Loss of ERβ expression as a common step in estrogen-dependent tumor progression

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Abbreviations: hERα or β, human estrogen receptor α or β; E2, 17β-estradiol; IHC, immunohistochemistry; ISH, in situ hybridization; Apc, adenomatosis polyposis coli; ERE, estrogen response element; SFRE, steroid factor response element ; AP-1, activator protein-1; wt, wild-type; SAOS-2, human osteoblast-like cells; HOSE, Human Ovarian Surface Epithelium; WHI, Women’s Health Initiative; RT-PCR, reverse transcription polymerase chain reaction; mRNA, messenger RNA; PARP, Poly (ADP-ribose) polymerase.
Abstract

The characterization of estrogen receptor beta (ERβ) brought new insight into the mechanisms underlying estrogen signaling. Estrogen induction of cell proliferation is a crucial step in carcinogenesis of gynecologic target tissues and the mitogenic effects of estrogen in these tissues (e.g. breast, endometrium and ovary) are well documented both in vitro and in vivo. There is also an emerging body of evidence that colon and prostate cancer growth is influenced by estrogens. In all of these tissues, most studies have shown decreased ERβ expression in cancer as compared to benign tumors or normal tissues, whereas ERα expression persists. The loss of ERβ expression in cancer cells could reflect tumor cell dedifferentiation but may also represent a critical stage in estrogen-dependent tumor progression. Modulation of the expression of ERα target genes by ERβ, or ERβ specific gene induction could indicate that ERβ has a differential effect on proliferation as compared to ERα. ERβ may exert a protective effect and thus constitute a new target for hormone therapy, e.g. via ligand specific activation. The potential distinct roles of ERα and ERβ expression in carcinogenesis, as suggested by experimental and clinical data, are discussed in this review.

Introduction

It is well documented that the mitogenic actions of estrogens are critical in the etiology and progression of human breast and gynecological cancers (Henderson et al. 1988, Pike et al. 1993). The promoting effect of estrogens was recently highlighted by the results of large prospective studies, showing that estradiol intake during menopause increased the risk of breast cancer (Nelson et al. 2002, Rossouw et al. 2002, Chlebowski et al. 2003, Beral et al. 2003). In ovarian cancer, although the question is still debated (Coughlin et al. 2000), several recent prospective studies have indicated a risk of ovarian cancer for women undergoing long-term estrogen replacement therapy (Rodriquez et al. 2001, Lacey et al. 2002, Anderson et al. 2003, Folsom et al. 2004). In contrast, estrogens appear to exert a protective effect on the risk of colon cancer (Rossouw et al. 2002).

The effects of estrogens are mediated by ERα and ERβ receptors, which are members of the nuclear steroid receptor superfamily. ERα and ERβ classically mediate their action by ligand-dependent binding to the estrogen response element (ERE) of target genes, leading to their transcription regulation (Green et al. 1986, Mosselman et al. 1996, Kuiper et al. 1996, Tremblay et al. 1997). Both of these proteins have a high degree of homology in the DNA binding domain (Mosselman et al. 1996), but differ considerably in the N-terminal domain and to a lesser extent in the ligand-binding domain (E domain) (Mosselman et al. 1996, Kuiper et al. 1996, Kuiper et al. 1996, Kuiper et al. 1996, Kuiper et al. 1996, Kuiper et al. 1996, Kuiper et al. 1996, Kuiper et al.
These differences suggest that the two receptors could have distinct functions in terms of gene regulation and biological responses and may contribute to the selective actions of E2 in different target tissues (Gustafsson et al. 2000).

Recently, various studies have shown decreased expression of ERβ mRNA and protein (or an increased ERα/ERβ mRNA ratio) in tumor versus normal tissues in many cancers, including breast, ovary, colon, and prostate (Brandenberger et al. 1998, Campbell-Thompson et al. 2001, Fixemer et al. 2003, Foley et al. 2000, Pujol et al. 1998, Roger et al. 2001, Rutherford et al. 2000). The ERα/ERβ gene expression ratio thus appears to increase during carcinogenesis, suggesting that ERα and ERβ specific pathways may have distinct roles in this process (Leygue et al. 1998). The differential expression of ERα and ERβ in cancer cells and experimental data on their respective roles on proliferation are reviewed in this report.

**Differential ERβ expression as a common feature of estrogen-dependent tumor progression in clinical studies**

**Analysis of ERα and ERβ expression in estrogen sensitive cancers (Tables 1 to 4)**

In breast tissues, several studies have indicated an increase in ERα/ERβ mRNA and protein ratios in cancer as compared to benign tumors and normal tissues. In immunohistochemical analyses, Roger et al. (2001) found a higher percentage of ERβ-positive cells in normal mammary glands as compared to non-proliferative benign breast disease (BBD) (85%), proliferative BBD without atypia (18.5%) and carcinoma in situ (33.8%). In contrast, an increase in ERα protein expression was noted during progression. Moreover, ERβ was inversely correlated with Ki67, a marker of cell proliferation. The authors thus suggest that ERβ has a protective role against the mitogenic activity of estrogens in mammary premalignant lesions. This conclusion is also supported by the results of another study (Shaw et al. 2002), which revealed lower ERβ protein expression in carcinomas and demonstrated that ERα but not ERβ protein expression was correlated with tumor grade. Similar findings were obtained at the mRNA level using the RT-PCR method in study of Iwao et al. (2000), who also showed that ERα mRNA is increased and ERβ mRNA decreased during breast carcinogenesis. Recently, Park et al. (2003) compared ERβ mRNA levels in various breast tissues using mRNA in situ hybridization. ERβ expression was decreased in breast cancer (BC) and metastatic lymph node tissues as compared with normal mammary and
benign breast tumor (BBT) tissues. The intensity and extent of ERβ expression were significantly higher in normal and BBT tissues than in BC or metastatic lymph node tissues (Park et al. 2003).

