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Mediates Focal Adhesion Formation in Breast Cancer Cells

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13. ABSTRACT (Maximum 200 Words) How progesterone and IGF signaling pathways cross-talk with each other to regulate breast cancer progression remains a critical question. In this study, it was found that progesterone enhances IGF-induced cell motility using PR-B-transfected C4-12 cells. To assess whether the progesterone effect is via regulation of IRS-1/2 expression and activation, I performed RT-PCR and western blot analysis. It was found that IRS-2 was sharply up-regulated by progestins through transcriptional mechanisms in MCF-7, T47D, ZR75, and especially in PR-B C4-12 cells while IRS-1 was not. This indicates that IRS-1 and IRS-2 are distinctively regulated by progestins. Moreover, IRS-2 and its downstream signaling elicited by IGF-I were enhanced by progesterone, which was shown by immunoprecipitation. These data, together with previous findings that IRS-2 is activated by integrins, provide a clue that IRS-2 may be involved in progestin increase of IGF-induced cell motility.				
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Introduction

Progesterone is critically involved in the development of the mammary gland and breast cancer, and its effects are mostly mediated by the progesterone receptor (PR) (1). Human PR normally exists in two isoforms, PR-A and PR-B, of 94 and 116 kDa (2), with PR-B containing an additional 164 amino acids at its N terminus. The two PR isoforms display different transcriptional activities and are unequally expressed in different tissues and tumors (3-5).

Progesterone is proliferative in the normal mammary gland, but its inhibition of breast cancer cell growth in tissue culture has been well documented (6-8). Interestingly, progestins have been found to exert a biphasic regulation of breast cancer cell growth — accelerating cells through the first mitotic cell cycle, then arresting them in G1 of the second cycle. Hence, it is proposed that progestins are inherently neither growth proliferative nor growth inhibitory, but rather sensitize breast cancer cells for growth factor and cytokine signals (9).

The insulin-like growth factors (IGFs) are key regulators of cell proliferation, survival, and differentiation (10). Numerous lines of evidence support a role for the IGFs in breast cancer pathogenesis (11). The IGF-I receptor (IGF-IR), upon activation by the IGFs, phosphorylates the insulin receptor substrates IRS-1 and IRS-2, which are multi-site docking proteins that link multiple downstream signaling pathways by binding to a variety of SH2 domain-containing proteins (12). IRSs are also involved in signaling of insulin, interleukins, interferons, and growth hormone, and are implicated in breast cancer growth (13-15). The IRS network of upstream and downstream signaling may place them in a central position to coordinate multiple signaling pathways. IRS-1 and IRS-2, despite their structural and functional similarities, are not completely interchangeable (16).

Recently, much study has been directed to cross-talk between the IGFs and the estrogen receptor (ER) signaling in breast cancer cells (17), and IRS-1, IRS-2, and IGF-IR have been shown to be induced by estrogen (18). However, how the IGFs interact with progesterone in breast cancer is less well defined. Recently, it was reported that progesterone induces focal adhesion in MDA-MB-231 breast cancer cells transfected with PR cDNA (19). In this study, as a first step to elucidate cross-talk and synergism between progesterone and IGF signaling in breast cancer cells, I plan to study whether progesterone regulates focal adhesion and/or cell motility in breast cancer cells and whether this effect is via its regulation of IRS-1/2 expression and activation.

Body

1) Determine whether progesterone regulates focal adhesion in different breast cancer cell lines with distinct PR levels.

My previous studies failed to find progesterone regulation of focal adhesion in breast cancer cells that contained estrogen receptor (ER) and PR. To eliminate the potential confounding effect of ER, I stably transfected a specifically selected MCF-7 cell line C4-12 which is ER-/PR-(20), with PR-A or PR-B. Generation of these stable transfectants was indicated in the last report and these cells have now been reported in two of my publications this year (see later). These cells are very valuable in that PR can be studied without the masking effect of ER, as endogenous PR

expression depends on estradiol. In addition, I can distinguish the effect of the two PR isoforms (A or B).

In contrast to MDA-231 cells transfected with both PR isoforms, the C4-12/PR-A or C4-12/PR-B cells do not display significantly increased formation of stress fibers. Additionally, they do not show any change in their ability to attach to matrices such as laminin or fibronectin. However, in collaboration with Doug Yee (University of Minnesota), he found using a modified Boyden chamber cell migration assay that C4-12/PR-B cells stimulated with progesterone exhibit markedly enhanced motility in response to IGF-I (see Figure 1).

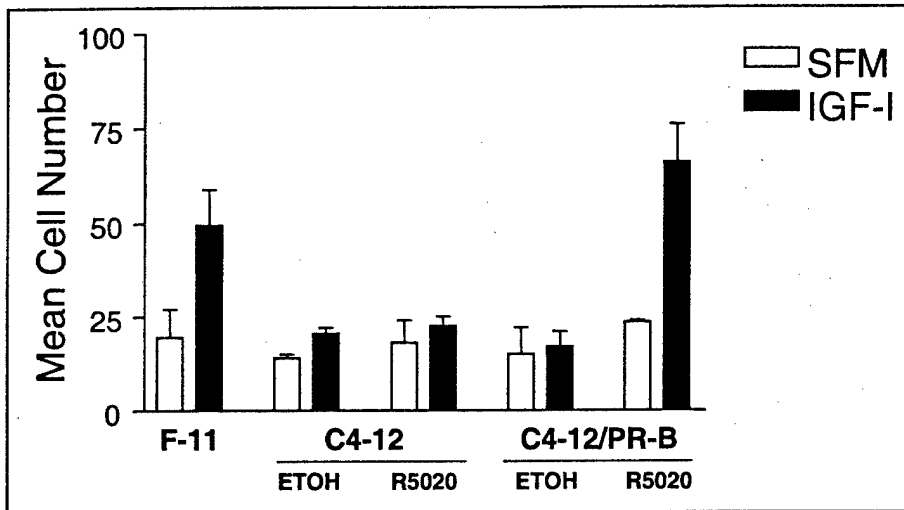


Figure 1: Progesterone sensitizes C4-12/PR-B cells to IGF-stimulated migration. Migration of C4-12, C4-12/PR-b and F-11 (variant of MDA-231 cells that migrate in response to IGF-I) was performed in a modified Boyden chamber assay with transwell coated with fibronectin. F-11 cells were used as a positive control. These cells were generated by successive passaging through mice via left ventricle heart

puncture and generation of highly metastatic cells that have been previously shown to migrate in response to IGF-I and this is correlated with their increased IRS-2 levels compared to parental MDA-231 cells (21). Cells were treated with either vehicle (ETOH) or R5020 (10nM) and then treated with or without IGF-I (10nM). Cells that migrated across a transwell were counted and represented as mean cell number (y-axis). Bars represent triplicate wells $\pm$ S.E.M.

This is very exciting and suggests that while PR may not regulate stress fiber formation similar to MDA-231/PR cells, that it may still regulate IGF-dependent signaling events that lead to changes in migration. We are studying how progesterone regulation regulates IGF signaling and this is detailed in Aim 2.

1) Analyze whether progesterone regulation of focal adhesion correlates with changes of IRS-1/2 expression and activation

I found that IRS-2 levels were markedly induced by progesterone and the synthetic progestin R5020 in C4-12/PR-B cells, not in C4-12/PR-A cells, whereas IRS-1 and IGF-IR were not induced. Similar but weaker effects were observed in PR(+) MCF-7, T47D, and ZR-75 cells, possibly due to lower PR levels compared with C4-12/PR-B cells and potential inhibitory effect of PR-A on PR-B activity (22). This progesterone up-regulation of IRS-2 is via transcriptional mechanisms. In addition, using immunoprecipitation with IRS-2 antibodies, I found that progestin treatment followed by IGF-I stimulation resulted in higher tyrosine-phosphorylated IRS-2 levels, increased binding of IRS-2 to Grb-2 and the PI3K regulatory subunit p85, and correspondingly enhanced ERK and Akt activation, as compared with IGF-I-only conditions. Since the similar results were obtained in C4-12/PR-B and other breast cancer cells with endogenous PR, it is reasonable to believe that the effect is a general characteristics of

progestins. The manuscript regarding this work has been accepted for publication in *Oncogene* and can be found in the appendix (Cui X et al. Progesterone Cross-talks with Insulin-like Growth Factor Signaling in Breast Cancer Cells via Induction of Insulin Receptor Substrate-2. In press *Oncogene*, 2003).

3) *Test the involvement of IRS-1/2 in focal adhesion induction by progesterone in breast cancer cells.*

We have shown thus far that progesterone can increase IRS-2 levels, sensitize C4-12/PR-B to IGF signaling, and sensitized C4-12/PR-B cells to IGF stimulated migration. We next plan to address whether the progesterone regulation of IGF-mediated migration is via the increase in IRS-2 levels. I plan to use Si-RNA strategies to eliminate IRS-2 levels in C4-12/PR-B treated by progesterone and to test whether this will impair or block progesterone regulation of cell motility induced by IGF-I. I speculate that IRS-2 is indeed involved in the progesterone effect, based on two recent publications. Jackson et al. showed that increased IRS-2 enhances IGF-I mediated cell motility (21). In another report, IRS-2 was found to be essential for the ability of integrins to promote cancer cell invasion (23). However, there two studies utilized invasive breast cancer cells. To investigate whether IRS-2 has similar roles in non-invasive cells, I have generated IRS-1 and IRS-2 stably transfected ZR-75 cells. Presently, I am comparing their IGF-induced motility with that of vector-transfected cells. I am also using various signaling inhibitors, e.g. U0126 (MEK inhibitor) and LY294002 (PI3K inhibitor) to examine which pathway downstream of IRS-2 is responsible for the progesterone-IGF regulation of cell motility in C4-12/PR-B cells.

While I was studying PR regulation of IRS-1 and -2, I also found that the IGFs regulate PR levels activity in breast cancer cells. This was noted in the last report, and this work has now been published in *Molecular Endocrinology* and is attached in the appendix (Cui X et al. Insulin-Like Growth Factor-I Inhibits Progesterone Receptor Expression in Breast Cancer Cells via the Phosphatidylinositol 3-Kinase/Akt/Mammalian Target of Rapamycin Pathway: Progesterone Receptor as a Potential Indicator of Growth Factor Activity in Breast Cancer. *Mol Endocrinol*. 2003 Apr;17(4):575-88.) This is a very exciting observation that may provide a new paradigm for regulation of PR in breast cancer and may in part explain the unusual phenotype of ER+/PR- breast tumors that are unresponsive to antiestrogen treatment.

In addition to my work on PR regulation of IRS-2 and cell motility, I also co-authored a review in *Clinical Cancer Research* on novel actions of tyrosine kinase inhibitors in breast cancer, and I assisted in a project examining estrogen-downregulation of E-cadherin which has been accepted for publication in *Cancer Research*. This manuscript ties in with my work concerning the ability of steroid receptors to regulate cell adhesion, migration and invasion.

Key research accomplishments

- Generation of C4-12 cells stably transfected with PR-A or PR-B
- Demonstration of progesterone induction of IRS-2 levels and increased sensitivity to IGF signaling in C4-12/PR-B cells
- Demonstration of progesterone induction of IGF-induced cell motility in PR-B transfected C4-12 cells.
- ZR-75 cells stably transfected with IRS-1 or IRS-2.

- Demonstration of IGF-I inhibition of PR levels and activity in breast cancer cells.

Reportable outcomes

- Manuscript (attached): **Cui X**, Lazard Z, Zhang P, Hopp T, Oesterreich S, Lee AV: Progesterone Cross-talks with Insulin-like Growth Factor Signaling in Breast Cancer Cells via Induction of Insulin Receptor Substrate-2. In press. *Oncogene* 2003.
- Publication (attached): **Cui X**, Zhang P, Deng W, Oesterreich S, Lu Y, Mills GB, and Lee AV. Insulin-Like Growth Factor-I Inhibits Progesterone Receptor Expression in Breast Cancer Cells via the Phosphatidylinositol 3-Kinase/Akt/Mammalian Target of Rapamycin Pathway: Progesterone Receptor as a Potential Indicator of Growth Factor Activity in Breast Cancer" in *Mol Endocrinol*. 2003 Apr;17(4):575-88.
- Manuscript (attached): Oesterreich S, **Cui X**, Deng W, Ivanova M, Hadsell D, Behrens J, Lee AV. Estrogen-mediated Downregulation of E-Cadherin in Breast Cancer Cells. In press. *Cancer Research*, 2003.
- Publication (attached): Lee AV, Schiff R, **Cui X**, Sachdev D, Yee D, Gilmore A, Streuli C, Oesterreich S, and Hadsell DL. New mechanisms of signal transduction inhibitor action: Receptor tyrosine kinase downregulation and blockade of signal transactivation. *Clinical Cancer Research*, 9: 516S-23S, 2003
- ZR-75 cells stably transfected with IRS-1 or IRS-2.

Conclusions

I have stably transfected C4-12 cells with different isoforms of PR and found that PR-B allows cells to respond to progesterone by dramatically upregulating IRS-2 levels. This increase in IRS-2 is associated with increased response of the cells to IGFs. Correlating with this, progesterone treatment of these cells also allows the cells to migrate in response to IGF-I. Current studies are aimed at determining whether it is the increase in IRS-2 levels by progesterone that allows the induction of IGF-mediated migration, and the signaling mechanisms responsible for this effect.

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Appendices

(See the attached publications)

Insulin-Like Growth Factor-I Inhibits Progesterone Receptor Expression in Breast Cancer Cells via the Phosphatidylinositol 3-Kinase/Akt/Mammalian Target of Rapamycin Pathway: Progesterone Receptor as a Potential Indicator of Growth Factor Activity in Breast Cancer

XIAOJIANG CUI, PING ZHANG, WANLENG DENG, STEFFI OESTERREICH, YILING LU, GORDON B. MILLS, AND ADRIAN V. LEE

Breast Center (X.C., P.Z., W.D., S.O., A.V.L.), Baylor College of Medicine; and Department of Molecular Therapeutics (Y.L., G.B.M.), University of Texas M. D. Anderson Cancer Center, Houston, Texas 77030

Although interactions between estrogen and growth factor signaling pathways have been studied extensively, how growth factors and progesterone regulate each other is less clear. In this study, we found that IGF-I sharply lowers progesterone receptor (PR) mRNA and protein levels in breast cancer cells. Other growth factors, such as epidermal growth factor, also showed the same effect. The decrease of PR levels was associated with reduced PR activity. Unlike progestins, IGF-I does not utilize the proteasome for down-regulating PR. Instead, the IGF-I-mediated decrease in PR levels is via an inhibition of PR gene transcription. In addition, the phosphatidylinositol 3-kinase (PI3K)/Akt/mammalian target of rapamycin (mTOR) pathway was found to be specifically involved in this IGF-I effect. Our data also suggest that the IGF-I down-regulation of PR is not mediated via a reduc-

tion of estrogen receptor (ER) levels or activity. First, IGF-I induced ligand-independent ER activity while reducing ER-dependent PR levels. Second, whereas PR and cyclin D1 are both ER up-regulated, IGF-I increased cyclin D1 levels while decreasing PR levels. Third, constitutively active PI3K or Akt induced ER activity but reduced PR levels and activity. Taken together, our data indicate that IGF-I inhibits PR expression in breast cancer cells via the PI3K/Akt/mTOR pathway. Because low or absent PR in primary breast cancer is associated with poor prognosis and response to hormone therapy, our results suggest that low PR status may serve as an indicator of activated growth factor signaling in breast tumor cells, and therefore of an aggressive tumor phenotype and resistance against hormonal therapy. (*Molecular Endocrinology* 17: 575-588, 2003)

THE IGF SYSTEM is composed of a complex interacting network of ligands, ligand binding proteins, and receptors (1). In different cell types, the IGFs can elicit distinct downstream signaling cascades, of which the phosphatidylinositol 3-kinase (PI3K)/Akt and Ras/MAPK pathways are the best studied (2). The IGFs can lead to cell proliferation, survival, and differentiation. As key regulators of cell cycle progression,

they also play an important role in malignant transformation and invasion (3, 4). Extensive study has demonstrated that the IGFs are mitogenic and antiapoptotic agents for breast epithelial cells *in vitro* (5) and are crucial for mammary gland development (6). Additionally, numerous lines of evidence have supported a role for the IGFs in breast cancer pathogenesis (7). First, breast cancer cell lines express all of the components required for eliciting a response to the IGFs, and this results in the IGFs being one of the most potent mitogens for breast cancer cells (8). Second, blockade of IGF action *in vitro* and *in vivo* can inhibit breast tumor growth (9, 10). Third, epidemiological study shows that circulating levels of IGF-I predict breast cancer risk (11). Finally, IGF components are expressed in primary breast tumors, and high expression of several of them are associated with poor prognosis (12).

Progesterone is also critically involved in the development of the mammary gland and breast cancer, and

Abbreviations: DCS, Dextran-charcoal-treated serum; DRB, 5, 6-dichlorobenzimidazole riboside; EGF, epidermal growth factor; ER, estrogen receptor; ERE, estrogen response element; GAPDH, glyceraldehyde-3-phosphatedehydrogenase; HIMOC, 1L-6-hydroxymethyl-*chiro*-inositol-(R)-2-O-methyl-3-O-octadecylcarbonate; HRG, heregulin; ICI, ICI 182,780; IGF-IR, IGF-I receptor; IMEM, improved MEM zinc option; IRSs, insulin receptor substrates; luc, luciferase; mTOR, the mammalian target of rapamycin; PBST, PBS plus 0.05% Tween-20; PI3K, phosphatidylinositol 3-kinase; PKA, protein kinase A; PKC, protein kinase C; PR, progesterone receptor; PR-A and PR-B, two isoforms of human PR; PRE, progesterone response element; Q-PCR, real-time quantitative RT-PCR; SFM, serum-free medium; tk, thymidine kinase.

its effects are mostly mediated via the progesterone receptor (PR; Refs. 13-15). Mice lacking PR display incomplete mammary ductal branching and failure of lobular-alveolar development (16). Although PR expression is estrogen receptor (ER) dependent (17, 18), some breast cancer cell lines constitutively express high levels of PR independent of estrogens (19). Human PR normally exists in two isoforms (PR-A and PR-B) of 94 and 116 kDa, originating from two PR promoters (20).

Progesterone is considered differentiative in the uterus but proliferative in the normal mammary gland (14). However, progestin inhibition of breast cancer cell growth in tissue culture has been well documented (21-23). High doses of progestins have been used to treat estrogen-mediated mammary carcinomas, even though their antitumor mechanisms are not clear (14). Interestingly, progestins have been found to exert a biphasic regulation of breast cancer cell growth—accelerating cells through the first mitotic cell cycle, then arresting them in G1 of the second cycle. At this stage, the cell cycle progression machinery is poised to restart, as expression of growth factors and their receptors is increased by progestins (21, 22). Thus, it is proposed that progestins are neither inherently growth proliferative or inhibitive, but rather sensitize cells for growth factor and cytokine signals (24, 25).

The presence of PR in breast tumors is an important indicator of likely responsiveness to endocrine agents (13, 26). Approximately two thirds of breast cancers express the ER, some of which are ER positive (ER+)/PR negative (PR-). Their likelihood of response to endocrine therapy drops significantly compared with those that are ER+/PR+. It has also been reported that absence of PR in primary breast tumors is associated with secondary breast cancer in postmenopausal women (27), and absence of PR correlated significantly with a less differentiated phenotype of breast tumors (G1/G2 grading) and the presence of ErbB2/HER2/neu (28). Abnormal expression of ErbB2 and other growth factor receptors is normally associated with more aggressive tumors and a poorer patient prognosis (29, 30). So is there an intrinsic correlation between PR and intensity of growth factor action? We hypothesize that PR status may reflect growth factor function: low or absent PR expression indicates high IGF, epidermal growth factor (EGF), and heregulin (HRG) activities, and this correlation is independent of ER status. This assumption, combined with the fact that progesterone may inhibit breast tumor invasion, might explain why absence of PR is a marker of an aggressive tumor phenotype (27).

