position +1. The transcriptional start site lies at position -203bp.
A. Modulation of the endogenous ERBB2 gene expression by AP-2 in breast cancer cell lines

Binding of a transcription factor to the endogenous chromatin embedded promoter region is the sine-qua non-requirement for its activity. We thus checked for AP2 association to breast cancer cells endogenous ERBB2 promoter by chromatin immunoprecipitation (ChIP). The chromatin from BT-474 cells was cross-linked, sonicated and immunoprecipitated with an AP-2 specific antibody. The AP-2 bound DNA fragments were PCR amplified with primers amplifying the region containing the proximal and the two distant AP-2 binding sites. The results show that AP-2 factors were bound to the proximal and the distal AP2BS (Begon et al, in press; Delacroix et al, in press). Thus, AP-2 factors are associated to the chromatin on the ERBB2 gene promoter in the cells expressing the gene. However, association to the promoter is not sufficient to prove that the factor is active.

To prove that AP-2 factors do contribute to ERBB2 overexpression, we measured ErbB2 mRNA levels in breast cancer cells where AP-2-α and -γ were down-regulated by siRNA. BT-474 breast cancer cells, which overexpress ERBB2, were transfected with AP-2α and AP-2γ siRNA, independently and in combination. After two to four days of treatment, AP-2α, AP-2γ, ErbB2 and VEGF (an AP-2 target gene) mRNAs were quantitated by real-time RT-PCR. The results are presented in Figure 3. AP-2α siRNA induced a rapid down-regulation of the corresponding protein, which became undetectable 2 days after the treatment, while AP-2γ levels were unmodified. In contrast AP-2γ was greatly reduced in cells treated with the specific siRNA, without significant changes in AP-2α content. Three days after treatment with both AP-2-α and -γ siRNAs both factors became undetectable (Figure 3A). The evolution of ErbB2 and VEGF transcript levels was measured in the cells transfected with the AP-2 directed siRNAs. Transfection with AP-2α siRNA inhibited AP-2α mRNA but did not modify significantly neither ErbB2 nor VEGF transcript levels (Figure 3B). Comparable results were obtained in cells transfected with AP-2-γ siRNAs (Figure 3C). In contrast, transfection of both AP-2-α and -γ siRNAs induced a transitory but significant reduction in ErbB2 and VEGF mRNA levels (Figure 3D).

In conclusion, the association of AP-2 factors with the endogenous gene promoter and the inhibition of expression by the down-regulation of AP-2α and AP-2γ are strong indications that AP-2 factors do contribute to ERBB2 overexpression in breast cancer cells. Our results further indicate that both AP-2α and AP-2γ are necessary for ERBB2 overexpression. However, clearly other transcription factors are involved in the increased ERBB2 gene expression observed in breast cancer cells (Delacroix et al, unpublished).

Cell lines present the advantage of being easily manipulated, however they might not reflect the properties of primary tumours. In the next sections we summarize results obtained on primary human breast cancers and in transgenic mouse models.

B. Correlation between AP-2 and p185\text{erbB2} levels in primary breast cancers.

A study using two antibodies recognizing specifically AP-2α and AP-2γ reported a positive correlation between the levels of p185\text{erbB2} on one hand and the presence of both AP-2α and AP-2γ on the other hand (Turner et al, 1998). A second study using a single antibody recognizing both AP-2α and AP-2β found a negative correlation between the receptor and the transcription factor levels (Gee et al, 1999).

A third report addressed the same question using a commercial anti AP-2α antibody. In only a proportion of tumours overexpressing ERBB2 were the AP-2 levels also increased. The overall survival was shorter in patients whose tumours overexpressed p185\text{erbB2} but not AP-2 (Pellikainen et al, 2004). Interestingly, we observed that in ERBB2 overexpressing MDA-MB-453 cells, AP-2 did not bind efficiently to DNA. ERBB2 overexpression in these cells might not be dependent on AP-2 factors (Grooteclaes et al, 1999).

