Binding of type II nuclear receptors and estrogen receptor to full and half-site estrogen response elements *in vitro*

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ABSTRACT

The mechanism by which retinoids, thyroid hormone (T$_3$) and estrogens modulate the growth of breast cancer cells is unclear. Since nuclear type II nuclear receptors, including retinoic acid receptor (RAR), retinoid X receptor (RXR) and thyroid hormone receptor (TR), bind direct repeats (DR) of the estrogen response elements (ERE) half-site (5′-AGGTCA-3′), we examined the ability of estrogen receptor (ER) versus type II nuclear receptors, i.e. RARα, β and γ, RXRβ, TRα and TRβ, to bind various EREs *in vitro*. ER bound a consensus ERE, containing a perfectly palindromic 17 bp inverted repeat (IR), as a homodimer. In contrast, ER did not bind to a single ERE half-site. Likewise, ER did not bind two tandem (38 bp apart) half-sites, but low ER binding was detected to three tandem copies of the same half-site. RARα, β or γ bound both ERE and half-site constructs as a homodimer. RXRβ did not bind full or half-site EREs, nor did RXRβ enhance RARα binding to a full ERE. However, RARα and RXRβ bound a half-site ERE cooperatively forming a dimeric complex. The RARα–RXRβ heterodimer bound the *Xenopus* vitellogenin B1 estrogen responsive unit, with two non-consensus EREs, with higher affinity than one or two copies of the full or half-site ERE. Both TRα and TRβ bound the full and the half-site ERE as monomers and homodimers and cooperatively as heterodimers with RXRβ. We suggest that the cellular concentrations of nuclear receptors and their ligands, and the nature of the ERE or half-site sequence and those of its flanking sequences determine the occupation of EREs in estrogen-regulated genes *in vivo*.

INTRODUCTION

Retinoic acid is critical in mediating differentiation and development (1,2). Retinoids inhibit the initiation and promotion of mammary tumors in rats treated with 7,12-dimethylbenz(a)anthracene or *N*-methyl-nitrosourea (3). Similarly, treatment of MCF-7 human breast cancer cells with all-*trans* retinoic acid (tRA), 9-*cis* RA and other retinoids; vitamin D$_3$ (VD$_3$) or four VD$_3$ analogs, inhibited

E$_2$-stimulated cell proliferation (4–6). However, the usefulness of retinoids is limited by their undesirable side effects and teratogenicity (reviewed in 7). These findings have generated a search for synthetic retinoids whose selectivity and efficacy might render them useful as chemopreventative or chemotherapeutic agents.

Retinoid action is mediated by nuclear receptor proteins, retinoic acid receptor (RARα, β and γ) and retinoid X receptor (RXRα, β and γ) (reviewed in 8), by cellular retinoic acid binding proteins I and II, and cellular retinol-binding proteins (reviewed in 9). Estrogen action is mediated by hormone binding to the estrogen receptor (ER), a transactivating enhancer protein that is a member of the ligand-activated steroid/nuclear receptor gene superfamily (8). RAR, ER and other nuclear receptors have two highly conserved regions: the ligand binding (E) and the DNA-binding (C) domains. Ligand binding initiates a series of steps leading to an 'activated', homodimeric E$_2$–ER that binds with high affinity to estrogen response elements (ERE). Sequence analysis of the 5′ regulatory regions of numerous estrogen responsive genes revealed a 13 bp minimal palindromic ERE consensus sequence: 5′-GGTCAnnnTGACC-3′ (EREc). EREc conferred estrogen responsiveness to reporter genes analyzed by transfection assay (10,11). Some genes, e.g. *Xenopus* vitellogenin A2 (12) and the human oxytocin gene (13), contain a single perfect or sequence variant copy of EREc. Other estrogen responsive genes, e.g. *Xenopus* vitellogenin B1 (14), the rat progesterone receptor (PR) (15) and human c-fos (16), contain multiple copies of EREc, usually with one or more base changes that function synergistically to induce E$_2$-dependent gene expression *in vivo* (15,17,18). Other estrogen regulated genes, e.g. ovalbumin and prolactin, contain multiple copies of the ERE half-site, but not the palindrome (19). These genes are also regulated by the type II nuclear receptors including RAR and RXR (19). Recent studies demonstrated that ER binds variously spaced direct repeats (DR) of the ERE half-site motif, albeit with significantly lower affinity than ER binding to EREc (19,20).

Once bound to DNA, the precise mechanism of transcriptional activation, or repression, by nuclear receptors is unknown. ER-mediated effects on transcription involve interaction between the DNA-bound ER and transcription factors, adaptor proteins, e.g. ERAP160, RIP140, SPT6, SRC-1, TIF1, SUG1 or components of the TATA binding complex including TFIIB and TBP (reviewed in 21).

Table 1. Sequences of estrogen responsive elements

Name	Sequence
EREc38	5′-C**AGGTCA**GAG**TGACCT**GAGCTAAAATAACACATTCAG-3′
EREm(–)	5′-C**GGTCA**CTC**TGACC**-3′
1/2EREc	5′-C**AGGTCA**GAG*CATTTC*GAG-3′
1/2EREc38	5′-C**AGGTCA**GAG*CATTTC*GAGCTAAAATAACACATTCAG-3′
1/2ERE3'c38	5′-C*CCTAAG*GAG**TGACCT**GAGCTAAAATAACACATTCAG-3′
VITB1ERU	5′-CCTCC**AGTCA**CTG**TGACCC**AACCC**AAGTTA**TC**ATGACCT**CTTACACATTCAG-3′
VIT 1B1	5′-CCTCC**AGTCA**CTG**TGACC**CAACCACACATTCAG-3′
VIT 2B1	5′-ACC**AAGTTA**TC**ATGACCT**CTTAACACATTCAG-3′
EREc3AΔT	5′-C**CAGGTCA**GAG**TGTCCTG**AGCTAAAATAACACATTCAG-3′
βRARE	5′-CGCGTGGGTAGG**GTTCAC**CGAAA**GTTCAC**TCGA-3′ (DR5)

The underlined nucleotides correspond to the minimal EREc. The *Xenopus* Vitellogenin B1 (Vit B1) gene estrogen responsive unit (ERU) consists of two imperfect EREs (67). The βRARE is a synthetic version of the mouse RAR type β gene (68).

The specificity of type II nuclear receptor–DNA binding is determined by the number of bases separating the direct repeats (DR) or inverted repeats (IR) of the ERE half-site: 5′-AGGTCA-3′ (reviewed in 22). Initial studies showed no binding of TRα or TRα–RXRα to an ERE (23), leading to the model that TR bound specifically to a DR with a 4 bp spacer (DR4) or an IR with no separation between the half-sites (IR0) (reviewed in 22,24). However, type II nuclear hormone receptors including TR (25) and peroxisome proliferator-activated receptor (PPAR) bind EREs as heterodimers with RXR (26,27). RXR also forms heterodimers with RAR and vitamin D_3 receptor (VDR) resulting in DNA binding cooperativity (22,23,28,29). In contrast, RXR did not enhance binding of ER to the vitellogenin ERE or form a heterodimer with the ER (30,31).

It is still unclear what nucleotide arrangements, or those of sequences flanking the recognition element, are essential for nuclear receptor binding and transactivation. Studies are needed to determine whether specific nuclear receptors synergize with or antagonize one another and the mechanisms behind such activities. For example, co-expression of *v-erbA* in MCF-7 cells inhibited E_2-mediated transactivation from an *ERE–CAT* reporter construct (32) and VDR and RAR were hypothesized to bind to the ERE or to indirectly impair ER–ERE binding (33). Recent work demonstrated that the '3, 4, 5 rule' of DR element spacing specificity of type II receptors is relaxed with DR spaced ≥10 bp apart, resulting in 'promiscuous elements' that bind and respond to RAR–RXR, VDR–RXR and ER, but not to TR–RXR or to progesterone receptor (PR) (19). Together, these results indicate a new dimension of 'cross talk' between nuclear receptors, e.g. competition for binding to 5′-AGGTCA-3′. The dissection of the molecular basis by which ER and other nuclear receptors activate or inhibit gene expression from this common motif is important for elucidating mechanisms controlling estrogen-regulated gene transcription.

