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Estrogen Regulates Adrenal Angiotensin AT_1 Receptors by Modulating AT_1 Receptor Translation

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Hypertension and associated cardiovascular disease increase after menopause. Angiotensin AT_1 receptor (AT_1R) antagonists are effective treatments, in part, by inhibiting angiotensin II (Ang II)-induced aldosterone release from the adrenal zona glomerulosa (ZG). Estrogen decreases the number of AT_1Rs in the adrenal gland and attenuates acute Ang II-induced aldosterone release. Here, we examined the effects of 17β-estradiol (E_2) on AT_1R gene regulation in the rat adrenal cortex (AC). Female rats were ovariectomized and injected with vehicle or E_2. Immunohistochemistry revealed the presence of both estrogen receptor (ER)α and ERβ in the ZG, and E_2 treatment increased the intensity of their nuclear staining. Under conditions in which AT_1R maximal binding capacity was decreased by 46%, chronic miniosmotic pump Ang II-induced aldosterone secretion was reduced by 43%. E_2 treatment had no effect on $AT_{1a}R$ and $AT_{1b}R$ mRNA levels in the AC, whereas the AT_1R mRNA polysome distribution in sucrose gradients was shifted to lighter fractions, indicating that E_2 treatment reduces AT_1R translation. RNA binding proteins (RBPs) in AC extracts formed complexes with the 5′ leader sequence (5′LS), coding region, and the 3′-untranslated region (3′UTR); however, only the activity of 5′LS RBPs was regulated by E_2 treatment. These data suggest that E_2, acting through its receptors in the ZG, reduces AT_1R density and Ang II-induced aldosterone release, primarily by inhibiting AT_1R translation, possibly by blocking ribosomal scanning caused by increased steric hindrance from 5′LS RBPs. Dysregulation of this posttranscriptional mechanism may contribute to the increased incidence of cardiovascular disease associated with menopause. (*Endocrinology* 144: 3251–3261, 2003)

IN WOMEN, THE incidence of cardiovascular disease dramatically increases after menopause (1). Although the recent findings from the Women's Health Initiative trial have questioned the role of combined estrogen-progestin hormone replacement therapy in protecting postmenopausal women against cardiovascular disease (2, 3), numerous studies indicate that estrogen deficiency in postmenopausal women increases the risk of developing hypertension, coronary atherosclerosis, and myocardial infarction (4–6). Furthermore, many studies suggest that estrogen therapy has cardiovascular protective benefits by lowering blood pressure, increasing cardiac output, and reducing the risk of developing coronary atherosclerosis and myocardial infarction (7–9).

Estrogen is associated with a lipid profile in women that includes reduced low-density and elevated high-density lipoprotein levels. This cardioprotective lipid profile contrasts with the atherogenic lipid profile that often develops after menopause. Estrogen is also associated with improved endothelial function. By elevating nitric oxide and prostaglandin levels, estrogen enhances vasodilation, inhibits proliferation of vascular smooth muscle cells, and reduces platelet aggregation and is thereby thought to attenuate atherosclerosis (10). Nonetheless, analyses of large-scale studies indicate that the benefits of estrogen on the lipid profile account for only 25–50% of the cardioprotective effects associated with the hormone, suggesting that additional factors are involved (11).

In addition to estrogen deficiency, another recognized factor implicated in the pathogenesis of hypertension, atherosclerosis, and congestive heart failure is overactivation of the renin-angiotensin system (RAS). Inhibition of the RAS by angiotensin-converting enzyme inhibitors and angiotensin AT_1 receptor (AT_1R) antagonists are effective treatment modalities for these disease states (12). Accumulating data indicates that estrogen regulates all of the known components of the RAS. The synthesis of angiotensinogen in hepatocytes is regulated by estrogen (13). Plasma renin levels and angiotensin-converting enzyme activity are significantly higher in estrogen-deficient (compared with estrogen-replete) rats and in postmenopausal women not receiving ERT (compared with women who do) (5, 6). Concordantly, circulating levels of angiotensin II (Ang II) are higher in estrogen-deficient monkeys and transgenic hypertensive rats, compared with their estrogen-replete counterparts (14, 15). We and others have shown that, in addition to regulating the components involved in synthesizing Ang II, estrogen also alters the expression of AT_1Rs in many target tissues (16–18). Estrogen attenuates vascular responses to Ang II (19), and we have recently observed that, in the presence of peak physiological levels of estrogen, when adrenal AT_1R expression is reduced by approximately 30% (18), adrenal responsiveness to acute Ang II surges is markedly attenuated (20); Ang

Abbreviations: AC, Adrenal cortex; Ang II, angiotensin II; AT_1R, angiotensin AT_1 receptor; Bmax, maximal binding capacity; CR, coding region; DAB, 3,-3′-diaminobenzidine tetrachloride dihydrate; E_2, 17β-estradiol; ER, estrogen receptor; 5′LS, 5′ leader sequence; ERE, estrogen response elements; FL, full-length; ns, not significant; nt, nucleotide(s); OAT, ornithine δ-aminotransferase; OVX, ovariectomized; RAS, renin-angiotensin system; RBP, RNA binding protein; RNase, ribonuclease; RPA, ribonuclease protection assay; UTR, untranslated region; ZF, zona fasciculata; ZG, zona glomerulosa; ZR, zona reticularis.

II-induced aldosterone production was reduced by 45% in 17β-estradiol (E_2)-treated ovariectomized (OVX) rats fed a NaCl-deficient diet, compared with estrogen-deficient animals.

Aldosterone serves as an important mediator of fluid homeostasis and blood pressure control, and recent studies indicate that rapid increases in circulating aldosterone can modify sympathetic outflow to the heart, vasculature, and kidney through effects in the brain (21). Rats treated chronically with mineralocorticoids develop hypertension (22). Accompanying features of mineralocorticoid-induced hypertension include several risk factors for cardiovascular events, such as increased vascular responsiveness to Ang II, increased vascular resistance, and decreased baroreflex sensitivity. Furthermore, inhibition of aldosterone receptors with spironolactone was recently shown, in the Randomized Aldactone Evaluation Study, to substantially reduce the risk of morbidity and mortality among patients with severe heart failure who were also receiving standard angiotensin-converting enzyme inhibition therapy (23). Thus, estrogen-induced decreases in acute levels of Ang II-induced aldosterone secretion may contribute to the cardiovascular benefits associated with estrogen by decreasing overall mineralocorticoid activity; and conversely, a loss in the ability to down-regulate AT_1Rs and Ang II-induced aldosterone release in estrogen-deficient states may represent a risk factor for hypertension and cardiovascular events associated with aging and menopause. In this study, we investigated the molecular mechanisms underlying E_2 regulation of AT_1R gene expression in the rat adrenal gland.

Materials and Methods

Animal treatment

Female Sprague Dawley rats, weighing approximately 250–300 g, were obtained from Harlan Inc. (Indianapolis, IN). All rats were subjected to ovariectomy; and the following day, they were treated with either a daily injection of vehicle (peanut oil) or vehicle containing E_2. In the time course study, animals were treated with 40 μg/kg E_2 for 2, 4, 8, and 16 d. In the dose response study, OVX rats were injected with E_2 at 10, 25, 40, and 50 μg/kg for 8 d. For all other studies, rats were injected with vehicle or E_2 at 40 μg/kg every day for 8 d. All rats were maintained on a phytoestrogen-free diet (TD95092, Harlan Inc.) and tap water *ad libitum*. After experimental treatments, rats were killed by decapitation, and tissues were rapidly excised, snap-frozen in liquid nitrogen, and stored at −80 C. For immunohistochemistry, the adrenal glands were removed and fixed with 4% paraformaldehyde for 3 h at room temperature.

Measurement of plasma E_2 levels

Blood (0.5–1 ml) was collected, and the plasma was separated by centrifugation. E_2 levels were measured according to the RIA protocol of Diagnostic Products (Los Angeles, CA).