An additional, thorough immunohistochemical analysis localized AP-2α and AP-2γ in healthy breast tissues, in ductal carcinoma in situ (DCIS) and in invasive carcinoma (IC). Higher expression levels were detected in the healthy breast and in DCIS than in IC. Moreover, the two isoforms were expressed in distinct cell types. Glandular epithelial cells expressed AP-2α, while myoepithelial cells expressed AP-2γ. AP-2α and ERBB2 levels were weakly but significantly correlated. In undifferentiated invasive carcinoma occasional co-expression of the two AP-2 isoforms was noted (Friedrichs et al, 2005). Interestingly, most breast cancer cell lines which overexpress ERBB2, overexpress both AP-2α and AP-2γ.

Finally, the relation between AP-2α gene methylation and expression was analyzed in breast cancer cells and a panel of normal breast, DCIS and IC samples (Douglas et al, 2004). AP-2α gene was unmethylated in most normal mammary epithelial cells and DCIS. AP-2α protein was detected in the nuclei of both these types of cells by IHC, with a tendency for overexpression in DCIS. In contrast, in 75% of invasive carcinoma AP-2α was hypermethylated and the protein was undetectable. These observations do not exclude an association between AP-2 and ERBB2 overexpression during breast cancer progression. Indeed, ERBB2 was overexpressed in a high proportion of DCIS (van de Vijver et al, 1988), while less than 30% of IC overexpress the gene.

In summary, AP-2 isoforms are expressed in healthy human breast cells, possibly in different cell types. These cells express low levels of p185\text{erbB2}. AP-2 and ERBB2 expression was increased in DCIS. Three out of four IHC analysis observed a tendency for a correlation AP-2 and p185\text{erbB2} levels in invasive carcinomas.

C. Transgenic overexpression of AP-2 in mice mammary gland

Mammary targeted overexpression of AP-2α inhibited the development of the gland. The expression
level of Neu, the mice ERBB2 ortholog, was not modified by AP-2α overexpression (Zhang et al., 2003). Transgenic overexpression of AP-2γ elicited hyper-proliferation of the epithelial cells, which was counterbalanced by increased apoptosis, the sum of these effects leading to hypoplesia of the gland. In these mice the transgene did induce a slight increase in Neu expression (Jäger et al., 2003).

However, the failure of AP-2 to stimulate Neu gene expression in mice mammary gland does not imply that the human ERBB2 is not regulated by these transcription factors.
factors. Indeed, as we have mentioned above, the AP2BS are missing from the mice Neu promoter (Figure 2).

The results of the experiments on the role of AP-2 transcription factors on ERBB2 gene overexpression in breast cancer cells are summarized in Table 1. In breast cancer cell lines AP-2 factors stimulate ERBB2 promoter activity. The factors are bound to the endogenous ERBB2 promoter and their down regulation inhibits the expression of the endogenous gene. Thus, in breast cancer cell lines, experimental evidence clearly indicates that AP-2 factors stimulate ERBB2 gene transcription. With one exception, a positive correlation was also reported between AP-2 and p185<sub>erbB2</sub> levels in primary breast cancers. As discussed above, the null effect of AP-2 overexpression on Neu expression in transgenic mice was probably due to the absence of AP2BS in the rodent promoter. These results indicate that AP-2 factors do contribute to ERBB2 gene overexpression in some human breast cancers.

VI. ERBB2 overexpression in non-breast cancer cells

The transcriptional mechanisms responsible for the increased ERBB2 expression in cancers others than the breast are poorly understood. We decided to use our knowledge on breast cancer cells to understand the mechanisms leading to ERBB2 gene overexpression in non-breast human cancer cells. We used three prostate, two ovary, five colon and seven pancreas cancer cell lines. To start, we compared the transcript and protein levels with the gene copy number. Next, we compared ErbB2 transcript and protein levels with those of AP-2 protein levels and DNA binding. Finally, we analyzed the activity of the ERBB2 promoter fragments which have been previously characterized in breast cancers (Vernimmen et al, 2003b).

We compared ERBB2 gene copy number, mRNA and protein levels in the non-breast cancer cells with those of well characterised breast cancer cells. ERBB2 gene amplification was detected only in SKOV-3 ovary cancer cells, where the amplification has been described previously. These cells contained the highest amounts of ErbB2 transcripts, comparable with those measured in breast cancer cells with a similar degree of gene amplification. Variable amounts of ErbB2 mRNA were detected in the other cells we have analyzed. The ErbB2 transcript levels in one colon cancer (COLO320) and in HepG2 liver cancer cells were comparable to those of ZR-75-1 breast cancer cells, which overexpress ERBB2 with a normal diploid set of genes.

