Estrogenically regulated LRP16 interacts with estrogen receptor α and enhances the receptor’s transcriptional activity

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Abstract

Previous studies have shown that leukemia related protein 16 (LRP16) is estrogenically regulated and that it can stimulate the proliferation of MCF-7 breast cancer cells, but there are no data on the mechanism of this pathway. Here, we demonstrate that the LRP16 expression is estrogen dependent in several epithelium-derived tumor cells. In addition, the suppression of the endogenous LRP16 in estrogen receptor α (ERα)-positive MCF-7 cells not only inhibits cells growth, but also significantly attenuates the cell line’s estrogen-responsive proliferation ability. However, ectopic expression of LRP16 in ERα-negative MDA-MB-231 cells has no effect on proliferation. These data suggest the involvement of LRP16 in estrogen signaling. We also provide novel evidence by both ectopic expression and small interfering RNA knockdown approaches that LRP16 enhances ERα-mediated transcription activity. In stably LRP16-inhibitory MCF-7 cells, the estrogen-induced upregulation of several well-known ERα target genes including cyclin D1 and c-myc is obviously impaired. Results from glutathione S-transferase pull-down and coimmunoprecipitation assays revealed that LRP16 physically interacts with ERα in a manner that is estrogen independent but is enhanced by estrogen. Furthermore, a mammalian two-hybrid assay indicated that the binding region of LRP16 localizes to the A/B activation function 1 domain of ERα. Taken together, these results present new data supporting a role for estrogenically regulated LRP16 as an ERα coactivator, providing a positive feedback regulatory loop for ERα signal transduction.

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Introduction

Estrogen plays a crucial role in the control of development, sexual behavior, and reproductive functions. Its effects have been linked to the progression of the majority of human breast cancers and acts as a potent mitogen for many breast cancer cell lines (Masood 1992, Prall et al. 1998a). Mechanistic studies on estrogen-induced mitogenesis have revealed multiple cell cycle regulatory pathways activated by estrogen (Foster & Wimalasena 1996, Planas-Silva & Weinberg 1997, Prall et al. 1997). The biological actions of estrogen are manifest through the transcriptional activation of the ligand-dependent estrogen receptor α and β (ERα and β; Mangelsdorf et al. 1998, McDonnell & Norris 2002). The activation of an ER results in an altered expression of its direct transcriptional targets, thereby affecting downstream secondary biological activities. It is believed that 75% of carcinoma in situ breast lesions and similar percentages of invasive breast cancers express elevated levels of ERα protein; whereas in normal breast epithelial cells, only 10% of cells express ERα and only at low levels (Allred et al. 2001). Patients expressing elevated levels of ERα are therefore suitable candidates for hormonal therapy, which aims to block estrogen stimulation of breast cancer cells (Deroo & Korach 2006).
ERα contains six domains named A through F. The structure of ERα is similar to that of other nuclear receptors (NRs), having three separate functional domains; a variable activation function 1 domain (AF-1) in the N-terminal A/B domain, a central DNA-binding domain (LBD, ligand-binding domain) located in the C domain and a C-terminal LBD, domain E that contains AF-2 (Nilsson et al. 2001). The AF-1 domain is regulated by growth factors and its activity depends on the cellular and promoter context, while the AF-2 domain is dependent on ligand binding (Lees et al. 1989, Shao & Brown 2004). The two activating domains act synergistically to generate maximum transcriptional activity of ERα (Danielian et al. 1992, Métivier et al. 2001). ERα-mediated transcription is a highly complex process involving multiple of coregulatory factors (Hall et al. 2001, Hall & McDonnell 2005). The cofactors can be broadly divided into subgroups of either coactivator which augments the function of an activated receptor or corepressors which sustain the inactivated state of a receptor. Transcriptional activation of ERα involves interactions with coactivator molecules and the basal transcription machinery in a sequential and cyclic fashion at the promoter region of responsive genes (Glass & Rosenfeld 2000, Shang et al. 2000, McKenna & O’Malley 2002, Métivier et al. 2003). The balance of ERα cofactors in target cells, coupled with different concentrations of ERα and its ligand, allows fine-tuning of target gene transcription in response to estrogen. Over the past decade, more than 20 coactivator molecules have been identified using biochemical approaches as well as yeast two-hybrid screens (Klinge 2000, Shao & Brown 2004). Most of the coactivators bind to the ERα AF-2 domain in a ligand-dependent fashion. Only two related coactivators specific to ERα AF-1 have been identified to date, p68 and p72 RNA helicases (Endoh et al. 1999, Watanabe et al. 2001). The LRP16 gene was originally isolated from human lymphocyte cells, and was identified as an estrogen-responsive gene by our group (Han et al. 2003). We have previously documented that 17β-estradiol (E2) upregulated the leukemia related protein 16 (LRP16) mRNA level in an ERα-dependent manner in MCF-7 human breast cancer cells (Han et al. 2003). One-half of the estrogen response element (ERE)/GC-rich Sp1-binding site and several GC-rich Sp1-binding sites within the promoter region of LRP16 gene were identified as the main contributors to the E2-responsive regulatory mechanism (Zhao et al. 2005, Si et al. 2006). Overexpression of LRP16 significantly stimulated MCF-7 cell proliferation by promoting the transition of G1 to S (Han et al. 2003). In primary breast cancer samples, our data indicated that LRP16 mRNA was overexpressed in nearly 40% of all samples. The clinicopathologic characteristics, including ERα/PR status, tumor diameter, and the involvement of axillary lymphoid nodes were tightly linked with LRP16 mRNA overexpression (Liao et al. 2006). Taken together, these data implied that LRP16 may play an important role in carcinogenesis and/or progression of hormone-dependent breast cancer.