In invasive breast cancer, other studies using IHC and ISH methods revealed that ERβ expression was associated with indicators of low biological aggressiveness (low tumor grade, low S-fraction, and negative lymph node status), suggesting that ERβ might be a good prognostic indicator (Jarvinen et al. 2000). In a study of Omoto et al. (2001), a survival analysis showed that patients with ERβ-positive tumors had increased disease-free survival at 5 years as compared with those with ERβ-negative tumors. Fuqua et al. (2003) studied ERβ expression using IHC in a pilot series of 242 breast cancer patients and showed that ERβ expression is not associated with clinical and biological parameters, including PR expression, tumor grade and S-phase fraction. ERβ was only found to be correlated with aneuploidy. The findings of this study suggested that ERβ could be a useful biomarker on its own in clinical breast tumors. To gain insight into the possible role of ERβ in breast carcinogenesis, Skliris et al. (2003) performed an IHC analysis of ERβ on 512 breast specimens. Moreover, real time PCR was used to investigate the ERβ gene methylation status in the ERβ-negative breast cancer cell lines SK-BR-3 and MDA-MB-435. The results suggested that the loss of ERβ expression is one of the hallmarks of breast carcinogenesis and that it may be a reversible process involving methylation. Zhao et al. (2003) also concluded that decreased ERβ mRNA expression may be associated with breast tumorigenesis and that DNA methylation is an important mechanism for ERβ gene silencing in breast cancer (Table 1). Collectively, ERβ expression decreases in the process of breast cancer development.

The ovary (Table 2) contains both ER isoforms but ERβ seems to be the predominant species expressed in normal ovary in rats (Byers et al. 1997) and humans (Kuiper et al. 1996, Enmark et al. 1997). Our laboratory (Pujol et al. 1998) documented an increase in the ERα/ERβ mRNA ratio in ovarian carcinomas as compared with normal ovaries and cysts and our findings suggested that overexpression of ERα relative to ERβ mRNA may be a marker of ovarian carcinogenesis. This conclusion was further supported by Brandenberger et al. (1998) and Rutherford et al. (2000). The latter study revealed that the balance between ERα and ERβ receptors might be essential for maintaining normal cellular function, suggesting that, as ERβ decreases, uncontrolled cellular proliferation leads to a metastatic state. In a study of Lau et al. (1999) no differences in ERβ mRNA expression were found between normal and cancer epithelial cells, but these authors only analyzed a few HOSE cell primary cultures (n=4) and ovarian cancer cell lines (n=3) using a non-quantitative PCR method. Decreasing levels of ERβ expression seems to be a common denominator between breast and ovarian carcinogenesis.
In prostate, it has been suggested that estrogens and their receptors may be involved in cancer development and progression (Santti et al. 1994, Farnsworth et al. 1999, Jarred et al. 2000). Estrogen exposure during prostate development may initiate cellular processes resulting in future neoplasia (Santti et al. 1994). In a study of Latil et al. (2001), ERα and ERβ mRNA expression were quantified by real-time RT-PCR in both benign and malignant prostate. ERβ mRNA level was decreased in most of the tumor samples as compared to normal prostate, suggesting that ERα and ERβ expression status could be used to identify advanced prostate tumor patients. This result is in agreement with those obtained at the protein level. Pasquali et al. (2001a) investigated ERβ expression in benign and malignant prostate tissue specimens using a polyclonal antibody directed against the C-terminal domain of the ERβ protein. In contrast to normal tissues, ERβ nuclear immunostaining was undetectable in all cancer sections, showing that malignancy seems to be associated with the disappearance of ERβ expression in prostate tissue. Horvath et al. (2001), using IHC, also found that the ERβ protein was progressively lost in hyperplasia and neoplastic lesions. This is in agreement with the results of Fixemer et al. (2003) in a study in which a new monoclonal antibody revealed the differential expression of ERβ in tissue sections from 132 patients with prostate cancer. Moreover, these authors showed partial loss of ERβ in high grade prostatic intraepithelial neoplasia (HGPIN) (Table 3). Once more the change in ERα/ERβ ratio seems to be correlated with malignancy.

