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

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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 (such as 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 with 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 explain that ERβ has a differential effect on proliferation as compared with ERα. ERβ may exert a protective effect and thus constitute a new target for hormone therapy, such as 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.

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(Brandenberger et al. 1998, Pujol et al. 1998, Foley et al. 2000, Rutherford et al. 2000, Campbell-Thompson et al. 2001, Roger et al. 2001, Fixemer et al. 2003). 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 1–4)**

In breast tissues, several studies have indicated an increase in ERα/ERβ mRNA and protein ratios in cancer as compared with benign tumors and normal tissues. In immunochemical analyses, Roger et al. (2001) found a higher percentage of ERβ-positive cells in normal mammary glands than in nonproliferative benign breast disease (BBD) (85%), proliferative BBD without atypia (18.5%) and carcinoma in situ (33.8%). In contrast, an increase in ER protein expression was noted during progression. Moreover, ERβ was inversely correlated with Ki67, a marker of cell proliferation. The authors thus suggest that ERβ protects 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 by the RT-PCR method by 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 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 BC, other studies using immunohistochemistry (IHC) and in situ hybridization revealed that ERβ expression was associated with indicators of low biologic 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). Omoto et al. (2001) in 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 BC patients and showed that ERβ expression is not associated with clinical and biologic parameters, including progesterone receptor (PR) expression, tumor grade and S-phase fraction. ERβ was found to be correlated only 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) did an IHC analysis of ERβ in 512 breast specimens. Moreover, real-time PCR was used to investigate the ERβ gene methylation status in the ERβ-negative BC 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 BC (Table 1). Collectively, ERβ expression decreases in the process of BC 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 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. Lau et al. (1999) found no differences in ERβ mRNA expression between normal and cancer epithelial cells, but these authors analyzed only a few HOSE cell primary cultures (n = 4) and ovarian cancer cell lines (n = 3) by a nonquantitative PCR method. Decreasing levels of ERβ expression seem 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 was quantified by real-time RT-PCR in both benign and malignant prostate.
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 SQ Ov</th>
<th>ERβ SQ Ov</th>
<th>Comments</th>
</tr>
</thead>
<tbody>
<tr>
<td>Roger et al.</td>
<td>Normal</td>
<td>118</td>
<td>IHC</td>
<td>+</td>
<td>++</td>
<td>ERβ positive</td>
</tr>
<tr>
<td>(2001)</td>
<td>NP-BBD</td>
<td>18</td>
<td>IHC</td>
<td>+</td>
<td>++</td>
<td>Cells decrease during</td>
</tr>
<tr>
<td></td>
<td>P-BBD</td>
<td>37</td>
<td>IHC</td>
<td>++</td>
<td>++</td>
<td>preinvasive tumor progression</td>
</tr>
<tr>
<td></td>
<td>P-BBDWA</td>
<td>13</td>
<td>IHC</td>
<td>++</td>
<td>+</td>
<td></td>
</tr>
<tr>
<td></td>
<td>CIS</td>
<td>25</td>
<td>IHC</td>
<td>++</td>
<td>+</td>
<td></td>
</tr>
<tr>
<td></td>
<td>High-grade CIS</td>
<td>35</td>
<td>IHC</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>Changes in ERβ1 and ERβ2 mRNA levels in breast cancer</td>
</tr>
<tr>
<td>(2000)</td>
<td>Cancer</td>
<td>112</td>
<td></td>
<td>+++</td>
<td>++</td>
<td></td>
</tr>
<tr>
<td>Park et al.</td>
<td>Normal</td>
<td>89</td>
<td>SH</td>
<td>++</td>
<td></td>
<td>ERβ mRNA level decreases during tumor progression</td>
</tr>
<tr>
<td>(2003)</td>
<td>BBT</td>
<td>11</td>
<td></td>
<td>+++</td>
<td></td>
<td>High ERβ level associated with poor differentiation</td>
</tr>
<tr>
<td></td>
<td>Breast cancer</td>
<td>85</td>
<td></td>
<td>/</td>
<td>+</td>
<td></td>
</tr>
<tr>
<td></td>
<td>Met. lymph node</td>
<td>10</td>
<td></td>
<td></td>
<td>+</td>
<td></td>
</tr>
<tr>
<td>Skliris et al.</td>
<td>Normal</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>PDCIS</td>
<td>16</td>
<td></td>
<td>+++</td>
<td></td>
<td>Loss of ERβ may be a reversible process involving methylation</td>
</tr>
<tr>
<td></td>
<td>Invasive cancers</td>
<td>319</td>
<td></td>
<td>++</td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td>Met. lymph node</td>
<td>31</td>
<td></td>
<td>/</td>
<td>+</td>
<td></td>
</tr>
<tr>
<td></td>
<td>Recurrences</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</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>
<tr>
<td>Gustafsson &amp;</td>
<td>Normal</td>
<td>30</td>
<td>RT-PCR</td>
<td>/</td>
<td></td>
<td>ERβ is the predominant form in normal mammary gland</td>
</tr>
<tr>
<td>Warner (2000)</td>
<td>Cancer</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