The goal of this study was to gain an understanding of the functional role of LRP16 in hormone-sensitive breast cancer cells. To do this, we investigated the expression of LRP16, its interaction with ERα and its effect on ERα-mediated signaling. First, we showed that both mRNA and protein expression levels of LRP16 are positively linked with estrogen action in several breast cancer cell lines. Next, the proliferation rate of ERα-positive MCF-7 cells, but not ERα-negative MDA-MB-231 cells, was shown to be related to LRP16 expression levels. Furthermore, we showed that LRP16 enhanced the transcriptional activity of ERα. This provided evidence that LRP16 is not only a target gene of ERα but also a novel ERα coactivator, thus creating a positive regulatory feedback loop. Therefore, LRP16 may play an important role in the proliferation of ERα-positive breast cancer cells by amplifying the function of ERα.

Materials and methods

Cell culture

All cell lines were purchased from American Type Culture Collection (ATCC, Rockville, MD, USA) and cultured according to the instructions. Pure estrogen antagonist ICI 182 780 was provided by Dr Qinong Ye (College of Military Medicine Science of China). E2 was purchased from Sigma. Phenol red-free DMEM and estrogen-deprived fetal calf serum (FCS) were prepared as described previously (Zhao et al. 2005).

Cell proliferation assay

Cells were seeded at 1×10^4 per well in 24-well plates. After cell attachment, the medium was replaced with 1 ml fresh DMEM supplemented with 1% FCS. For each cell line, cells from three dishes were counted daily to generate proliferation curves. For the E2-stimulated proliferation experiment, a total of 5000 cells were seeded and cultured in each well of a 24-well plate in phenol red-free DMEM supplemented with charcoal-stripped FCS (5%). After 12 h, cells were treated with E2 in the same fresh medium for 24 h. Cell proliferation rate
was quantified using CellTiter 96 Aqueous One Solution Cell Proliferation Assay (Promega). Each experiment was performed in triplicate and repeated on three occasions.

**Plasmids**

The mU6pro vector containing the mouse U6 snRNA promoter was kindly provided by Dr Turner from University of Michigan (Yu et al. 2002). Mammalian expression plasmid for ERα (pS5G-hERα) was provided by Prof. Hajime Nawata at Kyushu University, and the reporter 3×ERE-TATA-Luc was provided by Prof. Donald P McDonnell at Duke University Medical Center (Norris et al. 1998). The fragment of −101 to −24 bp from the LRP16 upstream regulatory region containing multiple GC-rich sites was cloned into pGL3 basic vector as described (Si et al. 2006).

Two siRNA-coding oligonucleotides against human LRP16 were designed and verified to be specific to LRP16 by a Blast search against the human genome. The LRP16-siRNA-374-targeting sequence is AAGCAGCGGGAG by a Blast search against the human genome. The LRP16-siRNA-668-targeting sequence is AAGCAGCGGGAG by a Blast search against the human genome. The LRP16-siRNA-374-targeting sequence is AAGCAGCGGGAG by a Blast search against the human genome. The LRP16-siRNA-668-targeting sequence is AAGCAGCGGGAG by a Blast search against the human genome. The LRP16-siRNA-374-targeting sequence is AAGCAGCGGGAG by a Blast search against the human genome. The LRP16-siRNA-668-targeting sequence is AAGCAGCGGGAG by a Blast search against the human genome.