In colon cancer, the protective effect of estrogen replacement therapy is supported by a number of clinical observations (Calle et al. 1995, Newcomb et al. 1995, Persson et al. 1996, Kampman et al. 1997), including the results of recent randomized studies named "WHI" (Nelson et al. 2002, Rossouw et al. 2002). These studies demonstrated that women with a history of current or past hormone replacement therapy had a significantly decreased risk of colon cancer. These findings have led many investigators to search for the biological mechanisms by which estrogen may influence the pathogenesis of colorectal cancer. Since ERα is reported to be minimally expressed in normal colon mucosa and colon cancer cells (Waliszewski et al. 1997, Campbell-Thompson et al. 2001), the effects of estrogen on colon cancer susceptibility may be mediated by ERβ. Campbell-Thompson et al. (2001) showed, using semi-quantitative RT-PCR, that ERβ is the predominant ER subtype in the human colon and that decreased ERβ1 (ERβwt) and ERβ2 (ERβcx) mRNA levels were associated with colonic tumorigenesis in women. In a recent study using IHC analysis (Konstantinopoulos et al. 2003), it was shown that ERβ expression was significantly lower in colon cancer cells than in normal colonic epithelium and that there was a progressive decline in ERβ expression, which paralleled the loss of malignant
colon cell dedifferentiation. These findings are in accordance with a previous study of Foley *et al.* (2000) who also detected a selective loss of ERβ protein in malignant human colon by Western immunoblotting. Weyant *et al.* (2001) worked with a model of mice bearing germline mutations in murine Apc. These mice develop multiple intestinal tumors that show loss of wild-type Apc protein. In this model, E2-induced prevention of Apc-associated tumor formation was correlated with an increase in ERβ protein and a decrease in ERα in target tissues. Altogether, these results strongly suggest that ERβ provides protection against colon carcinogenesis (Table 4).

**ERβ as a predictive factor for antiestrogen therapy?**

Although many reports suggest the protective role of ERβ against tumor progression, controversies have arisen regarding the clinical value of ERβ expression in terms of predicting the adjuvant hormonal therapy response in breast cancer. Some studies suggest that the ERβ status in breast cancer is a predictor of the response to tamoxifen (Leygue *et al.* 1998, Jarvinen *et al.* 2000, Mann *et al.* 2001) whereas others suggest that ERβ is significantly upregulated in tamoxifen resistant breast cells and could be involved in tamoxifen resistance (Speirs *et al.* 1999).

The type of analysis, patient selection criteria, the type of splicing variants detected in RNA analyses or the small number of patients analysed to date could ultimately explain these controversial results. The first findings were obtained in studies involving RT-PCR based techniques, but the quantification of gene expression at the mRNA level may not be directly linked qualitatively or quantitatively to the protein expression. There have been very few studies in which ERs were measured by Western immunoblotting or IHC because of the lack of reliable antibodies. Finally, the choice of statistical analysis and different parameters selected for analysis could also influence the results.

**ERβ as a potential tumor suppressor gene?**

The results of these different studies, showing a loss of ERβ expression in cancer as compared to normal cells, are in line with the hypothesis that the ERβ gene may act as a tumor suppressor (Iwao *et al.* 2000). This concept needs to be confirmed but could make sense in view of the location of ERβ on chromosome 14q (Enmark *et al.* 1997). A loss of 14q has been detected by comparative genomic hybridization in some breast cancers (Loveday *et al.* 2000, Burki *et al.* 2000). Interestingly, in ovarian cancer, two potential tumor suppressor
gene loci have been mapped to 14q (Bandera et al. 1997). 14q deletions are also observed in colon carcinoma (Young et al. 1993) and prostate cancer (Kasahara et al. 2002). These overall findings suggest a potential tumor suppressive function for ERβ. However, further studies are required before definitive conclusions on the tumor suppressive function of ERβ can be drawn.

What are the potential molecular mechanisms underlying ERα and ERβ differential actions?

Several in vitro studies have focused on the molecular mechanisms underlying the differential roles of ERα and ERβ. Differences in ligand affinity, transcriptional activation, interactions with cofactors or putative heterodimerisation have been proposed.

Structural properties of ERα and ERβ and consequences on their transcriptional activities

Estrogen receptors α and β belong to the large nuclear steroid/thyroid hormone receptor family. Like most other members of the family, ERs have a modular architecture of four interacting domains: the N-terminal A/B domain, the C or DNA binding domain (DBD), the D or hinge domain and the C-terminal E/F or ligand binding domain (LBD) (Fig. 1). There is only 56% amino-acid identity between the two receptors in the LBD whereas the homology in the DBD is 97%. This suggests that ERβ would recognize and bind to the same EREs as ERα but that each receptor might have a distinct spectrum of ligands (Kuiper et al. 1997a). A number of novel selective ER subtype ligands have now been developed. The propyl pyrazole triol (PPT) compound was found to be an ERα-specific agonist, activating gene transcription only through ERα (Sun et al. 1999, Stauffer et al. 2000). A number of other known ligands are also somewhat ERβ selective. Some phytoestrogens, such as genistein and coumestrol, show a higher affinity toward ERβ than ERα (Kuiper et al. 1997b). The diaryl-propionitrile (DPN) compound is a potency-selective agonist for ERβ with a more than 70-fold higher binding affinity for ERβ than ERα (Meyers et al. 2001). Recently, Ghosh et al. (2003) have investigated a novel series of heterocycle ligands for the ERs based on a diazene core motif. In this process, they have found diazenes that have high binding affinity for the ERs and some of these show preferential affinity for ERα or for ERβ.
The N-terminal domain of nuclear receptors encodes a ligand-independent activation function (AF-1) (Berry et al. 1990, McInerney et al. 1996a, Tora et al. 1989), a region of the receptor involved in protein-protein interactions (Onate et al. 1998), and transcriptional stimulation of target gene expression. The activation function-2 (AF-2) domain, located in the ligand-binding domain (Tora et al. 1989), is responsible for hormone-dependent activation through recruitment of coactivator proteins (Tremblay et al. 1997, White et al. 1997). There is very little conservation in the N-terminal AF-1 domain, which could explain why different sets of proteins in the transcription complexes may interact with ER\(\alpha\) and ER\(\beta\) and direct them to specific targets. Dissimilarity in the NH\(_2\)-terminal extremity of ER\(\alpha\) and ER\(\beta\) is one possible explanation for the difference in the response of the two receptors to various ligands. In fact, the two receptors are distinct in their responses to the synthetic antiestrogens tamoxifen, raloxifen and ICI-164, 384. On an ERE-based reporter gene assay, tamoxifen, 4-OH-tamoxifen, raloxifen, and ICI-164, 384 have an ER\(\alpha\)-selective partial agonist/antagonist function but pure E2 antagonist effect through ER\(\beta\) (Barkem et al. 1998, McDonnell et al. 1995, McInerney et al. 1998). Watanabe et al. (1997) showed that the agonistic effect of tamoxifen depends on the cell type, ERE-promoter context, and ER subtypes, and that this action is ER\(\alpha\) specific. Tamoxifen is an ER\(\alpha\) antagonist in breast (Jordan et al. 1992) but an agonist in bone (Love et al. 1992) and uterine tissues (Kedar et al. 1994). Raloxifene is also an ER\(\alpha\) antagonist in breast tissue, but it exerts agonistic activity in bone but not in uterine tissue (Black et al. 1994).