The number of + indicates the ER’s 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, ISH = in situ hybridization, IHC = immunohistochemistry, Met = metastatic, RT-PCR = reverse transcription polymerase chain reaction.

ERβ mRNA level was decreased in most of the tumor samples as compared with 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, Perssonet 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 biologic 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. Using semiquantitative RT-PCR, Campbell-Thompson et al. (2001) showed that ERβ is the predominant ER subtype in the human colon, and that decreased ERβ1 (ERβwt) and ERβ2 (ERβcx) mRNA levels are associated with colonic tumorigenesis in women. In a recent study using IHC analysis, Konstantinopoulos et al. (2003) showed 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

### 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 Borderline tumors Cancers</td>
<td>6</td>
<td>Competitive RT-PCR</td>
<td>+ ↑ +++</td>
<td>+ + +</td>
<td>ERα/ERβ mRNA ratio increases during tumor progression</td>
</tr>
<tr>
<td>Brandenberger et al. (1998)</td>
<td>Normal Cancer</td>
<td>10</td>
<td>Northern blot RT-PCR</td>
<td>++ ↑ ++</td>
<td>+++ +</td>
<td>ERβ mRNA level decreases in cancer</td>
</tr>
<tr>
<td>Rutherford et al. (2000)</td>
<td>Primary cancer Met. cancer</td>
<td>9</td>
<td>RT-PCR Western blot</td>
<td>++ ↑ ++</td>
<td>+++ +</td>
<td>ERβ mRNA and protein levels decrease in ovarian cancer and metastases</td>
</tr>
</tbody>
</table>

### Table 3 Relative expression of ER 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</td>
<td>Real-time PCR</td>
<td>++ ↔ +++</td>
<td>++ +</td>
<td>ERβ mRNA expression decreases in the hormone-resistant group</td>
</tr>
<tr>
<td>Pasquali et al. (2001a)</td>
<td>Normal Cancer</td>
<td>5</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</td>
<td>RT-PCR Western blot</td>
<td>++ ↔ ++</td>
<td>+++ +</td>
<td>ERβ mRNA expression decreases in cancer</td>
</tr>
<tr>
<td>Horvath et al. (2001)</td>
<td>Normal Hyperplasia Cancer</td>
<td>5</td>
<td>IHC</td>
<td>+++ ↓</td>
<td>– or +</td>
<td></td>
</tr>
<tr>
<td>Leav et al. (2001)</td>
<td>Dysplasia - moderate grade - high grade Carcinoma - grade III - grade IV/V Metastasis Total of 50 samples</td>
<td>159</td>
<td>RT-PCR</td>
<td>– ↔ ++</td>
<td>–/+ –/+ –/+</td>
<td></td>
</tr>
<tr>
<td>Fixemer et al. (2003)</td>
<td>HGPIN Adenocarcinoma Gleason grade: III IV V Metastatic</td>
<td>47</td>
<td>IHC Monoclonal antibody</td>
<td>++ ± ++ ± ±</td>
<td>– +</td>
<td></td>
</tr>
</tbody>
</table>