Immunohistochemistry of estrogen receptors (ERs)

After fixation, the adrenal gland was routinely processed to paraffin; 4-μM sections were cut and placed on 1% gelatinized slides. Sections were incubated with 10% nonimmune goat serum for 30 min at room temperature, then with the ERα (MC-20, rabbit polyclonal IgG; Santa Cruz Biotechnology, Inc., Santa Cruz, CA) or the ERβ (PAI-313, rabbit polyclonal IgG; Affinity BioReagents, Inc., Golden, CO) antiserums at 4 C overnight. The endogenous peroxidase was removed by incubation with 1% H_2O_2 for 10 min. After washes with PBS (3 × 5 min), the sections were incubated with biotinylated goat-antirabbit IgG (DAKO Corp., Copenhagen, Denmark) for 1 h at room temperature, followed by a 10-min treatment with 3,–3′-diaminobenzidine tetrachloride dihydrate (DAB) containing 3% H_2O_2. Sections were counterstained with Mayer's hematoxylin to allow anatomical definition of adrenal layers. A positive reaction was identified as a brown stain in the cytoplasm, or a black nuclear stain as a result of superimposition of the DAB reaction and the blue counterstain. Sections incubated with 10% nonimmune goat serum, instead of the primary antiserum, were used as negative controls. Sections were imaged by light microscopy.

Radioligand binding assay

The adrenal cortex (AC) was separated from the medulla, yielding a sample of AC that mainly contained the zona glomerulosa (ZG) and outer portions of the zona fasciculata (ZF). Cell membranes from whole homogenized adrenal glands or the AC were prepared and used in radioligand binding assays as previously described (18). ^{125}I-[Sar^1, Ile^8]Ang II (0.05–4.0 nM) was incubated with adrenal gland (15 μg) or AC (5 μg) membranes at room temperature for 3 h in binding buffer (100 mM NaCl; 10 mM Na_2HPO_4; 5 mM EDTA, pH 7.4) supplemented with 0.1% BSA in the presence of 5 μM of the type 2 angiotensin receptor antagonist, PD-123,319 (to determine only AT_1R densities). Nonspecific binding was determined in the presence of unlabeled Ang II at 250 nM (based on the fact that this concentration is 100 times the dissociation constant for Ang II at the AT_1R). AT_1R densities [maximal binding capacity (Bmax)] were determined by Scatchard analysis using a computerized nonlinear regression analysis of the saturation isotherm data software program, PRISM (GraphPad Software, Inc., San Diego, CA).

Measurement of chronic Ang II-induced aldosterone secretion

OVX rats were implanted with miniosmotic pumps (Alzet model 2001; Durect Corporation, Cupertino, CA) delivering vehicle (sterile 0.9% NaCl, n = 23) or Ang II at a rate of 200 ng/kg·min (n = 24). Half the animals in each group were treated with vehicle (peanut oil), and half were treated with E_2 at 40 μg/kg for 8 d. The resulting experimental groups were: OVX (n = 11), E_2-treated (n = 12), Ang II-infused (n = 12), and the combination E_2 treatment and Ang II-infusion (n = 12). On the 8th day, the rats were anesthetized with isoflurane (3% in O_2 flowing 0.5 liters/min), and heparinized blood was collected via cardiac puncture. The rats were immediately killed by decapitation. Plasma aldosterone concentrations were determined according to the RIA protocol of Diagnostic Products.

Preparation of radiolabeled RNA

The 5′ leader sequence (5′LS) and coding region (CR) of the rat $AT_{1a}R$ and $AT_{1b}R$ cDNAs were subcloned into the pCR3 vector by TA cloning (Invitrogen, Carlsbad, CA). The full-length (FL) rat $AT_{1a}R$ and $AT_{1b}R$ cDNAs were subcloned into the pcDNA1/Amp vector (Invitrogen) (24). Three regions of the CR (CR-1, 133–348; CR-2, 532–764; CR-3, 776–991) and 3 regions of the 3′ untranslated region (UTR) (3′UTR-1, 1396–1609; 3′UTR-2, 1590–1812; 3′UTR-3, 1954–2157) were randomly selected from the $AT_{1a}R$ cDNA and subcloned into pGEM-Teasy vector by TA cloning (Invitrogen).

To prepare ^{32}P-labeled antisense RNA probes for the ribonuclease (RNase) protection assay (RPA), the CR-$AT_{1a}R$ cDNA in pCR3 was linearized with Acc 1 to generate CR-4. The 3′UTR RNA probes were prepared from FL-$AT_{1a}R$ and FL-$AT_{1b}R$ cDNAs in the pcDNA1/Amp plasmid by linearizing with Bsa B1 and Psh A1, to generate 3′UTR-4 and 3′UTR-5, respectively. Linearized pTRI-β-actin plasmid was purchased from Ambion, Inc. (Austin, TX) (RPAIII kit). To prepare ^{32}P-labeled RNA sense probes for the RNA EMSA, the AT_{1a}- and AT_{1b}-5′LS pCR3 plasmids were linearized by Xho 1. The CR-1, CR-2, CR-3, 3′UTR-1, 3′UTR-2, and 3′UTR-3 in pGEM-Teasy plasmids were linearized by Sac II or Not I.

Linearized DNA templates (1 μg) were incubated with T7 or SP6 RNA polymerase and 50 μCi [α-^{32}P]GTP or [α-^{32}P]CTP, according to the protocol of Promega Corp. (Madison, WI) for *in vitro* synthesis of high-specific-activity single-stranded RNA probes. Radiolabeled RNA probes were purified on 8 M urea-5% polyacrylamide gels. Once eluted from the gels, RNA probes were precipitated with 7.5 M ammonium acetate, pH 6.0, and 100% ethanol (at a ratio of 0.1–3 X, respectively, where X is

the gel elution volume) and resuspended in diethyl pyrocarbonate-treated H_2O.

RPA

RNA from AC and pituitary was isolated by TRIZOL reagent (Invitrogen), and RNA concentrations were determined by the Ribogreen RNA quantitation method (Molecular Probes, Inc., Eugene, OR). Total RNA (20–30 μg) was incubated with approximately 30,000–40,000 cpm of 3′UTR-4 ($AT_{1a}R$) or 3′UTR-5 ($AT_{1b}R$) ^{32}P-labeled antisense probes, according to Ambion, Inc.'s RPA III protocol. RNA isolated from the sucrose gradient fractions was incubated with CR-4 ($AT_{1a}R$ and $AT_{1b}R$) ^{32}P-labeled antisense probe. The sizes of the 3′UTR-4, 3′UTR-5 or CR-4 radiolabeled probes were 462 nucleotides (nt), 469 nt, and 139 nt, whereas the protected sizes were 420 nt, 429 nt, and 89 nt, respectively (note, the protected fragments were slightly smaller than radiolabeled probes before treatment with T1 RNase because 40 nt of RNA encoded by the plasmid used to generate the probes was included in the probe; consequently, this plasmid RNA was degraded by T1RNase). A total of 25,000 cpm mouse pTRI-β-actin antisense probe (full probe size = 304 nt; protected size = 250 nt) was added to the incubations to control for RNA integrity and gel loading. In negative controls, 2.5 μg yeast RNA was hybridized with the antisense probes, followed by incubation with and without T1 RNase.

Samples were loaded onto 8 M urea-5% polyacrylamide gels and electrophoresed at 200 V for 90 min. Dried gels were exposed to a phosphorimager screen (Molecular Dynamics, Inc., Piscataway, NJ), and the abundance of AT_1R mRNA was quantitated by ImageQuant software (IQMac version 1.2; Molecular Dynamics, Inc.). We chose to analyze the autoradiograms by phosphorimaging over optical density measured by scanning densitometry, because phosphorimaging is more sensitive, and the magnitude of the linear range significantly greater, than optical density. Initially, we performed an RNA dose-response curve in the RPA. The doses we chose (AC, 30 μg; pituitary, 35 μg) were well within the linear range of the phosphorimaging analysis, even for the light $AT_{1a}R$ bands detected in the pituitary.