ER\(\alpha\) and ER\(\beta\) are capable of regulating gene transcription through a classical mechanism involving the consensus estrogen response element (ERE) but ER\(\beta\) seems to be a weaker transactivator (Cowley et al. 1999). Cowley and Parker (1999) have shown that the AF-1 activity of ER\(\beta\) is weak compared with that of ER\(\alpha\) on estrogen-responsive reporters, whereas their AF-2 activities are similar. In turn, when both AF-1 and AF-2 functions are active in a particular cell and/or on a particular promoter, the activity of ER\(\alpha\) greatly exceeds that of ER\(\beta\), whereas ER\(\alpha\) and ER\(\beta\) activities are similar when only AF-2 is required (Cowley et al. 1999, McInerney et al. 1998). ER\(\alpha\) and ER\(\beta\) have similar but also different effects on gene transcription mediated via the ERE. To date only a limited number of genes have been shown to be regulated by one of the two E2-ligated ER subtypes in this classical mode of action. In this way, gene encoding the catalytic subunit of human telomerase hTERT is regulated by ER\(\alpha\) and not by ER\(\beta\) in human ovary epithelium cells (Misiti et al. 2000) and in human prostate cancer (Nanni et al. 2002). In the same way, Lazennec et al. (2001) reported that, ER\(\alpha\), but not ER\(\beta\) was able to regulate c-myc proto-oncogene expression. The metallothionein gene is known to be specifically upregulated by E2 via ER\(\beta\) in SAOS-2 cells (Harris et al. 2001). However, recently, Stossi et al.
(2004) have compared the gene regulatory activities of ERα and ERβ in bone and showed a highly similarity but also significant differences in gene targets for these two ERs. Thus, genes encoding for cystatin D, autotaxin or stromal antigen 2 appear to be E2-regulated specifically by ERβ in human osteosarcoma cells.

Estrogens (and antiestrogens) also transcriptionally regulate target genes via ERs though a non-ERE mode of action. These effects are mediated through promoter elements that bind various transcription factors, including AP-1-binding sites (Webb et al. 1995), Sp1 binding sites (Porter et al. 1997), the SF1 response element (SFRE) (Vanacker et al. 1999), electrophilic/antioxidant response element (EpRE/ARE) (Montano et al. 1997) and cyclic AMP response element (CRE) (Sabbah et al. 1999). At AP-1 sites, ERα and ERβ could have opposite transcriptional effects in some circumstances (Paech et al. 1997). In fact, ERβ is able to potentiate an AP-1 containing reporter in the presence of the anti-estrogen tamoxifen but not in the presence of estrogens in a tissue-specific manner. ERα stimulates AP-1 activity in the presence of antiestrogens in endometrial cells (Webb et al. 1995, Paech et al. 1997), but antiestrogens decrease or have no effect on AP-1 activity in breast cancer cells (Philips et al. 1993, Webb et al. 1995). Of particular note, ERβ is more potent overall than ERα on AP-1 sites, whereas the contrary occurs on EREs (Paech et al. 1997, Cowley et al. 1999, Hall et al. 1999). Similar to AP-1, E2 binding to ERα induces transcriptional activation when associated with SP1 in GC-rich regions. However, E2 interaction with ERβ does not result in the formation of a transcriptionally active complex at a promoter containing Sp1 elements (Saville et al. 2000). Vanacker et al. (1999) described that the osteopontin gene promoter is stimulated through SFRE sequences by ERα but not by ERβ.

Consequently, these differences in ligand interaction or transcriptional activity between the two ER subtypes may account for the major differences in their tissue-specific biological actions. This complexity is further enhanced by ERβ isoforms, the ability of ERs to form homodimers and heterodimers, and their capacity to interact with various coregulators.