Recently, much effort has been directed to the study of the cross-talk between growth factors and ER signaling pathways in breast cancer cells (31), but how growth factors may interact with PR is less well defined. In this study, we have investigated the mechanisms for growth factor regulation of PR in breast cancer using IGF-I and MCF-7 cells because these cells are sensitive to the IGFs, have considerable PR levels, and possess intact

PI3K, MAPK, and other common signaling pathways. We find that IGF-I dramatically down-regulates PR through a transcriptional mechanism involving the PI3K pathway, independent of ER activity. Our data provide the first evidence that activation of a growth factor signaling pathway can directly reduce PR levels, and may explain why PR-negative tumors, which possibly have highly active growth factor signaling, poorly respond to endocrine therapy.

RESULTS

IGF-I Inhibits PR Expression

As a first step to investigate the effect of IGF-I on PR in breast cancer cells, we treated MCF-7 cells with IGF-I and then performed Western blot analysis to determine how PR expression was affected. We found that IGF-I treatment caused a dramatic decrease of both PR-A and PR-B protein levels in MCF-7 cells. The dose-response assay using a 24-h time point of treatment showed that maximal reduction of PR protein levels occurred with 10 nM IGF-I (Fig. 1, A and B), which is physiologically relevant to the circulating concentrations of IGF-I in women (11). Much lower concentrations of IGF-I, 0.1 nM, also resulted in an apparent reduction of PR protein levels. From a time course experiment using 10 nM IGF-I, it was found that PR protein levels began to drop after 6 h of IGF-I treatment and continued to decrease with time, whereas the untreated control cells did not display visible down-regulation of PR (Fig. 1, C and D). After 24 h, the sharp fall in PR protein levels stopped, but levels remained suppressed for at least 72 h. We also observed similar results in other PR+ breast cancer cells such as T47D and ZR75 (data not shown). Hence, these data indicate that IGF-I lowers PR levels in breast cancer cells.

To ascertain whether PR activity changed correspondingly with its protein levels after IGF-I treatment, we transiently transfected a progesterone response element (PRE)-luciferase construct into MCF-7 cells. Treatment with the synthetic progestin R5020 caused a more than 100-fold increase in reporter activity, which was almost completely blocked by the antiprogestin RU486 (Fig. 1E). IGF-I pretreatment for 6 h caused a 70% reduction in R5020-induced luciferase activity. This was most probably due to the decrease of PR protein levels elicited by IGF-I, which by itself, at the same time point, had no detectable activation of the reporter activity over the unstimulated control. Hence, these data suggest that IGF-I represses PR transcriptional activity through down-regulation of PR in MCF-7 cells.

Because MCF-7 cells also respond well to other growth factors like EGF and HRG (although response to EGF is not as sensitive as the response to HRG and IGF-I), and these growth factors share similar signaling pathways, we subsequently examined the effect of

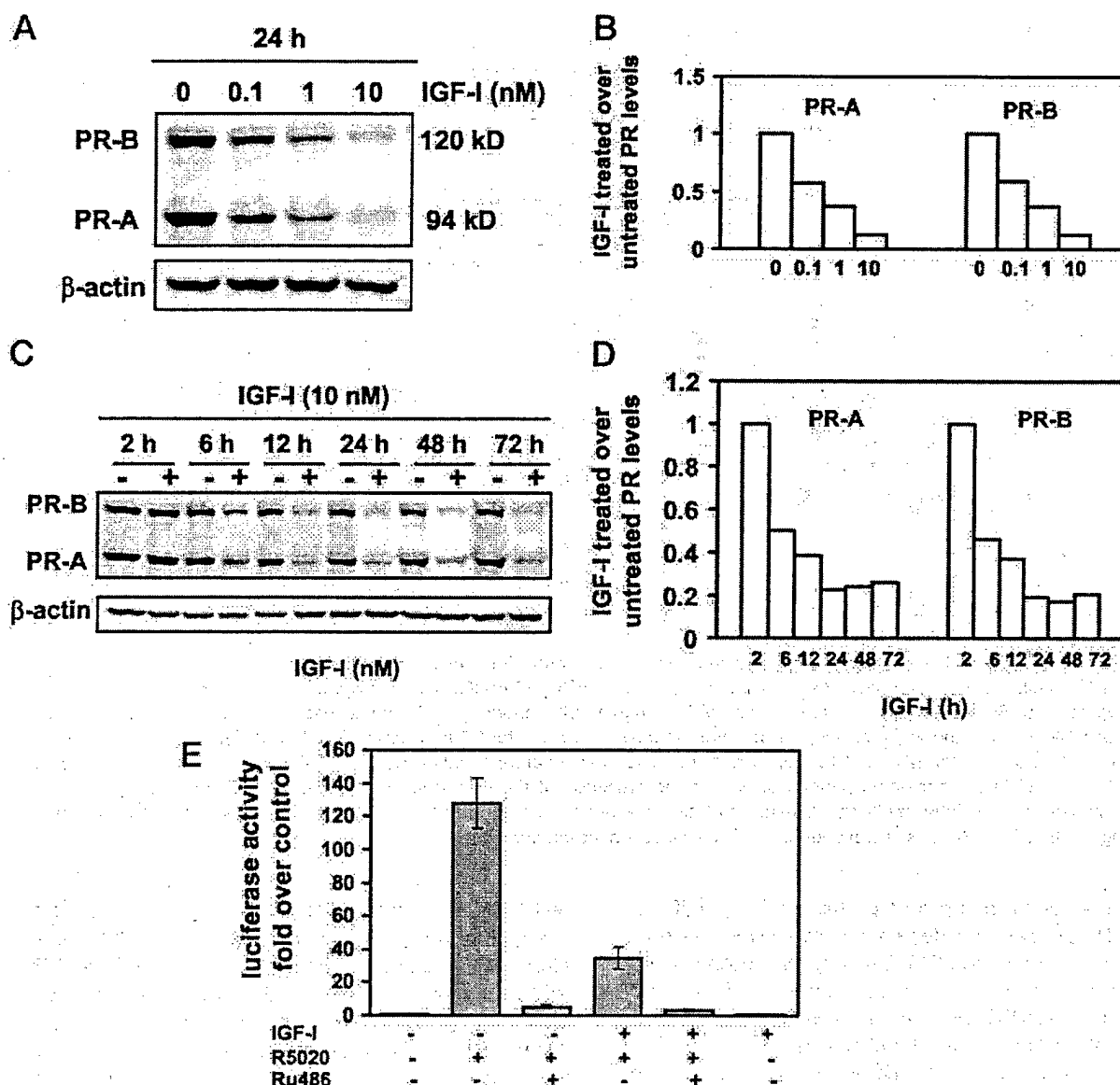


Fig. 1. IGF-I Down-Regulates PR in MCF-7 Cells

A, MCF-7 cells were stimulated for 24 h with increasing concentrations of IGF-I (0.1, 1, 10 nM). Cell lysate (40 μ g) was separated by 8% SDS-PAGE and immunoblotted with anti-PR antibody. β -Actin was used as a loading control. B, Graphical representation of data in panel A after densitometry and correction for β -actin expression. PR levels (represented by the densitometric readings) in IGF-I-treated samples were compared with those in the control sample. C, MCF-7 cells were stimulated with 10 nM IGF-I or vehicle for increasing periods of time. Cell lysates were immunoblotted with anti-PR antibody. D, Graphical representation of data in panel C after densitometry and correction for β -actin expression. PR levels (represented by the densitometric readings) in IGF-I-treated samples were compared with those in the control sample at each time point. E, MCF-7 cells in six-well dishes were transiently transfected with 0.2 μ g PRE-tk-luc vector. After treatment with 10 nM IGF-I for 6 h, cells were stimulated with 10 nM R5020, 100 nM RU486, or a combination for 12 h. Then, cells were lysed and luciferase assays were performed. The β -galactosidase expression vector pSV- β -Gal was used as an internal transfection control. Values are means $\pm$ SE of three independent experiments, each in duplicate.

EGF, HRG, and insulin on PR expression using Immunoblotting. As a control, we treated cells with R5020 and found the characteristic upward protein mobility shift (due to phosphorylation) and decrease in PR levels (due to proteasomal degradation—see Fig. 2B) as reported previously (32). Not surprisingly, HRG and EGF at similar concentrations to that of IGF-I also

markedly down-regulated PR (Fig. 2A), but insulin required 100-fold higher concentrations than IGF-I to achieve the same PR reduction. This suggests that the reduction of PR expression by IGF-I is a common effect shared by other growth factors in MCF-7 cells.

As reported previously, IGF-I can induce extensive phosphorylation of insulin receptor substrates (IRSs),

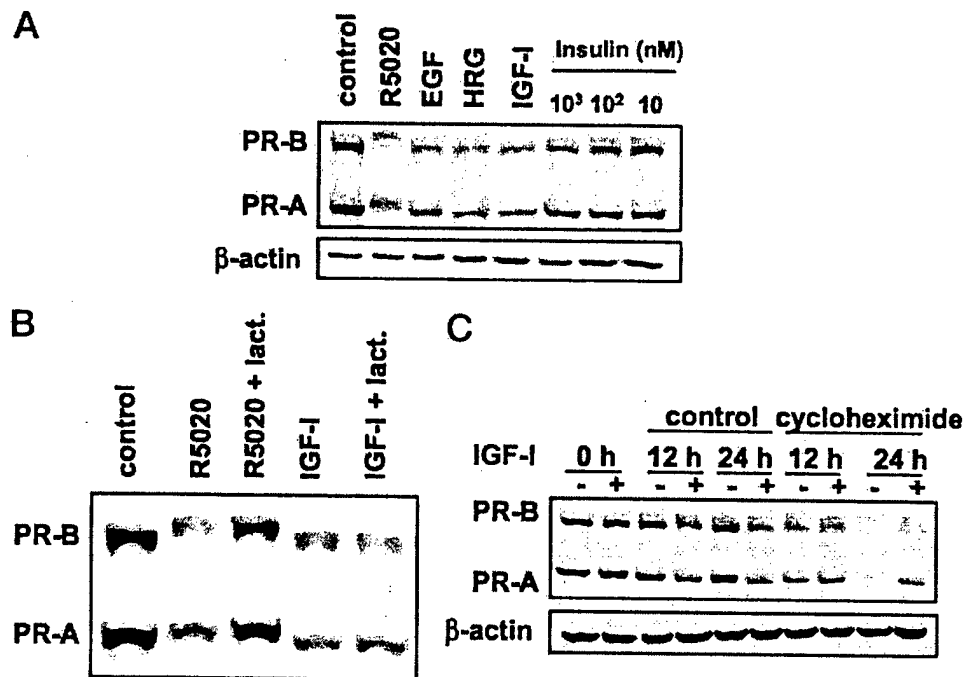


Fig. 2. IGF-I, EGF, HRG, and Insulin Down-Regulate PR by a Different Mechanism than R5020

A, MCF-7 cells were stimulated for 24 h with 20 nM EGF, 10 nM HRG, 10 nM IGF-I, increasing concentrations of insulin (10, 10^2 , 10^3 nM), or 10 nM R5020. Cell lysates were immunoblotted with anti-PR antibody. β -Actin was used as a loading control. B, Cells were first treated with the 26S proteasome inhibitor lactacystin (10 μ M) for 30 min before IGF-I and R5020 stimulation in the presence of lactacystin for 12 h. Cell lysates were immunoblotted with anti-PR antibody. C, MCF-7 cells were stimulated with 10 nM IGF-I or vehicle for increasing periods of time in the presence of the translation inhibitor cycloheximide (10 μ g/ml) after preincubation with cycloheximide for 30 min. Cell lysates were immunoblotted with anti-PR antibody. β -Actin was used as a loading control. This figure is representative of three independent experiments.

which leads to an upward protein mobility shift on SDS-PAGE gels and decreased IRSs levels via proteasomal degradation (33). Similarly, progestins cause phosphorylation and a mobility up-shift of PR, and they decrease PR levels via proteasomal degradation (32). Interestingly, IGF stimulation did not lead to a mobility shift of PR on SDS-PAGE gels, unlike the progestin R5020 (Fig. 2, A and B). Thus, the mechanism by which IGF-I down-regulates PR in breast cancer cells may be different from the 26S proteasome degradation pathway. This was confirmed by the inability of lactacystin, a 26S proteasome inhibitor, to block the decrease of PR protein levels by IGF-I (Fig. 2B). To further investigate how IGF-I affects PR protein stability, we used the translation inhibitor cycloheximide. Western blot analysis demonstrated that, in contrast to noncycloheximide conditions, PR protein levels were not lowered by IGF-I treatment compared with non-IGF treatment under cycloheximide conditions (Fig. 2C, see 12-h and 24-h lanes). This indicates that IGF-I does not impede PR protein stability, which is consistent with the result from the proteasome inhibitor assay (Fig. 2B).

IGF-I Represses PR Transcription

To investigate whether IGF-I suppresses PR protein levels by inhibiting PR transcription, we conducted

real-time quantitative RT-PCR (Q-PCR) to detect changes of PR mRNA concentrations in MCF-7 cells after IGF-I treatment. Because more than five PR mRNA transcripts with a wide range of sizes have been found in breast cancer cells and tumors, and it has not been clarified which codes for PR-A, PR-B, or both (20, 34), we chose primers and the fluorescent probe located near the 3' end of the PR coding region so as to detect all PR transcripts. We found that total PR mRNA transcript levels gradually decreased during the 24-h time period (Fig. 3A), which can probably be attributed to the fact that PR is ER dependent and estradiol is depleted in the serum-free medium (SFM) that was used in our cell stimulation experiments. However, compared with controls, PR mRNA levels dropped dramatically after 2 h of IGF-I treatment and continued to decrease with time, which was consistent with the change of PR protein levels in the IGF-I time course experiment (Fig. 1B). Interestingly, PR protein levels did not show a detectable drop at the 2-h time point, suggesting that the repression of PR mRNA levels by IGF-I occurred earlier than the reduction of PR protein levels. At any selected time point, PR mRNA levels under IGF-I-treated conditions were clearly lower than untreated controls. The decrease of PR mRNA levels by IGF-I was confirmed by Northern blotting using a probe at the 3' end of the PR coding

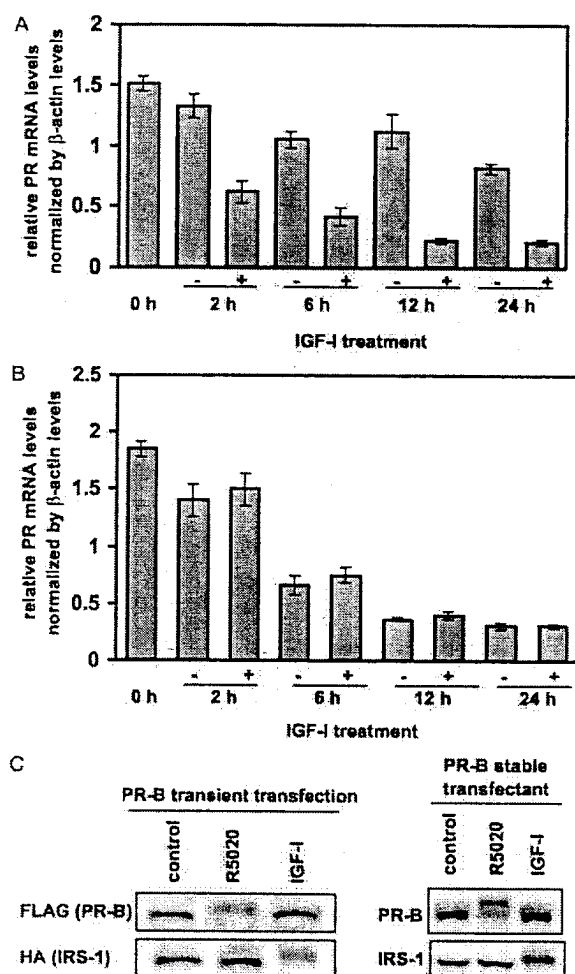


Fig. 3. IGF-I Down-Regulates PR mRNA Levels in MCF-7 Cells

A, MCF-7 cells were stimulated with 10 nM IGF-I or vehicle for increasing periods of time. Total RNA was isolated and PR mRNA levels measured by Q-PCR. PR mRNA levels in each sample were calculated from a standard curve and normalized using β -actin mRNA levels. B, MCF-7 cells were stimulated with 10 nM IGF-I or vehicle for increasing periods of time in the presence of the transcription inhibitor DRB (50 μ M) after preincubation with DRB for 30 min. Total RNA was isolated and Q-PCR was performed. C, FLAG-PR-B and HA-IRS-1 constructs were transiently cotransfected into MCF-7 cells. After 18 h, cells were stimulated with 10 nM IGF-I or 10 nM R5020 for 24 h. Similarly, stable transfectants of PR-B were stimulated with 10 nM IGF-I or 10 nM R5020 for 24 h. Cell lysates were immunoblotted with anti-FLAG, anti-HA, anti-IRS-1, and anti-PR antibodies. IRS-1 mobility shift and down-regulation was used as a marker for IGF-I responsiveness. This figure is representative of two independent experiments.

region (data not shown). These results indicate that IGF-I represses PR mRNA levels in breast cancer cells.

To determine whether posttranscriptional mechanisms are also involved in the IGF-I down-regulation of PR mRNA, we preincubated MCF-7 cells with the transcription inhibitor 5,6-dichlorobenzimidazole riboside (DRB), and then stimulated the cells with IGF-I in the

presence of DRB. Q-PCR showed that in the presence of DRB, PR mRNA levels dropped due to RNA degradation (Fig. 3B). However, in contrast to non-DRB conditions (Fig. 3A), PR mRNA levels under DRB conditions were not lowered by IGF-I compared with non-IGF-I treatment. The same result was confirmed by Northern blotting (data not shown). This suggests that IGF-I does not impair PR mRNA stability.

To confirm that IGF-I down-regulates PR through regulation of PR promoter activity, we transiently transfected a FLAG epitope-tagged PR-B cDNA and an HA epitope-tagged IRS-1 cDNA, both of which were driven by the cytomegalovirus (CMV) promoter, into MCF-7 cells. As expected, immunoblotting showed that IGF-I treatment did not reduce the exogenous PR protein levels that were generated from a heterologous promoter (CMV), whereas it did lower the exogenous IRS-1 levels and cause its mobility up-shift (Fig. 3C). As a control, the exogenous PR protein could still be regulated normally by R5020, *i.e.* PR protein levels were decreased and PR protein mobility was shifted upward. Furthermore, we stably transfected the PR-B cDNA into a specifically selected MCF-7 cell subline, which does not have detectable ER and PR but still responds to IGF-I (35). Similar to the transient transfection, IGF-I did not decrease PR-B levels in the stable transfectants but altered the endogenous IRS-1 levels and mobility (Fig. 3C). Then we transiently transfected a PRE-luciferase construct into these PR-B stable transfectants. Opposite to the data in regular MCF-7 cells, IGF-I could not inhibit the R5020-induced luciferase activity (data not shown).

In summary, these data show that IGF-I down-regulates PR mRNA transcription, and this is dependent upon the original PR promoter context.

