

AWARD NUMBER DAMD17-94-J-4372

TITLE: Splicing Variants Of Estrogen Receptor in Breast Cancer

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REPORT DATE: October 1998

TYPE OF REPORT: Annual

PREPARED FOR: U.S. Army Medical Research and Materiel Command
Fort Detrick, Maryland 21702-5012

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REPORT DOCUMENTATION PAGE			Form Approved OMB No. 0704-0188	
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1. AGENCY USE ONLY (Leave blank)		2. REPORT DATE October 1998		3. REPORT TYPE AND DATES COVERED Annual (30 Sep 97 - 29 Sep 98)
4. TITLE AND SUBTITLE Splicing Variants of Estrogen Receptor in Breast Cancer			5. FUNDING NUMBERS DAMD17-94-J-4372	
6. AUTHOR(S) Richard J. Miksicek, Ph.D.				
7. PERFORMING ORGANIZATION NAME(S) AND ADDRESS(ES) Research Foundation of SUNY Stoney Brook, New York 11794			8. PERFORMING ORGANIZATION REPORT NUMBER	
9. SPONSORING / MONITORING AGENCY NAME(S) AND ADDRESS(ES) U.S. Army Medical Research and Materiel Command Fort Detrick, Maryland 21702-5012			10. SPONSORING / MONITORING AGENCY REPORT NUMBER	
11. SUPPLEMENTARY NOTES				
12a. DISTRIBUTION / AVAILABILITY STATEMENT Approved for Public Release; Distribution Unlimited			12b. DISTRIBUTION CODE	
13. ABSTRACT (Maximum 200 words) Progress reported for year 4 of this award includes: 1) an analysis of ER- α mRNA variants in two cell lines (TG-1 and TG-3c) from the MCF10AT series (a model for preneoplastic breast disease), 2) PCR analysis of ER- α mRNA in M13 SV1 and R ₂ N ₁ cells (SV40 immortalized normal human breast epithelial lines developed as a model for breast stem cells), and 3) continued characterization of selected ER- α splicing variants, focusing on non-canonical estrogen response elements (EREs). The findings extend our work to include two new model systems for premalignant breast disease. In both models, a diverse array of splicing variants are seen at the RNA level, but the major variants differ compared with the MCF-7 system. We continue to investigate the significance of these findings by analyzing the behavior of transfected reporter plasmids in the TG-1, TG-3c, and M13 cell lines. Our analysis of the ability of ER- α splicing variants to modulate gene expression via non-classical (ERE-independent) pathways has also progressed. Data from transfection studies exploring the behavior of selected splicing variants on four reporter constructs that lack consensus EREs are summarized. A variety of behaviors are observed, including reporters that are activated primarily by ERAE3, primarily by ERAE5, or by both. These studies provide the first convincing evidence that ER- α variants are able to mediate positive regulation of gene expression on a subset of genes that contain non-canonical hormone response elements. They provide further evidence that ER- α splicing variants can contribute both to positive and to negative regulation of transcription, suggesting that their impact on the growth, differentiation, and neoplastic transformation of the breast deserves continued study.				
14. SUBJECT TERMS Breast Cancer			15. NUMBER OF PAGES 65	
			16. PRICE CODE	
17. SECURITY CLASSIFICATION OF REPORT Unclassified	18. SECURITY CLASSIFICATION OF THIS PAGE Unclassified	19. SECURITY CLASSIFICATION OF ABSTRACT Unclassified	20. LIMITATION OF ABSTRACT Unlimited	

FOREWORD

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Richard J. M. Smith 6/11/99
PI - Signature Date

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INTRODUCTION

Title: Splicing Variants of the Estrogen Receptor in Breast Cancer
 ID No.: DAMD-1794-J-4372
 PI: Richard J. Miksicek
 Period: 10/01/97 through 09/30/98

Summary of Administrative Matters

This USAMRDC Breast Cancer Research Award was made to Richard J. Miksicek, who currently holds an appointment as Assistant Professor of Physiology and Member of the Cancer Center at Michigan State University (MSU). This report summarizes the fourth year of this award, through 09/30/98. At the time this grant was awarded, Dr. Miksicek was on the faculty at the State University of New York (SUNY) at Stony Brook. During the first year of this award, the P.I. accepted a new position (effective 07/01/95) in the Department of Physiology at MSU. At that time, permission was requested from the US Army MRMCC through the awardee institution (The Research Foundation of SUNY) to effectively change the site of performance of this project from SUNY @ Stony Brook to MSU by establishing a research subcontract between these institutions. This research subcontract stipulated that Dr. Sandra Haslam (Professor of Physiology and Director of the MSU Breast Cancer Program) be named as Principal Investigator for the MSU subgrant with Dr. Miksicek continuing to serve as P.I. on the primary award to SUNY @ Stony Brook. In addition, Dr. Miksicek has been acting as Principal Co-Investigator at MSU with primary responsibility for the conduct of research and grant administration. This subcontract was accepted by both institutions on 03/28/96 to become effective retroactively to 07/01/95. Predictably, progress on this project was substantially delayed between 07/01/95 and 03/28/96 pending negotiation of the research subcontract and release of research funds at MSU. During 1996, the investigator's laboratory was re-established at MSU and the following research staff were recruited to resume work on this project. For the current reporting period (10/01/97 through 9/30/98):

Key Personnel:

<u>Name</u>	<u>Degree</u>	<u>Role</u>	<u>Effort</u>	<u>Period of Service</u>
MIKSICEK, Richard	Ph.D.	PI (SUNY) & Co-PI (MSU)	25%	09/94-present
ANKRAPP, David	Ph.D.	Postdoctoral Research Fellow	100%	07/96-09/98
BOLLIG, Aliccia	B.S.	Graduate Research Asst.	100%	10/95-present
MORRISON, Mary	M.S.	Research Asst.	15%	02/96-03/98

Dr. Miksicek received partial summer salary from this award for the period 6/98-8/98. Dr. Ankrapp and Ms. Bollig drew full salary support from this award during the reporting period. Ms. Morrison was supported primarily from a non-overlapping award (DAMD1794-J-4411), but she provided significant technical support to this project (until her retirement in 03/98), in the form of laboratory management, cell culture, media preparation, antibody preparation, DNA sequencing, and technical assistance. In addition, this award provided supplemental salary during year 4 for a part-time minority work study student, John Hicks. During 09/98, the PI requested a one year no-cost extension through SUNY at Stony Brook, the recipient of the primary award, in order to make up for time lost in moving this project from Stony Brook to MSU. Work planned for completion during this extension period will be largely limited to the remainder of Task 2b, involving functional analysis of the transcriptional stimulatory activity of ER- α splicing variants on non-classically regulated genes that contain estrogen-responsive AP-1 motifs.

Scope of the Project

Human breast tumors and tumor-derived cell lines contain a mixed population of estrogen receptor- α (ER- α) messenger RNAs (mRNAs), representing both correctly and aberrantly processed transcripts (1-3). The aberrant ER- α mRNAs are predicted to give rise to structurally altered receptor molecules that are likely to interfere with the normal estrogen response pathway present in breast tumor cells. Early reports speculated that these variants may provide a molecular explanation for the loss of estrogen responsiveness or the acquisition of resistance to tamoxifen and other estrogen antagonists (4,5), thereby reducing the effectiveness of hormonal adjuvant therapy of breast cancer. We received this award to undertake a detailed analysis of splicing variants of ER- α mRNA in selected human breast tumor specimens and to characterize the functional activity of these variants in transfected cells. During the course of this project, we have also attempted to refine techniques and develop reagents (both molecular and immunological) to enable further investigation of the clinical significance of these ER- α splicing variants.

The approach being used in this project involves amplification of complementary DNAs (cDNAs) using the polymerase chain reaction (PCR), followed by sequence analysis of the resulting clones. In parallel, plasmid vectors have been constructed to enable expression and functional characterization of selected ER- α splicing variants in both transiently and stably transfected cells. The original statement of work for this project included the following specific tasks:

Task 1, Identification of ER mRNA variants in breast tissue (months 1-24):

- a. Preparation of oligonucleotide primers for the analysis of ER mRNA splicing variants and optimization of PCR amplification conditions.
- b. PCR amplification of ER cDNAs prepared from tamoxifen-resistant tumors.
- c. PCR amplification of Progesterone Receptor cDNAs prepared from tamoxifen-resistant tumors.
- d. PCR amplification of ER cDNAs prepared from normal human breast tissue.

Task 2, Functional analysis of ER mRNA splicing variants (months 18-48):

- a. Construction of ER expression plasmids harboring variant ER cDNAs.
- b. Analysis of the transcriptional stimulatory activity or inhibitory activity of ER splicing variants by transient transfection.
- c. Production and characterization of cell lines that stably express the "constitutive" ERAE5 variant.

Work during the current reporting period involved primarily Tasks 1.d. and 2.b. For several reasons, the decision was made to substitute the M13 SV1 and MCF10A derivative cell lines as proxies for normal human breast tissue in Task 1.d.

EXPERIMENTAL METHODS

Cell lines and cell culture.

MCF10A/TG-1 and TG-3c cells, obtained from the Karmanos Cancer Institute (Detroit, MI), were cultured in a 1:1 mixture of Hams-F12:DMEM media containing 5% horse serum. M13 SV1 and M13 R₂N₁ cells, obtained from C.C. Chang (Dept of Pediatrics, MSU), were cultured as described in MSU media containing 10% fetal bovine serum. HeLa cells were cultured as described in previous annual reports in DMEM containing 10% calf serum. In addition, all cell lines were supplemented with 5 mM HEPES (pH 7.4), 100 units/ml penicillin, 100 µg/ml streptomycin, and 2 mM glutamine. Experiments involving DNA transfection, RNA extraction, and PCR analysis utilized cells that were subcultured fewer than 25 passages from receipt.

PCR analysis of ER-α mRNA splicing variants in premalignant breast epithelial cell lines.

Standard conditions were employed for PCR amplification of cDNA sequences using AmpliTaq DNA polymerase (GIBCO/BRL) and a Stratagene thermocycler. Synthetic primers used for the current experiments have been described in previous reports. Reactions typically involved 35-40 cycles of amplification, beginning with 30 seconds of denaturation at 94° C, followed by a 60 second annealing step (56-66° C) and 60 to 300 seconds of elongation at 74° C, depending on the length of the interval to be amplified. Annealing temperatures were carefully selected for each primer pair and were held as stringent as possible to optimize for the specificity and efficiency of amplification. Total RNA (for use in RT/PCR experiments) was prepared using Trisolve reagent (GIBCO/BRL) according to the manufacturer's instructions. Single-stranded cDNAs were synthesized using MLV reverse transcriptase from 10 µg aliquots of total RNA, priming variously with oligo(dT)₁₅ or a lower strand ER-α specific primer. In general, amplification reactions began with the cDNA equivalent of 1 µg of total RNA. No consistent differences in PCR yield or product profile were noticed comparing cDNAs made with oligo(dT) or with an ER-specific RT primer. Products of PCR reactions were routinely cloned using InVitrogen's pCR2-TOP kit according to manufacturer's instructions. When the goal was to perform a clonal analysis of the products of key PCR experiments, representative cDNA libraries were established by picking individual bacterial transformants into 96 well microtitre plates containing LB medium, incubating overnight at 37° C, and freezing at -70° C after the addition of glycerol to 10%. Individual transformants were picked, grown up, and used for miniprep DNA isolation. Plasmid DNA was subjected to a battery of restriction enzyme digests and, where appropriate, DNA sequence analysis.

Transient transfection analysis and reporter constructs.

Transcriptional activity of receptor variants was assessed by measuring their effect on the activity of chloramphenicol acetyltransferase (CAT) or luciferase (Luc) reporter genes expressed in HeLa cells. For transient transfection experiments, we used the calcium phosphate co-precipitation technique, as detailed in previous reports. Plasmids expressing wild type or variant ER-α cDNAs were transfected into recipient cells along with one of a variety of estrogen-responsive reporter plasmids (see below). Typically, 1.5 X 10⁶ cells were plated one day prior to transfection in 60 mm dishes and were treated with 0.5 µg of receptor expression plasmid and 10 µg of reporter plasmid. Total input DNA was normalized using an empty pCMV-4 vector, which also served as a negative control. Transfected cells were cultured for 48 hours in DMEM containing 5% charcoal-treated calf serum, in the absence and presence of 5 nM estradiol or 20 nM phorbol 12-myristate 13-acetate (PMA). For each experiment, CAT and Luc activities (corrected for protein concentration) were normalized to the basal level of expression seen for untreated pCMV-4 control transfections. The estrogen-responsive reporter plasmids used for these experiments included pERE-TK-CAT (6), pOvalb-Cat obtained from M. Sanders (7), pAP-1₃TK-CAT kindly provided

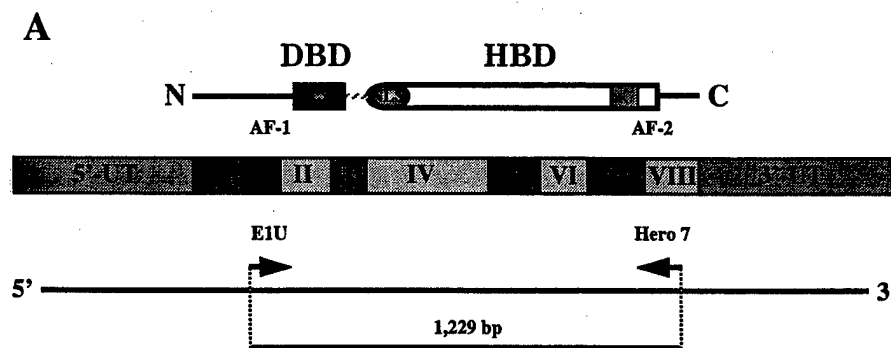
by L. McCabe (Dept. of Physiology, MSU), Coll73-Luc received from P. Kushner (8), and pIGF(1630)-Luc and pIGF(926)-Luc obtained from P. Rotwein (9).

RESULTS

Clonal analysis of variant ER- α transcripts in MCF10AT derivatives, TG-1 and TG-3c cells.