**ER isoforms**

Several groups have reported and cloned different ERβ isoforms with exon deletions (Lu et al. 1998), insertions (Hanstein et al. 1999), or C-terminal splice variants (Ogawa et al. 1998, Moore et al. 1998). These isoforms can also bind ligands, mediate estrogen signalling (Kuiper et al. 1997b, Paech et al. 1997, Cowley et al. 1999, Bollig et al. 2000) and exhibit different properties, thus further enhancing the complexity in the spectrum of potential cellular responses to estrogen. The key element lies perhaps in the balance between the expression of
these different variants and their relative quantities. It has been shown that ERβ splice variants have dramatically
different localization patterns in living cells and this localization can be altered by estrogen agonists and
antagonists (Price et al. 2000). Interestingly, Poola et al. (2002) recently showed that estrogen receptor β splice
variant mRNAs were differentially altered during breast carcinogenesis. ERβcx, which utilizes an alternative
exon 8, is the most extensively studied splice variant. Ogawa et al. (1998) showed that this isoform may act as a
potential inhibitor of ERα transactivation, possibly due to ERα/ERβcx heterodimer formation. Using IHC, it has
been shown that differential expression of ERβwt and ERβcx may be used as a prognostic marker in human
prostate (Fujirama et al. 2001). Peng et al. (2003) showed that all ERβ isoforms inhibited ERα transcriptional
activity on an ERE, while only ERβwt had transcriptional activity of its own. It has been shown, using cDNA
microarrays in MCF-7 cells stably transfected with ERβwt and ERβcx MCF-7, that these two isoforms inhibit
ERα function differently (Omoto et al. 2003). Consequently, it can be hypothesized that the differential
expression of ERβ isoforms may have a role in the modulation of estrogen action.

**ER homo- and hetero-dimers**

The functional formation of ERα and ERβ heterodimers has been demonstrated (Pettersson et al. 1997,
Cowley et al. 1997). They are able to bind to DNA with an affinity similar to that of ERα and greater than that
of ERβ homodimers, to interact with coactivators, and to stimulate the transcription of reporter gene in
transfected cells (Pettersson et al. 1997, Cowley et al. 1997). The possible involvement of ERα and ERβ
dimerization would increase the complexity of transcription activation in response to E2 and suggests the
existence of two previously unrecognized estrogen signaling pathways, i.e. via ERβ homodimers and ERα/ERβ
heterodimers. Moreover, it has been reported that various ERα and ERβ ratios in different cells, resulting in
different homodimer and heterodimer compositions, may constitute a key for gaining insight into the tissue-
specific effects of estrogen and antiestrogens (Kuiper et al. 1997a). Homodimers and heterodimers could bind to
distinct response elements and consequently activate specific gene expression patterns in given target tissues. For
such interactions, ERα and ERβ must be coexpressed in cells, as noted in breast, ovarian and endometrium
tissues. However, future studies will be required to determine the physiological roles of ERα and ERβ homo-
and heterodimers in vivo.
Interactions with coactivators and corepressors

There is one further confounding factor in the ER-mediated estrogen action equation. The ER-mediated transcriptional activity of estrogen is influenced by several regulatory factors, known as coactivators and corepressors, which activate or repress the transcription of ER-responsive genes (Klinge et al. 2000). The p160/SRC (steroid receptor coactivator) family is one of the most studied classes of coactivators, and includes SRC1, SRC2 (GRIP1/TIF-2) (McKenna et al. 1999) and other more recently described coactivators such as ACTR (Chen et al. 1997), RAC3 (Li et al. 1997), AIB1 (Anzick et al. 1997) and TRAM-1 (Takeshita et al. 1997). Most of interactions of these coregulators with the ER is ligand-dependent but some coactivators have also been shown to be recruited in a ligand-independent manner by the AF-1 domain of ERs (Mc Inerney et al. 1996b; Tremblay et al. 1999). SRC-1 activated ERβ AF-1 upon MAPK-induced phosphorylation of serine residues (Tremblay et al. 1999). Deblois et al. (2003) studied the steroid receptor RNA activator (SRA) and showed that SRA potentiated the estrogen-induced transcriptional activity of both ERα and ERβ. They demonstrated that the transcriptional activity of ERα can be enhanced by SRA in a ligand-independent manner through the AF-1 domain. However, this AF-1 dependent effect of SRA is not observed on ERβ. Very few receptor-specific ERβ cofactors have been identified so far. Warnmark et al. (2001) showed that TRAP220 displays a preference for ERβ and suggested that the coregulator selectivity of ER subtypes is an additional layer of specificity that influences the transcriptional response in estrogen target cells. Kurebayashi et al. (2000) also showed, using multiplex RT-PCR, that ERβ expression levels were correlated with some activators such as AIB1, CBP, P/CAF, and a corepressor, N-CoR, but the significance of this correlation is unclear. Nuclear receptors usually bind the corepressors N-CoR and SMRT in the absence of ligand or in the presence of antagonists. Agonist binding leads to corepressor release and coactivator recruitment. A recent study (Webb et al. 2003) demonstrated that, in vitro and in vivo, ERβ binds to N-CoR and SMRT in the presence of ER agonists such as estradiol and phytoestrogens like genistein, but not in the presence of antagonists. ERα and ERβ present completely distinct modes of action with coregulators, which could be of major importance in terms of potential effects on physiological behaviour (Webb et al. 2003).
What do we know about the role of ERβ in cell proliferation and death?