IGF-I Regulates PR Expression through the PI3K/Akt/Mammalian Target of Rapamycin (mTOR) Pathway

The transmission of IGF signals in breast cancer cells involves several well-characterized signaling cascades downstream of IGF-I receptor (IGF-IR), including the PI3K/Akt and Ras/MAPK pathways (2). To identify the signaling pathway implicated in the IGF-I down-regulation of PR, we used a series of potent signaling inhibitors against Akt, MEK, mTOR, p38 MAPK, PI3K, protein kinase A (PKA), and protein kinase C (PKC). These inhibitors have been widely used in signal transduction research including our own previous studies (33). MCF-7 cells were first preincubated with these inhibitors and then stimulated with IGF-I in the presence of the inhibitors. Western blot analysis showed that blockade of Akt with 10 μ M 1L-6-hydroxymethyl-*chiro*-inositol-(R)-2-O-methyl-3-O-octadecylcarbonate (HIMOC), of mTOR with 40 nM rapamycin, or of PI3K with 20 μ M LY294002, rescued IGF-I down-regulated PR to the control level (Fig. 4A). In contrast, the MEK inhibitor U0126, the p38 MAPK inhibitor SB203580, the PKA inhibitor H-89, and the PKC inhibitor GF109203X did not prevent IGF-I re-

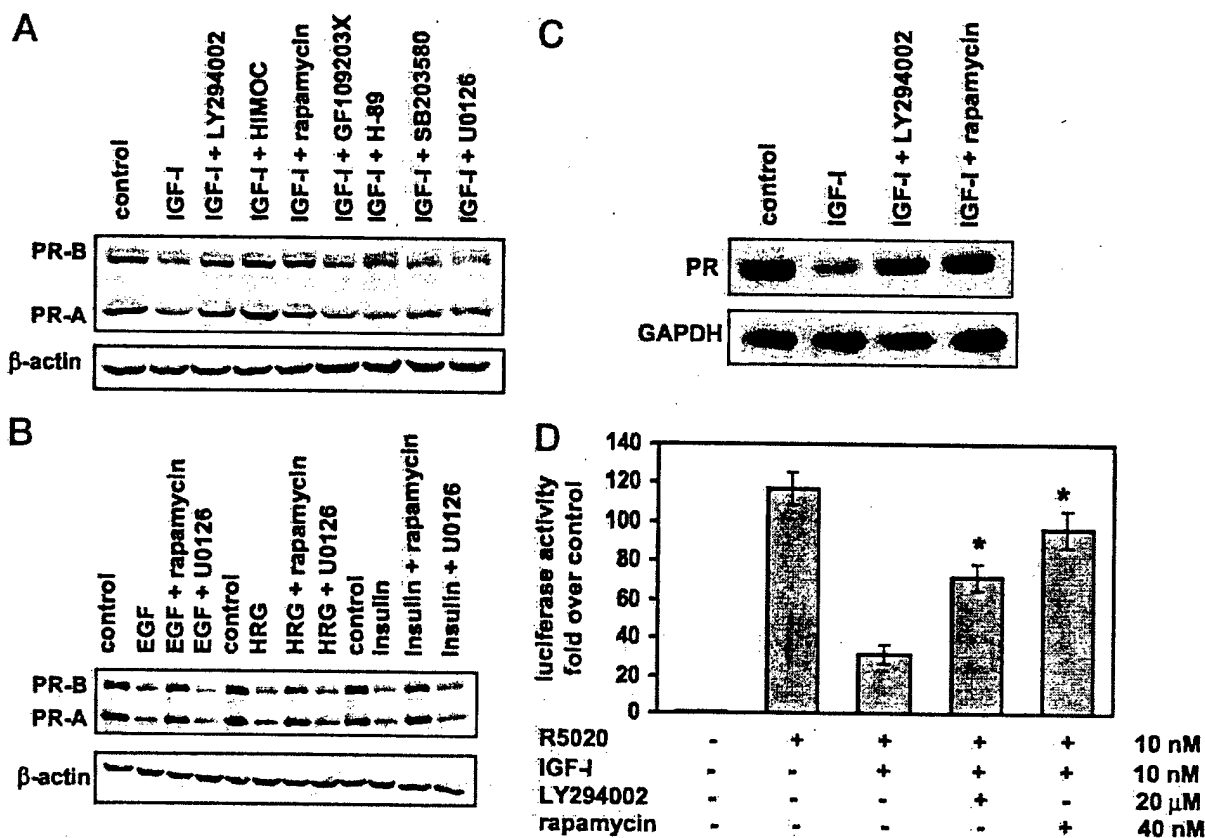


Fig. 4. The PI3K Inhibitor LY294002 and the mTOR Inhibitor Rapamycin Prevent IGF-I Down-Regulation of PR

A, MCF-7 cells were stimulated with 10 nM IGF-I for 24 h in the presence of the inhibitors after preincubation with 20 μM LY294002 (PI3K), 10 μM HMOOC (Akt), 40 nM rapamycin (mTOR), 5 μM GF109203X (PKC), 10 μM H-89 (PKA), 10 μM SB203580 (p38 MAPK), or 5 μM U0126 (MEK) for 30 min. Cell lysates were immunoblotted with anti-PR antibody. β-Actin was used as a loading control. B, MCF-7 cells were stimulated with 20 nM EGF, 10 nM HRG, or 1 μM insulin for 24 h in the presence of the inhibitors of mTOR and MEK. Cell lysates were immunoblotted with anti-PR antibody. β-Actin was used as a loading control. C, MCF-7 cells were stimulated with 10 nM IGF-I in the presence of the inhibitors for 12 h after preincubation with 20 μM LY294002 or 40 nM rapamycin for 30 min. Total RNA was isolated and RT-PCR was conducted. PCR product was visualized with ethidium bromide staining under UV light. GAPDH was used as an internal control for RT-PCR. D, MCF-7 cells in six-well dishes were transiently transfected with 0.2 μg PRE-tk-luc vector. The cells were preincubated with LY294002 and rapamycin for 30 min before IGF-I treatment for 6 h followed by R5020 stimulation for 12 h. Then, cells were lysed and luciferase assays were performed. pSV-β-Gal was used as an internal transfection control. Values are means ± SE of three independent experiments, each in duplicate. *, $P < 0.005$ as compared with IGF-I plus R5020 treatment.

duction of PR in MCF-7 cells. These results were confirmed using other common inhibitors against the same target kinases such as the MEK inhibitor PD98059, the PI3K inhibitor wortmannin, and the PKC inhibitor GO6983 (data not shown). As PI3K, Akt, and mTOR form a sequential signaling cascade activated by the IGF-IR (36), the IGF-I effect on PR appears to be specifically elicited via the PI3K/Akt/mTOR pathway. Not surprisingly, the same signaling pathway was found to be involved in the EGF, HRG, and insulin down-regulation of PR (Fig. 4B). Because IGF-I represses PR at the transcription level, we confirmed by RT-PCR that inhibitors of PI3K or mTOR abolished the decrease of PR mRNA by IGF-I (Fig. 4C).

As shown previously (Fig. 1E), IGF-I down-regulates R5020-induced PR transcriptional activity. To assess the role of PI3K and mTOR in this event, we transiently transfected a PRE-luciferase construct into MCF-7

cells. Subsequent stimulation experiments using R5020, IGF-I, and the PI3K and mTOR inhibitors showed that the inhibitors impaired IGF-I reduction of R5020-induced luciferase activity (Fig. 4D). Noticeably, luciferase activity did not fully recover, unlike the PR protein levels (Fig. 4A). We speculate that the toxicity of these inhibitors to transfected cells and to the transcription machinery on the PRE promoter may contribute to their partial effect.

To confirm that the PI3K/Akt/mTOR pathway is involved in IGF-I down-regulation of PR, we used MCF-7 cells stably transfected with either a kinase-defective Akt (KD-Akt) containing a K179M substitution or a constitutively active Akt (myr-Akt) containing a myristoylation membrane-targeting sequence. Western blot analysis showed that overexpression of KD-Akt moderately elevated PR levels in MCF-7 cells in SFM, whereas overexpression of myr-Akt dramatically de-

creased PR levels (Fig. 5A). Interestingly, ER α protein levels were not different in the parental and transfected MCF-7 cells. As expected, mTOR phosphorylation was attenuated in KD-Akt cells but enhanced in myr-Akt cells (Fig. 5A). These data are consistent with Akt having a role in IGF-I down-regulation of PR in breast cancer cells.

To examine how ER regulates PR in both stable transfectants, we treated the cells with estradiol. As shown in Fig. 5B, 10 nM estradiol induced PR expression over the basal control levels in both KD-Akt and myr-Akt cells, suggesting that ER functions properly in both cell lines and that the effect of mutant Akt on PR

is not mediated by influencing ER. Interestingly, LY294002 pretreatment displayed a stronger effect in blocking the IGF-I effect in KD-Akt transfectants than in myr-Akt transfectants, although rapamycin had a similar effect in both cells (Fig. 5B). This can be explained by the fact that Akt is downstream of PI3K and upstream of mTOR, and that myr-Akt activity is largely independent of growth factor and PI3K activation. Taken together, our data demonstrate that the PI3K/Akt/mTOR pathway uniquely mediates the alteration of PR expression elicited by IGF-I in breast cancer cells.

IGF-I Down-Regulation of PR Is Independent of ER Activity

It has been reported previously that IGF-I down-regulates ER levels in breast cancer cells (37, 38), which we also found (data not shown). Accordingly, this raised a question as to whether the IGF-I effect on PR was actually caused by the IGF-I effect on ER. This intriguing enigma prompted us to explore if there is a correlation between ER and PR expression regulated by IGF-I.

Initially, we had three pieces of evidence to suggest that the down-regulations of PR and ER are two independent events triggered by IGF-I. First, PR expression in T47D breast cancer cells, which is independent of ER (19), was also significantly reduced by IGF-I (data not shown). Second, as shown in Fig. 5, PR levels were markedly lower in myr-Akt stable transfectants than in KD-Akt cells, even though ER levels, and ER's ability to induce PR, were similar in both cells. Third, PR levels were remarkably lower when MCF-7 cells were grown in dextran-charcoal-treated serum (DCS: estradiol and other steroid hormones removed, but growth factors maintained) medium than in SFM, whereas ER levels were constant in both media (data not shown). Thus, to further test this separation of effects, we performed the following experiments.

Previous reports have shown that IGF-I can cause ligand-independent activation of ER via alteration of ER phosphorylation status in breast cancer and other cells, and even *in vivo* (39–41). To test this in our experimental system, we transiently transfected an estrogen response element (ERE)-luciferase vector into MCF-7 cells, which were then stimulated with estradiol, IGF-I, or the antiestrogen ICI 182,780 (ICI). As shown in Fig. 6A, luciferase activity was significantly increased by estradiol or IGF-I and was further elevated by the two together, whereas ICI blocked the effect of both estradiol and IGF-I, suggesting that the IGF-I-induced luciferase activity is mediated by ER and accordingly that IGF-I can directly induce the transcriptional activity of ER. Surprisingly, Western blot analysis showed that estradiol and IGF-I cotreatment severely attenuated estradiol-induced PR levels, which dropped even lower than that of the unstimulated control (Fig. 6B). This suggests that IGF-I may directly repress PR expression, even while it activates ER, and that this repression is dominant over ER ac-

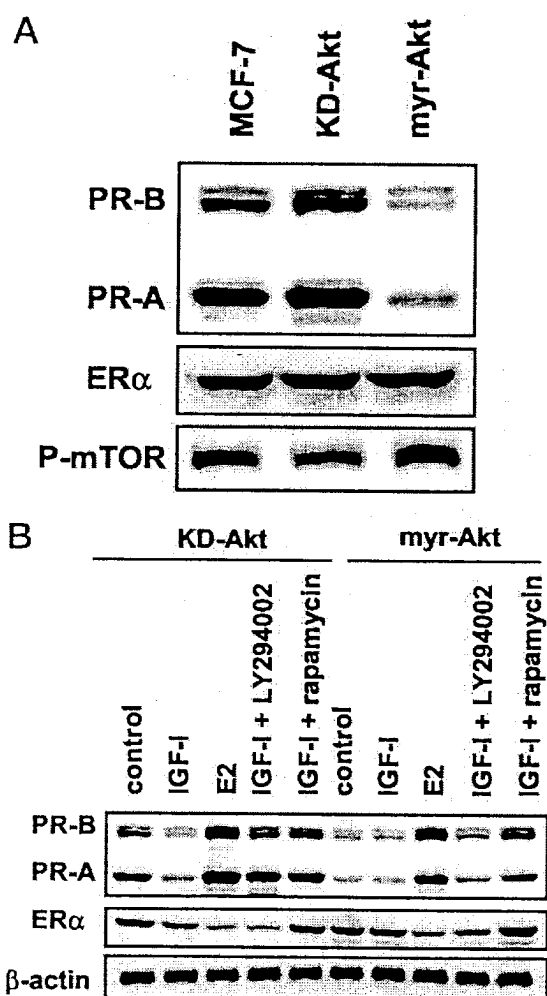


Fig. 5. Expression of KD-Akt and myr-Akt Alters PR Levels in MCF-7 Cells

A, Cell lysates from stable transfectants of KD-Akt and myr-Akt, and parental MCF-7 cells grown in SFM for 48 h were immunoblotted with anti-PR, anti-ER α , and anti-phospho-mTOR antibodies. B, KD-Akt and myr-Akt transfectants were stimulated for 24 h with 10 nM estradiol or 10 nM IGF-I in the presence of the inhibitors after preincubation with 20 μ M LY294002 or 40 nM rapamycin for 30 min. Cell lysates were immunoblotted with anti-PR and anti-ER α antibodies. β -Actin was used as a loading control. This figure is representative of three independent experiments.

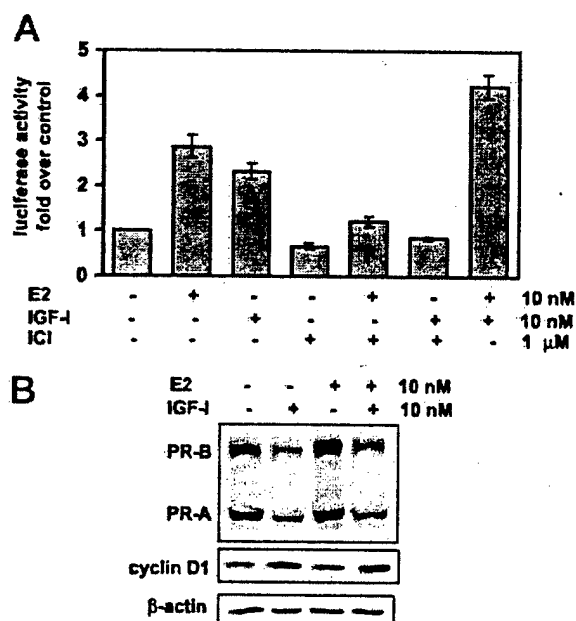


Fig. 6. IGF-I Induces Ligand-Independent ER Activity While Reducing Estradiol-Induced PR Expression

A, MCF-7 cells in six-well dishes were transiently transfected with 0.2 μ g ERE-tk-luc vector. After stimulation with 10 nM IGF-I, 10 nM estradiol, 1 μ M ICI, or their combination for 12 h, cells were lysed and luciferase assays were performed. pSV- β -Gal was used as an internal transfection control. Values are means $\pm$ SE of three independent experiments, each in duplicate. **B**, MCF-7 cells were stimulated with 10 nM IGF-I, 10 nM estradiol, or their combination for 12 h. Cell lysates were prepared and immunoblotted with anti-PR and anti-cyclin D1 antibodies. β -Actin was used as a loading control.

tivity on PR. In contrast to PR, expression of cyclin D1, which is also ER dependent (42), was increased by estradiol, IGF-I, and the two together (43, 44). Thus, IGF-I has opposite effects on ER-inducible PR and ER-inducible cyclin D1 expression, even though it activates ER transcriptional activity.

To elucidate the difference between the IGF-I effects on ER activity and PR levels, we transiently co-transfected ERE-luciferase with myr-Akt or a constitutively active PI3K catalytic subunit p110 (myr-PI3K) into MCF-7 cells. As shown in Fig. 7A, estradiol or IGF-I treatment caused a 2- to 3-fold increase of the reporter activity over the nontreated control, whereas overexpression of myr-Akt or myr-PI3K led to a similar or higher increase of the luciferase activity in the absence of estradiol. This was due to the ligand-independent activation of ER by Akt and PI3K (PI3K utilizes both Akt-dependent and Akt-independent pathways) (45, 46). On the other hand, when we transiently co-transfected PRE-luciferase with myr-Akt or myr-PI3K into MCF-7 cells, either IGF-I or overexpression of myr-Akt or myr-PI3K inhibited the R5020-induced luciferase activity (Fig. 7B). Thus, myr-Akt and myr-PI3K can mimic the effect of IGF-I in suppressing PR activity through down-regulation of PR. Taken together, these data indicate that IGF-I regulates ER activity and ER-

dependent PR levels in opposite ways, and that IGF-I down-regulation of PR expression is independent of ER (Fig. 8).

DISCUSSION

PR is an important factor in mammary gland and breast cancer development. Because PR is a highly ER-dependent gene, regulation of PR expression by other proteins and growth factors has been naturally regarded as indirect and attributed to changes of ER status. Here, we provide evidence showing that IGF-I down-regulates PR in breast cancer cells irrespective of ER activity through a transcriptional mechanism involving the PI3K/Akt/mTOR signaling pathway (Fig. 8).

In this study, we found that EGF, HRG, and insulin can also sharply reduce PR levels. An obvious common feature between IGF-I and these growth factors is that they all can activate the PI3K/Akt signaling cascade in breast cancer cells, which explains why they all display the same effect on PR expression. One could speculate that other growth factors like PDGF, which also activates the PI3K/Akt pathway through its receptors, may likewise down-regulate PR in breast cancer cells that express PDGF receptors (47). But why does insulin require much higher doses to achieve the same effect as IGF-I even though MCF-7 cells have relatively high levels of insulin receptor (48)? We found that IGF-I is more potent than insulin at the same concentration (10 nM) to induce phosphorylation of IRS-1 and Akt, an indicator of activated PI3K/Akt signaling (Ref. 33 and data not shown). Thus, high concentrations of insulin may be necessary for insulin to act through IGF-IR to decrease PR levels in MCF-7 cells because insulin has a relatively low affinity to IGF-IR (33, 49). Alternatively, high doses of insulin may simply enhance the insulin receptor-mediated PI3K/Akt signaling pathway.

It is a long-held rule of thumb that optimal estradiol stimulation of PR occurs in medium supplemented with 5% DCS (50). This may be attributed to the fact that DCS medium contains large amount of growth factors and consequently suppresses PR to barely detectable levels, whereas the basal level of PR is much higher in SFM. Hence, the fold-induction of PR with estradiol is seemingly more dramatic in DCS medium. This is perhaps also the reason behind the previous conflicting reports in which PR was used as a reporter gene monitoring ER activity in the study of IGF-I regulation of ER. Clayton *et al.* (37) showed that insulin and IGF-I considerably impaired the estradiol induction of PR mRNA in SFM, which is in line with our result. In another study that showed that IGF-I had a potentiating effect on the estradiol induction of PR mRNA (38), the cells were grown in DCS medium for 2 d. In this system, because PR transcription was already suppressed by growth factors, the observed IGF-I effect might actually indicate a change in PR

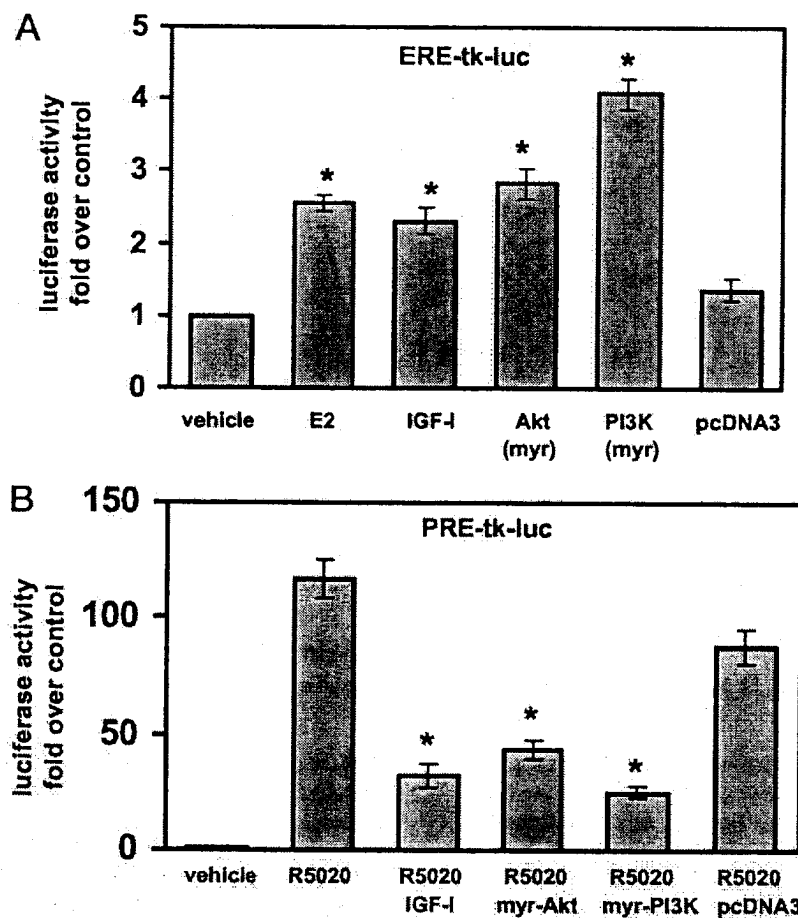


Fig. 7. Myr-Akt and myr-PI3K Mimic the IGF-I Effect on Ligand-Independent ER Activity and R5020-Induced PR Activity

A, MCF-7 cells in six-well dishes were transiently cotransfected with 0.2 μ g ERE-tk-luc and 0.5 μ g myr-Akt, myr-PI3K, or empty pcDNA3 vector. ERE-tk-luc-only transfected cells were stimulated with 10 nM estradiol or 10 nM IGF-I and were compared with nonstimulated ERE-tk-luc plus myr-Akt or myr-PI3K cotransfected cells in luciferase assay. Values are means $\pm$ SE of three independent experiments, each in duplicate. *, $P < 0.005$ as compared with pcDNA3 transfection. B, MCF-7 cells in six-well dishes were transiently cotransfected with 0.2 μ g PRE-tk-luc and 0.5 μ g myr-Akt, myr-PI3K or pcDNA3.1 vectors. Cells were treated with R5020 to induce PR activity. PRE-tk-luc-only transfected cells were stimulated with 10 nM R5020 or 10 nM IGF-I plus 10 nM R5020. Values are means $\pm$ SE of three independent experiments, each in duplicate. *, $P < 0.005$ as compared with pcDNA3 transfection.

mRNA and/or protein stability. Previously, Cho *et al.* (50) reported that IGF-I does not affect PR transcription but elevates PR protein levels in MCF-7 cells under SFM conditions. The discrepancy between their and our results may be due to the different cell culture conditions before IGF-I stimulation. In our study, before IGF-I treatment, cells were starved for 16 h after being switched to SFM from regular culture medium, whereas there was no delay of IGF-I treatment after the change to SFM from DCS medium in their studies.