ERβ protein and mRNA expression decrease in high-grade dysplasia and carcinoma.
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 protects 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 BC is a predictor of the response to tamoxifen (Leygue 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 analyzed 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 with 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 (Burki et al. 2000, Loveday 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 effects on their transcriptional activities**

ERα 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 & Gustafsson 1997). A number of novel selective ER subtype ligands have now been developed. The propyl pyrazole triol (PPT) com-

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**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</th>
<th>ERβ</th>
<th>Comments</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td></td>
<td></td>
<td></td>
<td>SQ Ov</td>
<td>SQ Ov</td>
<td></td>
</tr>
<tr>
<td>Campbell-Thompson</td>
<td>Normal</td>
<td>26</td>
<td>RT-PCR</td>
<td>+</td>
<td>↔</td>
<td>+</td>
</tr>
<tr>
<td>et al. (2001)</td>
<td>Cancer</td>
<td>26</td>
<td>Southern blot</td>
<td>+</td>
<td>+++</td>
<td>↓</td>
</tr>
<tr>
<td>Foley et al.</td>
<td>Normal</td>
<td>11</td>
<td>RT-PCR</td>
<td>+</td>
<td>↔</td>
<td>+++</td>
</tr>
<tr>
<td>(2000)</td>
<td>Cancer</td>
<td>11</td>
<td>Western blot</td>
<td>+</td>
<td>+</td>
<td>↓</td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td>Decrease ERβ protein but not mRNA expression in cancer</td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td>Post-transcriptional mechanism?</td>
</tr>
</tbody>
</table>
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 & Gustafsson 1997). The diarylpropionitrile (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) (Tora et al. 1989, Berry et al. 1990, McInerney & Katzenellenboigen 1996), 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 LBD (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, a fact which could explain why different sets of proteins in the transcription complexes may interact with ERα and ERβ and direct them to specific targets. Dissimilarity in the NH2-terminal extremity of ERα and ERβ 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 ERα-selective partial agonist/antagonist function but pure ER antagonist effect through ERβ (McDonnell et al. 1995, Barkem et al. 1998, 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 ERα specific. Tamoxifen is an ERα 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 ERα antagonist in breast tissue, but it exerts agonistic activity in bone, but not in uterine tissue (Black et al. 1994).
ERz and ERβ are capable of regulating gene transcription through a classical mechanism involving the consensus ERE, but ERβ seems to be a weaker transactivator (Cowley et al. 1999). Cowley and Parker (1999) have shown that the AF-1 activity of ERβ is weak compared with that of ERz 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 ERz greatly exceeds that of ERβ, whereas ERz and ERβ activities are similar when only AF-2 is required (McInerney et al. 1998, Cowley et al. 1999). ERz and ERβ 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-liganded ER subtypes in this classical mode of action. In this way, the gene encoding the catalytic subunit of human telomerase hTERT is regulated by ERz, and not by ERβ 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, ERz, but not ERβ, was able to regulate c-myc proto-oncogene expression. The metallothionein gene is known to be specifically upregulated by E2 via ERβ in SAOS-2 cells (Harris et al. 2001). However, recently, Stossi et al. (2004) have compared the gene-regulatory activities of ERz and ERβ in bone and showed high 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), 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, ERz 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 antiestrogen tamoxifen, but not in the presence of estrogens in a tissue-specific manner. ERz 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 BC cells (Philips et al. 1993, Webb et al. 1995). Of particular note, ERβ is more potent overall than ERz 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 ERz 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) found that the osteopontin gene promoter is stimulated through SFRE sequences by ERz, 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 biologic 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 (Moore et al. 1998, Ogawa et al. 1998). These isoforms can also bind ligands, mediate estrogen signaling (Kuiper & Gustafsson 1997, 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. 2001). Interestingly, Poola et al. (2002) recently showed that ERβ splice variant mRNAs were differentially altered during breast carcinogenesis. ERβΔcx, 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/ERβΔcx heterodimer formation. Using IHC, it has been shown that differential expression of ERβwt and ERβΔcx may be used as a prognostic marker in human prostate (Fujimura 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 ERβΔcx MCF-7, that these two isoforms inhibit ERα function differently (Oimoto 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 heterodimers

The functional formation of ERα and ERβ heterodimers has been demonstrated (Cowley et al. 1997, Pettersson 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 (Cowley et al. 1997, Pettersson et al. 1997). The possible involvement of ERα and ERβ dimerization would increase the complexity of transcription activation in response to E2, suggesting the existence of two previously unrecognized estrogen-signaling pathways, that is, 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 to gaining insight into the tissue-specific effects of estrogen and antiestrogens (Kuiper et al. 1997).