To determine whether type II nuclear receptors bind directly to EREs, we examined the binding of ER, TR, RAR and RXR to various EREs *in vitro*. The palindromic EREs used in these experiments include a perfect consensus ERE, featuring a 17 bp inverted repeat (IR) and flanked by a naturally-occurring AT-rich region (34), a 13 bp minimal ERE, an ERE half-site alone or in the presence of a naturally occurring AT-rich flanking region (35), and the estrogen response unit (ERU), featuring two imperfect EREs, of the *Xenopus* vitellogenin B1 gene (17). Our results demonstrate that individually RARα, β and γ, TRα or β and ER

bind fully palindromic EREs as a homodimer and that RAR and TR bind full and half-site EREs as heterodimers with RXR. The results of our studies suggest that the cellular levels of the nuclear receptors and their ligands and the nature of the nucleotide sequence of the promoter region are important for determining receptor–DNA interaction.

MATERIALS AND METHODS

Preparation of ERE containing plasmids

The sequences of synthetic ERE oligonucleotides are given in Table 1. Double stranded ERE oligomers were cloned into pGEM-7Zf(+) (Promega, Madison, WI) as described (35–37).

Preparation of estrogen receptor

ER was partially purified from calf uterus by heparin agarose affinity chromatography (35). ER was liganded with either 17β-[2,4,6,7,16,17-^{3}H]E_2 (142 Ci/mmol from NEN), (Z)-4-hydroxytamoxifen (4-OHT) (Research Biochemicals International, Natick, MA), or [ring-^{3}H]- tamoxifen aziridine ([^{3}H]TAz, 23 Ci/mmol from Amersham). The concentration of ER was determined by adsorption to hydroxyapatite (HAP) (47). All receptor concentrations refer to dimeric ER, i.e. with two molecules of ligand bound. All referrals to 'partially purified' ER indicate the post-heparin agarose ER. When using 4-OHT, the 4-OHT-ER was protected from exposure to light.

Preparation of RARα, RARβ, RARγ, RXRβ, TRα and TRβ

Full length human RARα, RARβ, RARγ and RXRβ were expressed in Sf9 insect cells using the baculovirus expression vector system (BEVS) (39). Sf9 cells in the log-phase of growth were inoculated with 10 p.f.u. of recombinant or wild-type baculovirus per cell and harvested 72 h post-infection. The cells were washed in 1× PBS and in 1× hypotonic buffer containing protease inhibitors. Following resuspension, the cells were allowed to swell in this buffer for 20 min at 4°C and lysed by Dounce homogenization. The cytoplasmic and nuclear pellet were separated by centrifugation. The nuclear pellet was resuspended in extraction buffer (0.05 M Tris–HCl pH 7.4, 10% glycerol, 0.01 M monothioglycerol, 1 mM EDTA, 1 mM PMSF and 2 µg/ml each of aprotinin, leupeptin and pepstatin), sonicated 3 × 10 s bursts, incubated 2–3 h (4°C) and sedimented at 100 000 *g* to obtain a soluble nuclear extract (NE) that was quickly frozen and stored at –80°C.

Preparation of TRα and TRβ

Purified, full length human recombinant TRα and TRβ, expressed in Sf9 insect cells using the baculovirus expression vector system, were obtained from Karo-Bio AB, Huddinge, Sweden.

Microtiter well plate assay of ER binding to plasmid DNA

The microtiter (well) plate assay for measuring [^{3}H]liganded-ER binding to DNA has been previously described (40). This is an equilibrium binding assay that quantitates ER–ERE binding based on [^{3}H]ligand and [^{35}S]DNA retention in specially treated microtiter wells. For each of the experiments presented here, plasmid DNA was linearized with *Eco*RI. Aliquots of *Eco*RI-digested plasmid DNA were labeled by incorporation of [^{35}S]dATP (>600 Ci/mmol, NEN) using the Klenow fragment of *Escherichia coli* DNA polymerase I (New England Biolabs, Beverly, MA) and mixed with unlabeled *Eco*RI-digested DNA for the desired final concentration.

Briefly, for saturation binding analysis, various concentrations of partially purified [^{3}H]E$_2$-ER was preincubated with ~0.22 nM of [^{35}S]DNA (plasmid DNA with or without ERE) for 2.5 h at 4°C, with shaking, in TDPK 100 buffer (TDP buffer containing 100 mM KCl) containing 0.1% NP-40. Aliquots of 50 μl of the receptor–DNA equilibrium mixture were then incubated in histone/gelatin-coated microtiter wells for 2.5 h at 4°C with shaking. Wells were rinsed, and the radioactivity in the wells was counted using EcoScint A (National Diagnostics, Atlanta, GA). Calculation of specific [^{3}H]E$_2$-ER, [^{3}H]4-OHT-ER, or [^{3}H]TAz-ER binding to EREs was previously described, with binding to pGEM-7Zf(+) plasmid alone subtracted from binding to plasmid containing an ERE (35,40).

Gel mobility shift assay

Gel mobility shift assays were performed as described (41–42), with the following ^{32}P-labeled DNA oligomers, obtained by *Eco*RI–*Bam*HI digestion of insert-containing pGEM-7Zf(+): EREc38, 1/2/EREc38 and 1/2ERE3'c38 (each 77 bp); EREm(–) (54 bp); 1/2EREc (54 bp); Vit B1ERU (85 bp), VIT 1B1 (66 bp) or VIT 2B1 (65 bp). Typical binding reactions contained 10 fmol (25 000 d.p.m.) ^{32}P-labeled DNA and ER and other reaction components indicated in the Figure legends. Reactions were incubated on ice for 2.5 h before 40 μl aliquots were loaded on 4% non-denaturing polyacrylamide gels and subjected to electrophoresis at 200 V in 0.5× TBE (0.05 M Tris, 41 mM boric acid, 0.5 mM EDTA, pH 8.3) for 2 h 20 min at 4°C. Gels were dried and autoradiographed on Kodak X-OMAT-AR film (Eastman Kodak Co., Rochester, NY) with an intensifying screen (Lightning Plus from DuPont, Wilmington, DE).

ER antibody H222, a generous gift from Abbott Laboratories (Abbott Park, IL), was diluted 1:10 in TE. One μl was added to confirm the identity of ER in ER–ERE complexes. Monoclonal anti-ER antibodies AER304, AER314, AER308, AER315, AER303, AER310, AER311, AER317 and AER320 were a generous gift of Neomarkers (Fremont, CA).

Antibodies for RARα. Synthesis and purification of the oligopeptides was as described previously (43). The antisera was tested by ELISA and those with a positive titer were tested by western blot analysis, sucrose density gradients and gel shift assays (39).

Two site-directed polyclonal antibodies to RARα were raised against two oligopeptides from the N-terminal region of RARα. Polyclonal antibody R1AB was raised against a polypeptide encompassing amino acids 63–77 (TQSSSSEEIVPSPPS). Polyclonal antibody γNTB (also called rNTAB) was raised against an oligopeptide corresponding to the residues between 55 and 68
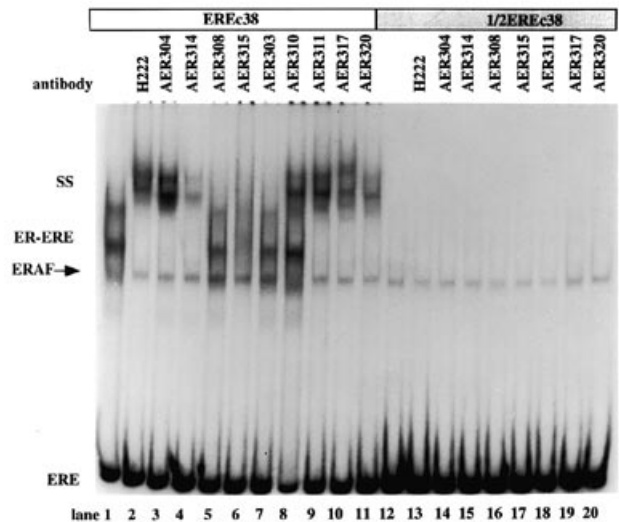
Figure 1. ER binds EREc38, but not 1/2EREc38. ^{32}P-oligomers of a single copy of EREc38 (lanes 1–11) or 1/2EREc38 (lanes 12–20) (25 000 d.p.m. per reaction) were incubated with partially purified E$_2$–ER (8.69 nM, 124 fmol/lane) for 2.5 h at 4°C. Anti-ER antibody H222 (0.1 μl) was added to the reactions for lanes 2 and 13. ER-specific AER antibodies (1 μl) were added to the reactions indicated. Aliquots (40 μl) of the reaction mixture were loaded onto 4% polyacrylamide gels and run as described in Materials and Methods. Each lane contained 10 fmol DNA. SS indicates the supershifted ER–ERE complex. COUP-TF binding to 1/2EREc38 is indicated by the arrow. This experiment was repeated using two different preparations of ER with identical results.