The expression levels differed significantly between cells derived from the same cancer type (Table 2). So, ErbB2 mRNA levels were about seven times higher in LNCaP than in PC-3 prostate cancer cells. The difference between ErbB2 mRNA content in COLO320 and HTm29 colon cancer cells was thirteen fold. Pancreas cancer cells presented a 40-fold difference between the cells expressing the highest and the lowest amounts of the transcripts.

P185<sub>erbB2</sub> was detected by western blot in the majority of the analyzed cells. Protein and mRNA levels were in good agreement in the non-breast cancer cells, with the exception of colon cancer cells (Table 2) (Vernimmen et al, 2003b).

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<tr>
<td>Endogenous ERBB2 promoter</td>
<td>AP-2 binding endogenous promoter proven by ChIP</td>
<td>Begon, 2005</td>
</tr>
<tr>
<td>AP-2-α and -γ directed siRNAs down-regulate ERBB2 expression</td>
<td></td>
<td>Delacroyx, in preparation</td>
</tr>
<tr>
<td>Immunohistochemistry on primary human breast cancer sections</td>
<td>Positive correlation between AP-2α and AP-2γ levels and p185&lt;sub&gt;erbB2&lt;/sub&gt; levels</td>
<td>Tumer, 1998</td>
</tr>
<tr>
<td>p185&lt;sub&gt;erbB2&lt;/sub&gt;/ AP-2α</td>
<td>Positive correlation in a fraction of the tumors</td>
<td>Pellikainen et al, 2004</td>
</tr>
<tr>
<td>p185&lt;sub&gt;erbB2&lt;/sub&gt; AP-2α</td>
<td>Weak correlation between AP-2α and p185&lt;sub&gt;erbB2&lt;/sub&gt; levels</td>
<td>Friedrichs et al, 2005</td>
</tr>
<tr>
<td>p185&lt;sub&gt;erbB2&lt;/sub&gt; and AP-2α + AP-2γ</td>
<td>Negative correlation</td>
<td>Gee, 1999</td>
</tr>
<tr>
<td>AP-2 overexpression in the mammary gland of transgenic mice</td>
<td>The development of the gland is inhibited</td>
<td>Zhang, 2003</td>
</tr>
<tr>
<td>AP-2α</td>
<td>Increased proliferation and apoptosis</td>
<td>Jäger et al, 2003</td>
</tr>
</tbody>
</table>
Table 2. Differences in ErbB2 mRNA and protein levels in human cancer cell lines of different origins. The transcript levels were measured by quantitative RT-PCR, while the protein levels were estimated by western blotting (adapted from Vermimmen et al, 2003b). For each cancer type two cell lines are presented, one containing the lowest the second the highest amounts of ErbB2 mRNA and protein. For each cancer type, the lowest transcript and protein amounts were considered as equal to one. The relative increase in expression was calculated by dividing the highest values by the smallest values measured in cells from the same cancer type.

<table>
<thead>
<tr>
<th>Origin</th>
<th>Ovary</th>
<th>Prostate</th>
<th>Colon</th>
<th>Pancreas</th>
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<tr>
<td></td>
<td>mRNA</td>
<td>Protein</td>
<td>Low</td>
<td>High</td>
</tr>
<tr>
<td>Cell line</td>
<td>Ovar-3</td>
<td>SKOV-3</td>
<td>(PC-3)</td>
<td>(LNCaP)</td>
</tr>
<tr>
<td>mRNA</td>
<td>1</td>
<td>60</td>
<td>1</td>
<td>7.3</td>
</tr>
<tr>
<td>Protein</td>
<td>1</td>
<td>13**</td>
<td>1</td>
<td>7.5</td>
</tr>
</tbody>
</table>

Next we compared AP-2 and p185erbB2 levels in the non-breast cancer cell lines to find out if the overexpression of the transcription factors contributes to ERBB2 overexpression. Contrary to breast cancer cells, AP-2 and p185erbB2 levels were not correlated in the non-breast cancer cells. Strikingly, HepG2 cells expressed fair amounts of erbB2 mRNA cells but were devoid of AP-2 (Vermimmen et al, 2003b).