**ERβ and cell proliferation**

Although the specific functions of ERβ in cancer are not known, there is some evidence that ERβ could have inhibitory effects on cellular proliferation. First, as indicated previously, the levels of ERβ are highest in normal tissue (breast, ovary, prostate) as well as in benign disease and it decreases during carcinogenesis (Table 1-3). Our laboratory obtained the first evidence that ERβ is an important modulator of proliferation and invasion of breast cancer cells, thus supporting the hypothesis that the loss of ERβ expression could be one of the events leading to breast cancer development (Lazennec et al. 2001). Whereas ERα was able to regulate reporter genes and endogenous genes in a ligand-dependent manner, ERβ inhibited MDA-MB231 cell proliferation in a ligand-independent manner. This suggests that the two ERs inhibit cancer cell proliferation via different mechanisms (Lazennec et al. 2001).

Omoto et al. (2003) recently developed cell lines expressing ERβwt and ERβcx by stable transfection of each expression plasmid in MCF7 cells and demonstrated that this constitutive expression significantly reduced the percentage of cell population in S-phase and the number of colonies in an anchorage-independent assay. Recently, two studies showed that the induced expression of ERβ in ERα-positive breast cancer cells inhibits their growth (Paruthiyil et al. 2004, Strom et al. 2004). These reports also suggest that ERβ might reduce cell proliferation by inhibiting cyclin D1gene, a key factor controlling the G1-S transition of the cell cycle, and thus cell proliferation. Strom et al. (2004) also indicated that numerous other components of the cell cycle associated with proliferation such as cyclin E or Cdc25A were decreased. These results are in accordance with the study of Bièche et al. (2001), showing a negative correlation between ERβ and CCND1 (cyclin D1) expression. In vitro studies are in agreement with the hypothesis of Liu et al. (2002) who showed that E2 activates cyclin D1 gene transcription through ERα, but inhibits cyclin D1 gene transcription through ERβ in HeLa cells.

The contrasting phenotypes observed in individual lines of ER knockout mice, i.e. ERαKO and ERβKO, which exhibit phenotypes that generally mirror the respective ER expression patterns, provides further evidence that the two ERs have distinct biological functions. Weihua et al. (2000) observed that, in immature uterus, ERα and ERβ are expressed at comparable levels in the epithelium and stroma, and E2 treatment decreases ERβ in the stroma. Increased cell proliferation and the exaggerated response to E2 in ERβKO mice suggested that ERβ plays a role in the modulation of the effects of ERα and also (or consequently) has an
antiproliferative function in immature uterus. A second study in ERβ-/− mice showed that ERβ is implicated in the regulation of epithelial growth, and its absence results in hyperplasia of the prostatic epithelium (Weihua et al. 2001). The inhibition of ERα transcriptional activity could be a molecular mechanism by which ERβ has antiproliferative effects. Previous in vitro data indicate that ERβ could act as a dominant negative regulator of ERα activity. Hall et al. (1999) have provided direct proof that ERβ modulates/represses ERα transcriptional activity in transient transfection cells. In bone, it has been shown that ERβ inactivation by gene targeting results in increased cortical bone formation. Windalh et al. (2001) showed that, when present, ERβ acts in a repressive manner on trabecular bone, possibly by inhibiting the stimulatory action of ERα. Finally, Lindberg et al. (2003) showed that in some mouse tissues, ERβ reduces ERα-regulated gene transcription, thus indicating that there is a balanced relationship between ERα and ERβ (Fig. 2).

**ERβ and apoptotic pathways?**

A decrease in the human cancer cell population in vitro or tumor regression in vivo reflects a change in the balance of cellular growth events and could involve arrested cell proliferation or an enhanced cell death or both. Several studies have suggested that estrogen may regulate apoptotic pathways in cancers (Kyprianou et al. 1991, Perillo et al. 2000, Choi et al. 2001). We could assume that E2 effects involve both proliferation induction and apoptosis inhibition. Choi et al. (2001) showed that E2 may be associated with upregulation of the anti-apoptotic bcl-2 gene at the mRNA level. It has been suggested that ERα may play a role in ovarian tumorigenesis by preventing apoptosis whereas the ERβ-induced inhibition of proliferation could be explained by the inhibition of the bcl-2 gene, as supported by a recent report of Nilsen et al. (2000). They showed that estradiol can function as a neuroprotective agent or an inducer of apoptosis, depending on the estrogen receptor-subtype present in the cell. ERα is thus associated with a neuroprotective effect, while ERβ mediates the induction of apoptosis in neuronal cells. Similarly, Sapi et al. (2002) demonstrated estrogen-induced upregulation of FasL, an apoptotic protein ligand, in ovary. This could seem paradoxical since estrogen is known to be anti-apoptotic in different cells. The authors proposed that in normal ovary the apoptotic protein ligand FasL is probably upregulated by ERβ, the predominant form of ER in this tissue (Fig. 3). Recently, we have demonstrated (Cheng et al. in press) that the expression of ERβ in prostate carcinoma cells triggers apoptosis, notably by increasing baxα levels as well as cleavage of PARP and caspase-3 expression.
Conclusions

Numerous clinical and in vitro studies suggest that imbalanced ERα/ERβ expression is a common feature and could be a critical step of estrogen dependent tumor progression. ERβ seems to play a key role in the mitogenic action of estrogen by providing protection against ERα-induced hyperproliferation. A role in apoptosis might also be possible.

ERα and ERβ have some overlapping tissue distribution but also display high relative tissue-specific expression. Moreover, a number of molecular mechanisms could be proposed to explain the differential roles of ERα and ERβ, including differences in ligand affinity and transactivation, distinct cofactor interactions and putative heterodimerisation. Splicing variant ERs isoforms may also be important in modulating the cellular response.