(STPSPATIETQSSS) of RARα. These antibodies recognized RARα by western blot and sucrose density gradient analyses. The antibodies did not recognize ER, PR, GR or AR, suggesting receptor specificity (39). Polyclonal antibody γNTB also recognized RARβ and RARγ by western blot and gel shift assays. Monoclonal antibodies to RARα and γ were prepared by standard hybridoma technology using partially purified RARα or γ as the antigen inoculated into mice. Western blot analysis with authentic RARα or γ was used to insure specificity.

PPAR antibody was a gift from Dr Michel Dauça (Université de Nancy I, France). RXR polyclonal antisera was a generous gift from Dr Pierre Chambon (CNRS, INSERM, Université Louis Pasteur, Strasbourg, France). Monoclonal antibody (9A7γ) to the VDR was a generous gift from Dr Mark R. Haussler of the University of Arizona. Monoclonal antibodies to TRα and TRβ were purchased from Affinity BioReagents (Golden, CO). Polyclonal antisera to COUP-TF was a generous gift from Dr Sophia Y. Tsai of Baylor University (Houston, TX).

The amount of receptor–DNA complex formed and that of free DNA were determined by excision of the entire corresponding regions from the dried gels and measuring the radioactivity present. The fraction of total [^{32}P]DNA in the receptor–DNA complex [F(t)] was calculated as follows (44): F(t) = (c.p.m. in the receptor–DNA complex)/(total c.p.m. in the lane), where the (total c.p.m. in the lane) = (c.p.m. in free DNA) + (c.p.m. in the receptor–DNA complex).

RESULTS

ER binds EREc38 but not an ERE half-site *in vitro*

We examined the ability of partially purified E$_2$-liganded ER (E$_2$-ER) to bind to a consensus ERE, EREc38 derived from three
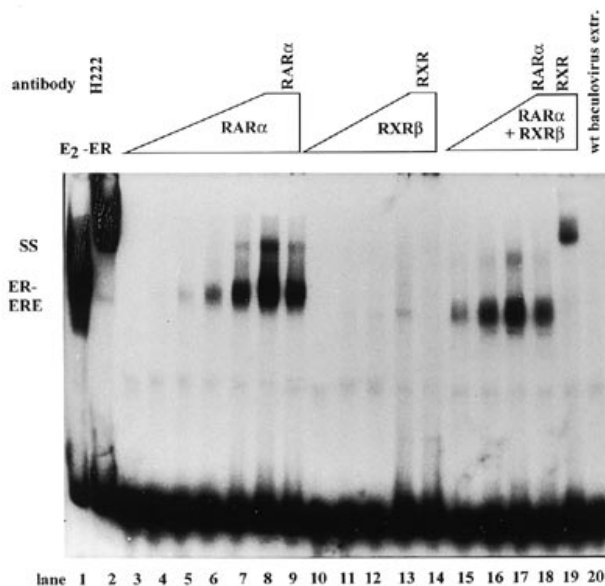
Figure 2. RARα binds EREc38 with higher affinity than RXRβ and RARα–RXRβ heterodimers *in vitro*. Gel mobility shift assay of receptor–EREc38 binding. Partially purified E$_2$–ER (162 fmol/lane) was incubated with EREc38 (lanes 1 and 2) and H222 (0.1 µl) was added to the reaction in lane 2. Increasing amounts of nuclear extracts from Sf9 insect cells expressing recombinant human RARα (0, 0.2, 0.5, 1, 2 and 3 µl per reaction for lanes 3–9) were preincubated with EREc38. Reactions in lanes 10–14 contained 0, 0.5, 1 and 1 µl RXRβ cell extract respectively, preincubated with EREc38. Lanes 9 and 14 included 0.5 µl MoAb antibody to RARα or RXR respectively. For the reactions in lanes 15–19 equal volumes (0.2, 0.5 and 1 µl in lanes 15–19) of RARα and RXRβ cell extracts were preincubated for 1 h at 4°C with [^{32}P]EREc38 and RARα MoAb (lane 18) or RXR MoAb (lane 19) (1 µl/reaction volume). Reactions were incubated for 2.5 h at 4°C prior to electrophoresis as described in Figure 1. The reaction in lane 20 included 4 µl nuclear extract from wt baculovirus-transfected Sf9 cells. Each lane contained 10 fmol DNA.

highly estrogen-responsive genes (34), versus a half-site ERE, 1/2EREc38 which lacked the 3′ERE half-site but was otherwise identical in sequence to EREc38 (Fig. 1, sequences in Table 1). We detected an ER–EREc38 binding complex of which 85% was supershifted by the ER-specific antibody H222. This result together with our previous work (35–37,41–43,45,46), in which we quantitated both the amount of receptor, based on [³H]ligand, and DNA, based on ³⁵S incorporation, indicates that E$_2$-ER binds EREc38 as a homodimer. Approximately 15% of the ER–ERE complex detected was not ER. This is indicated by the inability of H222, or any of the ER-specific antibodies tested, to shift or inhibit the appearance of this complex. Because these antisera recognize epitopes spanning the entire ER protein from N-terminal A/B to C-terminal F domains (47), this result appears to rule out the possibility that the non-supershifted complex is formed by an ER proteolytic product, unless the epitope is not recognized under these assay conditions. A complex of similar mobility, but that did not contain ER, was detected when examining the binding of partially purified ER to an ERE half-site (1/2EREc38; Fig. 1, lanes 12–20). Recent experiments revealed that this complex includes COUP-TF (data not shown). The specificity of COUP-TF–1/2EREc38 or EREc38 binding was demonstrated by competition with unlabeled EREc38, 1/2EREc38 and the 17 bp core ERE IR, but not by the AT-rich region that flanks the ERE IR in EREc38 or by the region in the
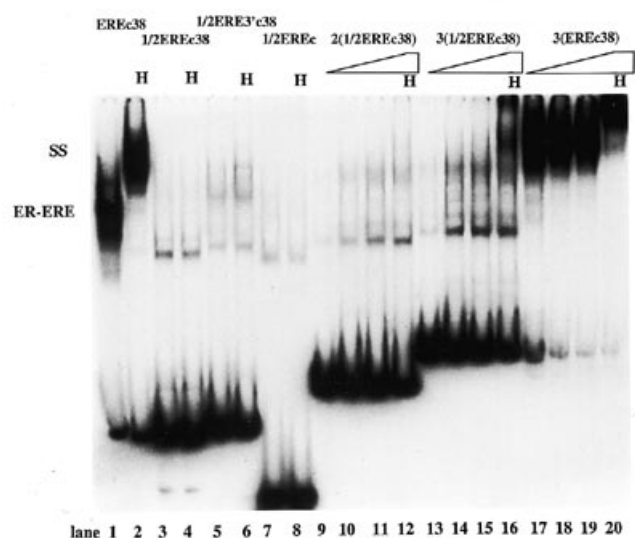

Figure 3. ER binds select ERE half-site constructs. Partially purified TAz-ER (100 fmol per lane) was incubated with ^{32}P-oligomers (25 000 d.p.m. per reaction) containing EREc38 (lanes 1 and 2), 1/2EREc38 (lanes 3 and 4), 1/2ERE3'c38 (lanes 5 and 6), 1/2EREc (lanes 7 and 8). Increasing concentrations of TAz-ER (50, 100, 126 and 126 fmol per lane for lanes [9–12, 13–16 and 17–20] respectively were incubated with ^{32}P-oligomers (25 000 d.p.m. per reaction) containing two tandem copies of 1/2EREc38 [2(1/2EREc38)] (lanes 9–12), three tandem copies of 1/2EREc38 [3(1/2EREc38)] (lanes 13–16) or three tandem copies of EREc38 [3(EREc38)] (lanes 17–20). Reactions in lanes 2, 4, 6, 8, 12, 16 and 20 included 0.1 µl H222 (indicated as an H at the top of the gel). Reactions were incubated under conditions as described in Figure 1 and separated on 4% polyacrylamide gels as described in Materials and Methods. Each lane contained 10 fmol DNA.

pGEM-7Zf(+) plasmid into which the EREs were cloned (data not shown).