In order to identify the factor(s) responsible for the increased ERBB2 expression in non-breast cancer cells, we compared the activity of ERBB2 promoter fragments in couples of cells of the same origin expressing low and high levels of the transcript. This approach lead to the identification of AP-2 and ETS factors involved in ERBB2 overexpression in breast cancer cells. We could carry out these experiments only in ovary and colon cancer cells, because of very low transfection efficiencies of the other cell types. Figures 4 B-E summarize our results (Vermimmen et al, 2003b). The differences in activities of the fragments between breast and non-breast cancer cells are striking. In breast cancer cells the activity of the promoter fragments from vectors 2 and 4 was related to ERBB2 expression levels (Figure 4B). In contrast, all promoter fragments displayed comparable activities in HCT116 (Figure 4C) and in COLO205 cells (Figure 4D), in spite of the 3 fold difference in their ErbB2 mRNA content. In the ovary cancer cells the activity of the 6kb promoter fragment was higher in OVCAR-3 (Figure 4E) than in SKOV-3 cells (Figure 4F), while only the latter overexpress ERBB2.

The low AP-2 levels might explain the low activity of the p176-LUC vector in colon and ovary cancer cells since AP-2 binding drives the activity of this fragment. These results indicate that different mechanisms lead to ErbB2 mRNA upregulation in cancerous cells of different origins.

The promoter fragments we have analyzed do not contain the sequences responsible for increased ERBB2 gene expression in colon and ovary cancer cells. It is possible that the transcription factors responsible for the differences in transcription levels recognize sequences outside the fragments we have studied.

Another possibility is that, contrary to breast cancer cells, post-transcriptional mechanisms might be responsible for the increased ErbB2 mRNA and protein levels in the ovary and colon cancer cells we have analyzed. Indeed SKOV-3 ovary carcinoma cells express a variant ErbB2 mRNA with an extended half-life (Doherty et al, 1999). These mechanisms will have to be taken into account for the understanding of ERBB2 gene expression regulation in non-breast cancer cells.

VII. Conclusions

p185erbB2 contributes to mammary carcinogenesis if present in very high amounts, reached by the combination of gene amplification and increased transcription rates. In other tumours, increased protein levels, in the highest range of the levels measured in breast cancers without gene amplification, might be sufficient for cancer progression, probably in cooperation with other oncogenic signalling pathways. Our results indicate that different mechanisms are responsible for increased receptor content in non-breast cancer cells and in breast cancer cells. These mechanisms are not known at present.

Recent data indicate that non-breast cancer cells might become resistant to chemotherapy by upregulating ERBB2 expression. Thus, understanding the mechanisms responsible for the increase in p185erbB2 levels in different cancer cells is important for the development of more efficient therapeutic strategies for cancerous and non-cancerous diseases involving this protein.

Acknowledgements

Our work was supported by the FNRS, the Belgian Federation against Cancer, the Centre Anticancereux près l’Université de Liège. LD and DV were recipients of Televie grants from the FNRS; BD was a recipient of FRIA fellowship and Televie grant; RW is Senior Research Associate (FNRS).
Figure 4. ERBB2 promoter activity in human cancer cells of different origins. A. Reporter vectors used in this study containing the luciferase (LUC) cDNA under the transcriptional control of 215 (1), 716 (2), 3798 (3) and 6007 (4) bp fragments of the human ERBB2 promoter. B. Relative luciferase activities induced by reporter vectors 2, 3 and 4 transfected into BT-474 breast cancer cells overexpressing ERBB2, reported to the activity induced by vector 1 considered as equal to one (Delacroix et al, in press). C. Relative luciferase activities induced by reporter vectors 2, 3 and 4 transfected into HCT116 colon cancer cells reported to the activity induced by vector 1 considered as equal to one. D. Relative luciferase activities induced by reporter vectors 2, 3 and 4 transfected into COLO 320 colon cancer cells, reported to the activity induced by vector 1 considered as equal to one. E. Relative luciferase activities induced by reporter vectors 2, 3 and 4 transfected into OVCAR-3 ovary cancer cells reported to the activity induced by vector 1 considered as equal to one. F. Relative luciferase activities induced by reporter vectors 2, 3 and 4 transfected into SKOV-3 ovary cancer cells overexpressing ERBB2 reported to the activity induced by vector 1 considered as equal to one (Vermimmen et al, 2003b).

References