The hairpin LRP16-siRNA-374, LRP16-siRNA-668 and GFP-siRNA oligonucleotides were chemically synthesized, annealed, and inserted into the mU6pro vector under the control of U6 snRNA promoter by BbsI and EcoRI sites. To construct the pcDNA3.1-K16. LRP16 cDNA was cloned into pGEX-6P-1 by EcoRI and HindIII sites and the supernatant was collected by centrifugation.

The human LRP16 full-length cDNA was cloned and inserted into the pcDNA3.1 expression vector as described previously (Han et al. 2003). The LRP16 cDNA with the Kozak sequence was also subcloned into the pcDNA3.1 expression vector to construct the pc3.1-K16. LRP16 cDNA was cloned into pGEX-6P-1 by EcoRI and HindIII sites to construct the glutathione S-transferase (GST)-LRP16 fusion. The truncated LRP16 fragment (coding 83–324 amino acids) was cloned into the pcDNA3.1 expression vector by KpnI and BamHI sites for prokaryotic expression. The full-length LRP16, ERα cDNA, and its truncated fragments coding for AB, ABC, and DEF domains were cloned into either pBIND or pACT vectors by BamHI and KpnI sites to construct pBIND- and pACT-LRP16, pACT-ERα, pACT-ERα-AB, pACT-ERα-ABC, and pACT-ERα-DEF vectors. All the constructions were confirmed by restriction enzyme mapping and DNA sequencing.

**Viral production and infection of target cells**

293GP2 cells were plated into 10 cm dishes and cultured until reaching 80–90% confluency. LPC-based plasmids (7.5 µg/well) and VSVG expression vector (2.5 µg/well) were transiently cotransfected into 293GP2 cells using Superfect transfection reagent (Qiagen) according to manufacturer’s protocol. After 2 days, the packaged pseudo-retrovirus in the supernatant was harvested by centrifugation at 8000 g for 10 min and was diluted 1:2 in DMEM. The retrovirus was then used to infect MCF-7 cells for an additional 48 h. Subsequently, MCF-7 cells were selected with 2 µg/ml puromycin (Invitrogen) for 2 weeks. All of the MCF-7 parental cells were killed by puromycin within this period. The selected cells were maintained as stably siRNA-expressing cells in DMEM supplemented with 1 µg/ml puromycin.

**RNA extraction and northern blot analysis**

Total RNA was extracted by TRIZOL reagent (Invitrogen) and analyzed by northern blot as described previously (Han et al. 2003). The membranes were probed to a 550 bp fragment of LRP16, a 1.6 kb fragment of ERα, 438 bp of c-fos, 744 bp of cathepsin D, 317 bp of RARα, 780 bp of MTA3, 440 bp of pS2, and a 515 bp of β-actin fragment labeled with [α-32P]dCTP by random priming.

**Generation of LRP16 rabbit polyclonal antibody**

The pRSET-C-LRP16 plasmid was transformed into the competent BL21 cells. Cells were cultured and 1 mM isopropyl-β-thiogalactoside (IPTG) was added to induce the synthesis of recombinant protein. The bacteria were harvested and were lysed by sonication and the supernatant was collected by centrifugation. Proteins samples were run on SDS-PAGE and negatively stained with KCl (250 mM). The gel segments containing human truncated LRP16 recombinant protein (28 kDa) were cut out. The recombinant protein was extracted from frozen gels by dialysis and dissolved in PBS. The protein was diluted 1:1 in complete Freund’s adjuvant for the first injection and incomplete Freund’s adjuvant for subsequent injections. ELISA was done to measure the titer of serum from immunized rabbits. Pooled serum from days 120, 135, and 147 was purified using the ImmunoPure...
IgG purification kit (Pierce Chemical Co., Rockford, IL, USA).

**Antibodies and immunoblotting**

Antibodies against β-actin, cyclin D1, ERα (Santa Cruz, Biotechnology, Santa Cruz, CA, USA), and c-Myc (Invitrogen) were used in this study. All immunoblotting procedures were performed as described (Han et al. 2003).