Following an approach previously described for the semiquantitative analysis of ER- α splicing variants in MCF-7 cells (see year 3 technical report), ER- α mRNA transcripts were similarly characterized in derivatives of the MCF10AT cell line, TG-1 and TG-3c. MCF10A cells represent a spontaneously immortalized (but non-tumorigenic) human mammary epithelial cell line established at the Karmanos Cancer Center (Detroit, MI) from a woman with benign fibrocystic breast disease (10). This woman remains in good health and is cancer-free. These cells were stably transfected with T24-HaRas to give rise to the MCF10AT cell line. When carried as (subcutaneous) xenografts in nude mice, MCF10AT cells give rise to histologically heterogeneous lesions with components that closely resemble human atypical hyperplasia, ductal carcinoma *in situ*, and invasive adenocarcinoma (11). As such, MCF10AT cells appear to represent a useful model for preneoplastic human breast disease whose progression can be followed in nude mice xenografts. The TG-1 and TG-3c sublines represent subcultures from first and third cycle of serial xenografts re-established from lesions that histologically resembled squamous carcinoma and carcinoma *in situ*, respectively. Like the parental MCF10AT cells, TG-1 and TG-3c cells also give rise to highly heterogeneous preneoplastic lesions in nude mice, including atypical hyperplasia. However, they appear to progress towards DCIS and invasive carcinoma with shorter latency and higher frequency than the MCF10AT line (12).

While the parental MCF10A cell line expresses such low levels of ER- α as to be essentially ER-negative, the Ras-transformed MCF10AT cells, as well as their xenograft derivatives TG-1 and TG-3c, are demonstrably positive with respect to expression of ER- α mRNA (11,12). Additionally, there is evidence that TG-3c cells are estrogen-responsive based on their increased cloning efficiency and larger colony size when cultured in soft agar in the presence of estradiol (11,12) and based on their more rapid progression to a neoplastic state when xenografted into animals receiving an estradiol implant (12). For these reasons, it was felt that a more detailed analysis of ER- α mRNA transcripts in TG-1 and TG-3c cells was justified. To do so, an RT/PCR approach was taken, followed by an extensive clonal analysis of the ER- α amplification products. As depicted in Fig. 1A, the PCR primers chosen for this analysis were targeted to exons I and VIII to permit a thorough analysis of the complete profile of known ER- α splicing variants. Fig. 1B shows that the PCR amplification products from both TG-1 and TG-3c cells are heterogeneous in size, and include full-length transcripts (1,229 bp) as well as discrete products shorter in size.



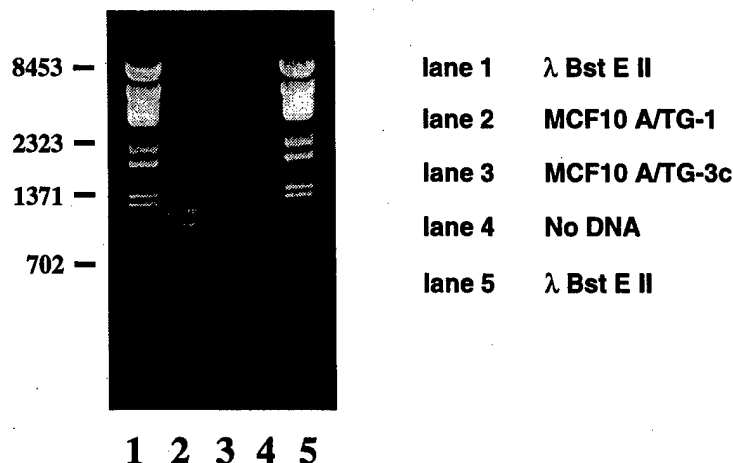
B

Fig. 1. RT/PCR amplification of ER α mRNAs present in MCF10A/TG-1 and TG-3c cells: A) design of the amplification experiment showing the locations of PCR primers, B) EtBr-stained agarose gel showing the size distribution of PCR products.

Products from these TG-1 and TG-3c amplification reactions were cloned without further purification into the pCR2-TOP cloning vector (InVitrogen, Inc.) and were analyzed as previously described for MCF-7 cDNA clones (see year 3 annual technical report). Approximately 100 white (insert-containing) colonies were picked for each cell line to enable characterization of their inserts and to confirm their identity as authentic ER- α cDNA clones. Clones were assigned using a battery of restriction digests and cDNAs representative of each insert size class were sequenced to confirm that they were correctly assigned. Data from this analysis are summarized in Fig. 2. While the profile of ER- α splicing variants that we observe in both TG-1 and TG-3c cells is reminiscent of the extensive transcript heterogeneity that we previously reported for the MCF-7 cell line (see year 3 annual technical report), two significant differences can be noted. In MCF-7 cells, correctly processed ER- α mRNA (hereafter referred to as wild type receptor, or wt ER- α) was easily the most abundant transcript observed, representing nearly 50% of the clones analyzed. In contrast, in both TG-1 and TG-3c cells, wt ER- α cDNAs were equaled or exceeded in abundance by four discrete splicing variants (ER Δ E2, ER Δ E3, ER Δ E4, & ER Δ E7). Additionally, clones isolated from TG-1 and TG-3c cells included only "simple" exon-skipped variants, although 15-20% of these variants harbored the loss of more than a single exon. A much more complex situation was observed in MCF-7 cells where approximately 10% of all the clones analyzed contained internal deletions that failed to mapped to known exon boundaries and therefore appeared to arise from the use of cryptic splice donor or acceptor sites (see year 3 annual technical report). Such cryptic splice products were not observed in either TG-1 or TG-3c cells. Our results confirm that both MCF10A/TG-1 and TG-3c cells appear to be ER- α positive and to express, at a fairly significant level, a wide array of splicing variants in addition to wt ER- α mRNA. Corroboration of these results at the protein level is underway and will involve immunoblot analysis using a battery of ER- α specific antibodies with non-overlapping epitopes. It is uncertain, however, if analysis at the protein level will give a clear picture due to the heterogeneity of protein variants predicted to occur based on the complexity of RNA variants that we observe.

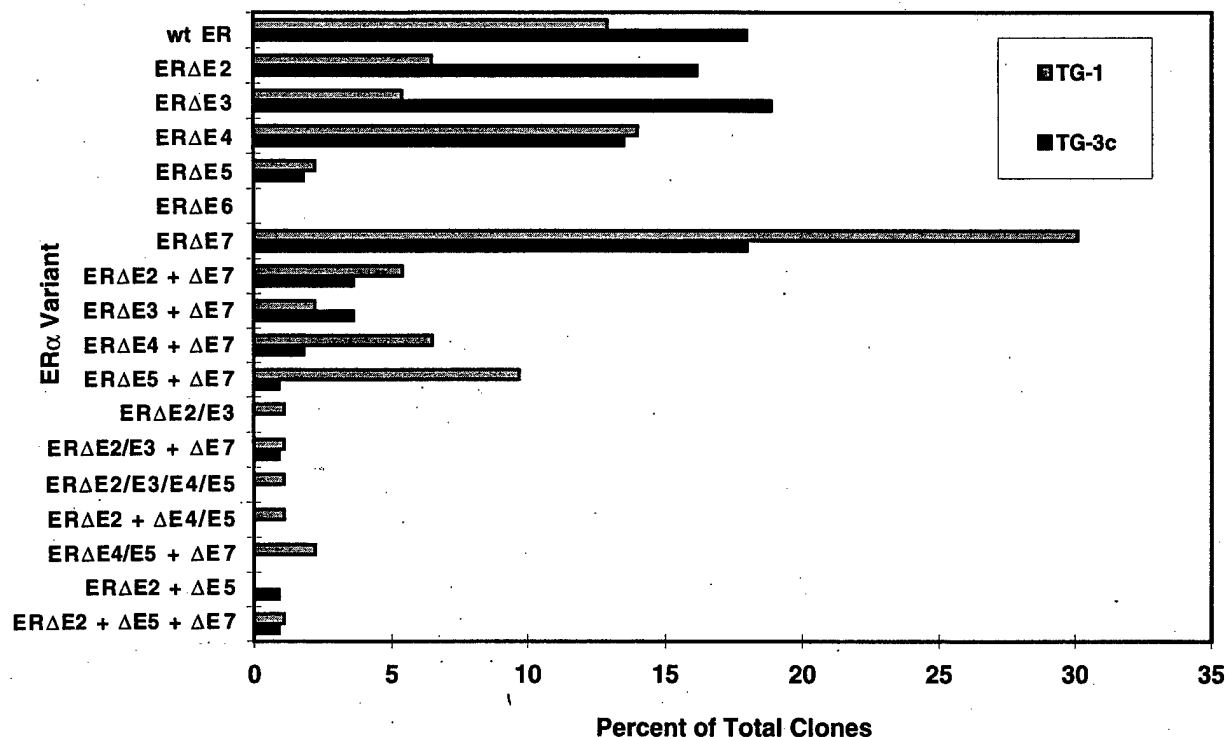


Fig. 2. Quantitative summary of the ER α cDNA clones from MCF10A/TG-1 and TG-3c cells. Clones were isolated from the PCR amplification experiment shown in Fig. 1B and characterized by restriction analysis and DNA sequencing. The numbers depicted indicate the percentage of total clones from the analyzed pool that were represented by each individual ER α splicing variant. A total of 111 ER α cDNAs were characterized for the TG-1 cell line and 93 cDNAs were characterized from TG-3c cells.

Analysis of variant ER- α transcripts in M13 SV1 cells.

As an additional model for ER- α expression in cells derived from the normal human breast, we chose to examine several cell lines developed in the laboratory of C.C. Chang (Dept. of Pediatrics, MSU). These cells originated from a reduction mammoplasty and represent a cell population (referred to as Type I cells) that display luminal and stem cell characteristics (13). When grown in Matrigel together with differentiated Type II breast epithelial cells, Type I cells form organoids that assemble into branching ducts that are capped by structures resembling terminal endbuds. Type I cells were immortalized by treatment with SV40 virus to give rise to a series of clones including M13/SV1, which are immortal but non-tumorigenic in nude mice (Fig. 3). The immortal cells were subsequently X-Ray irradiated and transformed with cErbB/Neu, giving rise to the tumorigenic M13/R₂N₁ cell line. Cells from this series express keratin 18, but not keratin 14 or α 6 integrin. Based on immunoblot and preliminary RT/PCR analysis both M13/SV1 and M13/R₂N₁ cells were shown to be ER-positive, but were reported to express a size variant of ER- α (14). For this reason, we chose to perform additional PCR analysis of ER- α transcripts in this cell line.

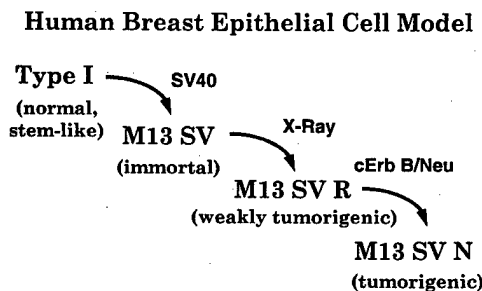


Fig. 3. Origin of M13 SV1 and M13 R2N1 breast epithelial cells

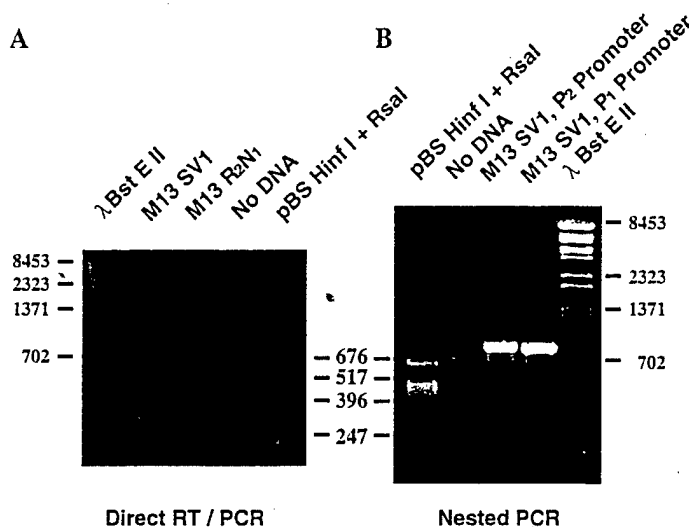


Fig. 4. Example of an ER α PCR experiment in M13/SV1 and M13/R2N1 cells, showing the heterogeneity in ER α transcript sizes encompassing exons 1 through 5. The panel on the left represents a direct RT/PCR experiment, while the panel on the right is from a nested PCR experiment using promoter-specific primers for the first round of PCR.

PCR amplification was performed as described above for MCF10A/TG-1 and TG-3c cells, using a variety of ER- α primer pairs. An example of one such experiment is given in Fig. 4, representing amplification of an 848 bp interval between exons 1 and 5. The majority of product corresponds to a band of the expected size, with a number of less intense bands smaller in size. The heterogeneity of PCR products is very reminiscent of what we observe in other ER-positive cell lines, such as MCF-7, and is consistent with species including ER Δ E2 (657 bp), ER Δ E3 (731 bp), ER Δ E4 (513 bp), and ER Δ E2/E3 (540 bp). Equivalent results were obtained with primer pairs encompassing the entire protein coding region (data not shown). As shown by a nested PCR experiment in which an initial round of amplification used P₁ or P₂-specific primers (from the 5'-untranslated regions) paired with an exon 8 lower stranded primer followed by reamplification with the exon 1/exon 5 primer pair, ER- α transcripts present in the M13 SV1 cell line originate from both the proximal (P₁) and distal (P₂) promoters. These promoters give rise to mRNAs with alternative 5'-untranslated exons that are spliced onto the body of the ER- α protein coding region. Due to the similarity between the pattern of ER- α transcripts in M13/SV1 and M13/R₂N₁ cells with what we previously observed in MCF-7 and MCF10A/TG-1 and TG-3c cells, further cloning and characterization of these PCR products was not performed. Our RT/PCR analysis of ER- α mRNA in cells of the M13 series therefore confirm previous conclusions regarding their ER-positive status, but failed to detect the presence of a predominant ER- α size variant as suggested by Kang, et al. (14). Rather, like other ER-positive cell lines, these cells appear to express predominantly wt ER- α along with a heterogeneous population of smaller ER- α variants.