In conclusion, the imbalance in ERα/ERβ expression in estrogen dependent cancer opens a new field in hormone therapy of cancer. Targeted ERβ therapies, including the development of ERβ specific ligands, may constitute a new therapeutic approach particularly for pre-invasive or proliferative lesions. The clinical value of ERβ in cancer prognosis and its possible usefulness for prediction of the hormone response should be assessed in large-scale and prospective clinical studies.

Acknowledgments

This work was supported by the “Ligue Nationale Contre le Cancer”, the “Centre Hospitalier Universitaire de Montpellier” (Grant # AOI7619), the “Association pour la Recherche contre le Cancer” (Grant n° 4302) and the “Institut National de la Santé et de la Recherche Médicale”.

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Vanacker JM, Pettersson K, Gustafsson JA & Laudet V 1999 Transcriptional targets shared by estrogen receptor-related receptors (ERRs) and estrogen receptor (ER) alpha, but not by ERbeta. EMBO Journal 18 4270-4279.


Table 1: Relative expression of ERα and ERβ in breast tumor progression.

<table>
<thead>
<tr>
<th>References</th>
<th>Tissues</th>
<th>Number</th>
<th>Methods</th>
<th>ERα</th>
<th>ERβ</th>
<th>Comments</th>
</tr>
</thead>
<tbody>
<tr>
<td>Roger et al.</td>
<td>Normal NP-BBD</td>
<td>18</td>
<td>SQ Ov.</td>
<td>++</td>
<td>+++</td>
<td></td>
</tr>
<tr>
<td></td>
<td>CIS</td>
<td>13</td>
<td>IHC</td>
<td>++</td>
<td>+</td>
<td></td>
</tr>
<tr>
<td></td>
<td>High grade CIS</td>
<td>25</td>
<td>SQ Ov.</td>
<td>++</td>
<td>-</td>
<td></td>
</tr>
<tr>
<td></td>
<td></td>
<td>35</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Iwao et al.</td>
<td>Normal</td>
<td>11</td>
<td>Real Time-PCR</td>
<td>++</td>
<td>+++</td>
<td>ERβ+ cells decrease during pre-invasive tumor progression.</td>
</tr>
<tr>
<td>Park et al.</td>
<td>Normal Breast Cancer</td>
<td>89</td>
<td>ISH</td>
<td>+++</td>
<td>+++</td>
<td>ERβ mRNA level decreases during tumor progression.</td>
</tr>
<tr>
<td></td>
<td></td>
<td>85</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td></td>
<td>10</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Skliris et al.</td>
<td>Normal PDCIS</td>
<td>138</td>
<td>IHC</td>
<td>++++</td>
<td>++++</td>
<td>Reduced expression of ERβ in invasive breast cancer.</td>
</tr>
<tr>
<td>(2003)</td>
<td>Invasive cancers</td>
<td>319</td>
<td></td>
<td>++</td>
<td></td>
<td>Loss of ERβ may be a reversible process involving methylation.</td>
</tr>
<tr>
<td></td>
<td>Met. lymph node Recurrences</td>
<td>31</td>
<td></td>
<td>+</td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td></td>
<td>8</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Speirs et al.</td>
<td>Normal</td>
<td>23</td>
<td>RT-PCR</td>
<td>+</td>
<td>+++</td>
<td>22% of normal breast expressing exclusively ERβ mRNA.</td>
</tr>
<tr>
<td>(1999)</td>
<td>Cancer</td>
<td>60</td>
<td>+++</td>
<td></td>
<td></td>
<td>50% of breast tumors coexpressing ERα and ERβ.</td>
</tr>
<tr>
<td>Leygue et al.</td>
<td>Normal (adjacent tissues)</td>
<td>18</td>
<td>Multiplex RT-PCR</td>
<td>+</td>
<td>++</td>
<td>Increase in ERα and decrease in ERβ during tumor progression.</td>
</tr>
<tr>
<td>(1998)</td>
<td>Cancer</td>
<td>18</td>
<td>+++/+++</td>
<td></td>
<td></td>
<td></td>
</tr>
</tbody>
</table>
The number of + indicates the ERs relative expression. The arrows indicate a decrease (↓), an increase (↑) or no variations in expression (↔) between normal and cancer tissues. SQ= semiquantitative, Ov= overall trends, BBD= Benign Breast Disease, NP-BBD= Non Proliferative BBD, P-BBD= Proliferative BBD, P-BBDWA= Proliferative BBD with atypia, BBT= Benign Breast Tumors, CIS= carcinoma in situ, HGPIN= High grade prostatic intraepithelial neoplasia, IHS= in situ hybridization, IHC= immunohistochemistry, Met= metastatic, RT-PCR= reverse transcription polymerase chain reaction.