**Protein–protein interaction assays in cell-free (GST pull-down) and cell systems (coimmunoprecipitation, CoIP)**

BL-21 bacteria were transformed with pGEX-6P-1 (GST alone) or GST-LRP16 and cultured in an incubator at 37 °C; 1 mM IPTG was added to the culture to induce expression of GST or GST-LRP16. Bacteria were pelleted and lysed in buffer (40 mM Tris–HCl (pH 7.5), 150 mM NaCl, 1 mM dithiothreitol, 1 mM EDTA, 0.5% NP40, 10% glycerol, 0.4 mM phenylmethylsulfonyl fluoride, 2 µg/ml leupeptin, and 2 µg/ml aprotinin) along with lysozyme (5 mg/l) and a bacterial protease inhibitor cocktail (Sigma). Suspensions were vortexed to resuspend the pellet, incubated on ice for 30 min, and sonicated for 5 min. The insoluble fraction was removed by centrifugation, and the supernatants incubated with glutathione-Sepharose beads (Amersham Bioscience) for 30 min at room temperature. For the pull-down assays, 30 µl of the 50% GST or GST-LRP16 bead slurry were incubated with 100 fmol of recombinant human ERα proteins (Invitrogen) supplemented with 10 nM E2 or DMSO at 4 °C for 3 h. To detect protein that bound specifically, the beads were washed six times with lysis buffer, boiled in SDS-PAGE samples buffer, and subjected to SDS-PAGE and analyzed by immunoblotting.

**CoIP studies were performed using transfected cell lines. Briefly, MCF-7 cells were cultured in phenol red-free and steroid-deprived medium for at least 3 days, and then plated in 3.5 cm dishes. MCF-7 or 293T cells were transiently cotransfected with the indicated vectors using Superfect transfection reagent. Luciferase activities were assayed as described previously.**

**Statistical analysis**

Experiments were performed in triplicate, and the results were expressed as the mean ± S.E.M. Statistical analysis was performed using Statview software. All data were evaluated for paired variables to compare two groups. P < 0.05 was considered to be statistically significant.

**Results**

Upregulation of LRP16 expression is dependent on estrogen action

Previously published work from our laboratory has demonstrated that E2 upregulated mRNA levels of the
human LRP16 gene in MCF-7 cells (Han et al. 2003). To assess the effects of anti-estrogens on the expression level of LRP16, a more selective steroidal estrogen antagonist, ICI 182 780 (10 nM), was used to treat proliferating MCF-7 cells. Total RNA over a 24 h time course was extracted, and northern blot analysis was used to determine the mRNA level of LRP16. Figure 1A demonstrated that the level of LRP16 mRNA decreased within 3 h of treatment. These results, combined with the induced effect of LRP16 expression by E2 as previously reported (Han et al. 2003), suggest that the LRP16 expression is dependent on estrogen action. To confirm this finding, we treated the endometrial cell line Ishikawa with E2 (10 nM) or estrogen antagonist ICI 182 780 (10 nM). The significant increase in LRP16 mRNA levels was observed after E2 stimulation; whereas, inhibition of ERα activity led to a decline in the expression of LRP16, but not β-actin (Fig. 1A). Next, we overexpressed ERα in Ishikawa cells cultured in normal medium, and observed an increase of LRP16 mRNA level (Fig. 1B). We also followed the expression patterns of LRP16 mRNA in ERα-positive and ERα-negative human breast cancer cell lines by northern blot. The LRP16 transcript was differentially expressed and was only abundant in the ERα-positive MCF-7 and T47D cell lines (Fig. 1C).

To confirm that the LRP16 mRNA levels were indicative of protein levels, we generated LRP16-specific antibodies using a truncated amino acid sequence highly specific for LRP16. Antibody specificity was confirmed through immunoblotting of protein extracts from MDA-MB-231 cells transfected with vector only or LRP16 cDNA with the Kozak sequence modified. As expected, high protein level of LRP16 in MDA-MB-231 cells transfected with the LRP16 expression vector was detected using this antibody (Fig. 1D). These data clearly demonstrate that estrogen regulates the expression of LRP16 and establish the dependence of LRP16 expression on estrogen action in breast cancer cell lines.