Characterization of the functional activity of ER splicing variants on "non-classical" estrogen responsive promoters.

We have previously reported that, while the ER Δ E5 splice variant may display modest transcriptional activity in some special contexts, it is largely devoid of transcriptional stimulatory effects that require it to bind directly to a palindromic estrogen response element (ERE). This is entirely consistent with the dramatically reduced DNA-binding affinity relative to wt ER- α that we observe in gel mobility shift experiments. Similarly, the remaining exon-skipped ER- α splicing variants (ER Δ E2, ER Δ E3, ER Δ E4, ER Δ E6, & ER Δ E7) appear to completely lack positive

transcriptional activity when tested in transient transfection assays with a pERE-TK-CAT reporter plasmid (see year 3 annual technical report). Indeed, we have concluded that the most prominent activity of two of the splicing variants (namely ERAE3 and ERAE5) on ERE-containing genes is to interfere with the transcriptional stimulatory activity of wt ER- α , acting as dominant-negative mutants with modest potency. The inhibitory activity of ERAE3 and ERAE5 is likely to result from their ability to form functionally inactive, mixed dimers with intact ER- α , to sequester steroid receptor coactivators or other limiting basal transcription factors into non-productive complexes, or by a combination of both mechanisms.

These results, however, leave open the possibility that some of the ER- α splicing variants may display transcriptional stimulatory effects on the growing list of estrogen responsive genes that lack a canonical ERE. For these genes, transcriptional stimulation by ER appears to be mediated by an indirect mechanism, involving synergistic protein-protein interactions with upstream transcription factors (such as AP-1 or SP-1) or nuclear receptor coactivators (including CBP/p300, SRC-1, TIF-2, GRIP1, or AIB-1). To further examine this possibility, we have tested the effect of co-transfecting individual ER- α splice variants, compared with an empty expression vector, on the activity of four reporter plasmids that were selected from the literature based on their ability to be transcriptionally induced by ER, despite their apparent lack of a canonical ERE. These plasmids included p(AP1)₃TK-CAT (driven by three consensus AP-1 sites upstream of the HSV thymidine kinase promoter), Coll73-Luc (driven by the -73/+63 human collagenase promoter), pIGF1630-Luc (driven by the -1630/+322 human IGF-1 promoter), and pOvalb-CAT (driven by a 1350 bp promoter fragment from the chicken ovalbumin gene). Data from experiments in which each of the ER- α splicing variants were individually tested on these four reporter constructs are summarized in Figs. 5-8. For screening purposes, HeLa cells were chosen as the host for transfection with each one of the reporters together with expression plasmids for wt ER- α , one of the splicing variants, or the empty pCVM-4 expression vector. Paired cultures were treated with 10 nM 17 β -estradiol (E) in combination with 20 nM phorbol 12-myristate 13-acetate (PMA), or with vehicle alone. This was done to ensure that an activating ligand (E) was present, if necessary, and that AP-1 was maximally stimulated in the event that promoter activation involved an AP-1 element. Of the reporter constructs that we examined, only pOvalb-CAT was consistently and significantly induced by wt ER- α ; however, all four reporter constructs displayed a reproducible transcriptional response to one or more of the ER- α splicing variants (either ERAE3 or ERAE5). These findings are detailed below.

As previously reported by Gaub et al. (15) and confirmed by the experiment shown in Fig. 5, efficient stimulation of ovalbumin transcription by wt ER- α in transfected HeLa cells requires both the presence of estradiol and activation of AP-1 by phorbol ester. A modest, but significant stimulation of this reporter is also observed in response to PMA treatment alone, but estradiol by itself is essentially without effect. Thus, estrogen regulation of the non-canonical hormone response element within the ovalbumin reporter involves strong transcriptional synergism between ER- α and AP-1. Mechanistically, this phenomenon is thought to involve a protein-protein interaction between ER- α and AP-1 (Jun/Fos heterodimers), acting through a consensus TPA response element (also known as a TRE, or an AP-1 site). Whether this involves a direct interaction between ER- α and the AP-1 components Jun and Fos, or an indirect interaction mediated through a bridging factor such as CBP/p300 or SRC-1 still needs to be clarified. Interestingly, while the chicken ovalbumin promoter contains a consensus AP-1 site, it lacks a palindromic ERE and doesn't appear to require the direct binding of ER- α to DNA. This finding was previously reported by Gaub and coworkers (15) who used genetically engineered receptor mutants to establish that the integrity of its DNA-binding domain was *not* required for ER- α to activate the AP-1 element within the ovalbumin promoter. Consistent with this fact, we observe that a *naturally* occurring ER- α splice variant (ERAE3) that contains an in-frame deletion within its DNA-binding domain is approximately 40% as active as wt ER- α on this reporter construct.

Similar to the wt receptor, the activity of ER Δ E3 requires the combination of estradiol and a phorbol ester. Among the other ER- α splicing variants tested with the pOvalb-CAT reporter (ER Δ E2 through ER Δ E7, data not shown), only the ER Δ E5 variant displayed some stimulatory activity. While the effect of ER Δ E5 was modest, this 3-fold stimulation (compared with vector controls) was reproducible and statistically significant. Since ER Δ E5 lacks an intact ligand-binding domain, its activity was unaffected by estradiol, but remained dependent upon treatment of cells with phorbol ester.

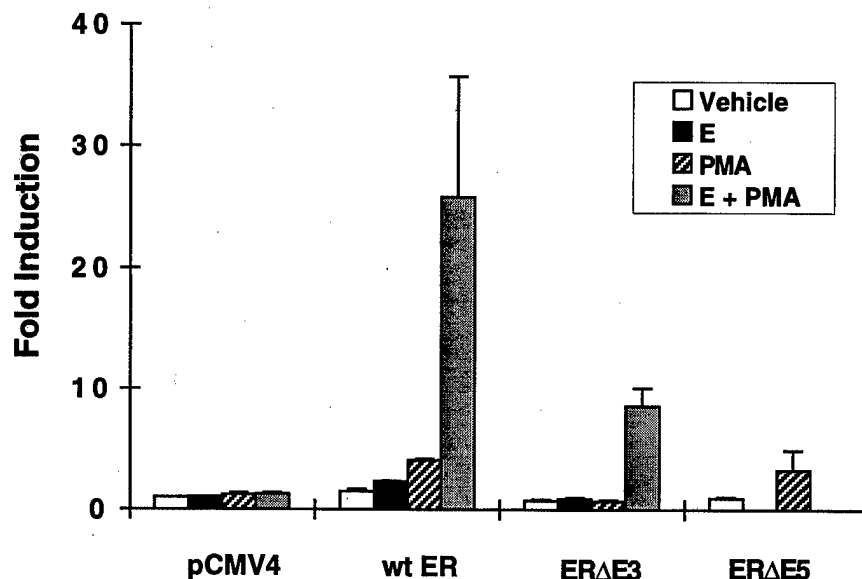


Fig. 5. Transcriptional stimulatory activity of wt ER α , ER Δ E3, and ER Δ E5 on a co-transfected pOvalb-CAT reporter plasmid. HeLa cells were transiently co-transfected with 10 μ g of reporter and 0.5 μ g of the indicated ER expression vector and were treated as indicated: vehicle control, 20 nM phorbol 12-myristate 13-acetate (PMA), 10 nM estradiol (E), or both (E + PMA). CAT assays were normalized for protein and values are expressed relative to vehicle-treated empty expression vector (pCMV-4) controls. Error bars represent the standard error of the mean of three independent experiments.

The Coll73-Luc (human collagenase) reporter represents a second well characterized AP-1 responsive reporter plasmid (8) that gave generally similar results with co-transfected ER- α splicing variants (see Fig. 6). Compared with the pCMV-4 vector control transfection which measures induction due to endogenous AP-1 in the absence of ER- α , the ER Δ E3 variant supported a 6- to 10-fold higher stimulation of Coll73-Luc expression in the combined presence of estradiol and phorbol ester. To a lesser extent, the ER Δ E5 variant also stimulated collagenase promoter activity. The stimulatory effect of ER Δ E5 was observed in both treated, as well as untreated cells, with phorbol ester producing an approximate doubling of the transcriptional response. The remaining splicing variants (ER Δ E2, ER Δ E4, ER Δ E6, and ER Δ E7) were indistinguishable from the empty vector control (pCMV-4). Somewhat unexpectedly, wt ER- α is largely without effect on the Coll73-Luc reporter construct in our hands (Fig. 6). Webb and coworkers (16) have described that intact ER- α in the presence of estrogen elicits a very modest (~2-fold) stimulation of the Coll73-Luc reporter in HeLa cells. These workers describe other conditions where a more robust response can be achieved. These include the use of collagenase promoter fragments containing additional upstream sequences (16), treatment with the antiestrogen tamoxifen instead of estradiol (16), or the use of agonist-liganded ER- β as opposed to ER- α (17). The apparent difference in the behavior of wt ER- α on this reporter construct are still under investigation. Our results with the Coll73-Luc reporter are nonetheless significant in that they indicate that two of the ER- α splicing variants (ER Δ E3 and ER Δ E5) actually appear to be more potent inducers of the

human collagenase reporter than the full-length ER- α protein. Further experiments are planned to separately characterize the need for ligand and phorbol ester to activate the ER- α variants on the collagenase reporter and to compare the activity of tamoxifen with estradiol.

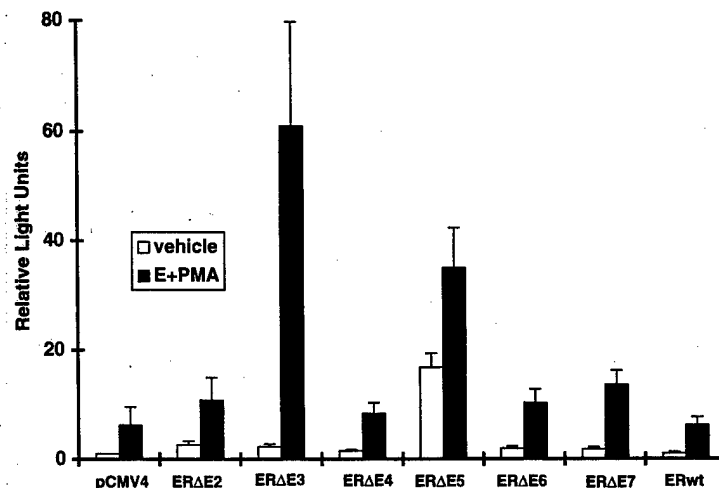


Fig. 6. Transcriptional stimulatory activity of ER α splicing variants on a co-transfected human collagenase reporter plasmid, Coll73-Luc. HeLa cells were transiently transfected as described in the legend to Fig. 5. Luciferase activities were normalized for protein and results are expressed relative to vehicle-treated empty expression vector (pCMV-4) controls. Error bars represent the standard error of the mean of three independent experiments.

A slightly different response pattern was observed when the ER- α splicing variants were tested with p(AP1)₃TK-CAT, an engineered reporter plasmid containing three consensus AP-1 elements upstream of the thymidine kinase reporter. As shown in Fig. 7, ERΔE5 was unique among the receptor constructs examined in its ability to induce the p(AP1)₃TK-CAT reporter in HeLa cells. In this case, it is significant that both wt ER- α and ERΔE3 *fail* to induce this reporter construct when treated with estradiol and phorbol ester. Indeed, there are subtle indications that wt ER- α and ERΔE3 may actually be inhibitory in this context although this inhibition does not reach statistical significance. Again, while there is a widespread impression that wt ER- α is able to act as an estrogen-dependent inducer of transcription through many AP-1 response elements, the data presented here are actually in good agreement with published reports using analogous reporter constructs.

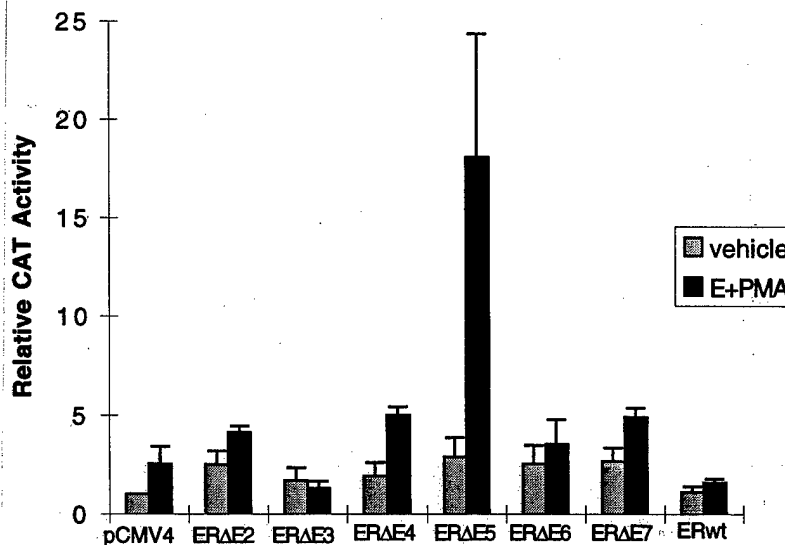


Fig. 7. Transcriptional stimulatory activity of ER α splicing variants on a reporter plasmid, p(AP1)₃TK-CAT, that contains three consecutive AP-1 elements upstream of the thymidine kinase promoter. HeLa cells were transiently transfected as described in the legend to Fig. 5, above. CAT activities were normalized for protein and values are expressed relative to vehicle-treated empty expression vector (pCMV-4) controls. Error bars represent the standard error of the mean of three independent experiments.

Specifically, Webb and coworkers (16) have shown that the collagenase AP-1 site, multimerized upstream of the HSV tk promoter (similar to the p(AP1)₃TK-CAT reporter used in our studies) displayed a modest (~2-fold) transcriptional response to antiestrogens (tamoxifen and ICI-164,384), but *not* to estradiol, when co-transfected with wt ER- α . We therefore feel that the 5-fold stimulation of CAT expression that we observe through a consensus AP-1 element (TGAGTCA) in response to the naturally occurring ER- α splicing variant (ER Δ E5) represents a highly significant finding. Preliminary experiments to dissect the requirements for this induction indicate that it depends upon treatment of transfected cells with phorbol esters and that, as expected for a variant that lacks an intact ligand-binding domain, it is unaffected by estradiol (data not shown). Further experiments to clarify this point and to assess the involvement of nuclear receptor co-activators in this phenomenon are underway.