RARα, β, γ and RXRβ bind EREc38, but not EREm(–)

To determine if select type II nuclear receptors are capable of binding a full length consensus ERE, the ability of baculovirus-expressed recombinant human RARα, RARβ, RARγ or RXRβ, individually and in combination, to bind to EREc38, 1/2EREc38 or EREm(–) was determined *in vitro*. These results were compared with those for the binding of partially purified calf uterine ER to the same constructs. ER, liganded with E$_2$, binds EREc38 with high affinity and a stoichiometry of one E$_2$–ER dimer per ERE (35–37,41–43). Incubation of EREc38 with RARα produced a complex, similar in mobility to that of ER–EREc38 (Fig. 2). Addition of a monoclonal antibody (MoAb) to RARα slightly inhibited the amount of complex formed. Addition of polyclonal RAR antibody R1AB supershifted and enhanced the amount of RARα homodimer bound to EREc38 (data not shown). Incubation of [^{32}P]EREc38 with NE from null baculovirus infected Sf9 cells formed only a rapidly migrating non-specific complex (Fig. 2). Binding specificity was also demonstrated by the ability of cold competitor EREc38 and βRARE to inhibit RARα–EREc38 binding in a dose-dependent manner (data not shown). RXRβ did not appear to bind EREc38 (Fig. 2). None of the RAR isoforms tested, i.e. α, β or γ, nor RXRβ bound to EREm(–) (data not shown).

Addition of equal amounts of NE containing RARα and RXRβ resulted in the formation of a complex whose migration was slightly faster than that of the homodimeric RARα–EREc38 complex (Fig. 2A). The amount of RARα/RXRβ–EREc38 complex formed was equal to that of the RARα–EREc38
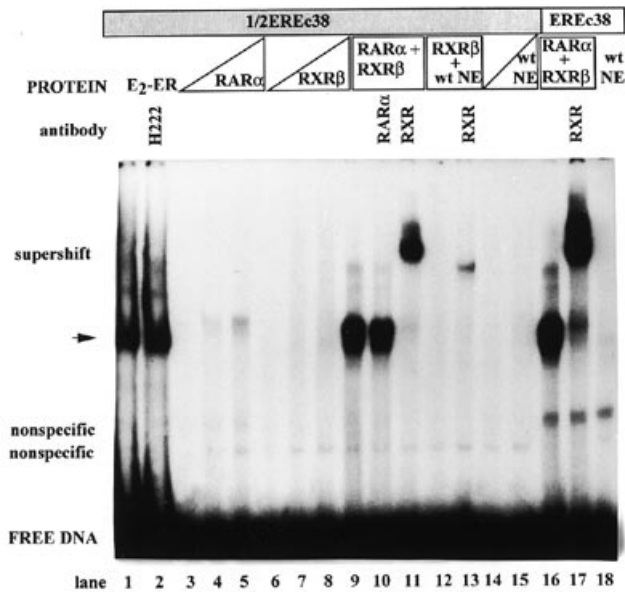
Figure 4. A heterodimer of RARα and RXRβ binds 1/2EREc38 with higher affinity than E₂–ER, RARα or RXRβ. Gel mobility shift analysis of ER, RARα or RXRβ binding to 1/2EREc38. Partially purified E₂–ER (162 fmol/lane) was incubated with 1/2EREc38 (lanes 1 and 2). H222, 0.1 µl, was added to the reaction in lane 2. The arrow at the left indicates the migration of ERAF bound to 1/2EREc38. Sf9 insect cell extracts containing RARα (lanes 3–5, 0.2, 0.4 and 0.8 µl respectively), RXRβ (lanes 6–8, 0.2, 0.5 and 1.0 µl respectively), RARα + RXRβ (lanes 9–11 and 16–17, 0.4 µl of each RARα + RXRβ per reaction per lane) were incubated with 1/2EREc38. MoAb to RARα (0.5 µl) was added to the reaction in lane 10. Antibody to RXRβ (0.5 µl) was added to the reactions for lanes 11, 13 and 17. Lanes 14, 15 and 18 include wt baculovirus-transformed Sf9 cell nuclear extract (0.4, 1.0 and 1 µl/reaction respectively) incubated with EREc38 (lanes 14 and 15) and EREc38 (lane 18). Reactions, containing 25 000 d.p.m. of [³²P]1/2EREc38, were incubated as described in Figure 1. Each lane contained 10 fmol DNA. Non-specific indicates complexes formed upon the addition of wt baculovirus-transformed Sf9 nuclear extract.

complex formed with the same amount of extract (Fig. 2B). The addition of a MoAb to RARα decreased the amount of complex formed. Addition of the R1AB RAR antisera, which did not itself bind EREc38, approximately doubled the amount of complex detected and supershifted ~50% of the bound complex (data not shown). Addition of a polyclonal RXR antibody supershifted the entire retarded complex, thus, demonstrating that the complex is a heterodimer of RARα and RXRβ.

ER does not bind to a single or two tandem copies of 1/2EREc38, but ER binds three tandem copies of 1/2EREc38

As shown in Figure 1, ER does not bind 1/2EREc38. Similarly, ER did not bind 1/2EREc or 1/2ERE3'c38, indicated by the lack of supershift with H222 (Fig. 3). In each case the binding activity detected to a half-site was attributable to COUP-TF (data not shown). Because recent reports indicate that ER can bind multiple ERE half-sites with variable spacing (19,20), we examined the ability of ER to bind two or three tandem copies of 1/2EREc38 (Fig. 3). ER did not bind two tandem copies of 1/2EREc38, but three tandem copies of 1/2EREc38 did bind ER. This is apparent by the formation of a slower migrating complex and the appearance of a 'supershifted' ER–ERE complex with the addition of H222 (Fig. 3, lane 16). This complex is also supershifted by AER304 (data not shown). The relative binding
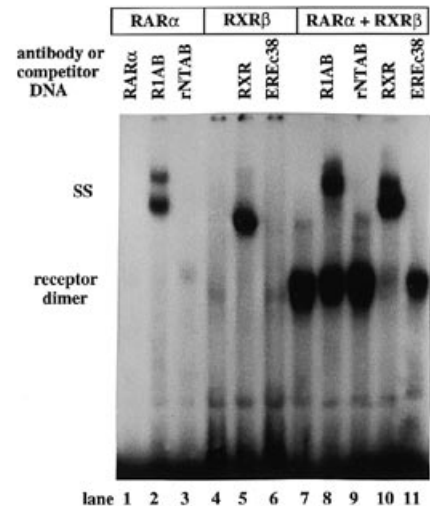
Figure 5. Specificity of the RARα–RXRβ heterodimer binding to 1/2EREc38. Gel mobility shift analysis of RARα or RXRβ binding to 1/2EREc38. Sf9 insect cell extracts containing RARα (0.5 µl/reaction for lanes 1–3), RXRβ (2.0 µl per reaction for lanes 4–6) or RARα + RXRβ (lanes 7–11, 0.4 µl of each per reaction) were incubated with [³²P]1/2EREc38 under conditions identical to those described in Figure 1. Antibody to RXRβ (1.0 µl) was added to the reaction for lanes 5 and 10. Polyclonal R1AB to RAR (1 µl) was added to the reactions in lanes 2 and 8 and polyclonal rNTAB to RAR (0.1 µl) was added to the reactions in lanes 3 and 9. 100-fold molar excess of EREc38 was added to the reactions in lanes 6 and 11.

affinity of ER for 3(1/2EREc38) is ~34% of ER binding to a single copy of EREc38 and 26% of that for ER binding to three tandem copies of EREc38 (data not shown). Based on our previous work (35–37,41–43), this yields an estimated K_d value of 0.92 versus 0.27 nM for ER–EREc38 interaction.