**Suppression of LRP16 expression reduces estrogen-mediated proliferation response of MCF-7 cells**

The dependence of LRP16 expression on estrogen activity led us to study different LRP16 expression levels and the proliferative properties of breast cancer. To do so, we chose several sequences in the coding region of the human LRP16 gene and designed short interfering RNAs (siRNA) targeted against each sequence. To test whether these siRNAs could suppress LRP16 expression in MCF-7 cells, we infected these cells with the retroviral vector transducing a DNA segment specifying such siRNA sequences and then selected the cells stably expressing the siRNA. An siRNA against GFP, whose sequence has previously been used as a control-siRNA in human cells (Yu et al. 2002), was also introduced into MCF-7 cells. As shown in Fig. 2A, siRNA-374 and siRNA-668 caused a specific reduction in LRP16 gene expression level,
leading to a 90 and 60% decrease respectively, of LRP16 mRNA relative to the control-siRNA. Consistent with the change in LRP16 mRNA, LRP16 protein was dramatically blocked by siRNA-374, and was partially silenced by siRNA-668.

We further examined the loss of LRP16 expression on the proliferation rate of MCF-7 cells. Growth rates of MCF-7 cells carrying either LRP16-siRNA-374 or LRP16-siRNA-668 were markedly decreased in contrast to the control cells carrying GFP-siRNA on the third day (Fig. 2B). This proliferation curve demonstrates a linear association between LRP16 expression level and the proliferation activity of MCF-7 cells, indicating that LRP16 is required for the proliferation of MCF-7 cells.

Next, we stably transfected LRP16 cDNA with a modified Kozak sequence into MDA-MB-231 cells and observed that MDA-MB-231 cells carrying either pcDNA3.1-KLRP16 or empty vector grew at a similar rate (data not shown), indicating that LRP16 is not required for the proliferation of MDA-MB-231 cells. Differential requirement of MCF-7 and MDA-MB-231 proliferation for LRP16 expression level as demonstrated above led us to speculate that the inhibition of MCF-7 proliferation by LRP16-siRNA resulted from the attenuated responsiveness of MCF-7 cells to estrogen. To test this hypothesis, the established stably transfected cell lines with different LRP16 expression levels were used to examine whether suppression of LRP16 has an anti-estrogenic activity on MCF-7 cell proliferation. E2 could stimulate proliferation of MCF-7 cells carrying either LRP16-siRNAs or control-siRNA in a dose-dependent manner, but the degree of stimulation of E2 on the cell proliferation of MCF-7 carrying LRP16-siRNAs was much less than that on the cell proliferation of MCF-7 carrying control-siRNA beginning from \(10^{-11}\) to \(10^{-7}\) M/l of E2 treatment (Fig. 2C). This indicated that LRP16 is required for the E2-stimulated proliferation of MCF-7 cells.

LRP16 modulates ER\(\alpha\)-mediated transactivation

The effect of LRP16 on the proliferative response of MCF-7 to estrogen suggested that LRP16 participates in the genetic program initiated by ligand-bound ER\(\alpha\). We reasoned that LRP16 might directly regulate the ER\(\alpha\) transcriptional activity. To address this question, the transcriptional activity of a 3×ERE-TATA-Luc reporter gene was first assayed. In the presence of estrogen, LRP16 enhanced ER\(\alpha\)-mediated transactivation of the reporter gene in a dose-dependent manner (Fig. 3A). However, this effect was abolished when estrogen was stripped from the culture media. In contrast to MCF-7 cells, the weak intrinsic activation of LRP16 for ER\(\alpha\)-mediated transcription was observed in a LRP16 dose-dependent manner in HeLa cells (Fig. 3A). To further test the requirement for LRP16 of ER\(\alpha\)-mediated transactivation in MCF-7 cells, we utilized RNA interference in the cotransfection system. Analysis of 3×ERE-TATA-Luc reporter
gene activities in this system revealed that the inhibition of LRP16 led to the decreased ERα-mediated transactivation in the presence of E2 (Fig. 3C). In the absence of E2, inhibition of the endogenous LRP16 in MCF-7 cells did not decrease the reporter gene activities, confirming that LRP16 has no intrinsic activity for ERα-mediated transactivation in MCF-7 cells.

To exclude selection for the promoter of ERα-mediated transactivation enhanced by LRP16, a promoter that lacked a classical ERE sequence but had E2 responsiveness was used. Several reports have demonstrated that the GC-rich region in the upstream regulatory region of ERα target genes is the main region to confer the E2 responsiveness (Watanabe et al. 1998, Safe 2001). The fragment from −101 to −24 bp of the LRP16 gene 5′-proximal region was identified to confer the E2-stimulated transcriptional activities through GC-rich sites, and we also confirmed that the transcriptional activity of LRP16 gene by E2 through this region is mediated through ERα–Sp1 interaction (Si et al. 2006). To test whether LRP16 is required for transcriptional activation of genes through ERα–Sp1 interaction, we utilized the LRP16 promoter (−101 to −24 bp)-luciferase fusion as a model promoter for this system. We observed the similar results by a GC-rich promoter and using the classical ERE promoter model in both MCF-7 and HeLa cells (Fig. 3B and C).