The IGF-1 gene is expressed in a variety of tissues, including the liver, bone, uterus and breast, where it contributes to the normal growth and differentiation of these structures (18). Some uncertainty remains regarding the sources of IGF-1 within the breast and with respect to its role in breast tumor growth. It is likely that the mammary epithelium is exposed to IGF-1 from systemic sources as well as from the breast stroma. In addition, some breast tumors produce IGF-1 and other growth factors of their own (19). Expression of IGF-1 (and other growth factors) appears to be deregulated in some tumors, contributing an autocrine component to tumor cell growth. The potential of ER- α splicing variants to stimulate transcription of the IGF-1 gene in breast tumor cells is therefore of potential clinical significance. Interestingly, we observe that ER Δ E5, but not ER Δ E3 or wt ER- α promotes expression of a co-transfected IGF-1 luciferase reporter plasmid (IGF1630Luc) in HeLa cells (Fig. 8). This stimulation is preserved on IGF-1 promoter fragments containing as little as 592 bp of upstream sequence (data not shown). As with the behavior of the p(AP1)₃TK-CAT reporter shown above, the activity of ER Δ E5 implicates the N-terminal activation domain (AF1) or the DNA-binding domain in this effect, while the inactivity of wt ER- α and ER Δ E3 suggests that presence of the C-terminal activation domain (AF2) prevents ER- α from stimulating IGF-1 expression. However, in contrast with the p(AP1)₃TK-CAT reporter, the failure of phorbol ester to stimulate the activity of ER Δ E5 on the IGF-1 promoter suggests that the AP-1 factor is unlikely to be involved and that transcription factors other than jun or fos must represent the targets for ER Δ E5 interaction. Experiments are in progress to map the cis element within the IGF-1 promoter that is responsible for regulation by ER Δ E5.

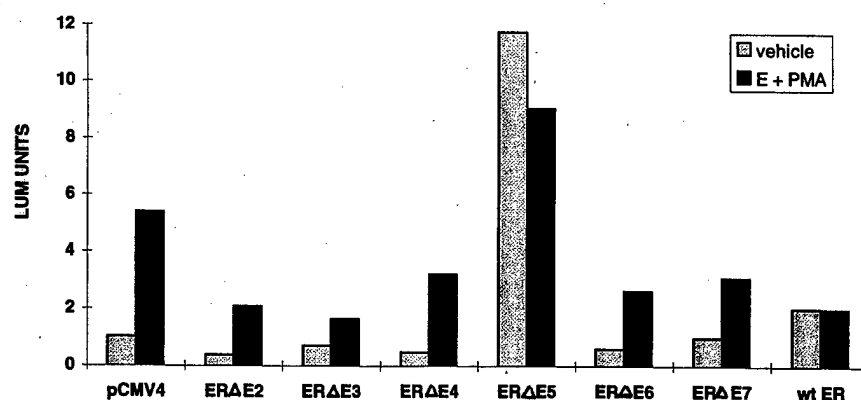


Fig. 8. Transcriptional stimulatory activity of ER α splicing variants on a co-transfected human IGF-1 reporter plasmid, pIGF(-1630)-Luc. HeLa cells were transiently transfected as described in the legend to Fig. 5, above. Luciferase activities were normalized for protein and values are expressed relative to vehicle-treated empty expression vector (pCMV-4) controls. Error bars represent the standard error of the mean of three independent experiments.

DISCUSSION

The major accomplishments for this reporting period include: 1) a thorough analysis of ER- α variants in TG-1 and TG-3c cells, two xenograft lines derived from the MCF10AT line, 2) the use of RT/PCR for a preliminary analysis of ER- α variants in M13 SV1 and R₂N₁ cells, 3) and continued characterization of the functional activity of two key ER- α splicing variants. The first two projects fall broadly within Task 1.d of our original statement of work, whose goal has been to clarify the status of ER- α splicing variants in normal breast epithelial cells. Since the inception of this project, several careful studies have been reported in the literature comparing ER- α mRNA species between breast tumors and normal human breast tissue (1,3). Based on these and earlier studies, a widespread consensus has emerged that ER- α splicing variants are not unique to the neoplastic breast, but appear to coexist with "correctly" processed ER- α mRNA in essentially all estrogen-responsive tissues and tumors that have so far examined. Rather than reproducing these published studies, we chose a slight redirection of our efforts to characterize ER- α transcripts in two fairly recently developed ER-positive mammary cell culture systems (derivatives of MCF10A and Type I M13 cells) that are being proposed as models for transformation and malignant progression in the normal human breast.

Work during this reporting period served to confirm and extend our previous conclusions by showing that ER- α transcripts in the MCF10A/TG-1, TG-3c, M13 SV1, and R₂N₁ cells are remarkably heterogeneous in nature, similar to MCF-7 and T47D breast tumor cells that we analyzed previously. In the majority of these cell lines, correctly processed ER- α mRNA is the single most abundant ER- α species observed. This is apparently *not* the case in MCF10A/TG1 and TG-3c cells, where the ERAE7 variant equals or exceeds wt ER- α in abundance (Fig 2). It is important to note, however, that in the aggregate ER- α splicing variants represent a significant fraction (usually $\geq 50\%$) of the total ER- α mRNA pool. Difficulty in documenting the existence of these variants at the protein level is often cited as evidence that ER- α variants may be unstable proteins that are of minor importance for estrogen signalling. The most likely reason for this is the finding that individually, most variants represent less than 5% of the structurally diverse pool of ER- α transcripts and are therefore predicted to give rise to an equally diverse population of low abundance variant ER- α proteins. While immunological detection techniques are generally suitable for detecting full length (67 kd) ER- α (which is usually the most abundant species), they are probably not sensitive enough to detect the lower abundance splicing variants. An ER- α species in the 48-52 kd size range reactive with many ER antibodies is observed by most investigators; however, it is generally dismissed as a probable proteolytic product. An alternative interpretation is that this band corresponds to the 52 kd ERAE7 variant that is consistently found to be the most abundant of the variant ER- α RNAs. In an effort to clarify this situation, studies are underway during the final award year to analyze cross-reacting ER- α proteins in these ER-positive cell lines using a battery of monoclonal antibodies that recognize defined epitopes within the ER- α polypeptide chain. In parallel, transfection studies using a variety of estrogen-responsive reporter plasmids are being conducted in the MCF10A/TG-1, TG-3c, M13 SV1, and R₂N₁ cell lines to assess their estrogen responsiveness.

The other major activity for this reporting period involved additional analysis of the transcriptional activity of ER- α splicing variants on promoters containing non-canonical estrogen response elements (Task 2.b). The traditional view of estrogen action depicts ER- α as the central player in target gene selection by virtue of its ability to bind to DNA containing a consensus estrogen response element (ERE). More recent evidence indicates that many estrogen regulated genes contain non-canonical hormone response elements organized around AP-1 or Sp1 sites (8,15). Among these targets are genes such as IGF-1, collagenase, cathepsin D, cyclin D1, c-fos, c-myc, and RAR α that are believed to play important roles both during normal breast development

and during tumor formation and progression. Of interest, the structural requirements for ER- α to regulate many non-canonical hormone response elements are less stringent than transcriptional stimulation through a consensus ERE. For this reason, we have examined the behavior of ER- α splicing variants on four reporter constructs containing non-canonical hormone response elements. In agreement with published reports, wt ER- α stimulated ovalbumin promoter activity. The dual requirement for estradiol and a phorbol ester indicate that this regulation occurs through an AP-1 site identified in the upstream region of the ovalbumin promoter (15) and involves a cooperative interaction between ER- α and the Jun/Fos heterodimer. A significant estradiol- and phorbol ester-dependent induction of ovalbumin activity was also supported by ERAE3, despite its lack of an intact DNA-binding domain. ERAE5 also supported a modest stimulation of ovalbumin activity that was phorbol ester-dependent, but estradiol-independent. These observations indicate that stimulation of the ovalbumin promoter by ER- α is mechanistically complex and includes both a phorbol ester-sensitive pathway involving the amino terminal activation domain (AF1) as well as an estradiol-sensitive pathway involving the carboxy terminal activation domain (AF2). While the activities of ERAE3 and ERAE5 imply that direct DNA binding by ERAE5 is not involved in regulation of ovalbumin gene expression, it is clear that neither of these splicing variants is as active as wt ER- α on this promoter construct.

In contrast to the situation with pOvalb-CAT, the activity of wt ER- α on the remaining three non-canonical hormone response elements was insignificant compared to the that of the ERAE3 or ERAE5 splicing variants. Specifically, both ERAE3 and ERAE5 were active on the Coll73-Luc reporter, while only ERAE5 was active on the pIGF(-1630)-Luc and p(AP1)₃TK-CAT reporter constructs. In the case of the collagenase promoter fragment, induction by ERAE3 required both estradiol and phorbol ester treatment. The stimulatory activity of ERAE5 required phorbol ester treatment for the p(AP1)₃TK-CAT reporter, was modestly enhanced by phorbol ester on the Coll73-Luc reporter, and was independent of phorbol ester treatment on the pIGF(-1630)-Luc reporter. This would appear to suggest that activation of AP-1, presumably by stimulation of protein kinase C and phosphorylation of Jun, plays different roles in the stimulation of these various reporter constructs by ERAE5. These data also suggest that the presence of a functional AF2 domain is detrimental for activation of some (but not all) non-canonical hormone response elements by ER- α since ERAE5, but not wt ER- α or ERAE3 stimulated the p(AP1)₃TK-CAT and pIGF(-1630)-Luc reporter plasmids. Our observations provide the first solid evidence that two ER- α splicing variants, namely ERAE3 and ERAE5, like wt ER- α can exert significant positive effects on gene transcription and raise the intriguing possibility that each one of these receptor isoforms may target a unique, but overlapping subset of genes for transcriptional regulation. In the final year of this project, our efforts will focus on understanding the mechanism(s) of gene regulation by ER- α splicing variants.

Publications From This Award

- 1) year 4 publication related to this award (copies included as an Appendix)
 - a) Bollig, A. and Miksicek, R.J. (1999) An estrogen receptor- α splicing variant mediates both positive and negative effects on gene transcription. *Mol. Endocrinol.*, submitted January 1999.
- 2) manuscripts currently in preparation from this award
 - a) Ankrapp, D.P., Morrison, M., Bollig, A.B., and Miksicek, R.J. MCF-7 and MCF10AT breast epithelial cells express a broad array of ER α mRNA size variants, in preparation.
- 3) previous publications related to this award
 - a) Bunone, G., Briand, P.-A., Miksicek, R.J., and Picard, D. (1996) Activation of the unliganded estrogen receptor by EGF involves the MAP kinase pathway and direct phosphorylation. *EMBO J.*, 15(9):2174-2183.
 - b) Elias, J.M., Hyder, D.M., Miksicek, R.J., Heimann, A., and Margiotta, M. (1995) Interpretation of steroid receptors in breast cancer: a case with discordant estrogen receptor results using ER1D5 and H222. *J. Histotechnology*, 18(4):331-335.
- 4) current publications unrelated to this award
 - a) Miksicek, R.J., Lee, C., and Morrison, M. Synthetic peptides derived from dimerization motifs within estrogen receptor- α interfere with receptor DNA-binding, in preparation.
 - b) Wang, S.F., Miura, K., Miksicek, R.J., Segraves, W.A., and Raikhel, A.S. (1998) DNA binding and transactivation characteristics of the mosquito ecdysone receptor-ultraspiracle complex. *J. Biol. Chem.*, 273:27531-27540.

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**An Estrogen Receptor- α Splicing Variant Mediates
Both Positive and Negative Effects on Gene Transcription**

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Keywords: Steroid Receptors, Coactivators, SRC-1, AP-1, Ovalbumin

ABSTRACT

Analysis of messenger RNA (mRNA) prepared from a variety of estrogen-responsive cell lines, breast tumor specimens, and normal breast tissue have established that estrogen receptor- α (ER α) mRNA is typically expressed as a mixture of transcripts. Using PCR amplification, this heterogeneity has been shown to result largely from an imprecise pattern of mRNA splicing that gives rise to a family of correctly processed and exon-skipped ER α transcripts. We have reconstructed ER α cDNAs representing the single exon-skipped variants ER Δ E2 through ER Δ E7 to enable their functional characterization in a well defined cell transfection system. All six of the ER α splicing variants can be efficiently and stably expressed in Cos7 cells, and each displays a characteristic pattern of subcellular distribution. Each of the variants displays a dramatic reduction in DNA-binding activity, as measured using transiently transfected Cos7 cell lysate and a consensus estrogen response element (ERE) in an *in vitro* gel mobility shift assay. While this DNA-binding defect appears to be complete for ER Δ E2, ER Δ E3, ER Δ E4, and ER Δ E6, weak DNA-binding is observed for ER Δ E5 and ER Δ E7, but only when DNA complex formation is stabilized by the addition of a bivalent antibody capable of recognizing the N-terminus of the ER α protein. Scatchard analysis of hormone-binding demonstrates that ER Δ E3 binds 17 β -estradiol (E₂) with a similar affinity to wild type ER α (wt ER α). Individual variants co-transfected with the pERE-TK-

CAT reporter gene (a consensus ERE-driven CAT reporter gene that is highly responsive to E_2 -liganded wt ER α) were ineffective at inducing CAT expression in ER-negative HeLa cells. Only ER Δ E5 showed indications of positive transcriptional activity on the pERE-TK-CAT reporter, but always this activity was limited to approximately 5% of the activity of wt ER α . When variants were expressed simultaneously with wt ER α , ER Δ E3 and ER Δ E5 were observed to have a dominant negative effect on wt ER α transcriptional activity. More compelling evidence that ER α splicing variants are transcriptionally active is observed with transfection experiments using a non-consensus estrogen-regulated reporter gene construct. Transcription from a region of the ovalbumin promoter, which contains an ERE half site and an AP-1 motif, is positively regulated by liganded wt ER α and ER Δ E3 in phorbol ester-treated, transiently transfected HeLa cells.