Polysomal distribution analysis

Polysome analysis was essentially carried out as previously described (25) and is based on the principle that the largest polysomes (multiple ribosomes bound to a single mRNA) are denser and, therefore, will sediment faster through a sucrose gradient than monosomes (one ribosome bound to a mRNA) or free ribosomal subunits not bound to mRNA (26). In brief, extracts from AC were homogenized in 3 ml ice-cold buffer A (20 mM Tris HCl, pH 7.5; 100 mM NaCl; 1.5 mM $MgCl_2$) supplemented with 10 mM EGTA, 500 μg/ml heparin, 0.5% Triton X-100, 100 μg/ml cycloheximide, 0.5% deoxycholic acid, and 160 U/ml RNAsin inhibitor. After centrifugation at 12,000 $\times$ *g* for 10 min at 4 C, the supernatants were loaded onto 10–50% linear sucrose gradients prepared in buffer A. In the polysome disruption experiment, the supernatant was loaded onto a sucrose gradient prepared in buffer A devoid of $MgCl_2$ and supplemented with 20 mM EDTA. The gradient was centrifuged at 243,000 $\times$ *g* in a SW40Ti rotor (Beckman, Fullerton, CA) at 4 C for 2 h. Six equal volume fractions were collected from the bottom to the top of the sucrose gradient, and equal volumes of buffer B (0.2 M Tris HCl, pH 7.5; 25 mM EDTA; 0.3 M NaCl; and 0.2% sodium dodecyl sulfate) were added to the sucrose fractions. After digestion with 500 μg/ml pronase (Sigma, St. Louis, MO) at 37 C for 30 min, RNA was extracted by phenol-chloroform and precipitated with 3 M sodium acetate (pH 5.2) and ethanol. The RNA pellet was dissolved in diethyl pyrocarbonate-treated H_2O.

The amount of AT_1R mRNA in each fraction was determined by RPA using the CR-4 radiolabeled antisense RNA probe (note, this probe detects both $AT_{1a}R$ and $AT_{1b}R$ mRNA levels attributable to the high nucleotide sequence homology in this region). Sample variation in cytoplasmic levels of AT_1R mRNA was controlled by normalizing the AT_1R mRNA recovered in each fraction, to the total amount of AT_1R mRNA recovered from the entire fractionation. Animal-to-animal variation was minimized, because each n value constituted a sucrose fractionation from the adrenals of six animals. Variation between fractionations was evaluated statistically by calculating the SE of the mean from multiple fractionations. At least three fractionations were performed for each experimental group. Sucrose gradient and RPA assays for each experimental group were run in parallel.

Preparation of cytosolic extract

Extracts from the AC were homogenized in a buffer containing 25 mM Tris HCl, pH 7.4; 0.1 mM EDTA; 1% Triton X-100; 40 mM KCl and supplemented with protease inhibitors, as previously described (18). Samples were layered on top of a 30% sucrose cushion and centrifuged at 230,000 $\times$ *g* for 3 h at 4 C. The supernatant (referred to as cytosolic extract) was collected and stored at −80 C. The protein concentration of the cytosolic extract was measured, using a colorimetric assay (Bio-Rad Laboratories, Inc., Hercules, CA), using BSA as a standard.

RNA EMSA

Cytosolic extracts from AC were incubated with 100,000 cpm ^{32}P-labeled 5′LS($AT_{1a}R$), 5′LS($AT_{1b}R$), CR-1, CR-2, CR-3, 3′UTR-1, 3′UTR-2, 3′UTR-3 RNA probes, as described previously (18). After T1 RNase treatment and heparin digestion, samples were electrophoresed at 200 V for 3 h in a 4% polyacrylamide gel. Dried gels were exposed to a phosphorimager screen (Molecular Dynamics, Inc.), and RNA binding protein (RBP) activity was quantitated by ImageQuant software (IQMac version 1.2; Molecular Dynamics, Inc.).

Statistical analysis

The value of each group was averaged, and the SEM was calculated. Results are expressed as the mean ± SEM. Statistical analyses were performed by one-way ANOVA, followed by Newman-Keuls test for multiple group comparison. Comparisons between two groups were made by unpaired *t* test. *P* values less than 0.05 were considered statistically significant, whereas values of at least 0.05 or greater were considered not significant (ns).

Results

E_2 increases the intensity of ERα and ERβ nuclear immunolocalization

To determine the effect of E_2 on ER subtype protein expression and location within the adrenal gland, we used an immunohistochemical approach. In OVX rats, ERα subtype immunoreactivity was found in many cells throughout the AC, including the ZG, ZF, and zona reticularis (ZR) (Fig. 1A), and in a few isolated cells of the adrenal medulla (not shown), whereas the ERβ subtype was confined mainly to the ZG (Fig. 1C). In contrast to the ERα staining that was found mostly in the cytoplasm, ERβ staining was observed more in cell nuclei. E_2 treatment markedly increased the number of cells with nuclear staining of ERα in the ZG and ZF (Fig. 1B), and revealed ERβ-positive nuclei in the ZF and ZR that were not observed in the estrogen-deficient OVX animals (Fig. 1D). No immunoreactivity was observed in any sections incubated with nonimmune serum instead of the primary antibody for ERα or ERβ, as evidenced by the presence of only *blue* counterstained stained cell nuclei in OVX (Fig. 1E) and OVX + E_2 (Fig. 1F) animals. No significant changes in either the intensity or the pattern of ERα or ERβ staining were seen in the adrenal medulla with E_2 treatment (not shown).

E_2 reduces adrenal AT_1R density in a time- and dose-dependent manner

To determine the time course and dose response of E_2 regulation of AT_1R density, saturation isotherms using ^{125}I-[Sar^1, Ile^8]Ang II (Fig. 2A) were performed on AC mem-