To address the necessity for LRP16 in estrogen induction of ERα target genes, we chose several ERα target genes including c-fos, MTA3, pS2, RARα, and cathepsin D to detect their estrogen...
response. All of the chosen targets genes are well-documented E2-induced genes in MCF-7 cells and their promoters contain either functional EREs or GC-rich Sp1-binding sites (Jeltsch et al. 1987, Weisz & Rosales 1990, Augereau et al. 1994, Sun et al. 1998, Fujita et al. 2004). Northern blot analyses demonstrated that the suppression of LRP16 gene expression in MCF-7 cells at least partially impaired the estrogen-mediated upregulation of all ERα target genes except cathepsin D at different culture conditions and time points (Fig. 4A). Cyclin D1 and c-myc are two well-known cell cycle-related genes (Weisz & Bresciani 1988, Sabbah et al. 1999, Vastro-Rivera et al. 2001). The protein levels of both cyclin D1 and c-myc were measured in LRP16-inhibitory MCF-7 cells by immunoblotting. There was an observed parallel depletion of growth recovery with estrogen after synchronization with ICI 182 780 (Fig. 4B). In addition, we also detected the ERα expression by immunoblotting, and the results confirmed that the suppression of LRP16 in MCF-7 cells did not change the ERα level (data not shown). These data excluded the fact that the attenuation of ERα-mediated transcription in LRP16-inhibitory cells could have been caused by the alteration of ERα expression itself. Finally, we concluded that LRP16 is required for ERα-mediated transactivation.

**LRP16 physically interacts with ERα**

The evidence that LRP16 enhances the function of ERα transactivation prompted us to examine whether LRP16 protein binds to ERα. As shown in Fig. 5A, LRP16 can bind to ERα in a GST pull-down assay, suggesting a direct interaction independent of estrogen stimulation in a cell-free system. By comparison of the intensity of the target bands in Fig. 5A, it was observed that the interaction of LRP16 and ERα proteins was enhanced in the presence of E2. Subsequently, MCF-7 cells were cultured with phenol red-free DMEM supplemented with steroid-stripped serum for at least 3 days and cotransfected with LRP16 and ERα cDNA to determine whether LRP16 and ERα interact in a cell system. We used a rabbit anti-human ERα antibody to immunoprecipitate LRP16 from cell lysates, and immunoblotting with an anti-LRP16 antibody confirmed the interaction between ERα and LRP16 in the cell system irrespective of the presence of estrogen (Fig. 5B). Next, we performed the same experiment in the reciprocal manner (i.e. immunoprecipitation with a LRP16 antibody and immunoblotting with a rabbit anti-human ERα antibody). Again we detected an interaction between LRP16 and ERα (Fig. 5B). A comparison of the intensity of the target bands in Fig. 5B confirmed that E2 enhanced the interaction of LRP16 and ERα since the cross-reaction of the IgG heavy chain with the secondary antibody serves as a loading control.

![Figure 4](https://www.endocrinology-journals.org/) Inhibition of LRP16 attenuates the estrogen-stimulated upregulation of ERα-induced target genes. (A) MCF-7 cells with stable LRP16-siRNAs or control-siRNA expression were grown in media stripped of steroids for at least 3 days, then treated with E2 (10 nM) for the indicated time. Northern blot analyses were performed to quantify the mRNA levels of MTA3 (24 h), pS2 (24 h), retinoic acid receptor α (RARA; 6 h), cathepsin D (6 h), and c-fos (3 h) genes. Total RNA loading was used as a loading control. These results are representatives of two independent experiments. (B) MCF-7 cells with different LRP16 expressions were first cultured in steroid-deprived medium for at least 3 days and subsequently treated with ICI 182 780 (10 nM) for 2 days for cells synchronization, as described previously (Sabbah et al. 1999) The cells were then released from the G0/G1 block by replacing the culture medium containing 10 nM E2. After 3 h, exposure of E2, cyclin D1, c-myc, and β-actin proteins was analyzed by immunoblotting. This experiment was repeated twice.
Involvement of A/B AF-1 functional domain in the interaction of ERα with LRP16