Recently, evidence is emerging to support our conclusion that IGF-I and other growth factors inhibit PR expression. First, it was found that overexpression of ER in a specifically selected ER-/PR- MCF-7 breast cancer cell subline did not restore PR expression, although ER did restore cyclin D1, IRS-1, and IGF-IR levels (35). These cells were grown in DCS medium, which might completely suppress PR expression after

long-term cell culture. Similarly, it was reported that in antiestrogen-resistant MCF-7 cells generated by continuous culture of the PR+ parental cells in antiestrogen-supplemented DCS medium, EGF receptor signaling was enhanced, whereas PR levels diminished (51). Interestingly, replacement of antiestrogen by estradiol failed to induce PR, whereas expression of other estrogen-responsive genes was significantly elevated. Conceivably, DCS medium plus enhanced EGF receptor signaling may permanently silence PR expression. In another interesting report, the mammary epithelial cells that retain stem/progenitor cell characteristics were found to lack PR (52). These cells rely on growth factors to continuously proliferate. Recently, in a study that confirmed that ER+/PR+ breast cancer patients respond better to hormonal therapy than ER+/PR- patients, Dowsett *et al.* (53) found that among ER+/PR- samples 25% are HER2+, com-

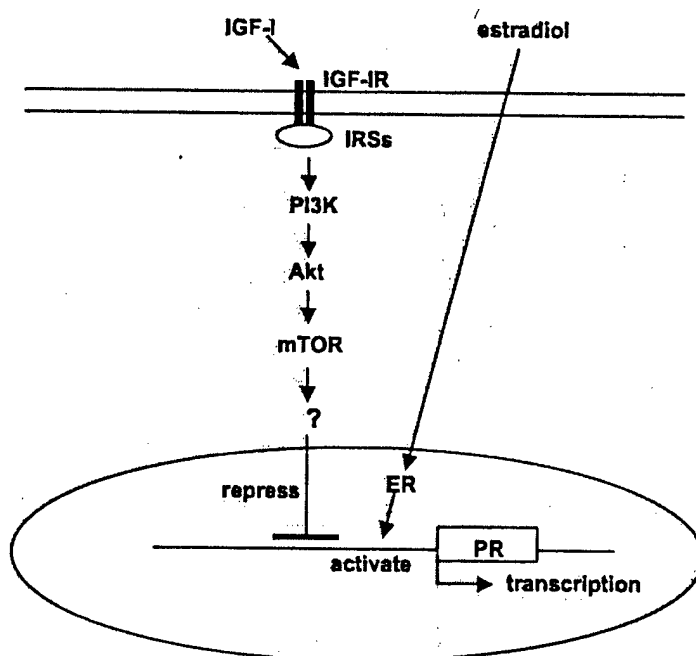


Fig. 8. Illustration of the IGF-I Signaling Pathway Repressing PR Expression

pared with 10% HER2+ among ER+/PR+. Moreover, HER2+/PR- patients responded much worse than HER2-/PR+ in hormonal therapy, again suggesting that PR status may reflect HER2 signaling.

Our result indicates that the PI3K/Akt/mTOR pathway is responsible for the IGF-I down-regulation of PR. In a relevant report, Shen *et al.* (54) showed that, although overexpression of MEKK1, through p42 and p44 MAPK, increased R5020-induced PR activity, it alone could not down-regulate PR. Thus, PI3K/Akt and Ras/MAPK pathways may play distinct roles in regulating PR activity in breast cancer cells. However, we only observed IGF-I down-regulation of PR despite IGF-I's ability to trigger both PI3K/Akt and Ras/MAPK pathways in MCF-7 and other breast cancer cells. This may be due to the finding that Ras can also bind to and activate PI3K (55), and the PI3K/Akt pathway is very potent in eliciting IGF-I signals in MCF-7 cells. Hence, the PI3K/Akt pathway is dominant in IGF-I regulation of PR. Interestingly, the PI3K/Akt/mTOR pathway is also involved in the IGF-I reduction of IRSs (33). The former event is mediated by a transcriptional mechanism, whereas the latter is via the 26S proteasome pathway for protein degradation. Different downstream proteins of mTOR may account for this seeming dilemma—although p70 S6 kinase is a typical target for mTOR, other kinases or signaling proteins may also function downstream of mTOR. For example, it has been shown that insulin regulation of IGFBP-1 gene expression is dependent on mTOR but independent of p70 S6 kinase activity (56). We hypothesize that mTOR may directly or indirectly activate a PR transcription repressor or inactivate a transcription activator to mediate the IGF-I effect on PR expression (Fig. 8).

The ER and PR status in breast cancer is highly correlated with the response to endocrine therapy. Key areas of study in breast cancer are those mechanisms that regulate ER and PR expression. The loss of PR gene expression has been attributed to loss of heterozygosity, loss of ER function, and methylation of a CpG island in the PR promoter (26). Our data provide implications for another theory, in which potent growth factor signaling, especially PI3K/Akt, may contribute to the PR down-regulation. This is reflected clinically with reduced PR levels in breast tumors with HER2 amplification (53). Because the IGF-I effect involves a transcriptional mechanism, whether IGF-I increases methylation of PR promoter and accordingly silences PR expression remains an intriguing question.

Low or absent PR in primary breast cancer is associated with faster disease progression and poor response to hormonal therapy. Our results suggest that low PR may be serving as an indicator of activated growth factor signaling in breast tumor cells, and therefore of an aggressive tumor phenotype and resistance against hormonal therapy.

MATERIALS AND METHODS

Materials

All general materials and chemicals were purchased from Sigma (St. Louis, MO) unless otherwise noted. IGF-I was purchased from GroPep Pty. Ltd. (Adelaide, Australia). ICI was a kind gift from Zeneca Pharmaceuticals (Macclesfield, UK). The inhibitors GF109203X, H-89, lactacystin, LY294002, HIMOC, rapamycin, SB203580, and U0126 were from Calbiochem (La Jolla, CA). All tissue culture reagents were purchased from Invitrogen (Carlsbad, CA) unless otherwise

stated. [³²P]deoxy-CTP (3000 Ci/mmol) was purchased from NEN Life Science Products (Boston, MA).

Cell Culture and Plasmids

MCF-7 cells have been maintained in our laboratory for many years (57). Cells were routinely maintained in improved MEM zinc option (IMEM) supplemented with 5% fetal bovine serum, 2 mM glutamine, 50 IU/ml of penicillin, 50 µg/ml of streptomycin, and 10 µg/ml insulin. SFM consists of IMEM without phenol red plus 10 mM HEPES (pH 7.4), 1 µg/ml of transferrin, 1 µg/ml of fibronectin, 2 mM glutamine, 50 IU/ml of penicillin, 50 µg/ml of streptomycin, and trace elements (BioSource Technologies, Inc., Camarillo, CA). Cells were kept at 37 °C in a humidified incubator with 5% CO₂. The estrogen-responsive reporter plasmid ERE-tk-luc contains a single consensus ERE upstream of a minimal thymidine kinase (tk) promoter and the luciferase (luc) gene (40). The PRE-tk-luc was constructed in the same way. The expression vectors for constitutively active myr-Akt and myr-PI3K were described elsewhere (58), and were gifts from Dr. Thomas Franke and Dr. Anke Klippel. The murine myr-Akt and myr-PI3K (p110α) each have a myristoylation signal at the N terminus to target the protein to the membrane.

Cell Stimulation and Lysis

Cells were plated at a density of 1.5×10^6 per 6-cm-diameter dish (Becton Dickinson and Co., Lincoln Park, NJ) and allowed to grow for 48 h. Then the medium was changed to SFM, and 16 h later, the cells were stimulated with 10 nM IGF-I, 20 nM EGF, 10 nM HRG, or insulin at 10, 100, or 10^3 nM for different periods of time. For experiments using inhibitors, cells were first preincubated separately with GF109203X (5 µM), H-89 (10 µM), lactacystin (10 µM), LY294002 (20 µM), a HIMOC (10 µM), rapamycin (40 nM), SB203580 (10 µM), and U0126 (5 µM) for 30 min before stimulation with EGF, HRG, IGF-I, and insulin in the presence of an inhibitor as described previously (33). For the translation inhibitor cycloheximide (10 µg/ml), the same procedure was followed. Control cells were incubated with a similar concentration of the vehicle dimethylsulfoxide alone. After stimulation, cells were washed twice with ice-cold PBS and then lysed in 200 µl of lysis buffer, which contained 50 mM Tris-HCl (pH 7.4), 1% Nonidet P-40, 2 mM EDTA, 100 mM NaCl, 10% glycerol, and a fresh protease inhibitor cocktail (Roche Applied Sciences, Indianapolis, IN). Cells were left on ice for 30 min, and then the cell lysate was clarified by centrifugation at $14,000 \times g$ for 15 min at 4 °C and stored at -20 °C. Protein concentration of the supernatant was measured by bicinchoninic acid assay in accordance with the manufacturer's instruction manual (Pierce Chemical Co., Rockford, IL).

Immunoblotting

Total protein (40 µg) was resuspended in denaturing sample loading buffer (3% dithiothreitol; 0.1 M Tris-HCl, pH 6.8; 4% sodium dodecyl sulfate; 0.2% bromophenol blue; 20% glycerol), separated by 8% SDS-PAGE, and electrophoretically transferred to a nitrocellulose membrane overnight at 4 °C. The remaining steps were all performed at room temperature. The membrane was blocked with PBS plus 0.05% Tween-20 (PBST) containing 5% nonfat milk for 1 h and followed by incubation with a 1:1000 dilution of anti-ER (Novocastra Laboratories, Newcastle upon Tyne, UK), anti-FLAG (Sigma), anti-HA (Covance Laboratories, Inc., Richmond, CA), anti-IRS-1 (Upstate Biotechnology, Lake Placid, NY), anti-PR (DAKO Corp., Carpinteria, CA), anti-β-actin (Upstate Biotechnology), and anti-cyclin D1 (Santa Cruz Biotechnology, Inc., Santa Cruz, CA) antibodies in blocking solution for 1–2 h. For phospho-mTOR detection, the membrane was first washed

three times for 5 min each with PBST and then incubated with a 1:1000 dilution of anti-phospho-mTOR antibody (Cell Signaling, Beverly, MA) in PBST. Subsequently, the membrane was again washed three times for 5 min each with PBST and then incubated with a horseradish peroxidase-linked secondary antibody (Amersham Pharmacia Biotech, Piscataway, NJ) at a dilution of 1:4000 in blocking solution. After the membrane was washed three times for 5 min each with PBST, bands were visualized by enhanced chemiluminescence according to the manufacturer's protocols (Pierce Chemical Co.).

RNA Blotting and RT-PCR

Cells were plated at a density of 5×10^6 per 10-cm-diameter dish and allowed to grow for 48 h. Then the medium was changed to SFM. After 16 h starvation, the cells were stimulated with IGF-I for an indicated time period. When the transcription inhibitor DRB (50 µM) and the signaling inhibitors LY294002 and rapamycin were used, cells were first preincubated with them for 30 min before IGF-I stimulation. Total RNA was prepared with RNeasy Midi kit (QIAGEN, Valencia, CA) according to the instruction manual. RNA integrity was checked by separation on a 1% agarose gel. For PCR of the 430-bp PR gene fragment, a pair of primers (5'-CAGTGGGCAGATGCTGTATTTTGC-3', 5'-GTGCAGCAATAACTTCAGACATC-3') was designed toward the 3' end of the PR coding region. Another pair of primers (5'-GGCTCTC-CAGAACATCATCCCTGC-3', 5'-GGGTGTCGCTGTTGAAGTCAGAGG-3') was used in PCR of the 299 bp glyceraldehyde-3-phosphatedehydrogenase (GAPDH) gene fragment (59). In the RT-PCR experiment, total RNA (2 µg) was used to produce cDNA with Superscript II reverse transcriptase (Invitrogen) in a 20-µl volume. Then, 1 µl from the cDNA synthesis reaction was added to PCR mixture, and PCR amplification was performed with PR and GAPDH primers with an annealing temperature at 60 °C and 30 cycles. Products were revealed by ethidium bromide staining under UV after agarose gel electrophoresis.

Q-PCR

Basically, reverse transcriptions of PR mRNA were performed in 96-well optical plates (PE Applied Biosystems, Foster City, CA) using Superscript II reverse transcriptase. All RNA samples were first treated with deoxyribonuclease I to eliminate residual genomic DNA. The reverse primer (5'-GGCTTAGGGCTTGGCTTTC-3') is at the 3' end of the PR coding region. Total RNA of 100 ng in a 10-µl reaction volume was added to each well. The plates were incubated at 50 °C for 30 min followed by 10 min at 72 °C. Then real-time quantitative TaqMan PCR of PR cDNAs was conducted using a PR-specific double fluorescence-labeled probe (5'-TCCCA-CAGCCATTGGCGTTC-3') in an ABI PRISM 7700 Sequence Detector (PE Applied Biosystems). ROX was used as a reference dye. The PCR mixture also contains 300 nM each of the forward primer (5'-GAGCACTGGATGCTGTTGCT-3') and the reverse primer. The plates were incubated at 94 °C for 1 min, followed by 40 cycles at 94 °C for 12 sec and 60 °C for 1 min. FAM was used as the fluorescent reporter coupled at the 5' end of the probe, whereas Block Hole Quencher was conjugated to the 3' end. Each experiment included three nontemplate controls to detect any template contamination. In addition, a control lacking reverse transcriptase was included for each sample to detect any residual genomic DNA. Standard curves for the quantification of PR and β-actin mRNAs were generated using serial 10-fold dilutions from 10^8 to 10^2 copies of synthesized templates. Q-PCR was performed in triplicate of each sample. The obtained PR mRNA concentration was normalized by the β-actin mRNA value.

Transfections

MCF-7 cells were grown for 48 h in IMEM + 5% FBS till 80% confluence before transfection. Stable transfectants of myr-Akt and KD-Akt, which contains K179M substitution, were gifts from Dr. Adriana Stoica (58). Using Lipofectamine (Invitrogen), a FLAG-PR-B expression vector pSG5-hPR1, which was a generous gift from Dr. K. Horwitz, was cotransfected with the neomycin resistant gene vector pcDNA3.1 (Invitrogen) in a 20:1 ratio (PR vector: neomycin vector). G418 of 600 µg/ml was used to select stable clones that were later verified by Western blot analysis with the PR antibody. All transient transfections were performed using Polyfect reagents (QIAGEN) according to the instruction protocols. For cotransfections with FLAG-PR-B and HA-IRS-1 constructs, 0.1 µg DNA of each plasmid was added to one well in six-well dishes. After 18 h, the culture medium was changed to SFM, and cells were incubated for 12 h before stimulation with 10 nM IGF-I and 10 nM R5020 for 24 h. For transfections with only ERE-tk-luc and PRE-tk-luc constructs, cells in six-well dishes were transfected with 0.2 µg DNA. After 5 h, the serum medium was switched to SFM, and cells were incubated for 6–8 h in the presence or absence of IGF-I. Then the cells were stimulated with 10 nM R5020 10 nM or 10 nM estradiol for 10–12 h. For the study of the inhibitors, cells were preincubated with LY294002 and rapamycin for 30 min before IGF-I treatment in the presence of the inhibitors. To examine the effect of myr-Akt and myr-PI3K on ER and PR activity, cells in six-well dishes were cotransfected with 0.2 µg reporter plasmids and 0.5 µg myr-Akt, myr-PI3K or empty pcDNA3 vector. Transfection time was extended to 16 h to allow sufficient time for exogenous Akt and PI3K expression. Then the serum medium was switched to SFM, and cells were stimulated with estradiol or R5020 for 12 h. Twenty nanograms of a β-galactosidase expression vector pSV-β-Gal (Promega Corp., Madison, WI) were cotransfected as an internal control. Luciferase and β-galactosidase assays were performed using the Promega Corp. assay system.

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New Mechanisms of Signal Transduction Inhibitor Action: Receptor Tyrosine Kinase Down-Regulation and Blockade of Signal Transactivation¹

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Abstract

The explosion of signal transduction research over the last 10 years has provided a unique insight into the complexity of these intricate pathways. Whereas intermediates of multiple signaling pathways have been identified, understanding their function and, in particular, the interactions between them has become a daunting task. The increasing evidence that many of these pathways can cross-talk with each other via signal transactivation inevitably raises the question of how cells determine specificity in signaling. Despite the mind-numbing complexity of these pathways, progress has been made in developing highly specific and potent signal transduction inhibitors (STIs). STIs show promise in the treatment of cancer in preclinical studies and are currently in a number of clinical trials. Whereas many of these agents were "rationally designed," we barely understand their mechanisms of action. This review will highlight how recent studies using these STIs have elucidated novel mechanisms of STI action that may be used in the development of new therapeutic strategies for the treatment of cancer.

Introduction

The complexity of development and growth of organisms can in part be attributed to the diverse and dynamic interactions between hormones, growth factors, cell contact, and other external stimuli that coordinate cell fate through cell surface

receptors. The explosion of signal transduction research over the last 10 years has deciphered the basic signaling mechanisms of a number of these receptors (1).³ However, although great progress has been made in identifying signaling intermediates and some of their functions, we are far from a complete understanding of many of these pathways. The sequencing of the human genome has allowed the identification of different members of various signaling pathways. Indeed, 11.2% of genes whose function can be predicted are directly involved in signal transduction (2). This is, however, an underestimate of the total number of genes involved because 41.7% of the genes in the human genome have unpredicted function, and many genes are important in multiple functions, such as cell attachment and ECM⁴ genes, and are not classified as signal transduction categories. Our increased knowledge of the human genome has far outpaced our ability to understand how these proteins and their pathways interact and function. Despite this, it is clear that the understanding of the human genome and, more importantly the human proteome will have a major impact on medicine and pharmaceutical discovery (3).

One of the most interesting, yet daunting, aspects of signal transduction discovered in the last 5 years is the realization that very disparate pathways can interact at multiple levels—this is often referred to as signal cross-talk. A search of Medline showed that the term "cross-talk" or "cross talk" first appeared in 1991 and has been used in over 3500 articles since then. It has become clear that most pathways are so intricate and complex, having multiple layers of regulation, that a complete understanding of any single pathway will only be accomplished by taking into account its global networks of interactions. It is anticipated that computer modeling programs such as neural networks will play a major role in signal transduction research in the future (4, 5).