INTRODUCTION

Estrogens are crucial for normal physiological development of the breast and this class of hormones plays a central role in breast oncology (1-5).

Binding of estrogen to the estrogen receptor (ER) elicits a change in receptor conformation that allows the receptor to bind DNA and enhance transcription from the promoters of regulated genes (6-8). ER-induced gene expression supports the proliferation and ultimately, the differentiation of target cells (2,3). Interference with these proliferative effects forms the basis for the chemotherapeutic actions of estrogen antagonists that are used to treat cancers of the breast and reproductive tract (4). The reported success of anti-estrogens such as tamoxifen and raloxifene in preventing breast tumors emphasizes a crucial role for ER in mammary carcinogenesis (1,5,9).

The transcriptional effects of estrogens are mediated by two closely related receptor isoforms, ER α and the more recently described ER β (10,11), each of which is encoded by a separate gene. While ER β is also being investigated for its potential role in various diseases including cancer, this study focuses solely on the ER α isoform. Analysis of mRNA prepared from a variety of estrogen responsive cells and tissues, including breast tumors, has established that ER α mRNA is typically expressed as a mixture of transcripts (12-15). This heterogeneity results largely from a pattern of alternative mRNA splicing that gives rise to a family of correctly processed and exon-skipped ER α mRNAs.

ER α mRNA comprises sequences from 8 coding exons and is translated to yield

a protein with discrete functional domains. An N-terminal transactivation function (AF1) encoded by exon 1 and a portion of exon 2 is thought to promote gene transcription by interacting with nuclear receptor coactivators and also with proteins integral to the transcription initiation complex (6,16,17). Derived from exons 2 and 3 is a centrally located zinc-finger motif (commonly referred to as the DNA-binding domain or DBD) that is essential for sequence-specific DNA-binding and transcriptional activation through canonical estrogen response elements (EREs) (18). Within the region encoded by exon 4 are the nuclear localization signals (NLS) and a hinge region which allows for receptor conformational flexibility (8,19). A ligand-binding domain (LBD) confers regulatory function to the receptor and is encoded by the C-terminal exons 4 through 8 (20). Exon 8 also includes determinants for subunit dimerization and a well characterized C-terminal transactivation function (AF2) which promotes gene transcription by recruiting coactivators (6,7,8,21). Like other nuclear receptors, ER α is a modular protein in that individual domains are capable of demonstrating autonomous function within receptor mutants, as well as when they are introduced into heterologous fusion proteins (6,18). It can reasonably be assumed that the exclusion of a particular exon will predictably result in a protein lacking the function ascribed to that exon. Additionally, it is probable that the loss of a particular exon will result in unpredictable functional deficits or perhaps even bestow a novel function on the variant receptor. This study examines the function of ER α splicing variants from the vantage point of what is known about the functional organization of wt ER α . We report results from

experiments designed to assess receptor capacity to translocate to the nucleus, bind to DNA, bind ligand and promote gene transcription.

Fuqua and colleagues have reported that ER Δ E5 (which contains the AF1 domain, but lacks AF2 and the regulatory functions imparted by the LBD), is constitutively active in promoting transcription from an ERE in a heterologous yeast reporter gene assay (22,23). These authors have also described that over-expression of ER Δ E5 in a stably transfected breast cancer cell line (MCF-7) supported greater proliferation compared to control cells, as well as imparting a tamoxifen resistant phenotype (24). In the human osteosarcoma cell line U2-OS, it has recently been reported that co-expression of ER Δ E5 significantly enhances ERE-directed reporter gene expression induced by wt ER α (25). The existence of a constitutively active receptor variant (such as ER Δ E5) able to exert a mitogenic effect in breast tumor cells in the absence of E₂ or in the presence of tamoxifen is an appealing explanation for the acquisition of anti-estrogen resistance observed in previously responsive tumors and cell lines (26,27). However, this model is challenged by conflicting observations that ER Δ E5 and closely related, genetically engineered ER α mutants do not efficiently induce transcription from an ERE reporter in transiently transfected ER-negative HeLa or CEF cells (7,28), or promote proliferation in stably transfected MCF-7 cells (28).

Recently a novel mechanism for mediation of an estrogen response has been reported to involve AP-1 directed regulation of transcription by ER (29-32).

AP-1 describes the fos / jun family of transcription factors that play a key role in transducing the effects of growth factors to regulate cell proliferation (33,34). A variety of estrogen-responsive genes have been described that lack a palindromic ERE, but instead contain one or more consensus AP-1 elements (5'-TGAG/CTCA-3'), with or without a degenerate ERE or ERE half site (5'-GGTCA-3' or 5'-TGACC-3'). Examples of such genes include ovalbumin which is induced by E₂ in chicken oviduct cells (35) and the insulin-like growth factor-I (IGF-I) gene whose expression is stimulated by E₂ treatment in cultured rat osteoblasts (36). An AP-1 enhancer motif identified in the chicken IGF-I promoter is essential for E₂ and phorbol ester stimulated gene transcription (31). Phorbol esters act directly on protein kinase C to initiate a signal transduction cascade that ultimately activates AP-1 (33). Reporter gene co-transfection studies with expression vectors for AP-1 isoforms and ER α in HeLa cells indicate that a similar mechanism regulates the human collagenase promoter (32). The minimal region of the collagenase promoter reported to be responsive to tamoxifen-liganded wt ER α , and to a variety of ER α mutants harbors a critical AP-1 element and lacks a consensus ERE. Additionally, the activity of ER α on the collagenase promoter was enhanced with AP-1 (c-jun or c-fos) over-expression (32). Further evidence that ER regulation converges with AP-1 directed gene transcription is provided by results from protein binding assays indicating that c-jun is able to bind to wt ER α *in vitro* (32).

Although evidence for function of ER α variants has been elusive, reports that ER Δ E5 can support weak, cell type-dependent activity (23,25,28), and that, when tested on an ERE, both ER Δ E5 and ER Δ E3 are dominant negative receptor forms in the presence of wt ER α (37,38) indicate that it is inaccurate to label these variants as transcriptionally inert. To investigate the capacity for ER α splicing variants to regulate gene transcription we have expanded our transcriptional focus to include the noncanonical ovalbumin promoter in addition to the consensus ERE. Here we present data indicating that individual variants display both similarities and differences compared with wt ER α , and that selected splicing variants (specifically ER Δ E3 and ER Δ E5) have the capacity to both positively and negatively regulate gene expression, depending on the cell and promoter context.

RESULTS

Construction of plasmids for efficient expression of individual ER α mRNA splicing variants

Numerous variant ER α cDNAs have now been cloned and sequenced from breast tumors and established tumor cell lines (12-15). The most common variants harbor a precise deletion of one of the internal exons from the eight that contribute to the structure of the mature ER α protein, suggesting that they arise as a result of imprecise splicing of the primary ER α mRNA transcript. ER α cDNAs with sequence deletions corresponding to exons 2, 3, 4, 5 and 7 have been identified, along with a large number of more complex variants (12-15). These basic variants will be referred to as ER Δ E2 through ER Δ E7, where the deleted exon is indicated numerically. While there has been extensive analysis at the RNA level of the pattern of expression and abundance of ER α splicing variants, limited information is available on their functional activity. We have therefore constructed CMV promoter driven ER α cDNA expression vectors representing the exon-skipped variants ER Δ E2 through ER Δ E7 to enable their functional characterization in a well defined cell transfection system. Our assembled pool of ER α splicing variants also includes the hypothetical receptor ER Δ E6 which is not readily identified *in vivo*. Figure 1 diagrams the ER α mRNA splicing variants showing the positions of deleted exons and their consequences with respect to protein structure. Deletion of exon 2, 5, 6 or 7 all

cause a frame-shift mutation resulting in premature termination of translation, thereby generating a diverse class of C-terminally truncated receptor forms. Omission of either exon 3 or 4 does not disrupt the mRNA reading frame, but produces a receptor protein with an internal deletion.

Transient expression in Cos7 cells demonstrates that each of these variants translates to a stable protein able to accumulate to readily detectable levels within transfected cells (Fig. 2). Based on immunoblot analysis with an N-terminal monoclonal antibody (Mab-17), which recognizes an epitope common to each of the variants (39), we observe the mobility of the six variant proteins is consistent with its predicted molecular weight.

Measurement of the DNA-binding activity of the ER α splicing variants

Efficient DNA binding by ER α requires the cooperation of several functional elements within this protein, including the centrally located DNA-binding domain and a ligand-inducible subunit dimerization motif located near the C-terminal end of the LBD (7,18). It is also possible that additional subunit contacts occur elsewhere in the protein. Because all of the ER α splicing variants sustained deletions within various regions of this protein, it was of interest to systematically assess the DNA-binding ability of each variant. For this purpose, gel mobility shift assays were performed using extracts prepared from E₂ treated, transiently transfected Cos7 cells. Extracts were incubated with a ³²P-labeled oligonucleotide containing a consensus estrogen response

element (AGGTCACAGTGACCT) from the xenopus vitellogenin A2 promoter. As expected, variants that harbor a mutation within the DBD (ER Δ E2 and ER Δ E3) are completely unable to recognize the ERE (Fig. 3, lanes 5-8). Less predictably, the loss of exons contributing to the LBD also result in a strong defect in ERE recognition (Fig. 3, lanes 9-16). For ER Δ E5 and ER Δ E7, however, this appears to be a quantitative defect in DNA binding. The addition of the monoclonal antibody, MAb-17, to the binding reactions consistently results in the recovery of weak DNA binding by ER Δ E5 (Fig. 3, lane 12). Presumably the role of the bivalent antibody is to stabilize the interaction of receptor subunits with their palindromic binding site, mimicking the function of the missing dimerization motif present within the C-terminus of the LBD. These results suggest the possible existence of cell-specific constituents that perform the same function *in vivo* and may account for the variable activity of ER Δ E5 and related constructs in different cell types (7,25,28). We have also observed the formation of a complex between ER Δ E7 and labeled ERE probe (Fig. 3, lane 16). The relative weakness of DNA-binding observed in these studies raises serious questions about the extent to which ER Δ E5 and ER Δ E7 are able to recognize and bind to a consensus ERE, *in vivo*.

ER Δ E3, like wt ER α binds ligand

To test the ability of the ER α mRNA splicing variants to bind hormone we performed a saturation binding assay on whole cell extracts from Cos7 cells transiently transfected with wt ER α or the ER α variants. Only wt ER α and ER Δ E3 were able to bind ^{3} H-labeled E $_2$ whereas all of the remaining variants demonstrated no specific ligand binding (Fig. 4A). The individual deletion of exons 2, 4, 5, 6 and 7 effectively eliminates all, or a significant portion of the LBD, consistent with their loss of hormone binding. We confirmed these results using an *in vivo* ligand-binding assay where the binding of a fluorescent estrogen analogue was visualized in cells cultured on cover slips. Cos7 cells transiently expressing the individual variants or wt receptor were treated with the fluorescent ligand, nitrile tetrahydrochrysene (nitrile THC) (40). Only those cultures transiently transfected with wt ER α or ER Δ E3 were observed to stain with this ligand. In both cases, staining was localized tightly within the nucleus. This suggests that among the variants examined, wt ER α and ER Δ E3 exclusively bind ligand and in both cases, ligand-bound receptors are translocated normally to the nucleus of expressing cells (Fig. 4B). With Scatchard analysis we compared the affinity of ER Δ E3 and wt ER α for ^{3} H-labeled E $_2$. The measured dissociation constants were 0.66 nM for wt ER α and 0.79 nM for ER Δ E3 (Fig. 4C).

Subcellular localization of ER α splicing variants

To more carefully assess the subcellular localization of ER α splicing variants, including those that fail to bind ligand, Cos7 cells were transiently transfected with expression vectors encoding wt ER α or individual variants. These receptors were detected in transfected cells by indirect immunofluorescence staining (using the MAb-17 monoclonal antibody) and confocal microscopy. Similar to wt ER α , ER Δ E3 and ER Δ E5 localize to the nuclei of transfected cells, though ER Δ E5 showed perinuclear as well as nuclear staining (Fig. 5). These results are consistent with the fact that each of these receptors retains the NLS immediately downstream of the DBD (8,19). Subcellular localization studies have also been completed for the exon 2,4,6 and 7 deletion variants. Each of these proteins can be readily detected in transfected cells, but they all possess dramatic defects in nuclear targeting (Fig. 5). Nuclear targeting of wt ER α is governed in large part by a tripartite karyophilic signal present within exon 4 (19). Loss of this signal is therefore consistent with the cytoplasmic pattern of distribution of mutants such as ER Δ E2 and ER Δ E4, both of which lack protein corresponding to exon 4 sequences. Inappropriate presentation or folding of this signal must account for the defects in nuclear localization seen with ER Δ E6 and ER Δ E7, since the NLS is retained in these variants.

Characterization of the Transactivation Function of ER α splicing variants on an ERE

HeLa cell co-transfection experiments designed to assess the transcriptional activity of individually expressed ER α splicing variants have failed to demonstrate any significant ability of variant receptors to support gene activation through an ERE, with the possible exception of the ER Δ E5 variant which appears to display a low level of constitutive transcriptional activity on an ERE driven reporter in some, but not all cell types examined (23,25,28). In our hands none of the variants were effective transcriptional activators of an ERE containing promoter. ER Δ E5 repeatedly showed only modest constitutive activity (approximately 5% of wt ER α induction) on an ERE-directed reporter plasmid co-transfected into HeLa cells (see Fig. 7, insert).