To define the individual domains of the ERα involved in binding to LRP16, mammalian two-hybrid assays were performed in MCF-7 and 293T cells. The ERα constructs were composed of amino acids 1–595 (pBIND-ERα), 1–263 (pBIND-ERα-ABC), 1–180 (pBIND-ERα-AB), and 263–595 (pBIND-ERα-DEF) fused to the DBD of GAL4; whereas, full-length LRP16 was fused to the VP16 activation domain (pACT-LRP16; Fig. 6A). As shown in Fig. 6B, the pG5-Luc reporter gene was induced in MCF-7 cells when pACT-LRP16 was cotransfected with pBIND-ERα, pBIND-ERα-ABC, or pBIND-ERα-AB construct but not with pBIND-ERα-DEF. The addition of E2 (10 nM) further enhanced the transcription by about 1.5-fold in the case of pBIND-ERα, but not with pBIND-ERα-ABC or pBIND-ERα-AB. In addition, results observed in 293T cells were similar to those described in MCF-7 cells (data not shown). To exclude possible vector-dependent transactivation (Finkel et al. 1993), we exchanged the vectors between LRP16 and the individual ERα domains and repeated the experiments. The results were consistent with the previous experiment (data not shown). These data indicated that LRP16 binds to the N-terminal A/B AF-1 but not AF-2 domain of ERα. Even though binding is not dependent on the presence of estrogens, E2 enhances LRP16 binding to the full-length ERα molecule, which is consistent with the results as shown in Fig. 5.

Discussion

ERα, a member of the NR family, has an established role in promoting breast cancer. ERα regulates the transcription of genes involved in breast cancer cell proliferation, invasion, and metastasis. In the complex regulation of ERα signal transduction, emerging evidence indicates that an auto-regulation loop could be an important model for ERα functional activity. For example, cyclin D1 is a well-documented estrogen target gene in many ERα breast cancer cell lines (Vastro-Rivera et al. 2001). Surprisingly, cyclin D1 has been shown to have a novel role in the growth regulation of estrogen-responsive tissues by activating ERα-mediated transcription in the absence of estrogen and enhancing transcription in its presence (Zwijsen et al. 1997). Several lines of evidence suggest that most
of the ERα cofactor expression levels are not hormonally regulated (Misiti et al. 1998, Thenot et al. 1999, Vienonen et al. 2003). Yet, there is evidence that a number of cofactors themselves are regulated by E2. For example, the expression of the corepressor SHARP (SMART/HDAC1 associated repressor protein) is increased by E2 (Shi et al. 2001) and expression of the coactivator AIB1 is decreased (Lauritsen et al. 2002). This self-regulatory model can also be extended to other NR members. For example, the expression of the SWI3-related gene product (SRG3), which is developmentally regulated in the prostate, is induced by androgen through the androgen receptor (AR). SRG3 in turn enhances the transactivation of AR, providing a positive feedback loop in a NR signaling pathway (Hong et al. 2005). Importantly and interestingly, our results now document one feedback-enhancing pathway regulating ERα-mediated transcriptional activity by an estrogen-responsive gene, LRP16. This pathway may be involved in the progression of ERα-positive breast cancer and may reflect the self-maintaining nature of ERα signaling in estrogen-sensitive target cells.

Previous studies have demonstrated that E2 induced the upregulation of LRP16 mRNA and the reporter gene activity in ERα-positive MCF-7 cells (Han et al. 2003). However, the expression pattern of LRP16 gene has been shown to be ubiquitous in multiple human tissues, not exclusively in hormone-dependent tissues (Han et al. 2001). In this study, using several breast cancer cell lines and ERα modulation, we provide evidence to confirm the positive relationship between LRP16 expression and estrogen action. We have demonstrated consistent changes in LRP16 expression at both mRNA and protein levels (Fig. 1). This link, initially derived from cell culture systems, is also supported by data from primary breast carcinomas. In clinical samples, LRP16 overexpression was observed in about 30–40% of primary breast carcinomas by northern blot and semi-quantitative RT-PCR analyses, and the positive status of ERα and PR were significantly linked to LRP16 expression level (Liao et al. 2006).