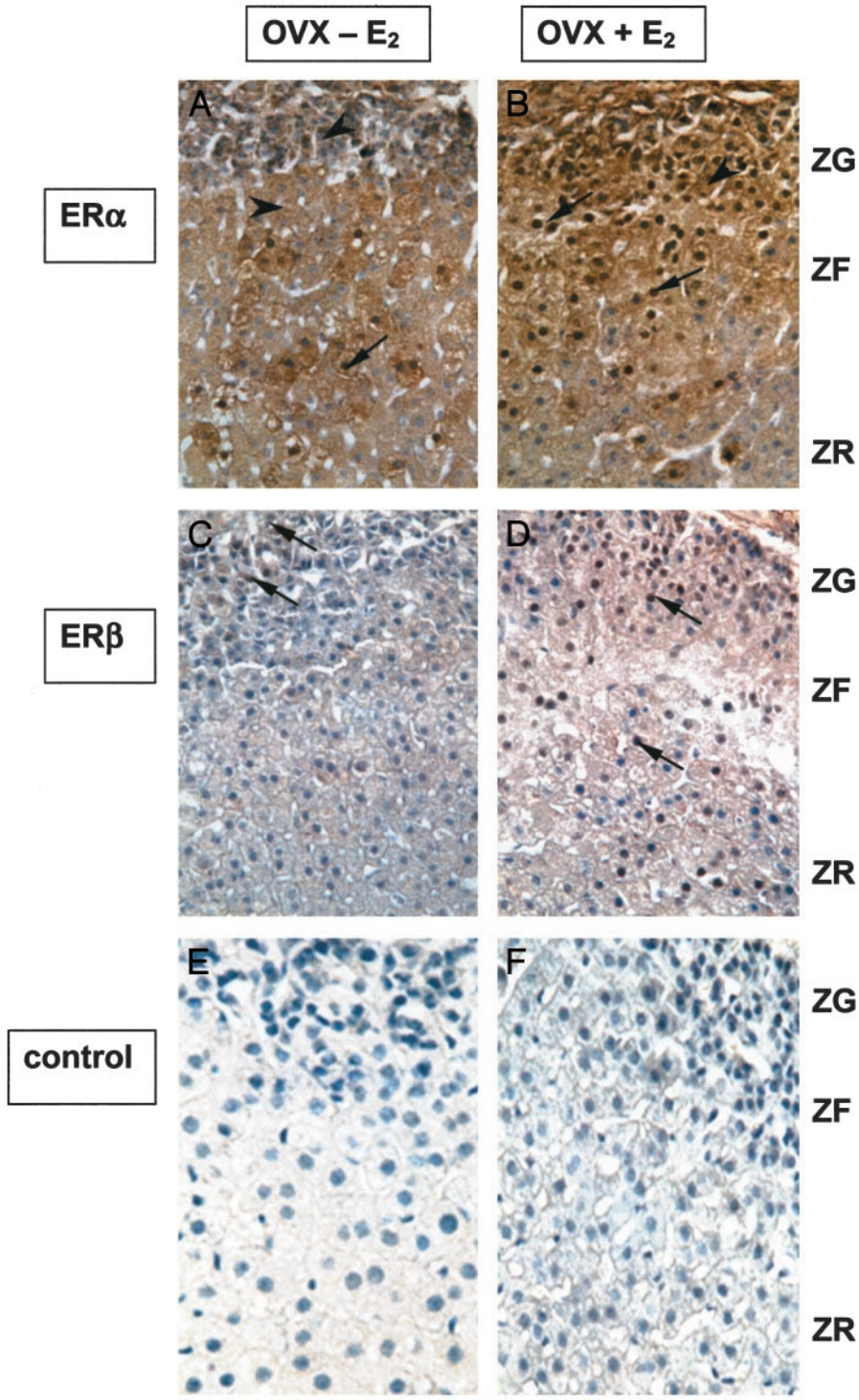

FIG. 1. Effect of E_2 treatment on localization of ERα and ERβ in the AC. All sections were counterstained with Meyers hematoxylin, so a positive reaction was identified as a *brown* stain in the cytoplasm, or a *brown-black* nuclear stain as a result of superimposition of the DAB reaction product and the blue counterstain. ERα immunoreactivity of vehicle-treated OVX animals (A) was observed in the cytoplasm of numerous cells of the ZG, ZF, and ZR (*arrowheads*), and, in a smaller number of cells, as nuclear staining (*arrows*). ERα immunoreactivity in the OVX+E_2 animals (B) was also observed in the cytoplasm (*arrowheads*) but was seen in the nucleus of a larger number of cells in all layers of the cortex (*arrows*). ERβ immunoreactivity of vehicle-treated OVX animals (C) was observed primarily in nuclei in the cells of the ZG (*arrows*). ERβ immunoreactivity in OVX+E_2 animals (D) was observed in the nuclei of a greater number of cells in the ZG and ZF (*arrows*). No immunoreactivity was observed in sections from OVX (E) and OVX + E_2 (F) rats that were incubated with nonimmune serum. Magnification, approximately ×400.

branes prepared from OVX rats injected with E_2 for 2, 4, 8, and 16 d (Fig. 2B). E_2 significantly decreased AT_1R Bmax, by 15%, after 2 d of treatment; maximum reductions in AT_1R number were obtained after 8 d (Fig. 2B). A dose-response study, after 8 d, showed that E_2 treatment reduced AT_1R Bmax in a gradual dose-dependent manner; significant reductions (18%) in AT_1R Bmax were observed at 10 μg/kg, and even greater reductions (41%) were observed at the peak dose of E_2 studied (50 μg/kg) (Fig. 2C).

Based on the time course and dose response, we carried out all further experiments in OVX rats treated with 40 μg/kg E_2 for 8 d, because these conditions caused a marked 30% decrease in adrenal AT_1R number without significantly altering receptor binding affinities (dissociation constant, pM: OVX, 100 ± 7; OVX + E_2, 88 ± 6, ns *vs.* OVX) (Fig. 2A). Radioligand binding on membranes prepared from AC homogenates showed that E_2 treatment similarly decreased AT_1R Bmax by 46% (fmol/mg: OVX,

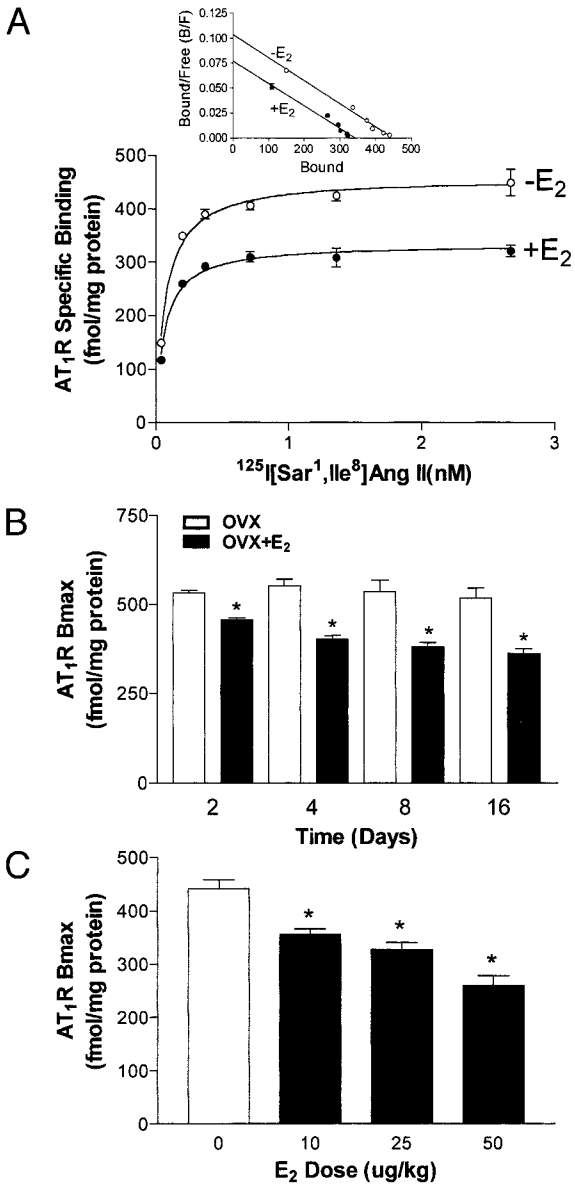

FIG. 2. Effect of E_2 treatment on adrenal AT_1R expression. Adrenal membranes were incubated with increasing concentrations of ^{125}I-[Sar^1, Ile^8]Ang II in the presence of saturating concentrations of the type 2 angiotensin receptor blocker, PD-123,319 (so only AT_1Rs were measured) in the absence (for determination of total receptor binding) or presence of 250 nM Ang II (for determination of nonspecific binding). A, Saturation isotherms. Shown are saturation isotherms of ^{125}I-[Sar^1, Ile^8]Ang II binding to adrenal membranes prepared from OVX rats treated with vehicle (peanut oil) (*open circles*) or E_2 at 40 μg/kg·d (*filled circles*) for 8 d. The data are averaged from three experiments, each performed in duplicate (each n value constitutes two animals/group; n = 3). *Inset*, Scatchard plot, derived from saturation binding data using the software program, PRISM. B, Time course. Shown are the Bmax values from OVX rats treated with vehicle (*open bars*) or E_2 at 40 μg/kg·d (*filled bars*) for 2, 4, 8, or 16 d. The values were derived by computerized nonlinear regression analysis of the saturation isotherm data (as in A), using the program, PRISM. *, $P < 0.001$, OVX *vs.* OVX + E_2; n = 6. C, Dose response. Shown are the Bmax values from OVX rats treated with vehicle (*open bar*) and E_2 (*filled bars*) at doses of 10, 25, or 50 μg/kg·d. The values were derived by a computerized nonlinear regression analysis of the saturation isotherm data (as in A), using the program, PRISM. *, $P < 0.01$, OVX *vs.* OVX + E_2, n = 3.

311 ± 18; OVX + E_2, 168 ± 14, $P < 0.05$ *vs.* OVX, n = 4). Under these conditions, plasma E_2 levels in vehicle-treated rats were only 3.4 ± 0.5 pg/ml (n = 10), which is the level typically detected at estrus, whereas plasma E_2 levels in E_2-treated OVX rats were 120 ± 10 pg/ml (n = 11), which represents the peak physiological level reached during the estrous cycle (27).