RARα, β and γ bind 1/2EREc38, but RXRβ does not

We next tested the ability of each RAR subtype, RXRβ, or combinations thereof, to bind a single ERE half-site *in vitro*. Although RARα was capable of binding 1/2EREc38 in a dose-dependent manner, more RARα was bound to EREc38 versus 1/2EREc38 (compare Figs 2, 4 and 5). Thus both halves of the ERE IR are required for RARα homodimer binding. Interestingly, RARα–1/2EREc38 corresponded in migration to a dimeric receptor complex. Addition of R1AB antibody enhanced the amount of RARα–1/2EREc38 detected (Fig. 5, lane 2). Similar results were detected for RARβ and RARγ (data not shown). The specificity of RARα binding was demonstrated by the ability of EREc38 and βRARE to inhibit RARα–1/2EREc38 binding, by the ability of the MoAb to RARα to decrease the amount of complex formed, and by the supershift of RARα with R1AB. RXR antibody had no effect on RARα–1/2EREc38 binding (data not shown), indicating that the Sf9 NE did not contain an RXR related activity. Neither R1AB nor the RXR antibody bound EREc38 or 1/2EREc38 (data not shown).

RXRβ did not appear to bind 1/2EREc38. This result indicates that binding of either EREc38 or 1/2EREc38 by RXRβ was of lower affinity compared with RARα and is consistent with the role of RXR as a dimerization partner for type II nuclear receptors that binds only certain RXREs as a homodimer (28). Addition of RXR antibody enhanced and supershifted the RXRβ–1/2EREc38 complex (Fig. 5, lane 5).

Table 2. Comparison of binding of 4-OHT–ER and RARα + RXRβ to Vitellogenin B1 ERU

| Fraction of total (d.p.m.) | Vit B1 ERU | | 1B1 | | 2B1 | | EREc38 | | 2(EREc38) | |
	ER	RARα + RXRβ	ER	RARα + RXRβ	ER	RARα + RXRβ	ER	RARα + RXRβ	ER	RARα + RXRβ
Bound	0.41	0.42	0.40	0.35	0.35	N.D.[a]	0.68	0.16	0.92	N.D.[a]
not SS by H222	0.24		0.26		0.17		0.07		0.02	
SS H222	0.48		0.22		0.24		0.78		0.94	

Receptor–ERE binding was determined by gel mobility shift assay and the total amount of shifted complex is given as F(t) values from two assays as described in Materials and Methods (44). ER (7.39 nM) was liganded with 4-OHT (84.4 fmol ER dimer per gel lane). Incubation of 4-OHT–ER with H222 increased the amount of complex formed.
[a]N.D., not determined.

RARα–RXRβ heterodimers bind cooperatively to 1/2EREc38, but not EREc38

Co-incubation of RARα and RXRβ with 1/2EREc38 produced a 5-fold increase in the amount of complex (Fig. 4, lanes 9–11 and Fig. 5, lanes 7–11). Similar results were obtained for RAR-α–RXRβ binding to 1/2ERE3'c38 and to two or three tandem copies of 1/2EREc38 (data not shown). The specificity of the RARα–RXRβ heterodimer was confirmed by the ability of R1AB and RXR antisera to supershift the complex. In addition, inclusion of 10-fold molar excess unlabeled EREc38 decreased complex formation by 41% (Fig. 5, lane 11).

Incubation of either 1/2EREc38 or EREc38 with NE from Sf9 cells transfected with wild-type (wt) baculovirus formed two complexes whose migration was faster than that of the ER–ERE complex (Fig. 3), and faster than the migration of the TR monomer complex (data not shown). In results similar to those for RARα alone, the amount of binding of the RARα–RXRβ to EREc38 was twice that of binding to 1/2EREc38. Addition of unlabeled competitor EREc38 or βRARE decreased the binding of RARα–RXRβ to EREc38 and 1/2EREc38, indicating binding specificity (data not shown).

RARα–RXRβ heterodimers bind naturally occurring EREs

We compared the binding of ER versus RARα or RXRβ to the *Xenopus* vitellogenin B1 estrogen responsive unit (ERU; Vit B1 ERU), consisting of two imperfect palindromic EREs, versus ER binding to each ERE alone (1B1 and 2B1) (sequences in Table 1). In contrast to the ability of two ER homodimers to bind to two tandem copies of EREc38, only a single homodimer of ER bound to the Vit B1 ERU (data not shown). The affinity of ER binding to the Vit B1 ERU was ~40% lower than binding to EREc38 (data not shown). To quantitate the affinity of ER binding to the Vit B1 ERU versus EREc38, equilibrium binding experiments were performed (40). E_2–ER bound Vit B1 ERU with considerably lower affinity than EREc38, $K_d = 7.17$ versus 0.24 or 0.27 nM, for Vit B1 ERU versus 1 or 2 tandem copies of EREc38 respectively (data not shown). The binding of ER to the individual EREs within the Vit B1 ERU, 1B1 and 2B1 was similar to that for ER binding to the Vit B1 ERU, i.e. one dimeric ER appeared to bind each construct. This is indicated by the proportion of [^{32}P]DNA complex retarded by ER gel shift assays shown in Table 2. These data also show that incubation with antibody H222 increased the amount of complex formed.

RARα and RXRβ appeared to bind cooperatively to VIT B1-ERU since the total complex formed in the presence of both was significantly greater than the sum of each alone (data not shown). RXRβ did not bind the Vit B1-ERU, 1B1 or 2B1 alone. Interestingly, the total RARα/RXRβ–VIT B1–ERU complex formed was twice that of RARα/RXRβ–EREc38 or RAR-α/RXRβ–1/2EREc38. However, the total amount of RAR-α/RXRβ–EREc38 complex was significantly less than that for ER–EREc38 and slightly lower than that for ER–VIT B1–ERU. By performing gel shift experiments in which the concentration of input [^{32}P]ERE was varied with a fixed volume of RAR NE, K_d values were calculated (data not shown). RARα bound EREc38 and 1/2EREc38 with $K_d = 1.24$ and 3.8 nM respectively. Similar values ($K_d = 0.77$ and 1.17 nM for EREc38 and 0.88 and 0.79 nM for 1/2EREc38) were obtained for RARβ and RARγ respectively. In comparison, a $K_d = 0.3$ nM was estimated for RARα–RXRβ binding to VIT B1 ERU (data not shown). We conclude that the RARα–RXRβ heterodimer binds VIT B1 ERU with higher affinity than EREc38 or 1/2EREc38.