The elucidation of growth factor signaling pathways and the observation that these pathways are often altered in human cancer have led to the development of a number of highly specific inhibitors for these pathways (6). These new compounds are often referred to as STIs. This review will discuss the complexity of signal transduction and highlight how new STIs are not only proving useful in the treatment of cancer but are

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⁴ The abbreviations used are: ECM, extracellular matrix; STI, signal transduction inhibitor; ER, estrogen receptor; RTK, receptor tyrosine kinase; IGF, insulin-like growth factor; IGF-IR, IGF-I receptor; EGFR, epidermal growth factor receptor; GPCR, G-protein-coupled receptors; MAPK, mitogen-activated protein kinase; EGF, epidermal growth factor; PDGFR, platelet-derived growth factor receptor; Prl, prolactin; GH, growth hormone; IRS, insulin receptor substrate; IGFBP, IGF-binding protein.

also elucidating novel mechanisms of signal transduction cross-talk.

Cross-Talk between Hormone Receptors and Growth Factors

An area of cross-talk that may have critical importance in breast cancer is interaction between hormone receptors and growth factors (7). The ER is a critical growth regulator in breast cancer and an excellent biological target for breast cancer prevention and treatment (8). Blockade of growth factor signaling represents a new and promising targeted biological therapy in breast cancer (9). Evidence that a RTK termed ErbB2 was amplified in breast cancer and that overexpression conferred a poor prognosis led to the pivotal development of inhibitors of ErbB2 receptor such as trastuzumab, which were successful in preclinical trials and are now used in breast cancer management (10).

Molecular studies have revealed that there are considerable interaction and cross-talk between hormone receptor and RTK signaling pathways (7). For example, the steroid hormone estrogen and the peptide growth factor IGF-I are both potent mitogens for a range of human breast cancer cell lines (11) and are both implicated in the growth and progression of breast cancer (12). Estrogen acts through a nuclear hormone receptor that upon activation increases transcription and expression of hormone-responsive genes (13). On the other hand, IGF-I acts through a transmembrane RTK (12) that signals via a series of phosphorylation events. Although the signal transduction pathways elicited by the two mitogens seem distinct, there appears to be considerable coordination and synergism between the two mitogens. Estrogen can increase IGF signaling, and, conversely, IGF-I can increase estrogen signaling (7). Recent studies have shown that these interactions can occur *in vivo*, with estrogen sensitizing the mammary gland to IGFs (14), and systemic IGF-I treatment of mice causing rapid activation of the ER (15).

Signal Transactivation

The original diagrams of linear signal transduction pathways have now been replaced with diagrams that start to incorporate the intricacies of signaling networks. Whereas many of the signals are transmitted in a linear fashion, there is now evidence that many connections may be made in a multidimensional manner. This type of signaling has recently been called "signal transactivation," and probably one of the best examples occurs within the EGFR pathway (16). The EGFR belongs to a family of tyrosine kinases termed EGFR/ErbB1, HER2/ErbB2/neu, HER3/ErbB3, and HER4/ErbB4 (we will use the term ErbB1-4). The four ErbB receptors can either homodimerize or heterodimerize in response to a number of different ligands (17). Dimerization results in receptor tyrosine phosphorylation that allows for the binding of downstream signaling molecules via Src homology-2 domain interactions. Different combinations of ErbB receptors can bind and activate different subsets of signaling intermediates, thus allowing signal diversification and specificity. Whereas many of these pathways have been extensively mapped and are becoming understood, recent evidence suggests that many other receptors can phosphorylate and activate ErbB receptors (Fig. 1) and that ErbBs may act as a conduit

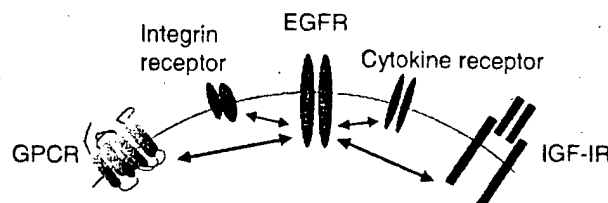


Fig. 1 Signal transactivation of ErbB receptors. ErbB receptors can be directly or indirectly activated by GPCRs, integrin receptors, cytokine receptors, or RTKs.

for multiple other signaling pathways (18).

Cross-Talk between ErbB Receptors and GPCRs

Perhaps the best evidence for signal transactivation of ErbB receptors comes from studies with GPCRs. Whereas GPCRs generally act through second messengers such as diacylglycerol and inositol triphosphate, many ligands for GPCRs (e.g., bombesin) can also activate the MAPK pathway (18). Furthermore, this activation of MAPK has been shown to occur via GPCR activation of ErbB1 (19), and the fact that ErbB1 is involved in bombesin-mediated proliferation (20) further emphasizes this signal transactivation. There appear to be multiple mechanisms whereby GPCRs can activate ErbB1 signaling. First, GPCRs can activate kinases such as Src, which directly phosphorylate ErbB1 (21). Second, GPCRs can also regulate calcium influx. This regulation has been linked to ErbB1 activation and signaling (22), possibly via increased protein kinase C (23) or pyk2 (24) activity. In addition to these direct mechanisms of activation, GPCRs can indirectly cross-talk with ErbB receptors by activating metalloproteinase that cleaves heparin-bound EGF, which can then bind and activate ErbB1 (25).

Cross-Talk between ErbB and Growth Factor Receptors

The ErbB family members are able to associate not only with themselves and other family members, but also with other RTKs. PDGFR is another RTK that has a similar structure to ErbB1 (single molecule that passes through the cell membrane once) and acts in a similar manner to ErbB receptors. ErbB1 and PDGFR can physically interact (26), and EGF can increase phosphorylation and activation of PDGFR (27). In contrast, platelet-derived growth factor has been shown to cause threonine phosphorylation of ErbB1 and inhibit its function (28). IGF-IR is another RTK that, in contrast to ErbB receptors and PDGFRs, always exists as a heterotetramer of two α and two β subunits (29). As such, IGF-IR does not undergo ligand-mediated dimerization but does respond to IGF ligands by activation of intrinsic tyrosine kinase activity. IGF-IR activation can lead to cross-talk with ErbB receptors because recombinant IGF rapidly but indirectly activates ErbB1 and its downstream MAPK signaling pathway (30). The mechanism for cross-talk has not been identified but does not appear to involve c-Src or metalloproteinase-mediated activation of ErbB1, as occurs with GPCR. However, IGF-IR has been shown to physically associate with other ErbB receptors such as ErbB2 (31), an association that is regulated by heregulins and IGF-I. Interestingly, IGF-IR-null cells are not able to respond to EGF (32), suggesting that the interaction between these two receptors may be critical for EGF to mediate its full signaling response. IGF-IR signaling can

induce an EGFR-dependent autocrine loop (33), and it has been shown that EGF can cause phosphorylation and activation of IGF-IR (34).

Cross-Talk between ErbB Receptors and Cytokine Receptors. Cytokines such as Prl and GH act through transmembrane receptors that do not contain intrinsic kinase activity (35) but recruit cytoplasmic intermediates such as Janus tyrosine kinase (specifically JAK2; Ref. 36). GH and Prl are able to increase phosphorylation of ErbB1 both in cell lines and in mice (37). GH activation of JAK2 results in direct phosphorylation of tyrosine 1068 in ErbB1, which is a binding site for Grb2. Prl can also cause JAK2-mediated phosphorylation of ErbB2, and this may account in part for the ligand-independent activation of ErbB2 that is seen in many breast cancers (38). Indeed, blockade of autocrine Prl production in breast cancer cell lines can reduce ErbB2 signaling, and breast tumors that express both ErbB2 and Prl have a poor prognosis (38). Finally another cytokine, interleukin 6, has been shown to increase ErbB2 activation, signaling, and cell migration in breast cancer cell lines (39). The biological relevance of this interaction is currently under investigation.

Cross-Talk between ErbBs, Integrins, and the ECM. The ECM controls cell growth, differentiation, and survival by signaling through integrin receptors (40). Whereas these interactions were initially viewed as "housekeeping" functions, it has become apparent that integrins activate intricate intracellular signaling pathways that equal or exceed the complexity of the RTK pathways (41). Most important, in several systems, ECM and integrins are higher-order controlling elements of other signaling pathways. For instance, binding of primary mammary epithelial cells to laminin is required for both Prl (42) and insulin (43) signaling, which are essential mediators of cellular differentiation. ECM can also control RTK action in a number of cell culture systems (44), and ligation of integrins is essential for RTK-mediated signal transduction (45). Part of this effect may come through direct association of integrin receptors with RTKs and their signaling intermediates. For instance, $\alpha_v\beta_3$ integrin physically associates with PDGFR (46) and also with the cytoplasmic signaling intermediate IRS-1 (47). Furthermore, IRSs can be activated by integrin ligation even in the absence of RTKs (48). $\alpha_6\beta_4$ integrin associates with ErbB2 after EGF stimulation of breast cancer cells, and treatment of cells with an antibody that binds and activates α_6 integrin causes increased association between ErbB2 and $\alpha_6\beta_1$ and promotes cell proliferation and invasion (49). Several of the IGFBPs have RGD sequence that is used in integrin receptor binding. IGFBP-1 can bind $\alpha_5\beta_1$ integrin and increase cell migration (50), but addition of excess recombinant IGFBP-1 can block IGF-I-mediated breast cancer cell motility (51).

STIs

Since the early discovery that a viral oncogene was also a mutated RTK in human cancer, a wealth of literature has implicated RTKs in cancer pathogenesis (6). This has led to the development of a number of inhibitors of RTK signaling pathways. RTK signaling has been blocked by a number of mechanisms *in vitro* including (a) blocking ligand binding to the RTK (using binding proteins such as IGFBP-1 or antibodies that bind

the RTK), (b) inhibiting RTK expression (using antisense oligonucleotides), or (c) inhibiting RTK activity (using kinase-dead and dominant negative RTKs or small molecule inhibitors). Clinical development has occurred with antibodies that block receptor activation and also recently with small molecules that block the tyrosine kinase activity of the RTK (52).

Predicting Response to STIs. Because these STIs have been designed against specific targets and show very high affinity and specificity in *in vitro* systems, it would be logical to expect that expression of the target of a STI may predict the sensitivity of a cell to that STI. For instance, antiestrogens are only effective in breast cancer cells that express ER and have very little or no effect in ER-negative breast cancer cell lines (53). This finding is reproduced in the clinical situation, where ER is an excellent predictive marker for response to antiestrogens (54). However, a greater understanding of the molecular biology of ER action has shown that antiestrogens can have dramatically opposing effects in different tissues due to other modulators of ER action, including coregulators, other growth factor pathways, and other isoforms of ER (55).

With regard to STIs, it has been found that response of breast cancer cells to the selective ErbB1 tyrosine kinase inhibitor ZD1839 (Iressa) does not correlate with ErbB1 status (56, 57). On normal mammary epithelial cells (MCF-10A) that are dependent on EGF for growth, ZD1839 has a growth inhibitory IC_{50} of 0.02 μM , consistent with its *in vitro* IC_{50} value. However, higher concentrations of 0.5–20 μM are needed for growth inhibition in breast cancer cell lines. Possible explanations for this are that (a) ZD1839 is inhibiting other ErbB receptor heterodimers, (b) other pathways are modulating EGFR activation, or (c) alterations in other signal transduction pathways reduce the dependence of these cells on EGF. It is clear that more studies of this nature are needed to identify the markers that predict response to specific STIs. These studies will no doubt involve the use of newly developed phospho-specific antibodies to activated growth factor signaling molecules and the use of gene array technology to measure global gene expression patterns.

STI Blockade of Signal Transactivation. Whereas STIs have shown promise in preclinical settings and are currently in clinical trials, we poorly understand their mechanisms of action. However, it is expected that these STIs will act as novel tools for dissecting and understanding RTK signaling and cross-talk. For example, Prl secreted by breast cancer cells can act in an autocrine manner and cause phosphorylation of ErbB2 via JAK2 (38). We know this in part because blockade of this signal transactivation, using STIs against either Prl receptor, ErbB2, or JAK2, results in reduced ErbB2 phosphorylation and decreased proliferation.

We have shown that blockade of ER using antiestrogens or blockade of IGF-I signaling using a neutralizing binding protein (IGFBP-1) can have dramatic effects on both signaling pathways. Antiestrogens are very effective at eliminating both estrogen and IGF signaling and growth (7). Additionally, whereas IGFBP-1 is effective at inhibiting IGF signaling and growth *in vitro* and *in vivo*, it also blocks IGF-I activation of the ER and inhibits estrogen-mediated growth (58). Other groups have similar findings (59).

Another example of blockade of signal transactivation, this

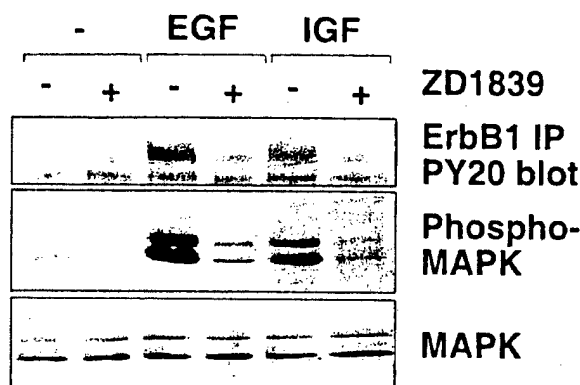


Fig. 2 ZD1839 inhibits IGF-I-mediated phosphorylation of ErbB1. Serum-starved FSK-7 cells were stimulated with EGF or IGF-I and treated with or without ZD1839 (1 μ M). ErbB1 was immunoprecipitated from cell lysates and immunoblotted for phosphotyrosine (top panel). Total cell lysates were immunoblotted for phospho-MAPK (middle panel) or total MAPK (bottom panel). This figure has been reproduced from Ref. 30 with permission.

time between ErbB1 and IGF-IR, has recently been shown using primary mammary epithelial cell cultures (30). In this system, EGF treatment results in phosphorylation of ErbB1 and MAPK, but phosphorylation also occurs when cells are treated with IGF-I (Fig. 2). The ErbB1 tyrosine kinase inhibitor ZD1839 completely blocks EGF signaling, as expected, but it also inhibits IGF-mediated phosphorylation of MAPK. This effect of ZD1839 is not through nonspecific inhibition of IGF-IR activation because phosphorylation of IGF-IR and its downstream signaling intermediate IRS-1 are not affected. The conclusion is that IGF interaction with IGF-IR causes phosphorylation of ErbB1, leading to activation of the MAPK pathway, and that the IGF-mediated activation of MAPK signaling can be blocked by inhibiting its cross-talk with ErbB1.

In primary mammary epithelial cell cultures, EGF and IGF-I are survival factors allowing cells to evade cell death. Interestingly, whereas ZD1839 is often thought of as an inhibitor of ErbB1-mediated cell growth, in primary mammary epithelial cells ZD1839 can block EGF-mediated protection from apoptosis by inhibiting phosphorylation of ErbB1 and activating the proapoptotic protein BAD (49). Importantly, ZD1839 is able to block IGF-I-mediated protection from cell death, substantiating the signaling cross-talk between IGF-I and ErbB1. This observation has important clinical implications for future approaches in which STIs are combined with other apoptosis-inducing agents (60).⁵ More studies are needed to fully understand the complex cross-talk between growth factor signaling pathways in both normal and neoplastic cells. These studies will have to define the mechanisms of action of these STIs and may predict potential toxic side effects and possible mechanisms of resistance.

STI-mediated Down-Regulation of RTKs. Careful characterization of STI action in cell lines has cast light on a

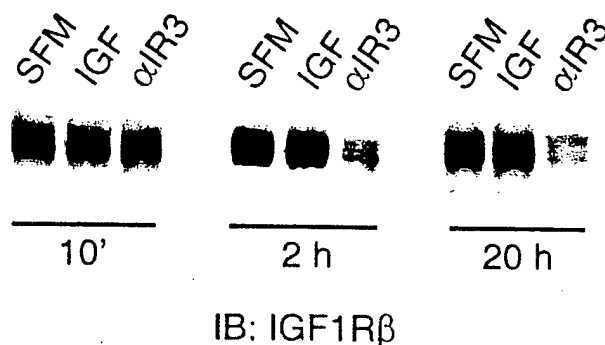


Fig. 3 Antibodies to IGF-IR cause receptor down-regulation. MCF-7 cells were serum starved overnight and then stimulated with IGF-I or α -IR3. Cells were harvested at various time points, and total cell lysates were immunoblotted for IGF-IR (β subunit).

novel mechanism of action that may unfold new avenues for designing alternative strategies to inhibit RTK function. Whereas RTK inhibitors were designed either to block ligand binding or receptor dimerization (e.g., using monoclonal antibodies such as trastuzumab) or to block the tyrosine kinase activity (e.g., by modifying the ATP binding site with CI-1033), it has been found that these strategies also result in down-regulation and proteasome degradation of ErbB2 (61). Whereas it is not unexpected that binding of an antibody at the cell membrane to ErbB2 puts the receptor in a unusual conformation that is recognized as abnormal by the cell and thus marked for degradation, it is unclear why an inhibitor of the tyrosine kinase activity would cause the same effect. Despite this, down-regulation of ErbB2 is clearly a very favorable outcome for blocking ErbB signaling because ErbB2 is a major signaling partner for the other ErbB family members. Interestingly, evidence suggests that ErbB2 may be such a potent signal transducer because after activation and endocytosis it is recycled to the cell surface, rather than being sent for degradation like ErbB1 (62). Blockade of ErbB2 function may disturb this process and thus block its potent activity. Whereas the mechanisms for trastuzumab- and CI-1033-mediated proteasome degradation are unclear, ErbB2 can also be targeted for proteasome degradation by geldanamycin, an ansamycin antibiotic that interferes with ATP binding to the Hsp90 chaperone and results in selective degradation of ErbB receptors (63). Citri *et al.* (61) showed that CI-1033 and geldanamycin act in an additive manner, using a common mechanism of chaperone-mediated degradation. This suggests that a common mechanism for ErbB2 degradation may be directly and specifically targeted.

Interestingly, antibodies that bind IGF-IR and block its signaling capacity also result in receptor down-regulation (Fig. 3). MCF-7 cells were treated with either IGF-I or a commercially available monoclonal antibody (α -IR3) that can block breast cancer cell growth *in vitro* and *in vivo* (64, 65). Neither IGF-I stimulation nor α -IR3 changed IGF-IR levels after 10 min, but after 2 h, α -IR3 caused a significant decrease in IGF-IR levels, whereas IGF-I did not. More studies are needed to define the biochemical mechanism of this reduction in IGF-IR levels, but the data suggest that down-regulation of RTKs may be a common feature after blocking receptor function. It is possible

⁵ <http://stke.sciencemag.org>.

that the antibodies force the RTK into an unnatural conformation that is then recognized by heat shock proteins, resulting in RTK ubiquitination and degradation. These *in vitro* studies simply that the agonist or antagonist biochemical properties of any such receptor binding antibody may not be important as long as binding results in down-regulation of cell surface receptor expression.

Targeted Down-Regulation of Signaling Intermediates.

The realization that STIs not only inhibit RTK action but also cause RTK down-regulation suggests that specifically targeting the mechanism of down-regulation may be a potential therapeutic strategy in breast cancer. Indeed, this is already being tested clinically with geldanamycin, an antibiotic that, as noted above, inhibits ATP binding of the chaperone Hsp90 and causes proteasomal degradation of many intracellular signaling intermediates including steroid receptors and RTKs (63). However, geldanamycin targets a relatively nonspecific form of protein degradation that may prove to be too nonspecific for therapeutic benefit.

Recent studies have shown that signal transduction pathways can initiate very specific targeted proteasomal degradation. Whereas the complete mechanisms are still to be elucidated, the SCF complex seems to be a key player in allowing phosphorylation-targeted ubiquitination of signaling intermediates (66). For instance, cell cycle components must be synthesized and degraded in a rapid and tightly controlled manner to allow cell cycle control. Many of the cyclins, cyclin-dependent kinases, and cyclin-dependent kinase inhibitors undergo rapid proteasomal degradation after phosphorylation on specific residues (67). Inhibitors of the proteasome have been developed and are being used in clinical trials for treatment of a number of cancers (68, 69).