E_2 attenuates chronic Ang II-induced aldosterone secretion

To determine the effect of E_2 on chronic aldosterone secretion, we measured plasma aldosterone levels in OVX ± E_2-treated rats after chronic infusion of Ang II via miniosmotic pumps (Fig. 3). E_2 treatment did not significantly alter basal plasma aldosterone levels (pg/ml: OVX, 150 ± 34, n = 11; OVX + E_2, 250 ± 56, n = 12, ns *vs.* OVX). In contrast, chronic Ang II infusion in OVX rats significantly increased plasma aldosterone concentration (by 221%, to 482 ± 64 pg/ml, n = 12, $P < 0.05$ *vs.* OVX). E_2 treatment significantly reduced Ang II-induced aldosterone secretion (by 43%, to 276 ± 93 pg/ml, n = 12, $P < 0.05$ *vs.* Ang II-infused OVX).

E_2 does not alter $AT_{1a}R$ and $AT_{1b}R$ mRNA levels in the AC

To distinguish between $AT_{1a}R$ and $AT_{1b}R$ mRNA expression, we developed an RPA that distinguished between $AT_{1a}R$ and $AT_{1b}R$ mRNA expression by designing AT_1R subtype-specific ^{32}P-labeled 3′UTR antisense probes (3′UTR-4 and 3′UTR-5, respectively). No cross-reactivity between $AT_{1a}R$ and $AT_{1b}R$ mRNA antisense probes was observed under the conditions of the RPA (data not shown). β-actin mRNA levels were also measured using a ^{32}P-β-actin probe, to control for RNA integrity and gel loading. The steady-state mRNA levels of $AT_{1a}R$ and $AT_{1b}R$ were expressed as the ratio of $AT_{1a}R$ or $AT_{1b}R$ mRNA to β-Actin mRNA.

Both AT_1R subtypes were enriched in the AC (Fig. 4, A and B). The results also demonstrate that, under conditions in which E_2 markedly decreased AT_1R density, E_2 had no significant effects on either $AT_{1a}R$ or $AT_{1b}R$ mRNA levels in the

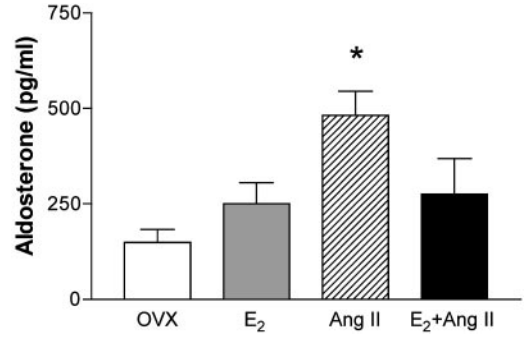

FIG. 3. Effect of E_2 treatment on chronic Ang II-induced aldosterone secretion. OVX rats were implanted with miniosmotic pumps delivering vehicle (sterile 0.9% NaCl) or Ang II at 200 ng/kg·min for the duration of the experiment. Half the rats in each group were treated with vehicle or E_2 at 40 μg/kg·d for 8 d (conditions that are identical to those shown in Fig. 2A). Plasma aldosterone was determined by RIA in the following experimental groups: OVX (n = 11) (*open bar*), Ang II-infused (n = 12) (*gray bar*), E_2-treated (n = 12) (*striped bar*), and combined E_2 treatment and Ang II-infusion (n = 12) (*black bar*). *, $P < 0.05$ *vs.* OVX, E_2, and E_2+Ang II.

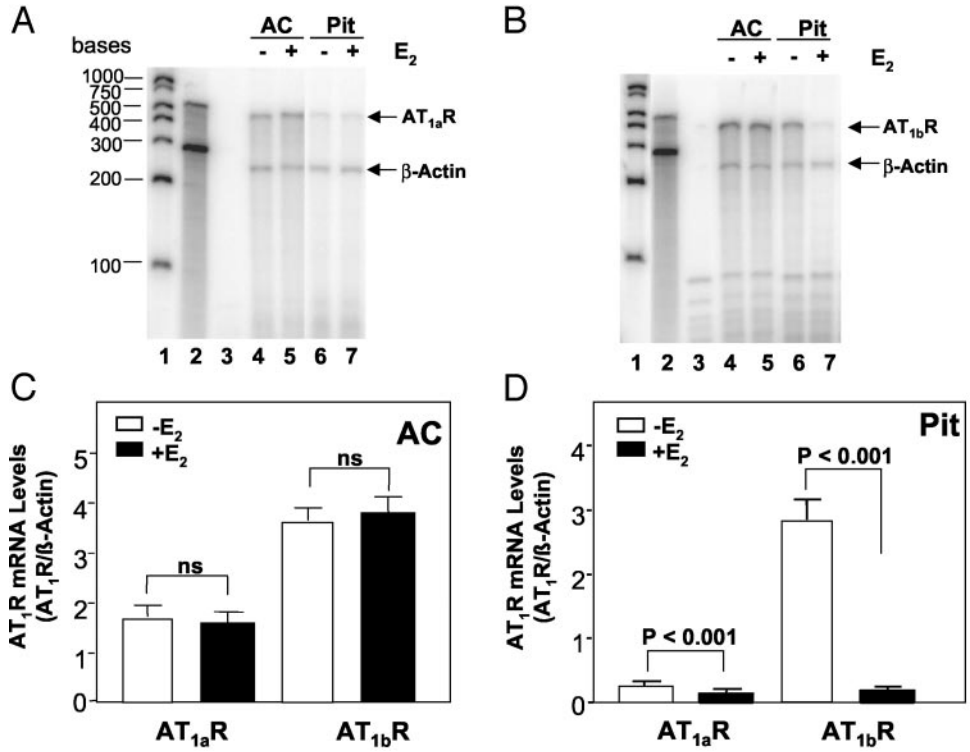

FIG. 4. Effect of E_2 treatment on $AT_{1a}R$ and $AT_{1b}R$ mRNA levels in the adrenal and pituitary. Total RNA isolated from AC (30 μg) (A and B, lanes 4 and 5) or pituitary (Pit) (35 μg) (A and B, lanes 6 and 7) from OVX rats treated with vehicle (lanes 4 and 6) or E_2 (lanes 5 and 7) (conditions identical to those shown in Fig. 2A) was incubated with 25,000 cpm β-actin and 35,000 cpm 3′UTR-4 ($AT_{1a}R$) (A) or 3′UTR-5 ($AT_{1b}R$) (B) ^{32}P-labeled antisense RNA probes. After incubation, all unprotected RNA (*i.e.* any RNA not hybridized to the antisense probes) was digested with RNase T1. Shown are the 420-nt $AT_{1a}R$ (A, lanes 4–7), 429-nt $AT_{1b}R$ (B, lanes 4–7), and 250-nt β-actin RNA (A and B, lanes 4–7) radiolabeled protected fragments analyzed on 5% denaturing polyacrylamide/urea gels (note, the protected fragments are a bit smaller than the probes not treated with T1 RNase, because of the presence of 40 nt of RNA encoded by the plasmid used to generate the probes). In negative controls, $AT_{1a}R$ (A, lanes 2 and 3) or $AT_{1b}R$ (B, lanes 2 and 3) ^{32}P-labeled antisense RNA probes (35,000 cpm) were hybridized with 2.5 μg yeast RNA, followed by digestion with (A and B, lane 3) or without (A and B, lane 2) T1 RNase. Lane 1 shows the molecular weight markers (note the molecular markers in A, lane 1, have run a bit high because of gel smiling). The amounts of $AT_{1a}R$- and $AT_{1b}R$-protected fragments were quantitated by phosphorimaging. Shown are the ratios of $AT_{1a}R$ and $AT_{1b}R$ to β-actin in the AC (C) and pituitary (D). Values are the mean ± SEM (n = 5).

AC (Fig. 4C). In contrast, E_2 significantly decreased steady-state levels of $AT_{1a}R$ and $AT_{1b}R$ mRNAs in the pituitary of these same rats, by 37% (OVX, 0.33 ± 0.01; OVX + E_2, 0.16 ± 0.01, $P < 0.001$ *vs.* OVX, n = 5) and 93% (OVX, 2.90 ± 0.30; OVX + E_2, 0.20 ± 0.03, $P < 0.001$ *vs.* OVX, n = 5), respectively (Fig. 4D).