It is important to acknowledge that the tissues and cell lines that express these variants also express wt ER α . We have previously reported that the ER Δ E3 variant acts as a dominant negative mutant when it is co-expressed with wt ER α in HeLa cells treated with E₂ (38). In the human breast epithelial cell line HMT-3522S1, ER Δ E5 has also been reported to disrupt transactivation by agonist-bound wt ER α of an ERE reporter gene (37). To clarify whether this is a function unique to these variants we completed a series of experiments to assess the likelihood that the remaining exon-skipped ER α variants also support transcriptional inhibitory effects. When tested in a HeLa cell co-

transfection assay in which the expression of pERE-TK-CAT was driven by E₂-bound wt ER α , a 5-fold molar excess of any of the splice variants lacking exons 2,4,6, or 7 failed to inhibit the E₂-dependent induction of CAT gene expression by intact receptor (data not shown). In agreement with previously published results, the ER Δ E3 and ER Δ E5 variants both demonstrated a dominant inhibitory activity at all molar ratios tested (Fig. 6). With the caveat that equal amounts of plasmid DNA support similar levels of variant receptor expression (see Fig. 2), it appears that ER Δ E3 and ER Δ E5 are nearly equivalent in their inhibitory activity in HeLa cells.

ER Δ E3 variant is a positive regulator of gene expression

The results presented above indicate that ER α splicing variants are either inactive (ER Δ E2, ER Δ E4, ER Δ E6 and ER Δ E7) or largely inhibitory (ER Δ E3 and ER Δ E5) in their effect on reporter constructs that contain a consensus ERE. Recent reports suggest that wt ER α is able to transactivate genes whose promoters do not contain an obvious ERE. In particular are promoters such as those that drive expression of the collagenase and ovalbumin genes that are regulated by wt ER α and contain a critical AP-1 element (29,32). Mutational analysis revealed that the DBD was not required for ER α -dependent expression of these genes. Clearly the mechanisms of ER α transcriptional activity and DNA targeting are complicated by these reports. We

propose that in order to assess the transactivating potential of ER α variants, the promoter focus must be expanded to include those containing non-canonical regulatory elements. These thoughts prompted us to test the activity of the ER α variants on the ovalbumin promoter which contains a complex hormone response element. We performed co-transfection experiments in HeLa cells using vectors expressing wt ER α or the exon-skipped variants ER Δ E2 through ER Δ E7 and a reporter construct driven by a fragment of the ovalbumin promoter (-1342 to +7 relative to transcription start site) described to encompass much of the regulatory sequence of this gene (35,41). Results from these experiments indicate that both wt ER α and ER Δ E3 support inducible gene expression from the ovalbumin promoter (Fig. 7) and that all of the remaining single exon-skipped variants are transcriptionally inactive on this reporter construct (data not shown). For wt ER α , this is consistent with previously published reports (29,35). Maximal activity was measured in cultures treated with both phorbol 12-myristate, 13-acetate (PMA, a phorbol ester) and E₂, where a 16-fold induction was observed. Similar to wt ER α , ER Δ E3 supported a marked 9-fold induction of this reporter, despite its lack of an intact DBD. In both cases the result of co-treatment with PMA and E₂ is highly synergistic as E₂ treatment alone has no significant effect and PMA treatment alone supports only modest induction for wt ER α (2.5-fold relative to vehicle control). Tamoxifen treatment of wt ER α - or ER Δ E3-transfected cultures, either alone or together with phorbol ester, had no

significant effect on pOvalb-CAT expression. In those cells not expressing ER α protein (i.e., controls transfected with an empty CMV expression vector), there was no PMA induction. This suggests that, in the absence of ER α , activated AP-1 alone does not support transcription from the ovalbumin promoter in these cells. Regulation of the reporter is only observed with PMA treatment when an ER α isoform is co-expressed.

DISCUSSION

Our efforts to functionally characterize exon-skipped ER α mRNA splicing variants have identified two receptor isoforms that possess the ability to modulate estrogen signaling on genes that are targeted by the estrogen receptor. Although their protein structure is significantly altered, the ER Δ E3 and ER Δ E5 splicing variants retain many of the activities attributed to the full length receptor. Loss of exon 3 results in a receptor protein with an internal deletion that lacks a major portion of the DBD and therefore prevents ER Δ E3 from binding to a consensus ERE, as confirmed by gel mobility shift analysis. However, ER Δ E3 retains the LBD and NLS thereby allowing it to bind hormone with an affinity similar to wt ER α and translocate to the nucleus. The deletion of exon 5 causes a frame-shift mutation and results in a C-terminally truncated form of the receptor. Loss of the LBD predictably renders ER Δ E5 unable to bind E₂. Nonetheless, ER Δ E5 also retains the NLS and immunofluorescence analysis shows nuclear staining in Cos7 cells transfected with this variant.

Rather than serving to stimulate transcription on a consensus ERE, results from transient transfection experiments in HeLa cells that combine either ER Δ E3 or ER Δ E5 with wt ER α and an ERE-driven reporter gene indicate that these isoforms actually function to inhibit transcriptional activation by wt ER α . These observations agree with our previous results and with those reported by others from similar experiments using HMT-3522S1 cells (37,38). A 70%

inhibition of transcriptional activation by E_2 -liganded wt ER α on an ERE-driven CAT reporter gene was observed in HeLa cells when ER Δ E3 and wt ER α expression vectors were co-transfected at a ratio of 5 to 1 (38). In the ER-negative cell line HMT-3522S1, co-expression of an equal amount of ER Δ E5 significantly inhibited stimulation of an ERE reporter construct by wt ER α (37). Increasing the ratio of transfected variant to wt ER α demonstrates that the repression of wt ER α by ER Δ E3 and ER Δ E5 is dose-related and becomes nearly complete when the variants are present in sufficient excess (37,38), a situation that is reported to occur in some breast tumor cells (22). The dominant negative character of ER Δ E3 and ER Δ E5 suggests that, like wt ER α , these variants are able to interact with at least one component of the ERE-directed transcription complex in a manner that disrupts positive gene regulation by wt ER α . Based on gel mobility shift assay analysis, it is unlikely that transcriptional interference by these variants involves binding to an ERE to the exclusion of wt ER α . Our DNA-binding analysis indicates that ER Δ E5 can bind only weakly to DNA, and only when the formation of this complex is stabilized by the addition of a bivalent antibody. The role of the antibody in this case is presumably to substitute for the missing dimerization interface and to tether receptor subunits together in a form more able to interact with DNA. DNA binding by ER Δ E7 similarly requires the addition of antibody, but this binding is even less efficient than binding by ER Δ E5. Interestingly, a correlation exists among the ER α

variants between their failure to translocate to the nucleus and their inability to inhibit wt ER α activity in mammalian cells (data not shown). As of yet, no clear function has been established for the ER Δ E7 variant in mammalian cells despite an earlier report that ER Δ E7 is a dominant inhibitor of wt ER α function in yeast (42). This is noteworthy since a number of quantitative studies have indicated that, as a rule, ER Δ E7 represents the most abundant of the ER α splicing variants (summarized in 15).

We have previously reported that although ER Δ E3 is unable to bind to an ERE itself, it can prevent wt ER α from binding to DNA (38). That ER Δ E3 inhibits both DNA complex formation and transactivation by wt ER α suggests that the potential targets of interaction by ER Δ E3 may include protein-protein contacts with wt ER α itself or interactions with nuclear receptor coactivators or other receptor-associated factors. ER α function may be disrupted when ER Δ E3, which lacks the DBD but retains the hormone-inducible dimerization domain, forms mixed dimers with wt ER α that are inefficient at binding stably to DNA. We are able to show that, in the presence of E₂, ER Δ E3 can form a stable complex with the ligand-binding domain of ER α fused to glutathione-S-transferase (GST), consistent with this model for inhibition by ER Δ E3 (Bollig and Miksicsek, unpublished data). We also observe that *in vitro* translated ER Δ E3 is able to associate in an E₂-dependent manner with a fragment of steroid receptor

coactivator-1 (SRC-1) containing the nuclear receptor (NR) boxes (amino acids 570-780) (43). SRC-1 is a potent enhancer of E_2 -bound $ER\alpha$ and is required for its full transcriptional activity (44,45). A site for SRC-1 interaction within wt $ER\alpha$ corresponds with the AF2 domain (46), a region that is retained in the $ER\Delta E3$ variant. Transfection experiments in E_2 -treated HeLa cell cultures demonstrate that co-expression of mutants containing the C-terminus of $ER\alpha$ can attenuate $ER\alpha$ -dependent gene expression and that this decreased activity can be overcome with simultaneous over-expression of the SRC-1-related coactivator TIF2 (47). These results suggest that coactivators are limiting factors for which the receptors are competing and that $ER\Delta E3$, like wt $ER\alpha$, is a target for SRC-1 binding.

In a surprising result from co-transfection studies using engineered mutants of $ER\alpha$, maximal expression of an ERE-containing reporter gene could be observed when SRC-1 was transfected simultaneously with separate N- and C-terminal fragments of $ER\alpha$, containing the AF1/DBD and the LBD/AF2 regions, respectively (48). This indicates that separate AF1- and AF2-containing $ER\alpha$ polypeptides can interact in a transcriptionally productive manner, provided they are brought together by SRC-1. These results offer initial indications that SRC-1 interacts separately and perhaps directly with both the AF1 and AF2 domains. More support for this is provided by recent reports that SRC-1 binds N-terminal polypeptides from $ER\alpha$ in solution (17). This

suggests the possibility that the inhibitory function of ER Δ E5, which itself is relatively inefficient at binding DNA or activating transcription through an ERE, may result from competition with wt ER α for interaction with SRC-1 or other cellular factors.

The most compelling evidence that several of the ER α mRNA splicing variants may indeed be transcriptionally active is seen in transfection experiments involving ER Δ E3 and reporter gene constructs containing a non-consensus hormone regulatory element. Recently a novel mechanism for mediation of an estrogen response has been reported to involve AP-1 directed regulation of transcription by ER α (29-32). AP-1 and its isoforms represent a family of nearly ubiquitous transcription factors whose activity is crucial for the efficient expression of a wide variety of genes. As an important downstream target for the MAPK signaling cascades, AP-1 is a central player in mediating the effects of serum and growth factors on cellular proliferation (33,34). A variety of estrogen-responsive genes have been described that lack a palindromic ERE, but instead contain one or more consensus AP-1 elements (5'-TGAG/CTCA-3'), with or without a nearby degenerate ERE or ERE half site (5'-GGTCA-3' or 5'-TGACC-3') (29,31,32). It should be noted that these imperfect EREs may in some cases serve dual function as cryptic AP-1 response elements whose consensus sequence bears superficial similarity to an ERE half-site (29,31,32).

An important observation from the analysis of genes regulated by non-canonical EREs is that the structure-activity requirements for activation by ER α (both for the ligand and for the receptor) are different than those for transcriptional activation through a palindromic ERE. Using a region of the collagenase gene promoter (-73/+63) that lacks an ERE but harbors an essential AP-1 element, Kushner and coworkers demonstrated that a DBD-deleted mutant of ER α was significantly more effective at supporting E₂-induced reporter gene expression than wt ER α in transfected HeLa cells (32). Similar to collagenase gene expression, ER α -dependent activation of the chicken ovalbumin promoter, which lacks a palindromic ERE, does not require an intact DBD (29). Furthermore, an ERE half-site was determined to be the site for synergistic regulation of the ovalbumin gene expression by AP-1 and ER α (29). Our studies involving co-transfection of an ER α splice variant with the ovalbumin promoter construct, pOvalb-CAT, agree with these findings. Results from Fig.7 demonstrate that, compared with mock-transfected HeLa control cultures, pOvalb-CAT is strongly activated by either wt ER α or ER Δ E3. A breakdown of treatments indicates that maximal activity of both wt ER α and ER Δ E3 clearly requires E₂ in addition to an AP-1 activator. Tamoxifen treatment had little or no effect on their activity, either with or without PMA co-treatment. This contrasts with results observed when wt ER α was co-transfected with a collagenase reporter construct in HeLa cells, where tamoxifen supported a

significant induction of reporter gene expression (32). The differences we observe between the relative activities of ER α isoforms on the ovalbumin promoter and the activation requirements reported for other AP-1 directed ER α regulated genes highlight the complexity of ER α signaling through this mechanism.

Our transfection results show that, while several of the ER α splicing variants are functionally incapacitated by their deletions, two of the variants clearly retain significant transcriptional activity. For the ER Δ E3 and ER Δ E5 variants, this activity is quite complex. Both of these variants represent stable receptor isoforms that, like the full-length receptor, localize efficiently to the nucleus where they can interact with the transcription apparatus. However, when acting through a consensus ERE, these variants completely lack (ER Δ E3) or show only weak (ER Δ E5) transcriptional stimulatory activity, consistent with their poor DNA-binding ability. On the contrary, both variants serve to blunt the ability of co-expressed wt ER α to promote transcription of ERE-containing genes. At the same time, the ability of ER Δ E3 (and presumably also ER Δ E5) to interact productively with nuclear receptor co-activators or other transcription factors gives these ER α splicing variants the potential to stimulate or otherwise modulate gene expression through non-consensus hormone response elements that are targeted by AP-1 motifs or other DNA-binding sites. We have clearly shown this to be true for ER Δ E3 and the chicken ovalbumin promoter

and believe that this is also likely to be true for many other genes, such as those encoding collagenase, cathepsin D, IGF-1, TGF- β , c-fos, HSP-27, and RAR- α , that lack an obvious ERE and yet still respond to estrogen. In this respect, ER α splicing variants may actually serve to redirect transcription away from ERE-containing genes to genes such as these that appear to be regulated non-classically by estrogens.

MATERIALS AND METHODS

Expression Vectors

Plasmids for ER α mRNA splicing variant cDNAs were generated as derivatives of pCMV4 (49) and pcDNA3.1 (InVitrogen Corp., San Diego, CA), which support high levels of receptor expression in HeLa and Cos7 cell lines (40). Plasmids expressing ER Δ E4, ER Δ E5, and ER Δ E6 were generated using synthetic oligonucleotides to construct the variant splice junctions within an otherwise wt ER α cDNA expression plasmid. The remaining plasmids were constructed with the use of flanking restriction sites to shuttle cloned cDNAs (38) into the appropriate expression vectors.