TRα and TRβ bind EREc38 as monomers, homodimers or as heterodimers with RARα and RXRβ

Since TR was reported to bind an ERE and inhibit E_2-dependent transactivation (25) and a heterodimer of TRα and RXRβ was reported to bind to the vitellogenin A2 ERE *in vitro* (31), we evaluated the ability of recombinant baculovirus-expressed human TR to bind EREc38 individually or with the addition of RARα or RXRβ (Fig. 6). In contrast to our findings with ER, RARα and RARα–RXRβ, two specifically retarded TR-containing bands were observed. The faster migrating band represents TR monomer and the more slowly migrating complex is TR dimer. The monomer complex appeared first with low concentrations of TR whereas both complexes were formed at higher TR concentrations (Figs 6 and 7 and data not shown). Thus, in the absence of T_3 as ligand, both TRα and TRβ bound EREc38 as monomers as well as dimers. Inclusion of a small amount of either TRα- or TRβ-specific antibody did not affect the migration or amount of complex formed. Inclusion of higher antibody concentrations supershifted the complex (data not shown). Addition of RARα to the TRβ–EREc38 binding reaction decreased the amount of retarded complex detected by 20% (Fig. 6, quantitation not shown). One explanation for this result is that TRβ forms a non-productive heterodimer with RARα that is unable to bind DNA. Neither preincubation of RARα with the RARα MoAb, for 30 min at 4°C, nor inclusion of RARα MoAb with the ERE affected migration or amount of complex detected. As seen in all gel shift assays performed, RARα-specific MoAb did not supershift the DNA-bound RARα, but rather minimally inhibited RARα–DNA binding. In contrast, polyclonal RAR antisera, rNTAB and R1AB, supershifted the RARα–DNA
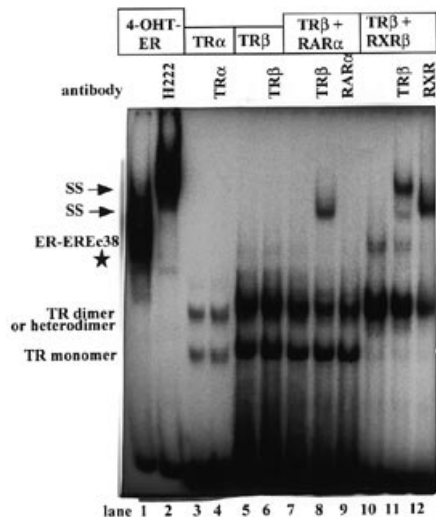
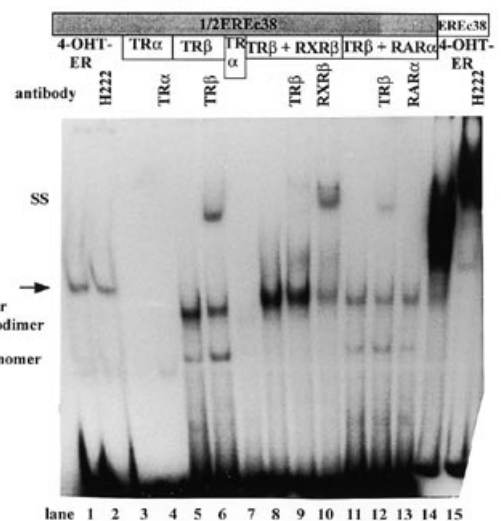**Figure 6.** TRα and TRβ bind as monomers, homodimers or as heterodimers with RARα and RXRβ to EREc38 *in vitro*. Gel mobility shift assay of ER or TR–EREc38 binding. Partially purified 4-OHT–ER (7.39 nM, 126 fmol/lane) was incubated with [^{32}P]EREc38 (lanes 1 and 2) or [^{32}P]1/2EREc38 (lanes 13–20) as described in Figure 1. In each reaction an identical concentration (25 000 d.p.m.) of [^{32}P]DNA was added (10 fmol/lane, final). H222, 0.1 μl, was added to the reaction in lane 2. Sf9 insect cell extracts containing recombinant baculovirus-expressed human TRα (5 μl, 20 nM monomer, 10 nM dimer) or TRβ (5 μl, 200 nM monomer, 100 nM dimer) were added to the reactions in lanes 3 and 4, and 5 and 6 respectively. Two μl of MoAb anti-TRα or anti-TRβ antibody was added to the reactions in lanes 4 and 6 respectively. Sf9 insect cell extract (0.4 μl) containing RARα was incubated with 5 μl TRβ for the reactions in lanes 7–9. Two μl MoAb anti-TRβ antibody and 5 μl MoAb RARα antibody were added to the reactions in lanes 8 and 9 respectively. RXRβ (0.4 μl) was incubated with 5 μl TRβ and [^{32}P]EREc38 for the reactions in lanes 10–12. Two μl MoAb anti-TRβ antibody and 0.3 μl anti-RXR antibody were added to the reactions in lanes 11 and 12 respectively. In addition to the TRβ dimer, a less mobile complex appeared with addition of RXRβ (star). SS indicates the supershifted complexes.

complex. Since this RARα MoAb works well in Western blots with denatured RARα, we believe that the RARα MoAb recognizes an epitope that is inaccessible or buried in the RARα–DNA complex.

When TRβ was incubated with RXRβ and EREc38, the monomer TR complex disappeared and concomitantly an increased amount of dimeric complex was detected (Fig. 6, lanes 10–12). This indicates cooperative binding. Interestingly, a small amount, ~13% of the total TRβ–RXRβ–EREc38 complex, migrated more slowly than the dimeric receptor (see the complex annotated by a star in Fig. 6, lanes 11 and 12). Addition of TRβ antibody reduced the intensity of this band and generated two supershifted complexes (Fig. 6, lane 11). The complex denoted by the star disappeared with RXR antisera (Fig. 6, lane 12) and did not appear in binding of TRβ–RXRβ to 1/2EREc38 (Fig. 7) or to 1/2EREc (data not shown). TRβ bound as a monomer and dimer to 1/2EREc38 (Fig. 7). However, only TR monomer binding was observed to 1/2EREc (data not shown). This indicates that the larger 'star' complex requires both halves of the ERE IR.

TR did not bind to EREm(–) which lacks the extended IR and the 3′ AT-rich region (data not shown). Thus, TR binding is dependent upon the presence of the 5′-A in the ERE half-site. It is important to note that co-incubation of ER with RARα, β and γ, TRα or TRβ, or RXRβ did not generate complexes of different mobility than that detected for ER alone. Moreover, the respective

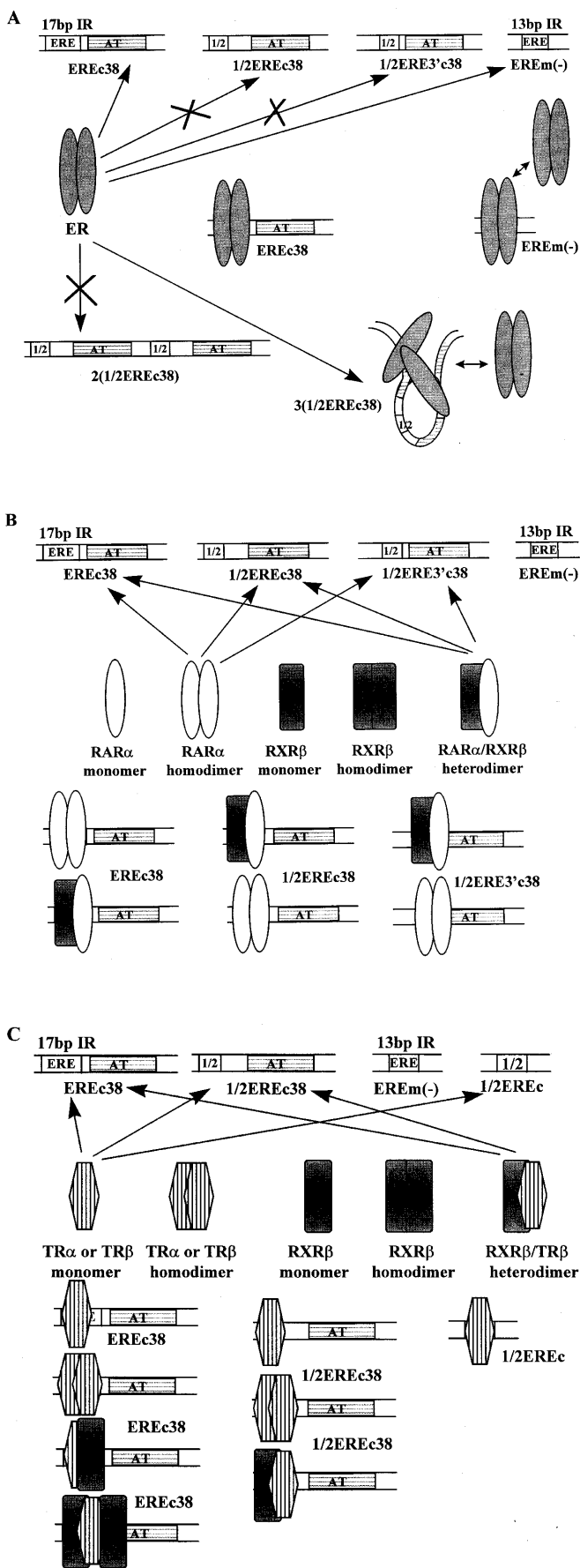**Figure 7.** TRα and TRβ bind as monomers, homodimers or as heterodimers with RARα and RXRβ to 1/2EREc38 *in vitro*. Gel mobility shift assay of ER or TR–1/2EREc38 binding. Partially purified 4-OHT–ER (7.39 nM, 126 fmol/lane) was incubated with [^{32}P]1/2EREc38 (lanes 1 and 2) or [^{32}P]EREc38 (lanes 14 and 15). In each reaction an identical concentration (25 000 d.p.m.) of [^{32}P]DNA was added (10 fmol/lane). H222, 0.1 μl, was added to the reactions in lanes 2 and 15. Sf9 insect cell extracts containing recombinant baculovirus-expressed human TRα (5 μl, 20 nM monomer, 10 nM dimer) and TRβ (5 μl, 200 nM monomer, 100 nM dimer), alone (lanes 3, 4 and 7, and 5 and 6 respectively), or TRβ plus RXRβ (0.3 μl RXRβ, lanes 8–10) or TRβ plus RARα (0.4 μl RARα, lanes 11–13) were incubated with [^{32}P]1/2EREc38 as described in Figure 1. Two μl MoAb anti TRα or TRβ antibodies were added to the reactions in lanes 4 and 6, 9 and 12 respectively. Polyclonal anti-RXR antibody (0.3 μl) was added to the reaction in lane 10. MoAb anti-RARα antibody (5 μl) was added to the reaction in lane 13. The arrow indicates the migration of the ERAF–1/2EREc38 complex. SS is the supershifted complex.