E_2 reduces AT_1R translational efficiency in the AC

Because E_2 did not decrease AT_1R mRNA levels in the AC, we investigated whether E_2 lowers AT_1R density by inhibiting receptor translation. AC cytosolic extracts from OVX and E_2-treated rats were layered onto sucrose gradients. After centrifugation, six equal fractions from A to F (with A comprising the heaviest polysome fraction and F, the lightest) were collected. Total RNA was extracted from each fraction and incubated with an antisense RNA probe that was complementary to an 89-nt stretch within both the $AT_{1a}R$ and $AT_{1b}R$ CRs (so both $AT_{1a}R$ and $AT_{1b}R$ mRNAs would be detected). The RPA results showed that the amount of AT_1R mRNA in the most dense fraction A was 63% less in E_2-treated OVX rats than in vehicle-treated OVX rats (% of total: OVX, 27 ± 2; OVX + E_2, 10 ± 3, $P < 0.005$ *vs.* OVX, n = 3); whereas in the lighter fraction C, there was 59% more AT_1R mRNA in the E_2-treated OVX rats than in the vehicle-treated OVX animals (% of total: OVX, 17 ± 1; OVX + E_2, 27 ± 2, $P < 0.005$ *vs.* OVX, n = 3) (Fig. 5).

To confirm that the AT_1 mRNA fractionation in the sucrose gradient represented decreasing amounts of ribosomes bound to the AT_1R mRNA from fractions A–F (rather than an artifact of RNA protein binding), AC extracts from OVX rats were run on sucrose gradients prepared in a buffer in which $MgCl_2$ was replaced by EDTA (Fig. 6) [the presence of EDTA causes mRNA and ribosomes to disassociate (28, 29)]. In these polysome disruption experiments, the AT_1R mRNA was redistributed, from the majority being in fractions A–C to the majority being in the lighter fractions (D–F), indicating that the distribution of AT_1R mRNA in the sucrose fractionation shown in Fig. 5 represented decreasing amounts of ribosomes bound to AT_1R mRNA from heavy to light fractions.

E_2 increases cytosolic $AT_{1a}R$ and $AT_{1b}R$ 5′LS RBP activity

To determine whether RBPs bind to the $AT_{1b}R$ 5′LS in a similar manner as that observed in the $AT_{1a}R$ 5′LS (18), we

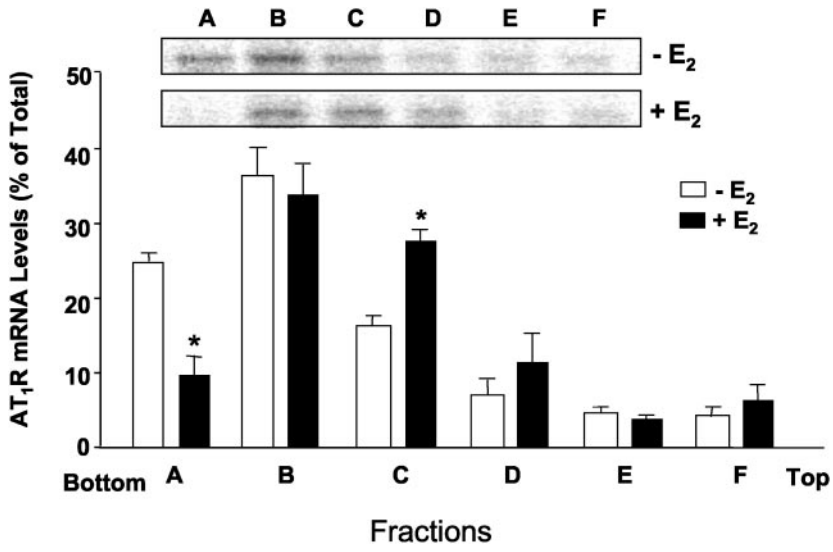

FIG. 5. Effect of E_2 treatment on the polysomal distribution of AC AT_1R mRNA. AC cytosolic extracts from OVX rats treated with vehicle (*open bars*) or E_2 at 40 μg/kg·d (*filled bars*) for 8 d were homogenized and loaded onto a 10–50% sucrose gradient. After centrifugation, six equal fractions (A→F) were collected from the bottom (fraction A) to the top (fraction F) of the gradient, followed by isolation of total RNA. The amount of AT_1R mRNA in each fraction was determined by RPA using the CR-4 AT_1R antisense probe, which hybridized to the CR of both the $AT_{1a}R$ and $AT_{1b}R$. Shown are the hybridization signals (*inset*) and the amount of AT_1R mRNA in each fraction expressed as a percentage of the total AT_1R mRNA recovered from all six fractions. *, $P < 0.005$, OVX *vs.* OVX + E_2; six animals/group constitutes one n value; n = 3.

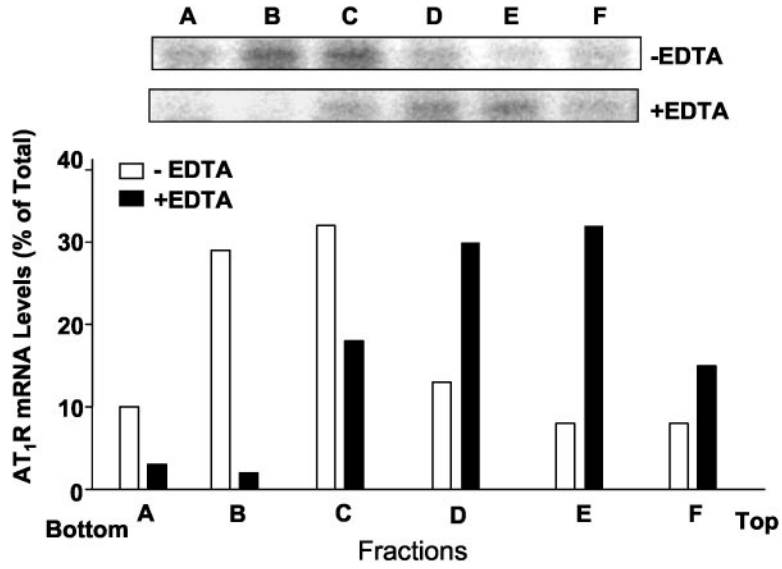

FIG. 6. Effect of EDTA on the polysome distribution of AC AT_1R mRNA. AC cytosolic extracts from untreated rats were homogenized, and half the samples were loaded onto a 10–50% sucrose gradient (*open bars*), whereas the other half were loaded onto a sucrose gradient in which $MgCl_2$ was replaced with EDTA in the gradient buffer (*filled bars*). AT_1R mRNA was determined from each sucrose fractionation, as in Fig. 5. Shown are the hybridization signals (*top*) and the amount of AT_1R mRNA in each fraction expressed as a percentage of the total AT_1R mRNA recovered from all six fractions (*bottom*).

examined the effects of E_2 on both $AT_{1a}R$ and $AT_{1b}R$ RBP activity in AC cytosolic fractions. We found that AC RBPs bound the 5′LS of both the $AT_{1a}R$ and $AT_{1b}R$ and that E_2 treatment significantly increased their RBP activity, by 148% (OVX, 1.0 ± 0.38; OVX + E_2, 2.48 ± 0.37, $P < 0.05$, n = 3) and by 68% (OVX, 1.0 ± 0.15; OVX + E_2, 1.68 ± 0.19, $P < 0.05$, n = 3), respectively (Fig. 7).

E_2 inhibits AT_1R RBP activity to the 5′LS but not to other regions of the receptor mRNA

To determine whether E_2 regulates RBPs that bind to other regions of the AT_1R mRNA, six different regions of the AT_1R, of approximately the same size as the 5′LS, were randomly selected from the AT_1R CR and 3′UTR and used as radiolabeled RNA probes to detect RBP activity. In contrast to the increased activity found in the 5′LS (OVX, 1.0 ± 0.27; OVX + E_2, 2.99 ± 0.75, $P < 0.05$, n = 3), E_2 did not significantly alter RBP activity in the CR or 3′UTR (Fig. 8).