Cell Culture, Transfection and CAT Assay

Cos7 and Hela cells were grown in phenol red-free Dulbecco's modified Eagle's medium (DMEM) supplemented with 10% calf-serum, 5 mM HEPES (pH 7.4), 2 mM glutamine, penicillin (50 U/ml), and streptomycin (50 μ g/ml). Cells were transfected by the CaPO₄ method, as previously described (50). HeLa cells (approximately 2×10^6 cells per 100 mm dish) were transfected with 1 μ g of the indicated ER α isoform expression plasmid and 16 μ g of the estrogen responsive reporter plasmid, pERE-TK-CAT (51) or pOvalb-CAT (a reporter gene construct containing -1342 to +7 bp of the chicken ovalbumin promoter relative to transcription start site) (41). Calf thymus DNA (10 μ g) was added as carrier. Following over-night incubation with DNA, culture medium was

replaced with 5% charcoal-treated serum supplemented DMEM containing the indicated hormones. After 24 hours incubation, cells were harvested and CAT assays were performed as previously described (52) using 100 µg protein. Quantification was performed by phosphorimage analysis of thin layer chromatographs (ImageQuANT, Molecular Dynamics, Sunnyvale, CA). Cos7 cells were similarly transfected with 10 µg of the indicated expression plasmid and 10 µg of calf thymus carrier DNA. After over-night culture with DNA, cells were cultured for 48 hours in 10% calf serum supplemented DMEM.

Estradiol Binding Analysis

Ligand-binding assays were performed as previously described (39). Whole cell extracts were prepared from transfected Cos7 cells that were resuspended and sonicated in extraction buffer. Aliquots containing 200 µg of protein were incubated over-night at 4°C with various concentrations (0.1 nM - 10 nM) of ³H-labeled 17β-estradiol (New England Nuclear) in the presence or absence of a 200-fold molar excess of unlabeled 17β-estradiol. Free ligand was separated from bound ligand by treatment with dextran-coated charcoal. For determination of equilibrium binding constants, these data were plotted according to the method of Scatchard (53).

DNA-Binding Assays

DNA-binding assays were performed as previously described (39). Aliquots containing 30 µg of protein from extracts prepared as above from transfected Cos7 cells were pre-incubated for 15 min at room temperature in 10 µl binding buffer [10 mM HEPES (pH 7.4), 1 mM MgCl₂, 1 mM dithiothreitol, and 20% glycerol] containing 1 µg poly (dl-dC), with or without added hER-specific monoclonal antibody (Mab17), generated as described by Neff (39). Approximately 6 fmol (40,000 cpm) of a ³²P-labeled double stranded ERE oligonucleotide (38) were added to the samples and incubated for 30 min at room temperature, followed by an additional 5 min incubation at 4°C. Samples were then loaded on a pre-electrophoresed non-denaturing 5% polyacrylamide gel that was run in 0.5 x Tris-Borate-EDTA at 275 V for 2 h. The gel was dried and exposed for autoradiography.

Immunoblot Analysis

Discontinuous 12% SDS-PAGE was carried out as previously described (54). After electrophoresis of 30 µg of protein from transfected Cos7 cell whole cell extracts, proteins were electrophoretically transferred to nitrocellulose filters with a Bio-Rad Trans Blot apparatus (Bio-Rad Laboratories, Richmond, CA) using the procedure of Erickson *et al.* (55). Immunoblots were probed with the ER-specific monoclonal antibody, Mab17 (39). Immunoreactive protein was visualized using enhanced chemiluminescence, following manufacturer's instructions (Amersham, Arlington Heights, IL).

Immunohistochemical and Cytochemical Analysis

Indirect immunofluorescence analysis was performed on Cos7 cells that were plated and transfected on glass cover slips. On the second day following transfection, cells were washed three times with Tris-buffered saline (TBS), fixed for 3 min in cold 95% methanol, rehydrated by three washes with TBS, and incubated 30 min at 37°C with primary antibody (Mab17 hybridoma supernate used at a 1:10 dilution in TBS). Bound antibody was detected by staining with a rhodamine-conjugated affinity-purified goat anti-mouse immunoglobulin G (Boehringer Mannheim, Indianapolis, IN) diluted 1:2000 in TBS, incubating for 30 min at 37°C in the presence of 0.02 µg/ml of 4', 6-diamidine-2-phenylindole dihydrochloride. Confocal images were recorded using the Odyssey system (Noran Instruments, Middleton, WI) on an Optiphot 2 Nikon microscope. Fluorescent ligand staining of transfected Cos7 cells was performed as described by Miksicek et al. (40), on live, whole-cell mounts treated in DMEM with 10^{-7} M nitrile THC. For these studies cells were visualized using a Nikon UFX microscope equipped with a 100 watt mercury lamp for fluorescence excitation, and a 40x 0.7 numerical aperture Plan objective.

Acknowledgements:

We are grateful to M. Sanders for kindly providing pOvalb-CAT. We would also like to thank M. Morrison and D. Ankrapp for helpful suggestions during the course of this work. This work was supported by award DAMD1794-J-4372 to RJM from the US Army Breast Cancer Research Program .

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FIGURE LEGENDS

Fig.1. Comparison of ER α mRNA Splicing Variants and wt ER α Structure

The diagram depicts the various functional domains of the receptor and the exon sequences from which they are derived. The variants are referred to by deleted exon and are labeled in the left column. The size and molecular weight of each variant is predicted from the translational reading frame of the sequenced cDNA clones. The nuclear localization signal is circled. The regions encompassing the DNA- and hormone-binding domains are marked by darkened and striped boxes, respectively, where they are expressed. The AF-1 and AF-2 domains are indicated where they reside within the N- and C-termini, respectively, of the wild type receptor.

Fig. 2. Efficient *In Vivo* Expression of wt ER α and ER α Splicing Variants

Immunoblot analysis indicates that the molecular weight of each variant is consistent with its predicted translational reading frame. Samples containing 20 μ g of protein from cell extracts were analyzed on a 10% SDS-polyacrylamide gel probed with the ER α -specific antibody, Mab-17. The figure is representative of three independent Cos7 transfection experiments.

Fig. 3. Gel Mobility Shift Assay to Assess the DNA-Binding Activity of ER α mRNA Splicing Variants

A gel mobility shift assay of lysate from 17 β -estradiol treated, transiently transfected Cos7 cells confirms that wt ER α binds efficiently to a ^{32} P-labeled consensus estrogen response element. Confirmation that the indicated band represents an authentic ER α /DNA complex is provided by the ability of an ER α -specific monoclonal antibody (Mab-17) to supershift this complex (compare lane 4 with lane 3). In contrast, all of the splicing variants display strong defects in DNA-binding. In this representative assay, weak binding of ER Δ E5 and ER Δ E7 to the ERE can only be observed when their respective DNA complexes are stabilized by the addition of the ER α -specific antibody (lanes 12 and 16). Position of the antibody-supershifted complex is indicated by an asterix.

Fig. 4. Ligand Binding of ER α and ER α mRNA Splicing Variants.

A, Ligand-binding capacity was assessed by measuring the specific association of 10 nM ^{3} H-17 β -estradiol with wt ER α and its splicing variants expressed in Cos7 cells, using the DCC method. Only wt ER α and the ER Δ E3 variant demonstrate specific binding of estradiol. B, Confirming the ligand binding results, ER Δ E3 and wt ER α are the only isoforms of the receptor observed to display specific cell staining using a fluorescent estrogen analogue (nitrile THC) to treat transiently transfected into Cos7 cells. C, Scatchard analysis shows that wt ER α and ER Δ E3 have similar affinities for 17 β estradiol.

Fig. 5. Localization of ER α and ER α Splicing Variants by Confocal Microscopy

Receptor isoforms were detected by immunofluorescence staining with an ER α -specific monoclonal antibody (Mab-17) and a rhodamine-conjugated secondary antibody. The upper left panel shows a representative field from control cells transfected with empty expression vector (pCMV4). Specific immunoreactivity can be observed in all other frames. Cells expressing wt ER α , ER Δ E3 and ER Δ E5 demonstrate strong nuclear staining in confocal sections. ER Δ E2, ER Δ E4, ER Δ E6 and ER Δ E7 are predominately localized to the cytoplasm. Bar, 10 μ m.

Fig. 6. ER Δ E3 and ER Δ E5 Inhibit Transactivation of a consensus ERE

Reporter by wt ER α in a Dose-Related Fashion

HeLa cells were cotransfected with 15 μ g of pERE-TK-CAT reporter gene, 1 μ g of wt ER α expression vector and increasing amounts of expression vectors for ER Δ E3 or ER Δ E5. The ratios of wt ER α to variant expression plasmid used in each transfection are indicated. The total amount of DNA in each transfection was held constant with the addition of empty expression vector, pCMV4. Reporter gene expression was normalized by measuring CAT activity in aliquots representing 100 μ g of soluble protein.

Fig. 7. Transcriptional Activity of wt ER α and Receptor Variants

Only ER Δ E3 and ER Δ E5 supports CAT gene expression from the ovalbumin promoter, similar to wt ER α . HeLa cells were cotransfected with 10 μ g of reporter (pOvalb-CAT) and 0.5 μ g of the indicated ER α expression vector followed by 24 hours of hormone treatment in the presence of 5% charcoal-treated calf serum. Cultures were treated as indicated: vehicle control; 2×10^{-8} M PMA; 10^{-8} M 17 β -estradiol (E); E+PMA; and 10^{-7} M Tamoxifen (T) or T+PMA. CAT assays were normalized for protein. Values are expressed relative to vehicle-treated empty expression vector, pCMV4. Error bars represent the standard error of the mean of three independent experiments. As shown in the insert, none of the ER α splicing variants tested are strong activators of the ERE driven CAT reporter gene (pERE-TK-CAT) in HeLa cells.