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 physiologic 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 it includes SRC1, SRC2 (GRIPI/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 are ligand-dependent, but some coactivators have also been shown to be recruited in a ligand-independent manner by the AF-1 domain of ERs (Mcinerney et al. 1996, 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. Using multiplex RT-PCR, Kurebayashi et al. (2000) also showed 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. Webb et al. (2003) recently 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, such as genistein, but not in the presence of antagonists. ERα and ERβ present completely distinct modes of action with coregulators, a fact which could be of major importance in terms of potential effects on physiologic behavior (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 and prostate) as well as in benign disease, and they decrease during carcinogenesis (Tables 1–3). Our laboratory obtained the first evidence that ERβ is an important modulator of proliferation and invasion of breast and ovarian cancer cells, thus supporting the hypothesis that the loss of ERβ expression could be one of the events leading to breast and ovarian cancer development (Lazennec et al. 2001, Bardin et al. 2004). 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 ERβ wt and ERβ cks 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 BC cells inhibits their growth (Paruthiyil et al. 2004, Strom et al. 2004). These reports also suggest that ERβ might reduce cell proliferation by inhibiting the cyclin D1 gene, 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 Bie`che et al. (2001), showing a negative correlation between ERβ and CCND1 (cyclin D1) expression. In vitro studies support 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−/− mice, that is, ERαKO and ERβKO, which exhibit phenotypes that generally mirror the respective ER-expression patterns, provides further evidence that the two ERs have distinct biologic functions. Weihua et al. (2000) observed that, in the immature uterus, ERz 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 suggests that ERβ plays a role in the modulation of the effects of ERz and also (or consequently) has an antiproliferative function in the 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 ERz 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 ERz activity. Hall et al. (1999) have provided direct proof that ERβ modulates or represses ERz transcriptional activity in transient transfection cells. In bone, it has been shown that ERβ inactivation by gene targeting results in increased cortical bone formation. Windahl et al. (2001) showed that, when present, ERβ acts in a repressive manner on trabecular bone, possibly by inhibiting the stimulatory action of ERz. Finally, Lindberg et al. (2003) showed that in some mouse tissues, ERβ reduces ERz-regulated gene transcription, thus indicating that there is a balanced relationship between ERz and ERβ (Fig. 2).

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

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 cancer (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 antiapoptotic bcl-2 gene at the mRNA level. It has been suggested that ER\textsubscript{a} may play a role in ovarian tumorigenesis by preventing apoptosis, whereas the ER\textsubscript{b}-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 ER-subtype present in the cell. ER\textsubscript{a} is thus associated with a neuroprotective effect, while ER\textsubscript{b} 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 may seem paradoxical since estrogen is known to be antiapoptotic in different cells. The authors proposed that in normal ovary the apoptotic protein ligand FasL is probably upregulated by ER\textsubscript{b}, the predominant form of ER in this tissue (Fig. 3). Recently, we have demonstrated (Cheng et al. in press) that the expression of ER\textsubscript{b} in prostate carcinoma cells triggers apoptosis, notably by increasing bax\textsubscript{x} levels, as well as cleavage of PARP and caspase-3 expression. We also observed pro-apoptotic effects of ER\textsubscript{b} in ovarian cancer cells (Bardin et al. 2004).

**Conclusions**

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

ER\textsubscript{a} and ER\textsubscript{b} have some overlapping tissue distribution but also display high relative tissue-specific expression. Moreover, a number of molecular mechanisms may explain the differential roles of ER\textsubscript{a} and ER\textsubscript{b}, including differences in ligand affinity and transactivation, distinct
cofactor interactions and putative heterodimerization. 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.

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