We have investigated the proteasomal degradation of IRS-1, a signaling intermediate that is regulated by hormone receptors and has ominous prognostic significance in breast cancer (70). Cell line studies have shown that, after activation, IRS-1 is ubiquitinated and then degraded by the proteasome (71). Importantly, the signal that mediates this degradation is the phosphatidylinositol 3'-kinase/Akt/mTOR pathway (72, 73), and the signal may actually be direct phosphorylation of IRS-1 on serine/threonine residues by one of these signaling proteins (74, 75). Interestingly, IRS-1 is upstream of the phosphatidylinositol 3'-kinase/Akt/mTOR pathway, and so down-regulation of IRS-1 represents a rapid and potent negative feedback mechanism for shutting off this pathway. Additional studies on the biology of IRS-1 have revealed that its level is hormonally regulated in the normal mammary gland.⁶ In particular, we have shown that IRS-1 proteins decline dramatically when the mammary gland undergoes involution (76). This decrease occurs within 6 h and occurs in the absence of changes in mRNA levels, suggesting that this represents protein turnover or degradation, similar to observations in cell culture.

Blockade of IRS-1 action in breast cancer may be difficult because IRS-1 has no intrinsic kinase activity, and interrupting protein-protein interactions with small molecules is technically

challenging. In contrast, lowering IRS-1 levels by stimulating degradation may be an ideal mechanism for inhibiting IRS-1 action. We are performing *in vitro* and *in vivo* studies to better understand the molecular pathways that are critical for IRS-1 degradation, with the goal of designing small molecules that will enhance IRS-1 degradation. Whereas phosphorylation-directed degradation probably uses common mechanisms for destroying proteins, e.g., the 26S proteasome, we believe that specificity is obtained through the combination of unique phosphorylation motifs and E3 proteins, thus allowing highly specific phosphorylation-targeted proteasome degradation for each signaling intermediate. Perhaps we can harness the power of naturally occurring negative feedback systems to stimulate degradation pathways that will allow the selective degradation of certain signaling intermediates.

Summary

STIs show promise in preclinical studies and are currently in a number of clinical trials. Whereas many of these agents were "rationally designed," we barely understand their mechanisms of action. Part of this is due to our limited understanding of cross-talk among receptor systems and the key pathways necessary for cell growth. For example, trastuzumab has clinical activity only in a minority of patients that overexpress the HER2 target. The reasons for *de novo* resistance are not understood and must be elucidated if we are to optimally use these new strategies. A greater understanding of signaling interactions and networks will be needed to better predict how inhibitors will affect neoplastic cell growth and death, and it is anticipated that careful *in vitro* studies with these specific high-affinity inhibitors will elucidate novel mechanism of signal cross-talk that will then lead to the development of new inhibitors that will block these new interactions. Once identified *in vitro*, these findings can be tested in clinical settings to make rational treatment choices for cancer patients.

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Open Discussion

Dr. Adrian V. Lee: The theory is that the IGF-I activates the IGF receptor, which then transphosphorylates the EGFR and causes EGFR signaling. If you give Iressa (ZD1839), you block EGFR signaling, which shows it's a specific blocker, but it also takes out the IGF signal as well.

Dr. Kent Osborne: Does it take out the IGF receptor or just the IGF downstream signaling?

Dr. Lee: That is a very critical question. It has practically zero effect on IGF receptor or IGF signaling downstream. So this is really proof of IGF receptor transphosphorylation of EGFR. Previous data came from transfection studies, but now in mammary epithelial cells, it's been shown that IGF activates the EGF pathway, and Iressa can wipe that out.

Dr. Carlos Arteaga: But that suggests that that cross-talk still requires the EGFR kinase, and so the activation of the receptor by IGF-I. Is that your interpretation?

Dr. Lee: That depends on whether that receptor is only taking out the kinase or whether it's a down-regulated receptor.

⁶ A. V. Lee and D. L. Hadsell, manuscript in preparation.

These inhibitors also cause down-regulation and destruction of the receptor.

Dr. Arteaga: Iressa doesn't. Just to underscore that these small molecules are not "me too" drugs, we have done similar experiments with OSI-774 and Iressa, and there's really no EGFR or HER2 down-regulation from the cell surface whatsoever. So there is something unique about this inhibitor that is doing that.

Dr. Steven Come: Well, I think now you see why we're anxious to go ahead and put Iressa into a clinical trial. It's looking better and better.

Dr. Arteaga: The Eastern Cooperative Oncology Group Phase II trial of Herceptin plus Iressa in HER2-overexpressing metastatic disease is accruing. The rationale is based on preclinical data indicating that when you block both receptors at the same time, you induce very profound apoptosis in culture, and there is also synergistic activity in xenograft and transgenic models. We have some data using a human mouse mammary tumor virus HER2 transgenic nude mouse from Genentech showing that tumors as big as 2 cm³ disappear with the combination of Herceptin and OSI-774, which is similar to Iressa. With either drug alone, there's little or no effect. So tumor cells may be smart, but they're not that smart. It would be logical that the first compensatory mechanism they use would be receptors of the same network, and that would be the EGFR. That could have been anticipated from the biochemistry of the EGFR/HER2 network.

Dr. Stephen Johnston: If HER2 is really critical and you take out HER2, the tumor cells couldn't get around it. If HER2 is really the prominent dimerization partner, then maybe they have to switch to another network.

Dr. Mitch Dowsett: The data you presented are provocative and also pretty discouraging in terms of applying these agents in the metastatic setting because of these multiple escape pathways.

Dr. Lee: We talked about that at last year's meeting, about whether metastatic disease is the right setting for testing these agents. That's a classic finding with Iressa working really well on normal cells and then having a different IC₅₀ in tumor cells. So maybe that's why these agents should be tested in the neoadjuvant setting. We understand why chemotherapy works in the metastatic setting, because it's completely nonspecific. In targeting a very defined pathway, either we're going to have to find the predictive biomarkers, which again is going to take time, or we have to try it in the adjuvant setting before any data come out.

Dr. Dowsett: The problem with a lot of these agents is a lack of long-term safety data because the metastatic studies are often quite short.

Dr. Kathleen Pritchard: But you have to take them into the adjuvant setting without long-term safety data anyway, so the question always is whether there's enough justification to take that big experiment with lots of patients when you don't know what the data are.

Dr. Come: The best thing by far, at least in this country, would be some sort of inter-SPORE (Specialized Program of Research Excellence) cooperation to do basically what Dr. Dowsett is doing. Once you resolve the institutional review board issues, involve several institutions that have the capacity

to do these studies, in which we decide we're going to get two pathologic specimens on each patient, that we're going to use these biomarkers to make meaningful measurements in that window. So then we'd be able to select what to go forward with in an adjuvant trial.

Dr. Eric Winer: I think it's the institutional review board and the safety issues that impede us.

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SHORT REPORT

Progesterone crosstalks with insulin-like growth factor signaling in breast cancer cells via induction of insulin receptor substrate-2

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Both progesterone and the insulin-like growth factors (IGFs) are critically involved in mammary gland development and also in breast cancer progression. However, how the progesterone and IGF signaling pathways interact with each other to regulate breast cancer cell growth remains unresolved. In this study, we investigated progesterone regulation of IGF signaling components in breast cancer cells. We found that insulin receptor substrate-2 (IRS-2) levels were markedly induced by progesterone and the synthetic progestin R5020 in MCF-7 and other progesterone receptor (PR) positive breast cancer cell lines, whereas IRS-1 and the IGF-I receptor were not induced. The antiprogestin RU486 blocked the R5020 effect on IRS-2 expression. Ectopic expression of either PR-A or PR-B in C4-12 breast cancer cells (estrogen receptor and PR negative) showed that progestin upregulation of IRS-2 was mediated specifically by PR-B. The IRS-2 induction by R5020 occurred via an increase of IRS-2 mRNA levels. Furthermore, progestin treatment prior to IGF-I stimulation resulted in higher tyrosine-phosphorylated IRS-2 levels, increased binding of IRS-2 to Grb-2 and the PI3K regulatory subunit p85, and correspondingly enhanced ERK and Akt activation, as compared with IGF-I-only conditions. Taken together, our data suggest that IRS-2 may play an important role in crosstalk between progesterone and the IGFs in breast cancer cells.

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Keywords: breast cancer; IGFs; IRS-2; phosphorylation; progesterone; R5020

Progesterone is critically involved in the development of the mammary gland and breast cancer, and its effects are mostly mediated by the progesterone receptor (PR) (Graham and Clarke, 1997). The presence of PR in breast tumors is an important predictive indicator of likely responsiveness to endocrine agents (Lapidus *et al.*, 1998). Human PR normally exists in two isoforms, PR-A and PR-B, of 94 and 116 kDa (Kastner *et al.*, 1990), with PR-B containing an additional 164 amino acids at its N terminus. Although the two PR isoforms exhibit similar hormone- and DNA-binding properties, they

display different transcriptional activities and are unequally expressed in different tissues and tumors (Wen *et al.*, 1994; Richer *et al.*, 2002).

Progesterone is proliferative in the normal mammary gland (Graham and Clarke, 1997), but its inhibition of breast cancer cell growth in tissue culture has been well documented (Musgrove *et al.*, 1991; Groshong *et al.*, 1997; Lin *et al.*, 1999). Interestingly, progestins have been found to exert a biphasic regulation of breast cancer cell growth – accelerating cells through the first mitotic cell cycle and then arresting them in G1 of the second cycle. At this stage, the cell-cycle progression machinery is poised to restart, as expression of epidermal growth factor and its receptor is increased by progestins (Musgrove *et al.*, 1991; Groshong *et al.*, 1997). Hence, it is proposed that progestins are inherently neither growth proliferative nor growth inhibitory, but rather sensitize breast cancer cells for growth factor and cytokine signals (Lange *et al.*, 1998).

The insulin-like growth factors (IGFs) are key regulators of cell proliferation, survival, and differentiation (LeRoith, 1996). They play an important role in malignant transformation and invasion (Baserga, 1995). Numerous lines of evidence support a role for the IGFs in breast cancer pathogenesis (Lee and Yee, 1995). The IGF-I receptor (IGF-IR), upon activation by the IGFs, phosphorylates the insulin receptor substrates IRS-1 and IRS-2, which are multisite docking proteins that link multiple downstream signaling pathways by binding to a variety of SH2 domain-containing proteins (Yenush and White, 1997). IRSs are also involved in signaling of insulin, interleukins, interferons, and growth hormone, and are implicated in breast cancer growth (Surmacz and Burgaud, 1995; Rocha *et al.*, 1997; Chang *et al.*, 2002). The IRS network of upstream and downstream signaling may place them in a central position to coordinate multiple signaling pathways. IRS-1 and IRS-2, despite their structural and functional similarities, are not completely interchangeable (Bruning *et al.*, 1997).

Recently, much study has been directed to crosstalk between the IGFs and the estrogen receptor (ER) signaling in breast cancer cells (Dupont and Le Roith, 2001), and IRS-1, IRS-2, and IGF-IR have been shown to be induced by estrogen (Lee *et al.*, 1999). However, how the IGFs interact with progesterone in breast cancer is less well defined. In an attempt to elucidate crosstalk and synergism between progesterone and IGF

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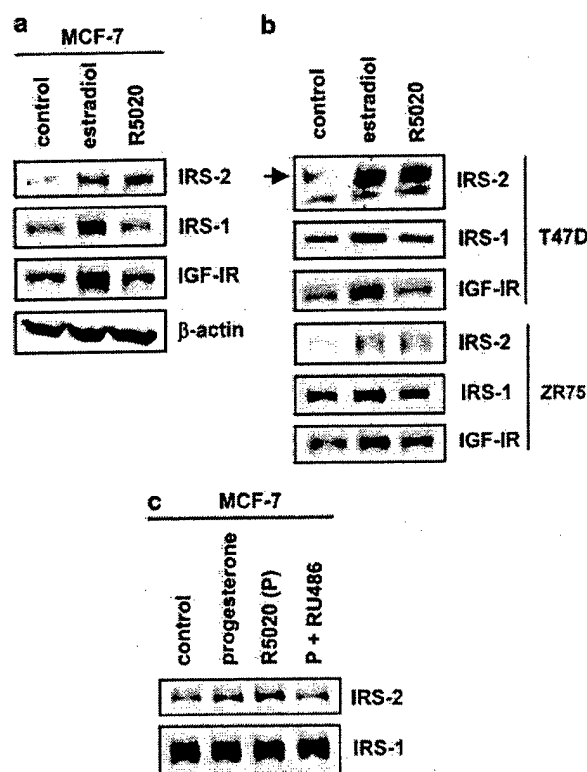


Figure 1 Progesterone induces IRS-2 expression in breast cancer cells. (a) MCF-7 cells were grown as described previously (Lee *et al.*, 1999). Cells were first starved for 16h in serum-free medium (SFM), and then treated for 24h with 10^{-8} M estradiol or 10^{-8} M R5020. Cell lysate proteins (40 μ g) were separated by 8% SDS-PAGE and immunoblotted with antibodies against IRS-1 (Upstate, Lake Placid, NY, USA), IRS-2 (Upstate, Lake Placid, NY, USA), and IGF-IR (Santa Cruz Biotechnology, Santa Cruz, CA, USA). β -actin was used as a loading control. (b) T47D and ZR75 breast cancer cells were also treated as in (a) and subjected to Western blot analysis of IRS-1, IRS-2, and IGF-IR. (c) MCF-7 cells were treated for 24h with 10^{-8} M progesterone, 10^{-8} M R5020, or 10^{-8} M R5020 plus 10^{-6} M RU486. Cell lysates were subjected to Western blot analysis of IRS-1 and IRS-2.

signaling in breast cancer cells, we have now investigated progesterone regulation of the IGF signaling pathway.

As a first step, we treated ER and PR positive (ER+/PR+) MCF-7 cells in serum-free medium with the synthetic progestin R5020, and then tested how expression of IRS-1, IRS-2, and IGF-IR was affected. Immunoblot analysis of total cell lysates demonstrated that a single dose of 10^{-8} M R5020 for 24h remarkably increased IRS-2 levels in MCF-7 cells, while it did not alter the expression of IRS-1 and IGF-IR (Figure 1a). This is in contrast to the effect of estradiol, which upregulates all these proteins. The R5020 effect on IRS-2 was also observed in other ER+/PR+ breast cancer cell lines like T47D and ZR75 (Figure 1b). Similar but slightly weaker induction of IRS-2 also occurred with a single dose of 10^{-8} M progesterone (Figure 1c), probably due to progesterone's much shorter half-life in cell culture than R5020 (Groshong *et al.*, 1997). Moreover, the antiprogestin RU486 blocked the IRS-2 upregulation by R5020 in MCF-7 cells (Figure 1c), suggesting

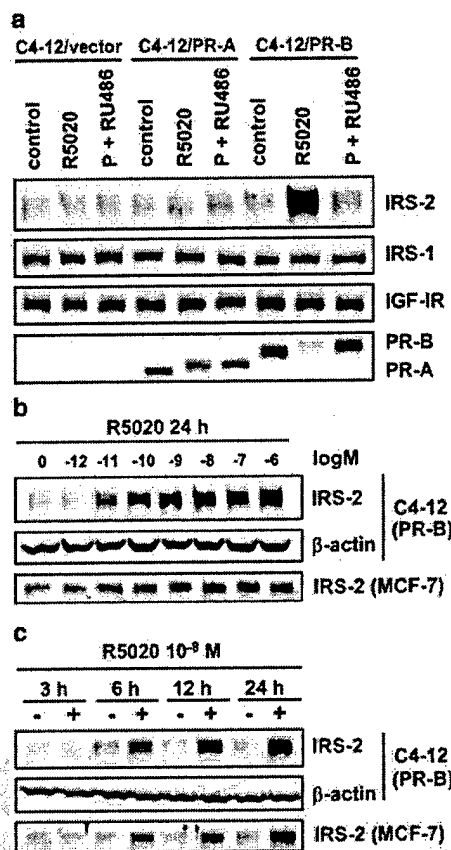


Figure 2 PR-B mediates the progesterone upregulation of IRS-2 in breast cancer cells. PR-A or PR-B cDNA was stably transfected into a specially selected MCF-7 cell sub-line C4-12 which is ER-/PR-. (a) Vector-, PR-A-, and PR-B-transfected C4-12 cells were stimulated for 24h with 10^{-8} M R5020, 10^{-6} M RU486, or both together. Cell lysate proteins (40 μ g) were separated by 8% SDS-PAGE and immunoblotted with antibodies against IRS-1, IRS-2, IGF-IR, and PR (DAKO, Carpinteria, CA, USA). (b) C4-12/PR-B and MCF-7 cells were stimulated for 24h with increasing concentrations of R5020 in a dose response experiment. Cell lysate proteins were separated by 8% SDS-PAGE and immunoblotted with IRS-2 or β -actin antibodies. (c) C4-12/PR-B and MCF-7 cells were stimulated with 10^{-8} M R5020 or vehicle for increasing periods of time in the time course assay. Cell lysates were immunoblotted with IRS-2 or β -actin antibodies.

that, as expected, the IRS-2 induction by progestins is mediated by PR in breast cancer cells.

To better define the role of progesterone and the two PR isoforms on IRS-2 in breast cancer cells, we established the expression of either PR isoform by stably transfecting PR-A or PR-B cDNA into C4-12 cells, a specifically selected MCF-7 cell subline that does not have detectable ER or PR (Oesterreich *et al.*, 2001). In PR-B-transfected C4-12 cells, IRS-2, but not IRS-1 or IGF-IR, was upregulated significantly by R5020 (Figure 2a), while PR-B by itself had no ligand-independent induction of IRS-2 expression. In addition, the antiprogestin RU486 completely blocked the IRS-2 upregulation by R5020 in the C4-12/PR-B cells. As expected, the R5020 effect on IRS-2 was not observed in parental or vector-transfected C4-12 cells. The R5020-

mediated effects were similar in several different C4-12/PR-B clones. In contrast, ectopic expression of PR-A in C4-12 cells did *not* render IRS-2 progestin-inducible (Figure 2a), which re-emphasizes the fact that the two PR isoforms possess distinct gene transcriptional activities and that PR-B is transcriptionally more active (Richer *et al.*, 2002). Thus, our data suggest that it is PR-B that mediates the progestin effect on IRS-2 upregulation. The induction of IRS-2 by R5020 over the untreated control was noticeably stronger in C4-12/PR-B cells than in MCF-7 cells (see Figure 1), perhaps due to the finding that C4-12/PR-B cells have 3–5-fold higher PR-B protein levels than MCF-7 cells. Another explanation may be that the PR-A also present in MCF-7 cells might act as a repressor of PR-B in regulating IRS-2 expression (Vegeto *et al.*, 1993).

To extend the study of progesterone regulation of IRS-2 in C4-12/PR-B cells, we performed a dose response assay using a 24 h stimulation. As shown in Figure 2b, R5020 at concentrations as low as 10^{-11} M dramatically increased IRS-2 levels. Maximal induction of IRS-2 expression occurred at 10^{-9} M R5020 and higher. In a time course experiment using 10^{-8} M R5020, we found that elevated IRS-2 protein levels were visible after 6 h of R5020 treatment and continued to increase throughout the 48 h time period (Figure 2c). Similar dose response and time course results were also observed in MCF-7 cells (Figure 2b and c). Taken together, these data suggest that the induction of IRS-2 is very sensitive to progesterone in PR-B-expressing breast cancer cells.

To assess whether progesterone uses transcriptional mechanisms to modulate IRS-2 levels, we first examined changes of IRS-2 mRNA concentrations in MCF-7 cells treated with R5020. RT-PCR analysis demonstrated that 10^{-8} M R5020 treatment for 3 h significantly increased IRS-2 mRNA levels, while RU486 impaired this IRS-2 mRNA induction by R5020 (Figure 3a). In the earlier time course experiment, IRS-2 protein was barely upregulated by R5020 by the 3 h time point, suggesting that the elevation of IRS-2 mRNA levels occurs prior to that of IRS-2 protein. To confirm that the progestin upregulation of IRS-2 was via transcriptional mechanisms, we preincubated MCF-7 cells with the transcription inhibitor 5,6-dichlorobenzimidazole riboside (DRB), and then stimulated the cells with R5020 in the continual presence of DRB. Not surprisingly, the IRS-2 mRNA upregulation by R5020 was suppressed by the DRB pretreatment (Figure 3a). The result was also confirmed by RNA protection assay (data not shown). In line with this, immunoblotting showed that the IRS-2 protein increase by R5020 was also blocked by the DRB pretreatment (Figure 3b), confirming that induction of IRS-2 mRNA synthesis is a prerequisite for the IRS-2 protein increase by progestins.