antibodies to these type II nuclear receptors had no effect on ER–ERE binding. This indicates that bovine ER did not heterodimerize with any of these type II nuclear receptors.

The MoAb to TRβ supershifted ~28% of the total TRβ–1/2EREc38 complex and enhanced the total amount of TRβ–1/2EREc38 detected by 41%. Addition of RXRβ to the TRβ + [^{32}P]1/2EREc38 reaction generated only the dimeric receptor binding form. Antibodies to either TRβ and RXR supershifted the complex. Addition of RARα to the TRβ + [^{32}P]1/2EREc38 binding reaction decreased the amount of complex detected by 26%. This indicates that interaction of RARα with TRβ either inhibited TRβ binding to 1/2EREc38 or competed away a co-factor required for TR–DNA binding. Addition of the MoAb to RARα inhibited the amount of TRβ–1/2EREc38 complex detected by 12%. This may be due to some cross-reactivity between the RARα MoAb and TRβ.

DISCUSSION

Because nuclear type II receptors bind various arrangements of the ERE half-site (reviewed in 41), we postulated that the inhibitory effects of retinoids (4–6) and the stimulatory effects of T$_3$ (48,49) on breast cancer cell replication could be mediated, at least in part, by RAR, primarily through RARα (6), or TR binding to EREs. In this model, type II nuclear receptors compete with estrogen-liganded ER for ERE binding and thus preclude subsequent transactivation of genes essential for cell replication. As a first step in elucidating these

A

17bp IR
| ERE | AT |
EREc38

| 1/2 | AT |
1/2EREc38

| 1/2 | AT |
1/2ERE3'c38

13bp IR
| ERE |
EREm(–)

ER

| AT |
EREc38

EREm(–)

| 1/2 | AT | 1/2 | AT |
2(1/2EREc38)

3(1/2EREc38)

B

17bp IR
| ERE | AT |
EREc38

| 1/2 | AT |
1/2EREc38

| 1/2 | AT |
1/2ERE3'c38

13bp IR
| ERE |
EREm(–)

RARα monomer   RARα homodimer   RXRβ monomer   RXRβ homodimer   RARα/RXRβ heterodimer

| AT |
EREc38

| AT |
1/2EREc38

| AT |
1/2ERE3'c38

| AT |

| AT |

| AT |

C

17bp IR
| ERE | AT |
EREc38

| 1/2 | AT |
1/2EREc38

13bp IR
| ERE |
EREm(–)

| 1/2 |
1/2EREc

TRα or TRβ monomer   TRα or TRβ homodimer   RXRβ monomer   RXRβ homodimer   RXRβ/TRβ heterodimer

| AT |
EREc38

| AT |
1/2EREc

| AT |
EREc38

| AT |
1/2EREc38

| AT |
EREc38

| AT |
1/2EREc38

| AT |
EREc38

mechanisms, we compared the ability of ER, RAR, RXR and TR to bind to palindromic EREs or ERE half-sites *in vitro*.

ER did not bind to a single copy of the 1/2EREc38 or 1/2ERE3'c38 half-sites, regardless of ligand, even at concentrations of up to 200 fmol ER dimer in a binding reaction including 10 fmol ERE half-site oligomer. This confirms our previous results (35–37,40–42,45,46,50) and those of other investigators that the ER homodimer requires both arms of the ERE IR. We did detect the binding of COUP-TF, present in the partially, but not highly, purified bovine ER, to 1/2EREc38. COUP-TF is one of the best characterized of the orphan nuclear receptors that competes for 5′-AGGTCA-3′ elements with other nuclear receptors and inhibits gene expression (51).

Although it was long dogma that ER bound only to EREs containing an IR+3 sequence, recent work demonstrated ER binding to half-sites as DR (19,20). We did not observe ER binding to a single or two tandem (head-to-tail) copies of 1/2EREc38, but low ER binding was detected to three tandem copies of 1/2EREc38. Since ER was reported to bind DR half-sites of 5 or 6 nt (20) and up to 300 nt apart (19), the reason for the failure of ER to bind the second half-site in two tandem 1/2EREc38 is unclear. It is possible that the helical spacing between half-sites is important. When there are two tandem copies of 1/2EREc38, the distance between each 5′-AGGTCA-3′ motif is 38 nt. Assuming 10.5 bp/turn in B-form DNA (52), this indicates that the half-sites are 3.6 helical turns apart, on opposite faces of the DNA helix. When a third half-site is present, the first and third half-sites are located 72 nt, 6.9 helical turns, apart on the same face of the helix. This may enhance ER binding stability in a way analogous to the co-operativity of E_2-ER binding to three, but not two, tandem copies of EREc38 (35–37,41,46). A model depicting this possibility is shown in Figure 8A.

Our results provide the first demonstration that RARα, β or γ bind as homodimers to an ERE half-site in the absence of ligand *in vitro*. It is unlikely that the RARα– 1/2EREc38 complex detected was the result of heterodimerization between RARα and a protein in the Sf9 NE because addition of increasing amounts of NE from cells infected with wt baculovirus did not enhance RARα–DNA complex formation. Additionally, RXR antisera had no effect on the complex formed. Two previous reports showed RAR binding to a half-site. RARα bound a single half-site as a monomer (53).