Discussion

Most of the currently demonstrated diverse effects of estrogen are mediated by the genomic pathway involving the interaction of estrogen with a nuclear receptor protein (30). Two ER subtypes (ERα and ERβ) have thus far been cloned and characterized (31). ERα and ERβ have similar affinities for E_2 and bind to the same estrogen response elements (ERE), although the hormone binding domains are only 53% homologous (32). Both tissue-specific expression of ER subtypes and differences in transcriptional activation influence the effects of E_2 on different tissue types.

RT-PCR and RPA studies have shown that both ERα and ERβ mRNAs are present in the adrenal gland; however, protein expression was not examined in this study (33). Our results indicate that ERα and ERβ immunoreactivity is prominently expressed in the ZG of the rat AC (Fig. 1). Our findings are therefore consistent with an early radioligand binding study that demonstrated the presence of ERs in rat adrenal gland membranes; however, the radioligand used

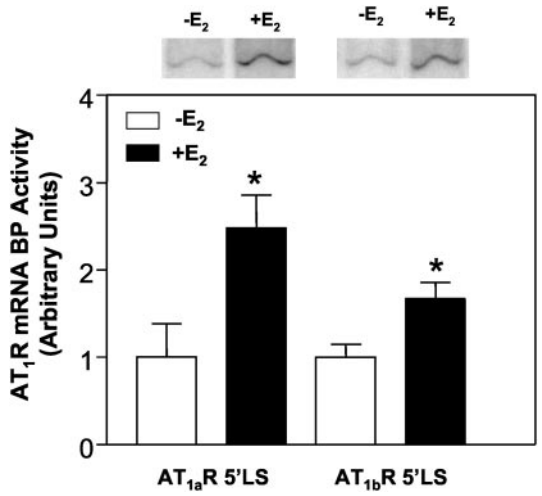

FIG. 7. Effect of E_2 treatment on AC AT_1R 5′LS RBP activity. RNA EMSA was performed using 5′LS ($AT_{1a}R$) or 5′LS ($AT_{1b}R$) ^{32}P-labeled RNA probes (100,000 cpm) and AC cytosolic extracts (40 μg) prepared from OVX rats treated with vehicle (*open bars*) or E_2 at 40 μg/kg (*filled bars*) for 8 d. Shown are EMSA autoradiograms (*top*) quantitated by phosphorimaging (in arbitrary units) and expressed as a ratio of radioactivity from the E_2-treated OVX rats normalized to the average radioactivity from the OVX group ($-E_2$). *, $P < 0.05$, OVX *vs.* OVX + E_2; two animals/group constitutes one n value; n = 3.

could not differentiate between ERα and ERβ subtypes (34). Our findings also support a previous immunohistochemistry study in rhesus monkey adrenal glands that showed ER immunoreactivity using an antibody that did not distinguish between ER subtypes (35). Our demonstration that both ER subtype antigens are expressed suggests that both the ERα and ERβ mRNAs found in the adrenal gland (33) are translated into protein. Furthermore, our finding that ERα and ERβ immunoreactivity is present in the ZG suggests that either of these ER subtypes could play a role in E_2 modulation of AT_1R density and Ang II-induced aldosterone release from the ZG, whereas any estrogen action in the adrenal medulla is likely to be ERα-mediated, because ERβ was undetectable in this region.

The apparent increase in immunoreactive nuclear staining for both ER subtypes in the E_2-treated OVX rats suggests that E_2 may up-regulate the expression of its own receptors in the AC (Fig. 1). This observed increase in immunoreactive nuclear staining for ERα, after E_2 treatment, is consistent with previous reports in human myometrium and mouse testis showing that estrogen can up-regulate ERα expression (36, 37). However (unlike our finding that E_2 treatment also increased ERβ expression in the ZG), in the myometrium and testis, estrogen treatment decreased ERβ (36, 37). Of interest is the observation that the intensity of ERα staining was more prominent in the nucleus than in the cytoplasm after E_2 treatment, suggesting that E_2 induces the relocation or retention of ERs into the cell nuclei. Changes in the cytoplasmic pattern of ERα immunolocalization were also observed in a cultured rat pituitary tumor cell line (38).

Recent studies showed that ERβ mRNA expression was markedly increased after intravascular balloon injury (39), and a recent report (40) demonstrated that ERβ-deficient mice have abnormal vascular function and develop hypertension with increasing age. These provocative new findings suggest that ERβ may play a role in the vascular protective effects of E_2.

We previously showed that 1 wk of E_2 treatment in OVX rats significantly reduced AT_1R expression in adrenal gland membranes (18, 41). In this study, we found significant effects of E_2 on AT_1R density after only 2 d of E_2 treatment in OVX rats; however, maximal effects were not observed until after 1 wk of treatment (Fig. 2). This relatively long time course suggests that AT_1R expression is altered by mechanisms involving gene expression, such as transcription, translation, and protein turnover, rather than by rapid regulation of signal transduction pathways.

At doses of E_2 that reflect peak physiological levels in female rats (27), AT_1R expression was inhibited by approximately 30% in the whole adrenal gland and by 46% in the AC. Under these conditions, we found that E_2 decreased aldosterone release by 43% in rats infused chronically with Ang II (Fig. 3). These new findings support our previous studies demonstrating that E_2 treatment of OVX rats significantly reduced acute Ang II-induced aldosterone release (41). The fact that estrogen also reduced plasma aldosterone levels after chronic Ang II infusions further supports the concept that attenuation of aldosterone responses contributes to the cardioprotective effects associated with estrogen. Thus, it will be very interesting to determine whether ERβ-deficient mice have abnormal Ang II-induced aldosterone responses that might contribute to their vascular function defects and the hypertension that develops in these animals with age (40).

Two highly homologous subtypes of the AT_1R (95% at the amino acid level), termed $AT_{1a}R$ and $AT_{1b}R$, have been cloned in rodents (24). These receptors are pharmacologically and functionally highly similar; and, thus far, immunohistochemistry and radioligand binding techniques have not been able to distinguish between them; however, their mRNAs are distinguishable because of lack of homology in the 5′LS and 3′UTRs. Whereas the $AT_{1a}R$ is widely distributed, the $AT_{1b}R$ is predominantly localized to the pituitary and adrenal gland; $AT_{1b}Rs$ comprise 52% of the total AT_1R mRNA population ($AT_{1a}R$ + $AT_{1b}R$) in the adrenal (42) and represent the majority of AT_1R mRNA in the anterior pituitary (43).

E_2 markedly decreased $AT_{1a}R$ and $AT_{1b}R$ mRNA in the rat pituitary, suggesting that E_2 decreases AT_1R densities in that tissue by inhibiting receptor transcription. Both the ERα and ERβ receptors modulate gene transcription through ERE and AP-1 enhancer elements present in estrogen-regulated genes; and both receptor subtypes were shown to be present in the pituitary, by immunohistochemistry and Western blotting (44). Thus, estrogen could regulate $AT_{1a}R$ gene transcription in the pituitary at these ERE and AP-1 regulatory elements, because they have been identified in the 5′ flanking region of the $AT_{1a}R$ gene (45, 46). Because the 5′ flanking region of the rat $AT_{1b}R$ gene is yet to be characterized, it is unknown whether these same elements also exist in the $AT_{1b}R$. Though both ERs activate gene transcription through ERE, ERα and ERβ function in opposition through AP-1 sites. ERβ actually suppresses the function of ERα through AP-1-mediated gene transactivation (47). The finding that estrogen coordinately