Furthermore, when hemagglutinin (HA) epitope-tagged IRS-2 cDNA driven by the CMV promoter was either transiently or stably transfected into MCF-7 and other breast cancer cell lines, R5020 could not upregulate HA-IRS-2 levels in the transfected cells (data not shown), suggesting that the progesterone impact on IRS-2 expression in breast cancer cells does not occur

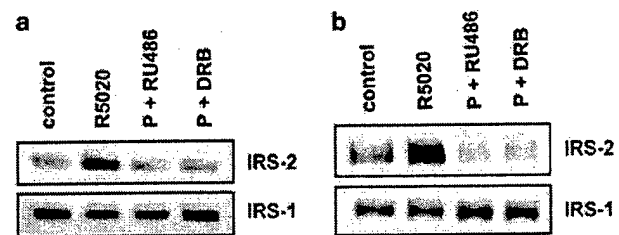


Figure 3 Progesterone induces IRS-2 mRNA levels. (a) MCF-7 cells were stimulated for 3 h with 10^{-8} M R5020, R5020 plus 10^{-6} M RU486, or R5020 in the presence of the transcription inhibitor DRB (50 μ M) after preincubation with DRB for 30 min. Total RNA was then isolated and 100 ng RNA was used in RT-PCR of IRS-1 and IRS-2, which was conducted using Superscript II reverse transcriptase (Invitrogen) and gene-specific primers (IRS-1: 5'-GCTGCTAGCATTTGCAGGCCTAC-3', 5'-CTGACGGTCCTCTGGCTGCT-3'; IRS-2: 5'-TTGACGTCGGGCGTGAAGAGGCT-3', 5'-CTCTTTCACGATGGTGGCCTCC-3'). The PCR was performed at an annealing temperature of 60°C and was subjected to 30 cycles. Products were revealed by ethidium bromide staining under UV after agarose gel electrophoresis. (b) MCF-7 cells were stimulated for 24 h with 10^{-8} M R5020, R5020 plus 10^{-6} M RU486, or R5020 in the presence of DRB after preincubation with DRB for 30 min. Cell lysate proteins were separated by 8% SDS-PAGE and immunoblotted with IRS-2 or IRS-1 antibodies

via alteration of protein translation or stability, but rather relies on the original IRS-2 promoter context.

In summary, these data suggest that the progesterone effect on IRS-2 in breast cancer cells is mediated by transcriptional mechanisms. Surprisingly, IRS-2 was not among the 94 progesterone-regulated genes identified in a recent study using T47D breast cancer cells and cDNA microarrays (Richer *et al.*, 2002). One explanation for the apparent discrepancy between this and our studies might be that IRS-2 mRNA is in low abundance in T47D cells and thus may not have been detected in the microarray analysis.

Since the IGFs utilize IRSs to transduce their signals in cells, we next examined how progestin's alteration of the IRS-2 levels might sensitize breast cancer cells to IGF signals. We preincubated MCF-7 cells with 10^{-8} M R5020 for 24 h and then stimulated the cells with 100 ng/ml IGF-I for 10 min. Immunoprecipitation with IRS-2 antibodies followed by immunoblotting demonstrated that R5020 pretreatment increased IRS-2 levels and consequently, the levels of tyrosine-phosphorylated IRS-2 induced by IGF-I. IRS-2 mobility was also shifted upward due to phosphorylation (Figure 4a). R5020 by itself could not activate IRS-2. An important feature of the IRS-mediated response to IGF-I is docking of Grb-2 and the PI3K regulatory subunit p85, which leads to activation of the Ras/ERK and PI3K/Akt signaling pathways. As shown in Figure 4a, R5020 enhanced the IGF-I-triggered association of p85 and Grb-2 with tyrosine-phosphorylated IRS-2, most probably due to upregulation of activated IRS-2 levels, since total cellular p85 and Grb-2 levels were not changed by R5020 (Figure 4a). In contrast, the association of p85 and Grb-2 to IRS-1 (not induced by progestins) after IGF-I stimulation was not enhanced by R5020. Moreover, upregulation of IRS-2 did not

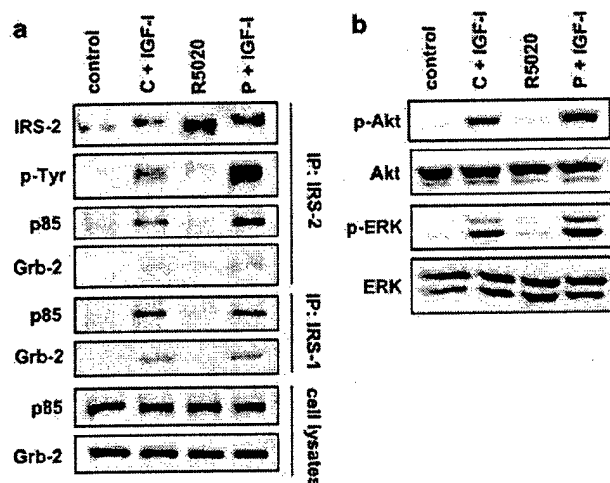


Figure 4 Progesterone enhances IGF-I signaling mediated by IRS-2. (a) MCF-7 cells were first treated for 24 h with vehicle or 10^{-8} M R5020, and then stimulated with 100 ng/ml IGF-I for 10 min. Cell lysates (500 μ g) were immunoprecipitated with IRS-2 antibodies at a 1:100 dilution. Aliquots of the immunoprecipitates were subjected to immunoblot analysis with the p85 (Upstate) and Grb-2 (Upstate) antibodies. Tyrosine phosphorylation of IRS-2 was detected with the specific phosphotyrosine antibody PY20 (Transduction Laboratories, Lexington, KY, USA). As a comparison, the association of p85 and Grb-2 with IRS-1 was also examined using immunoprecipitation with IRS-1 antibodies. (b) MCF-7 cells were first treated for 24 h with vehicle or 10^{-8} M R5020, and then stimulated with 100 ng/ml IGF-I for 10 min. Cell lysates were separated by 8% SDS-PAGE and immunoblotted with antibodies against total Akt and ERK (Cell Signaling, Beverly, MA, USA) and their corresponding phosphorylation-specific antibodies (Akt: Ser 473; ERK: Thr202/Tyr204).

impede the association of p85 and Grb-2 to IRS-1 upon IGF-I stimulation.

Since elevated IRS-2 levels were associated with increased p85 and Grb-2 binding, we measured subsequent Akt and ERK activation, using their phospho-specific antibodies. Immunoblot analysis revealed that activation of ERK and Akt triggered by IGF-I was higher after R5020 pretreatment, even though levels of total ERK and Akt were unaffected (Figure 4b). Nor did R5020 by itself cause detectable phosphorylation of ERK and Akt. We consistently obtained similar results, that is, R5020 treatment led to 50–100% increase of IGF-I-stimulated phospho-Akt and phospho-ERK. It may be that we did not observe a more dramatic increase of Akt and ERK activation under the R5020 condition because the basal amount of IRS-1 is much higher than that of IRS-2, and IRS-1 is the predominant signaling molecule activated by IGF-I in MCF-7 as well as other ER+ breast cancer cells (Jackson *et al.*, 1998). Despite a considerable increase in expression after R5020 treatment, IRS-2 is still unable to fully overcome the dominant role of IRS-1 in IGF signal transduction.

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It is also noted that estradiol seems to have a more prominent effect than progestins on enhancing IGF-I-induced activation of ERK in MCF-7 cells (Lee *et al.*, 1999; Dupont and Le Roith, 2001), which is probably due to estrogen's induction of IRS-1 and IGF-IR, as well as IRS-2, whereas progesterone only induces IRS-2. Taken together, these data suggest that R5020 potentiates IGF-I signaling in breast cancer cells through upregulation of IRS-2. Given that IRS-2 has been shown to interact with and be activated by other pathways such as integrins (Shaw, 2001), it is possible that progesterone also sensitizes breast cancer cells to IRS-2-mediated integrin signaling.

Previously, IRS-2 was identified as a progesterone response gene in PR-transfected HeLa cells, using differential display (Vassen *et al.*, 1999). So far, only a few PR-regulated genes have been characterized in breast cancer. This study represents the first attempt to characterize progesterone regulation of IRS signaling in breast cancer cells. Since IRSs are involved in effects of the IGFs, insulin, growth hormones, interleukins, and interferons, increased IRS-2 in cells may contribute to the promotion of cell proliferation, survival, and motility by these mitogens. Recently, the Women's Health Initiative, after a study of more than 16 000 women, concluded definitively that combined estrogen and progestin hormone therapy increases the risk of invasive breast cancer by 25% as compared to women taking placebo (Rossouw *et al.*, 2002). In another study (Schäirer *et al.*, 2000), it was found that the risk of developing breast cancer was higher in women on estrogen and progestin therapy than in women who used estrogen therapy alone, which was confirmed by Ross *et al.* (2000). These findings raised the question of why the addition of progestin to hormone replacement therapy would markedly enhance the risk of breast cancer relative to estrogen use alone. This enigma might be partly explained by the notion that progestins prime cells for extracellular signals through upregulation of pivotal cell signaling components. Our data presented here imply that progesterone may sensitize cells to signaling pathways that involve IRS-2 function. Future studies will be needed to determine the importance of the progesterone regulation of IRS-2 in breast cancer initiation and progression as well as normal mammary epithelial cell growth.

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Estrogen-mediated downregulation of E-cadherin in breast cancer cells

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Abstract

E-cadherin is an important mediator of cell-cell interactions, and has been shown to play a crucial role in breast tumor suppression. Its inactivation occurs through instability at its chromosomal locus and mutations, but also through epigenetic mechanisms such as promoter hypermethylation and transcriptional silencing. We show here that the potent mitogen estrogen causes downregulation of E-cadherin levels in both normal and tumorigenic breast epithelial cells, and that this downregulation is reversed by antiestrogens. The reduction in E-cadherin levels is via a decrease in promoter activity and subsequent mRNA levels. Chromatin immunoprecipitation assays revealed that estrogen receptor and corepressors were bound to the E-cadherin promoter, and that overexpression of corepressors such as SAFB resulted in enhanced repression of E-cadherin. We propose that estrogen-mediated downregulation of E-cadherin is a novel way of reducing E-cadherin levels in ER-positive breast cancer.

Introduction

E-cadherin is a glycoprotein with a large extracellular domain, a transmembrane domain, and a short intracellular domain which interacts with catenins. Recently there has been increased interest in E-cadherin as a mediator of cell-cell adhesions, and as a tumor suppressor gene (reviewed in (1). E-cadherin maps to a region on chromosome 16q22.1 which shows frequent loss of heterozygosity (LOH) in sporadic breast cancer. While LOH-concurrent mutations have been found on the second allele in lobular breast tumors, very few mutations have been found in ductal breast carcinoma (1). This finding suggests that other epigenetic mechanisms such as hypermethylation and transcriptional silencing might play a role in E-cadherin inactivation. Indeed, methylation of the E-cadherin promoter has been shown to correlate with loss of E-cadherin expression in breast cancer cell lines and primary ductal and lobular breast cancers (2, 3). However, the decrease of E-cadherin expression is not only attributable to hypermethylation since treatment with 5-aza-2'-deoxycytidine fails to reactivate E-cadherin expression (4). Increased internalization and degradation via Hakai overexpression (5) as well as overexpression of transcriptional repressors known to inactivate the E-cadherin promoter such as Snail (6, 7) and SIP1/ZEB2 (8) are alternative mechanisms for its inactivation in breast tumors. Indeed, a recent study by Fujita et al. (9) showed that aberrant expression of Snail in estrogen receptor α (called ER throughout the manuscript)-negative breast cancer cell lines results in loss of E-cadherin expression.

In this report we show that, in ER-positive breast cancer cell lines, the steroid hormone estradiol downregulates levels of E-cadherin protein and mRNA. This downregulation can be reversed by antiestrogens used in the clinical management of breast cancer. We have evidence that the observed downregulation depends not only on estrogen receptor (ER) but also on the crosstalk with other pathways since it can only be observed when cells are kept in serum-containing media but not in

serum-free media. The downregulation involves direct recruitment of ER and ER corepressors at the most proximal E-cadherin promoter. This study is intriguing since a) few estrogen-*down*regulated genes have been described to date, b) it provides evidence for a direct involvement of ER-corepressors (such as SAFB) in estrogen-mediated downregulation of genes, and finally c) it presents a novel mechanism for E-cadherin inactivation in breast tumors.

Material and Methods

Cells, transfections, and CAT assay

Human breast cancer cells (MCF-7L, MDA-MB-231, MDA-MB-435, T47D, ZR75) were maintained in IMEM supplemented with 10% FBS (Hyclone, Logan, Utah), 200 I.U./ml penicillin, 200 µg/ml streptomycin, and 6 ng/ml insulin. The immortalized human breast epithelial MCF10A cells were kept in DMEM/F12 media supplemented with 5% horse serum, 10 ng/ml insulin, 20 ng/ml EGF, 100 ng/ml cholera toxin, 2mM glutamine, 500 ng/ml hydrocortisone, 200 I.U./ml penicillin, 200 µg/ml streptomycin. To express ER in these cells, 5×10^5 cells were plated in a 6 cm dish, and transfected with 1 µg of HA-tagged ER (ER-HA-pcDNA3.1) for 5 hrs. To generate the ER-HA-pcDNA3.1 plasmid the ER-HA cDNA was released from pcDNA3.1/V5/His-TOPO (10) with EcoRI, and ligated into pcDNA3.1. After 24 hrs recovery, the cells were placed in phenol red free IMEM containing 5% charcoal-stripped serum (CSS) (Hyclone, Logan, UT) for a further 24 hrs and then stimulated with 10^{-8} M estradiol for another 24 hrs before being lysed in 5%SDS for subsequent immunoblotting (see below). The experiments were performed three independent times.

For reporter assays, cells were transiently transfected using Fugene (Roche, Indianapolis, IN) following the manufacturer's protocol. One day before transfection, cells were plated at 2×10^5 in 6-well plates. For estradiol (E2) induction experiments, the cells were treated either in serum-free medium (SFM) which consisted of phenol-red-free IMEM + 10mM HEPES pH7.4 + 1 µg/ml fibronectin (Invitrogen, Carlsbad, CA) + trace elements (Biosources, Worcester, MA) + 1 µg/ml transferrin (Invitrogen) or in phenol red free IMEM containing 5% charcoal-stripped serum (CSS) (Hyclone, Logan, UT). Most estradiol induction experiments were performed at least twice, the experiments in MCF-7L cells were performed at least three times each. For the promoter analysis 1 µg E-cadherin promoter (-178 / +92 bp) CAT construct (11) was transfected and twenty-four hours later

the medium was replaced with IMEM + 5% CSS containing the appropriate ligand. Forty-eight hours later cells were washed twice with PBS and CAT activity was measured using the CAT ELISA from Roche (Indianapolis, IN). Values were corrected for protein concentrations, and are presented as relative CAT activity. For transient transfections, triplicate samples were measured in each experiment. The data are presented as the average $\pm$ SEM, and are representative of three independent experiments.

SAFB1 overexpression in MCF-7 cells

In order to transiently overexpress SAFB1, sub-confluent MCF-7L cells plated in a 10 cm dish were transfected overnight with 2 μ g SAFB1-HA-pcDNA1 (12, 13) using Fugene (Roche, Indianapolis, IN) following the manufacturer's protocol. The next morning, media was changed, and 24 hrs later the cells were lysed in 5%SDS. The generation of MCF-7 cells expressing and inducible HA-SAFB1 has recently been described elsewhere (13).

Western and northern blot analysis.

Proteins were resolved on 8% SDS-PAGE, and electrophoretically transferred to nitrocellulose. The membrane was blocked in PBS/0.1% Tween 20 (PBST) + 5% milk for one hour at room temperature. Antibodies to E-cadherin (Santa Cruz, Santa Cruz, CA), insulin-receptor substrate 1 (IRS-1) (Upstate Biotechnology Inc., Waltham, MA), HA (Covance), SAFB (Upstate Biotechnology Inc.), progesterone receptor (PgR) (Santa Cruz), ER (Vector, Novacastra, Burlingame, CA), and β -actin (Sigma, St. Louis, MO) were diluted at 1:1,000, 1:1,000, 1:1,000, 1:500, and 1:5,000, respectively, in PBST + 5% milk. After washing 6x5 min with PBST, the membrane was incubated with HRP-linked anti-mouse IgG (Amersham Pharmacia Biotech, Piscataway, NJ) at 1:1000 in PBST

+ 5% milk and washed 6x5 mins, and the signal was developed using enhanced chemiluminescence according to the manufacturers instructions (Pierce, Rockford, IL).

For northern blots, 10 μ g total RNA were separated by electrophoresis in a 1.2% formaldehyde-agarose gel. RNA isolation (CsCl gradient) and northern blotting was performed following standard procedures. The human E-cadherin probe for hybridization was purchased from Research Genetics (Clone ID 2286727), and fold changes in RNA levels were determined using software on the Molecular Imager FX (Biorad). The presented northern blot is representative of two independent experiments.

Chromatin Immunoprecipitation (ChIP) assays

3×10^6 MCF-7 cells were plated in 15 cm dishes in phenol red-free DMEM supplemented with 10%CSS. After 36 hrs, the cells were transfected with 250 ng plasmid DNA (mouse E-cadherin promoter, pCAD-Ecad-3000) (11, 14) using Lipofectamine, and following the manufacturer's protocol. The next morning, the cells were treated with vehicle only, 10^{-8} M estradiol, or 10^{-6} M 4-hydroxytamoxifen for 45 mins. After washing the cells with PBS (3x), they were crosslinked with 1% formaldehyde for 10 min at room temperature. Cells were rinsed with ice-cold PBS (3x), collected into 100 mM Tris-HCl (pH 9.4), 10 mM DTT, incubated for 15 min at 30°C, and centrifuged for 5 min at 2000 g. Subsequently, cells were washed sequentially with 1 ml of ice-cold PBS, buffer I (0.25% Triton X-100, 10 mM EDTA, 0.5 mM EGTA, 10 mM HEPES, pH 6.5) and buffer II (200 mM NaCl, 1 mM EDTA, 0.5 mM EGTA, 10 mM HEPES, pH 6.5). Cells were then resuspended in 0.3 ml of lysis buffer (1% SDS, 10 mM EDTA, 50 mM Tris-HCl, pH 8.1, protease inhibitors), sonicated three times for 10 s each followed by centrifugation for 10 min. Supernatants were diluted in 1% Triton X-100, 2 mM EDTA, 150 mM NaCl, 20 mM Tris-HCl, pH 8.1, and 250 μ g were precleared with 2 μ g sheared salmon sperm DNA and protein G-sepharose (40 μ l of 50% slurry) for 2 hr at 4°C.

Immunoprecipitation was performed overnight at 4°C with specific antibodies (2 µg protein/each). After immunoprecipitation, 50 µl protein G-Sepharose and 2 µg of salmon sperm DNA were added and the incubation was continued for 1 hr. Precipitates were washed sequentially each in TSE I (0.1% SDS, 1% Triton X-100, 2 mM EDTA, 20 mM Tris-HCl, pH 8.1, 150 mM NaCl), TSE II (0.1% SDS, 1% Triton X-100, 2 mM EDTA, 20 mM Tris-HCl, pH 8.1, 500 mM NaCl) and buffer III (0.25 M LiCl, 1% NP-40, 1% deoxycholate, 1 mM EDTA, 10 mM Tris-HCl, pH 8.1). Precipitates were then washed with TE buffer (3x), extracted with 1% SDS, 0.1 M NaHCO₃, and heated at 65°C for at least 6 hr to reverse the formaldehyde cross-linking. After DNA purification (QIAquick Spin Kit), the proximal E-cadherin promoter (-234 to +62bp) was amplified using the following primer set: forward primer 5'-TCCTTTGTA ACTCCATGTCTCCCGT-3' and reverse primer 5'-CGGGCAGGAGTCTAGCAGAAG-3'. The PCR of the pS2 promoter was performed as previously described (15). The antibodies for the Chip assays were purchased from Santa Cruz (ER, NCoR, rabbit IgG) and UBI (SAFB). The experiments were performed three times.