This study provides the first evidence for a functional role of LRP16 gene in strengthening the ERα-responsive gene activation and estrogen-dependent proliferation of breast cancer cells. Previously, we demonstrated that the ectopic expression of LRP16 promoted the proliferation of MCF-7 cells as well as a G1/S transition, meanwhile stimulating cyclin E expression but not p53, p21, and Rb expression (Han et al. 2003). In contrast, herein we show by siRNA knockdown approaches that inhibition of the endogenous LRP16 gene in MCF-7 cells suppresses cell growth. The experimental results including the fact that inhibition of LRP16 attenuated the E2-stimulated
responsiveness of MCF-7 cells and that the enforced expression of LRP16 in ERα-negative MDA-MB-231 human breast cancer cells did not stimulate cell proliferation strongly suggest that LRP16 participates in ERα signaling. This prompted us to investigate the primary cell cycle checkpoint proteins that confer the mitogenic role of estrogen. Cyclin D1 and c-myc, two well-known ERα target genes, are believed to be sufficient to recapitulate the effects of estrogen on cell cycle progression (Prall et al. 1998b, Carrol et al. 2002). We show herein that the inhibition of LRP16 attenuated the induction of cyclin D1 and c-myc expression by E2 in MCF-7 cells (Fig. 4B). In addition, the response defect of several ERα-induced genes for estrogen stimulation was also observed in LRP16-inhibitory MCF-7 cells (Fig. 4A). In addition, we show by both ectopic expression and siRNA knockdown approaches that LRP16 enhances the transactivation of ERα-targeting promoters (Fig. 3). In general, results from the cell growth study point to the possibility of LRP16-mediated modulation of the ERα-responsive transcription in cancer development.

The ligand-dependent activation of ERα requires the ligand-dependent association of coactivator complexes (Beato et al. 1995, Horwitz et al. 1996, Mckenna et al. 1999, Glass & Rosenfeld 2000). Presently, most transcriptional mediators and cofactors have been identified as interacting with and activating the AF-2 activity of ERα in a ligand-dependent fashion (Klinge 2000, Shao & Brown 2004). Although it has previously been reported that the full activation of the AF-1 domain containing in ERα can stimulate the proliferation of breast cancer cells (Fujita et al. 2003), less is known about the coactivators for N-terminal A/B AF-1 domain. The enhancement of ERα-mediated transactivation by LRP16 can be attributed to the formation of an LRP16/ERα functional complex. By cell-free and cell system assays, we first demonstrated that LRP16 physically interacts with ERα in a manner that is estrogen independent but appears to be enhanced by E2 (Fig. 5). Further analyses showed that the region interacting with LRP16 was specifically located in the A/B region that contained the AF-1 domain of ERα. In addition, E2 enhanced the binding of LRP16 to the full-length ERα molecule but not to the AF-1 domain alone (Fig. 6), suggesting that the interaction of LRP16 and certain cofactors was recruited to the AF-2 domain upon E2 stimulation. These results emphasized the possible mechanism of LRP16 modulating the cooperative interaction of AF-1 and AF-2 by interacting with other cofactors, since the maximally transcriptional activity of ERα was exhibited. The coactivator complex recruited for AF-2 that may interact with LRP16 after E2 treatment is being investigated in our laboratory. However, the differing impact of LRP16 on ERα-mediated transcriptional activity in the absence of E2 between MCF-7 and HeLa cells was observed in this study (Fig. 3A), indicating cell-specific intrinsic activity of ERα by functional interaction of LRP16/AF-1 domain.

Over the past decade, a large number of proteins have been identified that interact with and regulate transcriptional activity of ERα (Klinge 2000, Dobrzycka et al. 2003, Shao & Brown 2004). To our knowledge, there has been no recognition of an ERα cofactor regulated directly by ERα where the expression level is dependent on estrogen activity. ERα directly activates transcription of LRP16 in response to estrogen stimulation. Interestingly, LRP16, in turn, binds to ERα and enhances its transcriptional activity in the presence of a ligand signal. Ultimately, one biological output of estrogen signaling through the interaction of LRP16 and ERα manifests in the magnification of the ERα-mediated transactivation signal and the expression modulation of ERα target genes. The ability of ERα target gene LRP16 to functionally modulate ERα-mediated transcriptional activity contributes both to the complexity and the plasticity of the regulatory circuit.

Our findings could potentially have clinical benefits since an understanding of the activation linked to the expression of ERα may be important for endocrine therapy of ERα-positive breast cancer. Based on the mechanism of the ERα/LRP16 regulatory loop, we would like to propose that patients with high LRP16 expression might benefit from LRP16 targeting alongside with anti-estrogen therapy. LRP16 targeting could potentially improve the initial efficacy of therapy or delay the emergence of therapeutic resistance.

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