Table 2: Relative expression of ERα and ERβ in ovarian tumor progression

<table>
<thead>
<tr>
<th>References</th>
<th>Tissues</th>
<th>Number</th>
<th>Methods</th>
<th>ERα SQ Ov.</th>
<th>ERβ SQ Ov.</th>
<th>Comments</th>
</tr>
</thead>
<tbody>
<tr>
<td>Pujol et al. (1998)</td>
<td>Normal Cysts</td>
<td>6</td>
<td>Competitive</td>
<td>+</td>
<td>+++</td>
<td>ERα/ERβ mRNA ratio increases during tumor progression</td>
</tr>
<tr>
<td></td>
<td>Borderline tumors</td>
<td>24</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td>Cancers</td>
<td>3</td>
<td>Competitive</td>
<td>++</td>
<td>++</td>
<td></td>
</tr>
<tr>
<td></td>
<td></td>
<td>10</td>
<td>RT-PCR</td>
<td>++</td>
<td>+</td>
<td></td>
</tr>
<tr>
<td>Brandenberger et al. (1998)</td>
<td>Normal Cancer</td>
<td>10</td>
<td>Northern Blot</td>
<td>++</td>
<td>++</td>
<td>ERβ mRNA level decreases in cancer</td>
</tr>
<tr>
<td></td>
<td></td>
<td>10</td>
<td>RT-PCR</td>
<td>+++</td>
<td>+</td>
<td></td>
</tr>
<tr>
<td>Rutherford et al. (2000)</td>
<td>Normal Primary cancer</td>
<td>9</td>
<td>RT-PCR</td>
<td>++</td>
<td>++</td>
<td>ERβ mRNA and protein levels decrease in ovarian cancer and metastases</td>
</tr>
<tr>
<td></td>
<td>Met cancer</td>
<td>8</td>
<td>Western Blot</td>
<td>++</td>
<td>+</td>
<td></td>
</tr>
<tr>
<td></td>
<td></td>
<td>8</td>
<td>Western</td>
<td>+++</td>
<td>-</td>
<td></td>
</tr>
</tbody>
</table>

Table 3: Relative expression of ERα and ERβ in prostate tumor progression

<table>
<thead>
<tr>
<th>References</th>
<th>Tissues</th>
<th>Number</th>
<th>Methods</th>
<th>ERα SQ Ov.</th>
<th>ERβ SQ Ov.</th>
<th>Comments</th>
</tr>
</thead>
<tbody>
<tr>
<td>Latil et al. (2001)</td>
<td>Normal Cancer</td>
<td>4 23</td>
<td>Real-time PCR</td>
<td>++</td>
<td>++++</td>
<td>Decreased expression of ERβ mRNA in the hormone-resistant group</td>
</tr>
<tr>
<td>Pasquali et al. (2001a)</td>
<td>Normal Cancer</td>
<td>5 10</td>
<td>IHC</td>
<td>/</td>
<td>+++</td>
<td>ERβ protein expression decreases in cancer</td>
</tr>
<tr>
<td>Pasquali et al. (2001b)</td>
<td>Normal Cancer</td>
<td>6 5</td>
<td>RT-PCR</td>
<td>++</td>
<td>++</td>
<td>ERβ mRNA expression decreases in cancer</td>
</tr>
</tbody>
</table>
Horvath et al. (2001) identified normal hyperplasia and cancer with IHC scores of +++ or +, indicating loss of ERβ protein expression during tumor progression.

Leav et al. (2001) observed dysplasia and carcinoma with RT-PCR scores of +/- or +/-, suggesting a decrease in ERβ protein and mRNA expression in high-grade dysplasia and carcinoma.

Fixemer et al. (2003) noted HGPIN and adenocarcinoma with IHC scores of +++ or +, showing ERβ protein expression decreases during tumor progression.

Table 4: Relative expression of ERα and ERβ in colon tumor progression

<table>
<thead>
<tr>
<th>References</th>
<th>Tissues</th>
<th>Number</th>
<th>Methods</th>
<th>ERα SQ</th>
<th>ERβ SQ</th>
<th>Comments</th>
</tr>
</thead>
<tbody>
<tr>
<td>Campbell-Thompson et al. (2001)</td>
<td>Normal cancer</td>
<td>26</td>
<td>RT-PCR</td>
<td>+</td>
<td>+++</td>
<td>ERβ1 and ERβ2 mRNA expressions decrease in cancer</td>
</tr>
<tr>
<td>Foley et al. (2000)</td>
<td>Normal Cancer</td>
<td>11</td>
<td>RT-PCR</td>
<td>+</td>
<td>+++</td>
<td>Decrease ERβ protein but not mRNA expression in cancer. Post-transcriptional mechanism?</td>
</tr>
</tbody>
</table>

ERα and ERβ gene structures are provided with the relevant domains and functional regions.
Figure 1 Schematic representation of the structure of human ERα and ERβ nuclear receptors. The A/B domain at the NH-2 terminal contains the ligand independent transcriptional-activation function AF-1, the C domain represents the DNA-binding-domain. D corresponds to the hinge region, E domain contains the hormone binding domain and the hormone-dependent transcriptional-activation function AF-2. Numbers outside each box refer to amino acid number whereas the number inside each box of ERβ refers to the percentage of amino acid identity. The arrow indicates the translation starting site in ER cDNA.

Figure 2 Schematic representation of ERα and ERβ imbalance in estrogen-dependent tumor progression

Hypothetical mechanism of antiproliferative effect of ERβ

- **Direct effect on gene transcription**
  - ERβ
  - ERE, AP-1, SP1

- **Indirect effect by modulation of ERα action**
  - ERα
  - ERE, AP-1, SP1

**Regulation of genes involved in apoptosis**
- Inhibition of genes involved in cell proliferation
- Induction of pro-apoptotic gene expression
- Inhibition of ERα induced cell proliferation
Figure 3 Hypothetical mode of ERβ action on cell proliferation pathways.