Animals, treatments, and tissues

Animal care was in accordance with institutional guidelines. Four to six week old female ovariectomized Balb/c athymic nude mice (Harlan Sprague-Dawley Inc., Madison, WI) supplemented with estrogen pellets (0.25 mg, Innovative Research, Rockville, MD) were inoculated subcutaneously with 5 X 10⁶ MCF-7 cells as previously described (16). When tumors reached a diameter of 7-9 mm (2-4 weeks), the animals were randomly allocated to continue estrogen treatment or to estrogen withdrawal by removal of the estrogen pellets. In this tumor model estrogen stimulates tumor growth and estrogen withdrawal results in tumor growth inhibition. Tumors were removed during estrogen treatment (E2 tumor group) and at 3 weeks after estrogen withdrawal treatment (-E2 tumor group) and kept at -70°C for later analyses. Tumor powders were manually homogenized in a 5% SDS solution.

After boiling and microcentrifugation, clear supernatants were collected, protein concentration was determined by the bicinchoninic acid method (Pierce, Rockford, IL.), and western blotting was performed as described above. This *in vivo* experiment was performed once.

Results

Estrogen downregulates E-cadherin protein levels in MCF-7 cells *in vitro* and *in vivo*. To analyze whether E-cadherin protein levels are regulated by estradiol, we placed ER-positive MCF-7L cells in medium containing charcoal stripped serum (CSS) and treated them with estradiol at a concentration ranging from 10^{-12} to 10^{-7} M for 24 hrs. Immunoblot analysis was performed using E-cadherin-specific antibodies, as well as β -actin antibodies for a loading control. As shown in Fig. 1A, estradiol treatment resulted in a dose-dependent decrease of E-cadherin. Interestingly, we never observed this estradiol-mediated downregulation of E-cadherin in the absence of serum, i.e. when the cells were kept in serum-free medium (SFM) (Fig. 1B). This result suggests that the estradiol-mediated downregulation of E-cadherin depends on other factors present in the serum, possibly "crosstalking" with ER.

Next we asked whether the downregulation could be reversed by antiestrogens. Therefore, we treated MCF-7 cells with estradiol only, with the non-steroidal antiestrogen 4-hydroxytamoxifen (TAM) only, or with a combinations of both (Fig. 1C). As expected, the addition of antiestrogen to estradiol-treated cells blocked E-cadherin downregulation, reflecting the inactivation of ER activity. We observed the same effect with the pure steroidal antiestrogen ICI 182,780 (data not shown). As a control we immunoblotted for the estrogen-inducible proteins IRS-1 and PgR, levels of which were both potently increased by estrogen. Additionally, confirmation of ER function was shown by the downregulation of ER (Fig. 1C) which is known to be degraded by estradiol and stabilized by TAM (17).

Interestingly, treatment with TAM alone increased levels of E-cadherin protein over baseline, reflecting the inhibitory effects of the residual estradiol in the charcoal-stripped serum (CSS). Indeed,

CSS can contain up to 10^{-11} M estradiol (data sheet from manufacturer). Further supporting this is our finding that increasing amounts of CSS resulted in a dose-dependent decrease of E-cadherin levels (Fig. 1D). We believe that this is due to residual estradiol as a) it can be reversed by TAM (and Fig. 1C and data not shown), and b) treatment with a range of growth factors such as epidermal growth factor (EGF), insulin-like growth factor-I (IGF-I), or heregulin in SFM did not lower in E-cadherin levels (data not shown).

Next we asked whether this estrogen-mediated downregulation of E-cadherin in MCF-7 cells in tissue culture could also be observed when MCF-7 cells were grown as xenografts in athymic mice. Therefore, athymic ovariectomized mice were injected with MCF-7 cells, and tumors were allowed to grow in the presence of estradiol (+E2). When the tumor reached 7-9 mm (2-4 weeks), the pellet was removed (-E2), and the tumors stopped growing as previously reported (16). We analyzed E-cadherin expression estrogen-stimulated (n=4) and estrogen-deprived tumors (n=4). As shown in Fig. 1E, the E-cadherin levels were significantly lower in the +E2 group as compared to the -E2 group (Fig. 1E). Thus, estrogen treatment results in downregulation of E-cadherin protein not only in MCF-7 cells grown in tissue culture, but also *in vivo*. While numerous (direct and indirect) factors can influence gene expression in an *in vivo* situation, we believe that these data, together with our *in vitro* experiments, strongly support an estrogen-mediated downregulation of E-cadherin.

Estrogen downregulates E-cadherin levels in both normal and transformed breast epithelial cell lines. To exclude that the effect seen in MCF-7 was cell line-specific, we measured E-cadherin levels in two ER-negative breast cancer cell lines (MDA-MB231 and MDA-MB-435) and two other ER-positive breast cancer cell lines (T47D and ZR75). There was no expression in the ER-negative cell lines (data not shown), a finding that was recently described and analyzed by Fujita et al

(9). However, in the ER-positive cell lines, we detected estrogen-mediated downregulation of E-cadherin, which was reversed by antiestrogen treatment (Fig. 2A).

We next asked whether this repression is specific for transformed cells, or whether it could also be found in cell lines with less severe genetic abnormalities. Since normal or immortalized breast epithelial cell lines do not express ER, we transiently transfected immortal but non-transformed MCF10A cells with ER to study E-cadherin regulation (Fig. 2B). Transient transfection of these cells with a GFP-tagged ER construct revealed transfection of up to 10% of cells (data not shown). No ER was detected in vector alone transfected cells. Stimulation of ER-transfected cells with estradiol resulted in an increase in expression of the estrogen-regulated gene IRS-1, and a minor decrease in ER levels. This confirmed that the ER was active in these cells. Furthermore, these cells also showed a decrease in E-cadherin levels. In other experiments the transient expression of ER alone (i.e. not simulated with estradiol) also caused a downregulation, which is presumably due to residual estradiol action, however decreased E-cadherin levels were always noted after estradiol stimulation. Therefore, estrogen-mediated repression of E-cadherin levels can be detected in both immortalized breast epithelial and cancer cell lines.

Estrogen treatment results in decreased E-cadherin RNA levels and promoter activity. In order to determine whether estrogen decreased E-cadherin at the mRNA level, we treated MCF-7L cells with estradiol or a combination of estradiol and antiestrogen for 6 hrs and then isolated total RNA. Northern blot analysis was performed using an E-cadherin probe, with GAPDH as a loading control. As shown in Fig. 3A, E-cadherin RNA levels were decreased 2 fold in the presence of estradiol. Substantiating the estrogen regulation at the RNA level is the finding that TAM treatment blocked the estradiol-mediated downregulation, and when given alone caused an increase of the E-cadherin levels.

This finding encouraged us to analyze whether the E-cadherin promoter might be estradiol-regulated in transient reporter assays. A number of studies have previously been conducted using a series of promoter constructs. We decided to use the most proximal E-cadherin mouse promoter construct (-178 / +92 bp) which was previously shown to have strong activity in epithelial cells (11), however it does not contain any classical estrogen response elements. This construct was transfected into MCF-7 cells, cells were treated with estradiol (10^{-9} M and 10^{-8} M), or with estradiol (10^{-8} M) and TAM (10^{-6} M) for 24 hrs, and CAT activity was measured. As shown in Fig. 3B, promoter activity was decreased in the presence of estradiol, and again this repression was relieved by the addition of TAM. Thus, E-cadherin is an estrogen-downregulated gene, and the downregulation is mediated through the proximal promoter region.

ER corepressor proteins are recruited to the E-cadherin promoter, and corepressor overexpression results in enhanced E-cadherin repression. To analyze whether the decreased promoter activity was the direct result of recruitment of ER and corepressors, we performed ChIP assays. Therefore, we transfected MCF-7 cells with a plasmid containing the E-cadherin fragment known to be repressed upon estrogen treatment. The cells were then treated with estradiol for 45 mins, and recruitment of ER and corepressors (N-CoR and SAFB1) was analyzed by ChIP (Fig. 3C) as described in Material and Methods. We also examined the recruitment of ER and corepressors at the pS2 promoter. As described previously (15), estrogen treatment resulted in strong recruitment of ER to the pS2 promoter. We repeatedly detected a low level of ER binding in the absence of estradiol, possibly reflecting low levels of estradiol in the stripped serum. Corepressors (N-CoR and SAFB1) showed constitutive binding to the pS2 promoter, which was released upon estradiol treatment. In stark contrast to results obtained with the pS2 promoter, the E-cadherin promoter showed strong

constitutive binding of ER in the absence of estrogen. Estradiol treatment of cells with estrogen for 45 mins did not result in release of corepressors, as observed for the pS2 promoter (Fig 3B).

To directly test whether the corepressors may modulate E-cadherin levels, we transiently overexpressed the ER corepressor SAFB1, and also generated stable tetracycline-inducible SAFB1 overexpressing breast cancer cell lines (Fig. 3D). Transient overexpression of SAFB1 in MCF-7L cells resulted in stronger estrogen-mediated repression of E-cadherin, as shown in Fig. 3D, top panels. We confirmed this data in MCF-7 RTA ("tet on") cells which consistently showed 3-fold overexpression of SAFB1 upon doxycycline treatment (Fig. 3D, bottom panels). Thus, ER corepressor levels are a major determinants in the regulation of E-cadherin expression.

Discussion

In this study we have shown that E-cadherin is an estrogen-downregulated gene in human breast cancer cells. A number of studies in various tissues and cell lines have previously described connections between steroid receptor pathways and E-cadherin. Habermann et al have shown that developmental exposure to estrogen was associated with changes in epithelial cell adhesion and decreased E-cadherin levels in the adult rat prostate (18, 19). Estradiol treatment resulted in a decrease of N-cadherin (20) and increase of E-cadherin (21) levels in the mouse ovary. In breast cancer cells, estrogen treatment was reported to induce cytoskeletal rearrangements (22) including delocalization of E-cadherin (23). Interestingly, tamoxifen restored the function of E-cadherin in an MCF-7 subline with a functionally inactive cell surface E-cadherin (MCF-7/6); however this was an extremely rapid event (30 mins) and did not require protein synthesis (24). Thus, while a number of reports have addressed a potential effect of estrogen on E-cadherin, our study represents the first attempt to investigate estrogen-mediated downregulation of E-cadherin as a novel mechanism of its inactivation in human breast cancer.

In contrast to the well characterized estrogen *induction* of a number of genes, estrogen-mediated *downregulation* of genes has only recently gained more attention. In a SAGE study using estrogen-treated MCF-7 cells, an equal number of induced and repressed genes were identified (25). A recent study has shown that transcription of the nuclear coactivator src-3/AIB1 (amplified in breast cancer 1) is repressed by estradiol (26). We believe that estrogen-mediated repression of genes is a critical regulatory pathway in ER-positive cells, and that deregulation of this repression in breast cancer may have dramatic effects such as promotion of transformation and metastasis. The observation that a number of genes, including E-cadherin, have been described as both induced and repressed might be explained by our finding that the repression can only be seen in the presence of serum but not in serum-free medium, suggesting that crosstalk with other pathways is necessary. For

instance, kinases can regulate ER and coregulators (for a recent review see 27), and the absence or presence of a specific kinase might determine whether the gene becomes induced or repressed upon estrogen treatment. We hypothesize that there are three distinct set of genes; one which can only be induced by estrogen, one which can only be repressed, and one which can be induced or repressed depending on cellular context. Experiments are ongoing to test this hypothesis.

As for the mechanism of estrogen downregulation of gene expression, our ChIP analyses suggest an involvement of ER corepressors and ER in a complex at the E-cadherin promoter. Several previous studies have suggested that a balance of coactivators and corepressors may modulate ER action, and may be deregulated in breast cancer and in particular in endocrine resistance. Our data support this hypothesis by showing that an excess of SAFB1 enhances the ability of ER to downregulate E-cadherin levels. Thus, our data so far implicate that a critical balance between ER and ER cofactors is determinant in the regulation of E-cadherin levels in breast cancer. However, a potential caveat of our experiments is the use of transiently transfected promoter. Studies analyzing the recruitment of both coactivators and corepressors to the endogenous E-cadherin promoter in mouse and human cell lines are ongoing.

The connection between ER and E-cadherin is obviously very complex. ER-negative cell lines are often (but not always as shown in Fig. 2B in MCF10A cells) E-cadherin-negative, and this has recently been analyzed in more detail: The repressor MTA3 is an estrogen-regulated gene, which regulates Snail expression, which in turn represses E-cadherin (9). Thus, in the absence of ER (and MTA3), aberrant expression of Snail results in loss of expression of E-cadherin. Additionally, as shown here, in ER-positive tumors, estrogen can result in downregulation of E-cadherin expression. How do these finding relate to known clinical data? Not surprisingly, there is little consensus between numerous studies addressing the relationship between hormone receptor status and E-cadherin expression. There have been studies showing positive (28), negative (29), or no correlation (30)

between E-cadherin and ER levels. This might, at least in part, be explained by the analysis of "mixed samples", ER-positive *and* ER-negative samples. As clearly shown by Fujita et al (Fig. 7 in reference 9), ER-positive and ER-negative tumors display very different and even opposite correlations between ER, E-cadherin, snail, and MTA3. We would like to propose that this, at least in part, results from the estrogen-mediated downregulation of E-cadherin in ER-positive samples. More clinical studies analyzing either only ER-positive or only ER-negative cases are needed to support these models. Potentially, our findings could have clinical impact, since restoration of E-cadherin expression might be an important result of antiestrogen therapy, and thus selective estrogen receptor modulator (SERMs) should be tested regarding their effects on E-cadherin expression.

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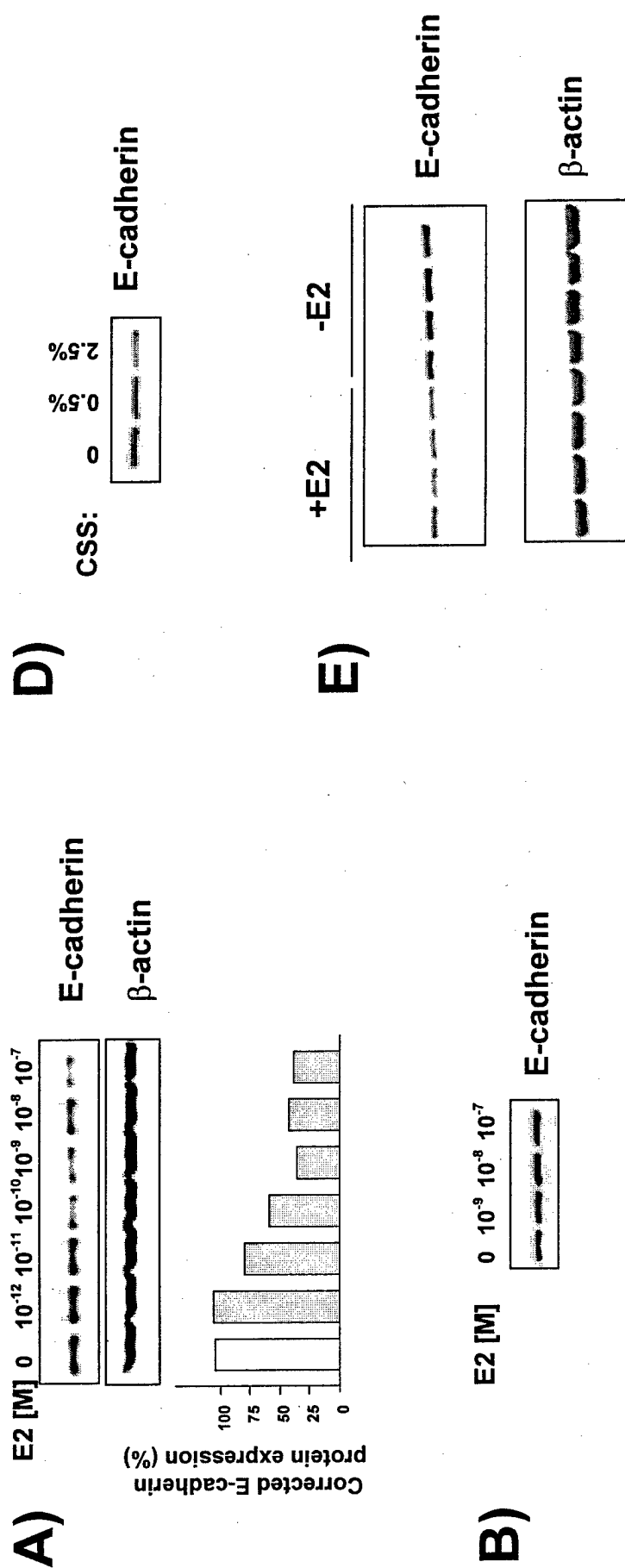
Figure Legends

1) **Effect of estradiol and antiestrogen on E-cadherin protein levels in MCF-7 breast cancer cells grown in tissue culture and *in vivo* (xenograft).** Proteins were extracted from MCF-7L cells and immunoblotting was performed using specific antibodies to E-cadherin (A through E), β -actin (A and E), IRS-1 (C), PgR (C), and ER (C). After ECL, images were captured using a CCD video camera (Fluorimager 8000, Alpha Innotech) and pixel intensity values were obtained using this machine. Values for E-cadherin were corrected for loading by dividing the E-cadherin pixel intensity by the β -actin pixel intensity. A) Cells were grown for 48hrs in 5%CSS, and then treated with increasing concentrations of estradiol (E2) for 24 hrs. B) Cells were grown in SFM, and then treated with estradiol for 24 hrs as indicated. C) Cells were grown for 48hrs in 5%CSS, and then treated with estradiol (E2) and/or 4-hydroxytamoxifen (TAM) for 24 hrs as indicated. D) Cells were grown for 24 hrs in medium supplemented with increasing amounts of charcoal-stripped serum (CSS). E) Flash frozen MCF-7 xenografts, grown in the presence and absence of estradiol, were pulverized, and SDS extracts analyzed by immunoblotting.

2) **Estrogen regulation of E-cadherin in immortalized and breast cancer cells.** A) ER-positive breast cancer cell lines T47D and ZR75 were incubated in 5%CSS for 48 hrs, and subsequently treated for 24 hrs with vehicle only, estradiol (10^{-8} M) (E2), or estradiol (10^{-8} M) (E2) and Tamoxifen (10^{-6} M) in 5%CSS. β -actin was used as a loading control. B) Immortalized MCF10A cells were transfected with ER-HA-pcDNA1, and treated with estradiol (10^{-8} M) (+E2) for 24 hrs. Cells transfected with empty vector only (pcDNA) served as negative control. SDS extracts were prepared, and immunoblotted as indicated.

3) **Effect of estradiol on transcriptional regulation of E-cadherin.** A) MCF-7L cells were treated with estradiol and Tamoxifen as indicated for 10 hrs. Following Northern blot analysis,

data were quantified using a phosphorimager, and corrected for GAPDH. B) MCF-7L cells were transiently transfected with the E-cadherin promoter construct (-178/+92), treated for 24 hrs as indicated, and CAT activity was measured. C) For the Chromatin immunoprecipitation analysis (ChIP), MCF-7 cells were transfected with the estrogen-responsive E-cadherin promoter. The next day, cells were treated for 45 min with vehicle only or 10^{-8} M estradiol (E2), crosslinked, and subjected to immunoprecipitation and PCR as described in Material and Methods. D) Top panels: MCF-7L cells were transiently transfected with vector only, or SAFB1pcDNAI, and treated with estradiol (E2) for 24hrs. SDS extracts were immunoblotted as indicated. E-cadherin levels were quantified as described in Figure legend Bottom panels: MCF-7 cells that express tet-inducible SAFB1 (13) were treated with doxycycline for 48hrs, and overexpression was confirmed by immunoblotting with HA and SAFB antibodies. Subsequently, cells were pretreated with doxycycline for 48 hrs, followed by treatment with vehicle only, 10^{-8} M estradiol (E2), or 10^{-8} M estradiol and 10^{-6} M Tamoxifen. E-cadherin levels were quantified as described in Figure legend 1.



A)

B)

T47D

MCF-10A

ZR75