Figure 1

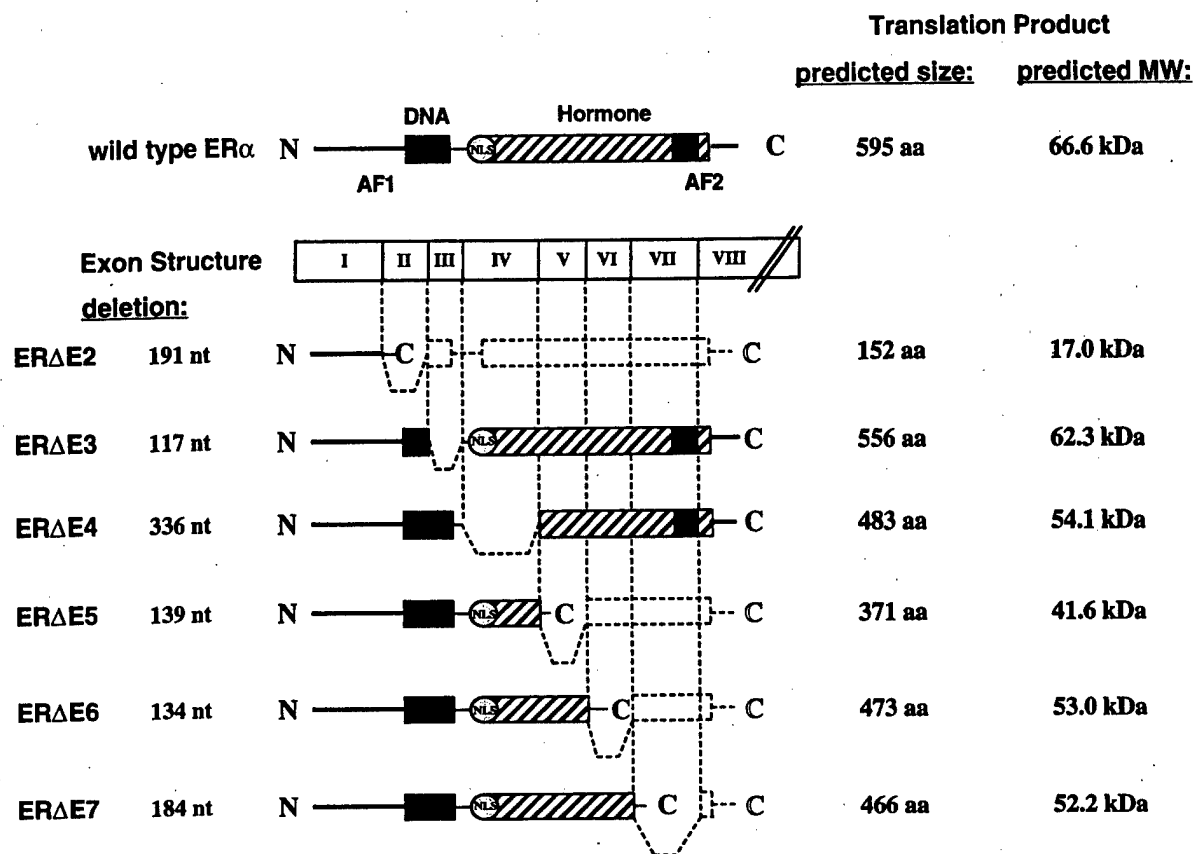


Figure 2

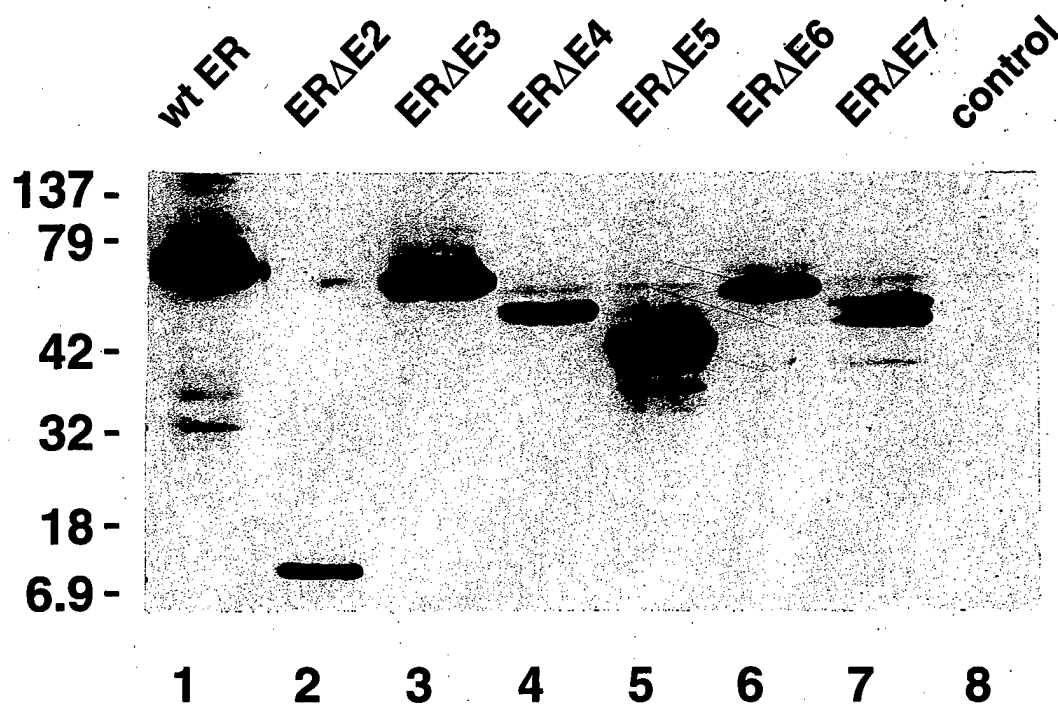


Figure 3

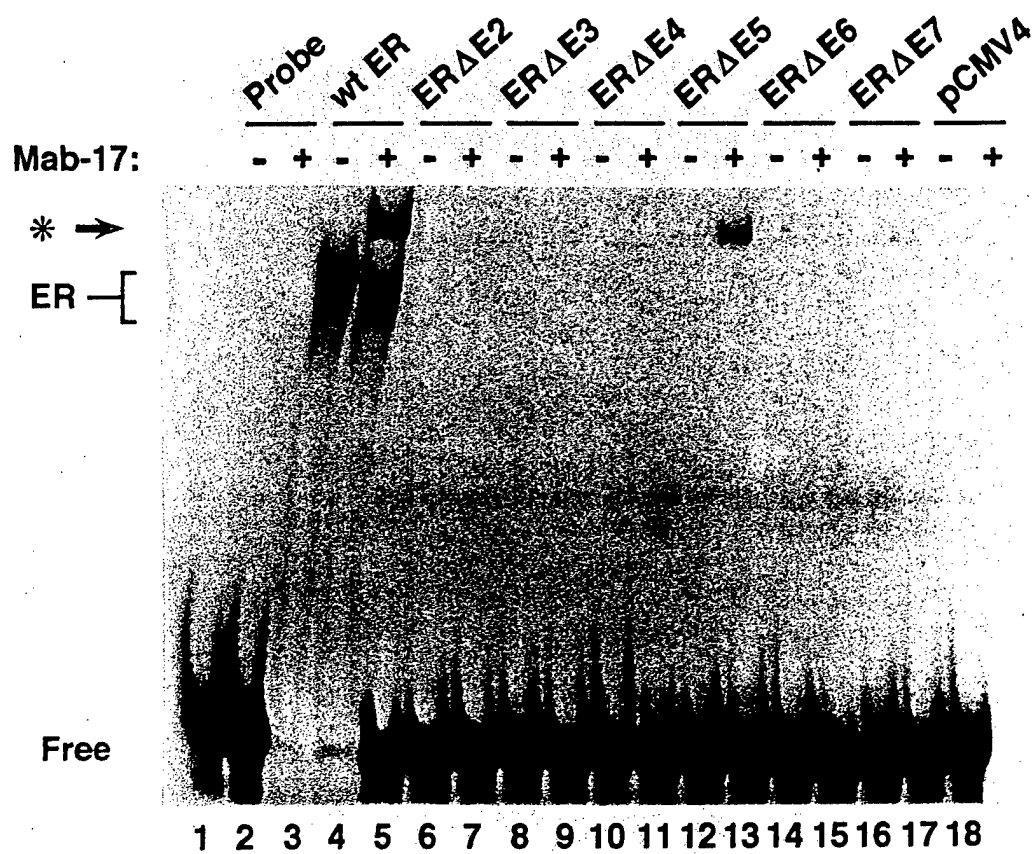
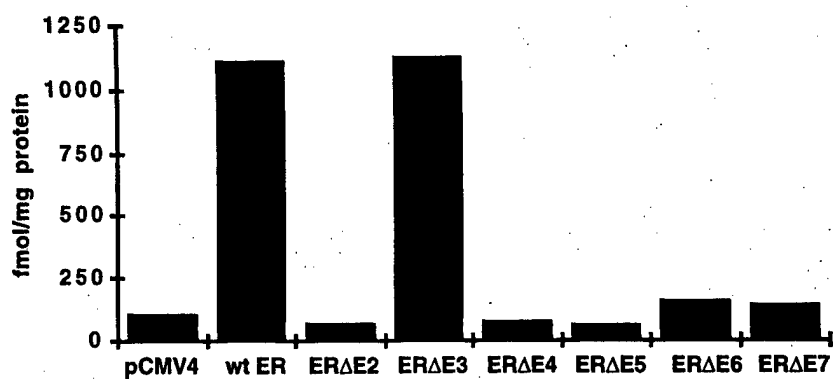
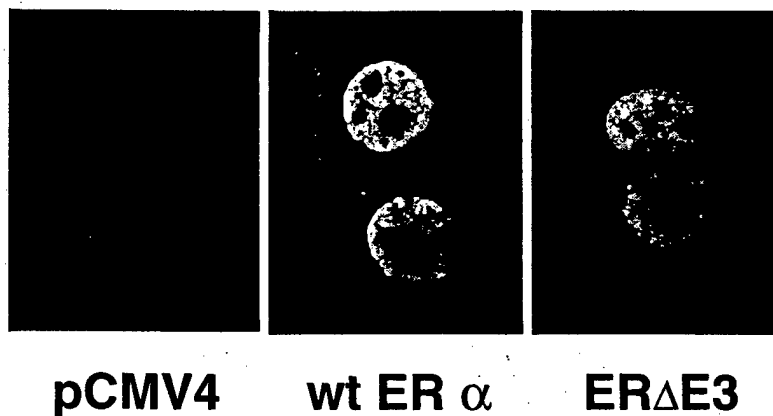


Figure 4

A.



B.



C.

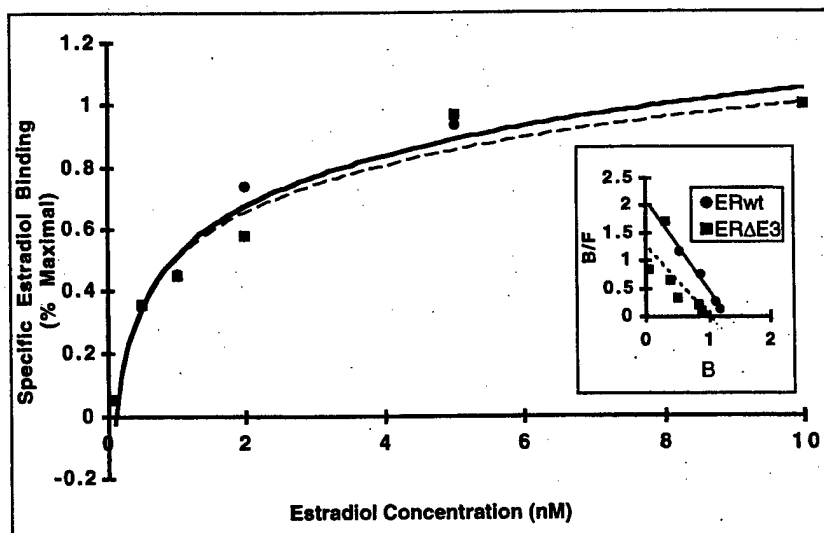


Figure 5

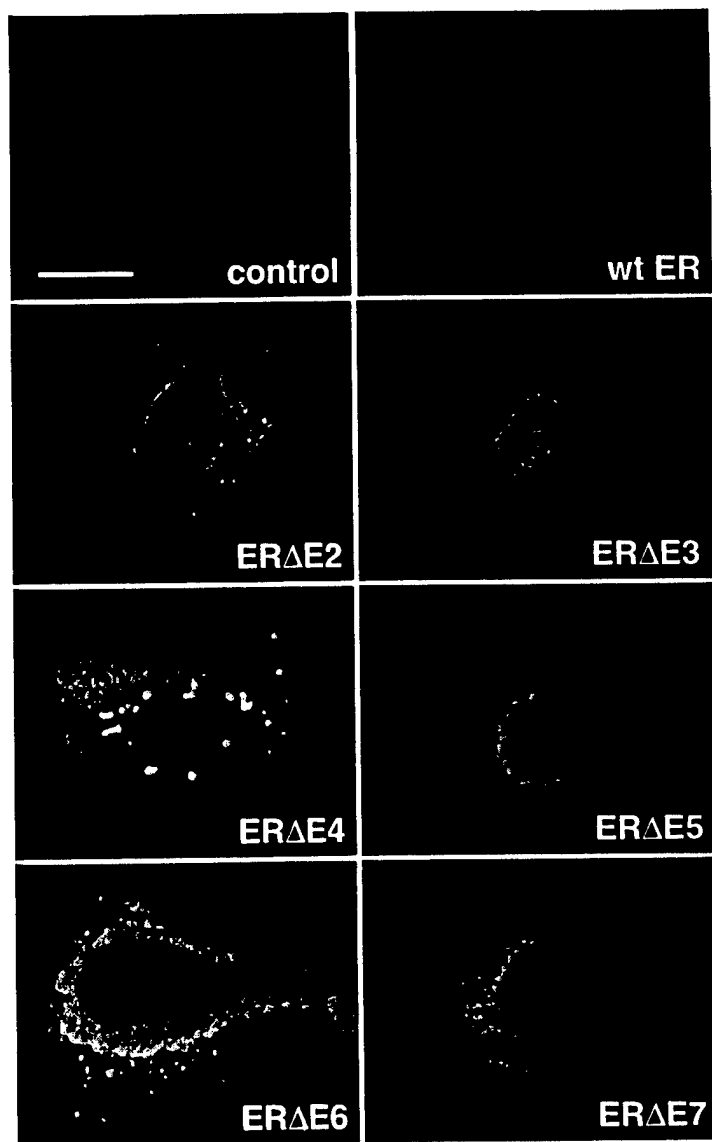


Figure 6

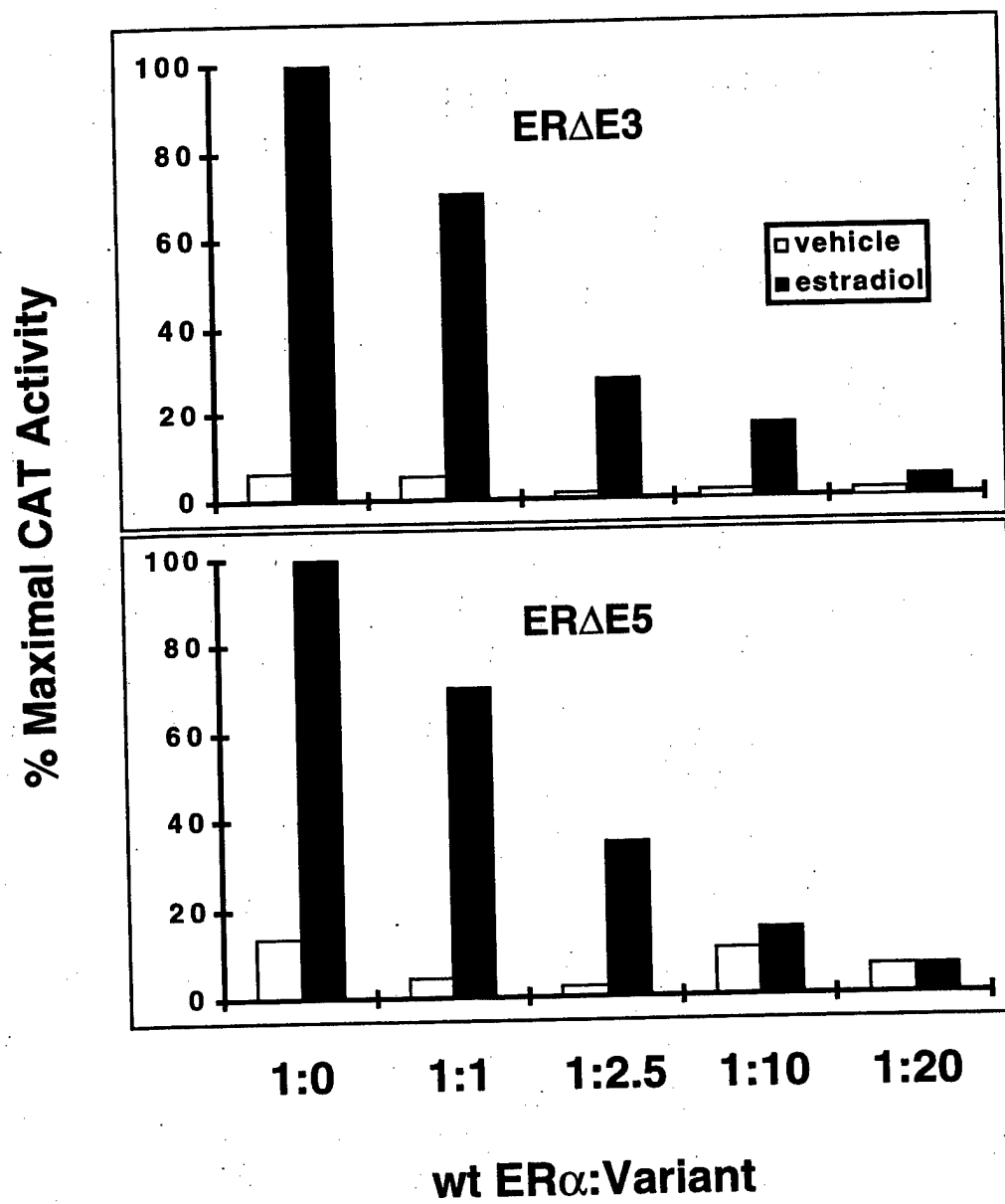


Figure 7