Figure 8. Model of ER and type II nuclear receptor interaction with ERE and ERE half-sites. (**A**) The ER homodimer (grey ovals) binds only to the full palindromic ERE (EREc38, the consensus AT-rich region is indicated with the grey stripes) and not to a single half-site (1/2EREc38 or 1/2ERE3'c38). ER does not bind two head-to-tail tandem copies of 1/2EREc38 (2(1/2EREc38)), but low specific binding was observed to [3(1/2EREc38)]. We suggest that DNA bending may be involved in this event. If two half-sites occur on the same face of the DNA helix, each ER monomer in the dimeric ER can contact the two half-sites. The broad Xs indicate no binding. The single arrows between the ER homodimer and the various EREs indicate ER binding. The double arrows indicate that ER binds with lower affinity to that ERE. (**B**) RARα homodimers (open ovals) bind the indicated full ERE and half-sites, but not the 13 bp ERE, EREm(–). RXRβ (grey rectangles) does not bind any of these constructs. An RARα–RXRβ heterodimer binds EREc38, 1/2EREc38 and 1/2ERE3'c38, but not EREm(–). Symbols are identical to those in part A. (**C**) TRα and TRβ (indicated as striped ovals) as monomers or homodimers, or as heterodimers with RXRβ, bind full and half-site EREs as indicted, but not EREm(–). Our data suggest that the RXRβ–TRβ heterodimer also interacts with an additional RXRβ monomer to form a complex composed of three receptor monomers, i.e. two RXRβ monomers plus one TRβ monomer on the EREc38 element. This binding is dependent on the presence of the two half-sites within the ERE palindrome and the adjacent AT-rich region. Symbols are identical to those in (A).

The molecular species of RARα, β or γ bound to 5′-GTTCA-3′ in the *zif268* gene promoter was not stated (54). In contrast to the binding of RAR homodimers to 1/2EREc38, RXRβ did not bind 1/2EREc38 in the absence of ligand *in vitro*. These binding data are modeled in Figure 8B.

Interestingly, the RARα–RXRβ heterodimer bound cooperatively to 1/2EREc38 and differs from previous reports suggesting that cooperative binding of RAR, TR and RXR occurred only on elements with specific spacing between the half-sites (55–56). RAR–RXR forms in solution and binds more efficiently than homodimers to a number of RA response elements *in vitro* (e.g. 23,24,29,30,49). Thus, our observation of cooperative binding of RARα–RXRβ to a single ERE half-site with an adjacent AT-rich region is unique. An earlier report predicted such binding (57), but this was, to our knowledge, not reported until now. Because we did not observe cooperative RARα–RXRβ binding to 1/2EREc, we believe that the proximity of AT-rich region and the half-site is responsible for enhancing binding. One possible mechanism for the AT-effect involves possible enhanced receptor-induced DNA bending. Both RAR and RXR bend DNA (reviewed in 58).

TR monomers and homodimers bound to 1/2EREc38. Similarly, a TR homodimer or TR–RXRβ heterodimer bound to a single half-site within the murine MHC Class I region II promoter (30). In contrast, only monomeric RAR or TR bound an ERE half-site (53) and TR required a HeLa cell protein, TRAP, to bind to an imperfect half-site (59). We suggest that sequences flanking the half-site influence the stability of dimeric TR binding. This is true for ER–ERE binding (35–37,41,46) and a recent report demonstrated that the sequences immediately flanking the half-site modulate RXR–TRα binding (60). Again, one possible mechanism involves TR-induced DNA bending (58).

While both TRα and TRβ bound 1/2EREc38 as monomers and homodimers *in vitro*, RARα inhibited TRβ–1/2EREc38 binding. Likewise, RARα inhibited TRβ–EREc38 binding. These results appear to correlate with the ability of RAR to inhibit T3 responses from DR4 (26,61). One explanation may be competition between receptors for DNA binding. Alternatively, heterodimerization between RARα and TRβ may result in an 'incorrect' orientation of the receptor monomers. For both RXR–RAR and RXR–TR heterodimers, binding cooperativity depends on RXR bound 5′ to its cooperating partner (56). RXR stimulated the binding of TR to TRE (26,29) and, as shown here, TR–ERE or half-site binding.

RARα, β and γ bound EREc38 as homodimers, but RXRβ did not bind to EREc38. In contrast, neither A/B-domain truncated RARα nor RXRβ bound to the vitellogenin ERE, but did bind the ERE as a heterodimer (62). This implicates sequences in the N-terminal region as necessary for the three-dimensional conformation of RARα for ERE binding. Neither RARα nor RXRβ bound EREm(–), indicating the importance of the 5′A nucleotide of the 6 bp half-site. It is currently unclear whether the liganded RAR homodimer or RAR–RXR heterodimer transactivate gene expression from an ERE. One report showed that RAR bound an ERE, but activated transcription only from DR+3, thus indicating that RAR–DNA binding is not necessarily correlated with transcriptional activation (63). However, since ER has only an ~4-fold higher affinity for binding EREc38 compared with the RARα–RXRβ heterodimer, our findings indicate that RAR–ERE binding could block ER binding and subsequent signal transduction depending on the cellular concentrations of each receptor and its ligands.

We observed greater binding of RARα–RXRβ heterodimers to the Vit B1 ERU compared with a single copy of EREc38. However, ER-Vit B1 ERU binding was greater than that of RARα–RXRβ. Similarly, Ozato's group (30) reported that RXRβ bound the Vit B1 ERU with higher affinity compared with *Xenopus* Vit A1 (34–36). One reason for this result is that the Vit B1 ERU contains two imperfect EREs. Each ERE could bind one RARα–RXRβ heterodimer. However, using gel shift assays, neither Marks and co-workers (30) nor we have observed a complex comparable in mobility to that for two RARα–RXRβ heterodimers bound to the two EREs. On the other hand, methylation interference (30) and DNase I footprinting (64) showed that both EREs in the Vit B1 ERU were protected by TR and TR–RXR or ER. We did not detect the binding of two ER dimers to the Vit B1 ERU by either gel shift or plate assays. Differences in the sensitivity of the assay systems seem likely to account for these observations.

A small amount of the TRβ–RXRβ heterodimer–EREc38 binding complex, migrated more slowly than the dimeric receptor form (see the complex denoted by a star in Fig. 6). We believe this to be a unique observation, distinct from the larger complex formed between a JEG cell extract and the rat α-myosin heavy chain, malic enzyme or human α subunit elements (65). A similar complex was observed by chemical cross linking using a C-terminal truncated RXRβ co-incubated with TR and the region I of the murine MHC class I genes that contains no apparent perfect half-site (30). Similar to our results, region I did not bind RXR but did bind TR homodimer and the RXR–TR heterodimer.

Results from experiments using RXR and TR antisera indicate that the complex denoted by a star in Figure 6 represents the binding of an additional RXRβ monomer with the TRβ–RXRβ heterodimer to EREc38. The exact sequence specificity of this binding is unknown. However, this complex did not appear when we examined the binding of TRβ–RXRβ to 1/2EREc38 (Fig. 7) or to 1/2EREc (data not shown), indicating that its formation requires both halves of the ERE IR.

TR was reported to bind the ERE as a monomer and dimer (25). Later work showed binding of a TR monomer, but not the TR dimer, either to a single half-site or to an IR3 ERE. Previous reports indicated that RXRβ did not enhance TR binding to a RARE (23), but did enhance TR–TRE binding (23,28,29,48,55). We showed that TRβ–RXRβ–ERE binding was significantly greater than that of TRβ alone, indicating binding cooperativity for the heterodimeric form. These results corroborate and extend earlier reports on TR–ERE binding (49,66).

TR did not bind to EREm(–) (data not shown). Thus, in results identical to those for RAR, TR binding is dependent upon the presence of the 5′-A in the ERE half-site. It is important to note that co-incubation of ER with RARα, β and γ, TRα or TRβ, or RXRβ did not generate the appearance of complexes of different mobility than that detected for ER alone and that antibodies to these receptors had no effect on ER–ERE binding. This indicates that bovine ER does not heterodimerize with any of these receptors.

In conclusion, our results suggest that RARα, β and γ, TRα, TRβ and RXRβ, and likely other type II nuclear receptors compete for binding to full and half EREs and may thus contribute in an elaborate manner to control the expression of estrogen-regulated genes. Our observations suggest the mechanism accounting for the E2 antagonistic properties of retinoids, and possibly the stimulatory effect of T3, is by binding competition between RAR, RXR, TR

and ER for fully palindromic EREs and may involve RAR, RXR and TR binding to half-site EREs in a number of naturally occurring estrogen-responsive genes.

ACKNOWLEDGEMENTS

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