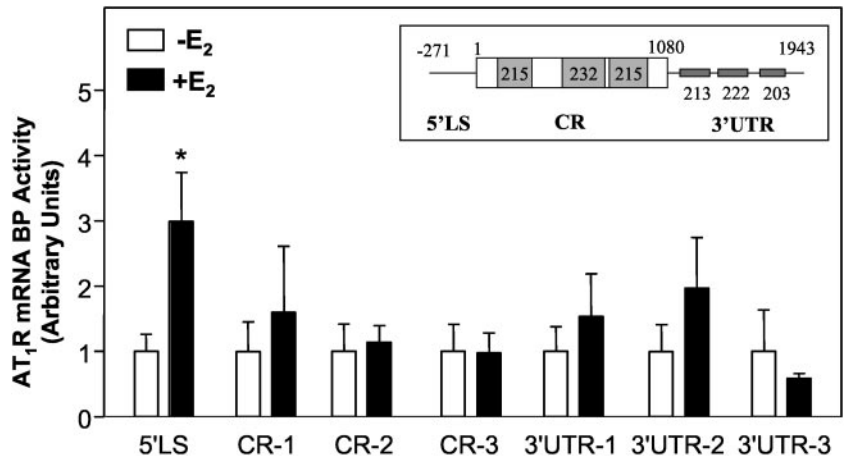

FIG. 8. Effect of E_2 treatment on AC AT_1R 5′LS, CR, and 3′UTR RBP activities. RNA EMSA was performed using 5′LS ($AT_{1a}R$), CR-1, CR-2, CR-3, 3′UTR-1, 3′UTR-2, or 3′UTR-3 ^{32}P-labeled RNA probes (100,000 cpm) and AC cytosolic extracts (40 μg) prepared from OVX rats treated with vehicle (*open bars*) or E_2 at 40 μg/kg (*filled bars*) for 8 d. Shown are EMSA autoradiograms quantitated by phosphorimaging (in arbitrary units) and expressed as a ratio of radioactivity from the E_2-treated OVX rats normalized to the average radioactivity from the OVX group ($-E_2$). *, $P < 0.05$, OVX *vs.* OVX + E_2; two animals/group constitutes one n value; n = 3. *Inset*, Location of the RNA probes within the $AT_{1a}R$ cDNA.

decreases the mRNA for both the $AT_{1a}R$ and $AT_{1b}R$ subtypes in the pituitary suggests that differential estrogen regulation through AP-1 sites is not occurring.

The surprising finding that E_2 did not decrease expression of either $AT_{1a}R$ or $AT_{1b}R$ mRNA in the AC (Fig. 4) suggests that E_2 does not down-regulate AT_1R number primarily by inhibiting AT_1R transcription in this tissue. Though the possibility remains that E_2 decreases adrenal AT_1R transcription at the same time as stabilizing AT_1R mRNA, resulting in equivalent steady-state levels of adrenal AT_1R mRNA, this scenario is unlikely, because inhibition of transcription is commonly accompanied by reduced mRNA expression.

One explanation for these tissue-specific differences is that the function of the AT_1R is different in these tissues. In the adrenal, the AT_1R mediates aldosterone secretion in response to rapid changes in Ang II levels. Under conditions of changing Ang II levels, the body must respond quickly to preserve fluid and electrolyte homeostasis to maintain stable blood pressure and cardiac output. Thus, having cellular stores of AT_1R mRNA that are ready to be translated would represent a more rapid method for changing AT_1R protein expression in response to acute stimuli than having to wait for the cell to first transcribe the DNA before translating the mRNA into AT_1R protein. In contrast, in the pituitary, AT_1Rs are involved in more chronic responses, such as mediation of prolactin and TSH secretion. Thus, transcriptional regulation of AT_1Rs in the pituitary may represent an appropriate mechanism for controlling AT_1R expression there.

The lack of AT_1R mRNA regulation by E_2 in the AC suggested that E_2 mediates its inhibition of AT_1R number in the ZG by posttranscriptional mechanisms. Therefore, we developed a polysome distribution assay to study the effects of E_2 on AT_1R translational efficiency *in vivo*. During translation initiation, 40S and 60S ribosome subunits assemble on the mRNA to form an 80S monosome or ribosome. The ribosome moves along the mRNA and then dissociates into subunits upon termination. Sucrose density gradients can separate polysomes according to their size, which is determined by the number of ribosomes bound to the mRNA. The mRNAs with the most polysomes bound will be the heaviest and, thus, found in the bottom fraction of the sucrose gradient, whereas the top fractions generally consist of monosomes, ribosomal subunits, and material sedimenting more slowly than the ribosomal subunits.

The fact that E_2 treatment of OVX rats shifted the AT_1R mRNA profile from the denser to lighter polysome fractions (Fig. 5) suggests that E_2 reduces the efficiency of AT_1R translation initiation, because the extent of ribosome loading on a mRNA depends primarily on the rates of translation initiation. Thus, mRNAs found in the heaviest sucrose fractions are translated more efficiently than those mRNAs located in the lighter sucrose fractions (25, 26), and a block in translation would result in the accumulation of small-sized polysomes and monosomes (26). However, the caveat remains that if elongation or termination were inhibited under these conditions, the rate of ribosome movement would slow down, as would the rate of protein synthesis; this scenario, however, is unlikely, because inhibition of elongation and termination are rarely rate limiting. Taken together, the results of the RPA and polysomal distribution analysis strongly suggest that E_2 modulation of AT_1R density in the AC is mediated at the posttranscriptional level by inhibiting receptor mRNA translation.

Although most reported studies of estrogen action have focused on control of gene expression at the level of transcription, estrogen has also been shown to act posttranscriptionally at the level of mRNA stability and translation. Estrogen activates a polysome-associated endonuclease and thereby destabilizes serum protein mRNAs in estrogen-treated frogs (48). Estrogen has also been shown to shift the distribution of ornithine δ-aminotransferase (OAT) mRNAs in neuroblastoma cells to denser fractions on a polysome gradient, suggesting that estrogen acts to increase OAT translation initiation (49). Our results are particularly interesting because, to our knowledge, this is the first study suggesting that E_2 can also modulate G protein-coupled receptor translation.

In genes that are regulated posttranscriptionally, RNA *trans*-acting factors are found to play a key role in gene expression by altering translational efficiency and/or mRNA stability (50, 51). We previously showed that cytosolic proteins in the adrenal bind to the 5′LS of the $AT_{1a}R$ and that the activity of these RBPs is modulated by E_2 in whole adrenal cytosolic extracts (18); however, we did not determine

whether cytosolic RBPs also bind to the $AT_{1b}R$ or whether these cytosolic proteins are located in the ZG, the tissue responsible for Ang II-induced aldosterone release. The observation that 5′LS AT_1R RBP activities are up-regulated under conditions in which the polysome distribution analysis indicates that E_2 is inhibiting AT_1R translation efficiency (Fig. 5), suggests that these 5′LS RBPs play a role in the mechanism by which E_2 reduces Ang II-induced aldosterone secretion from the ZG.

Numerous studies have shown that RBPs can recognize sequences in the CR and 3′UTR of mRNAs. A 50-kDa protein was shown to bind the CR of the LH/human chorionic gonadotropin receptor mRNA and was associated with destabilization of the receptor mRNA (52). In addition, FOS and MYC mRNAs contain a 180–320 purine-rich nucleotide segment in their CRs for RNA protein binding (53). Proteins were also found to bind with high specificity to the stem-loop structure located in the 3′UTR of the histone mRNA and to affect the histone mRNA transport, translation, and half-life (54). RBPs has been reported to bind to the 3′UTR of AT_1R and to regulate mRNA stability. In rat vascular smooth muscle cells, RPBs specifically bound to the distal 350 bases of the $AT_{1a}R$ mRNA and are likely involved in the Ang II-induced $AT_{1a}R$ mRNA destabilization (55). In Chinese hamster ovary cells, a major cellular protein of 55 kDa was identified and found to specifically interact with the 3′UTR of the $AT_{1a}R$, to control mRNA stability (56). In human vascular smooth muscle cells, the RNA binding protein, AUF1, has been shown to bind the AU-rich regions of the 3′UTR of AT_1Rs and to regulate receptor expression by altering mRNA levels (57).

According to the so-called scanning theory of protein translation (58), the formation of RBP activity in the 5′LS of receptor mRNAs could cause steric hindrance and thereby block the scanning of small ribosomal subunits toward the downstream open reading frame, so that translation efficiency is reduced. Posttranscriptional regulation by 5′LS BPs has been reported to be an efficient way to regulate ferritin, erythroid 5′-aminoevulinate synthase, and folate receptor-α expression (59, 60). Thus, the observation that E_2 does not regulate RBP activity in the CR or 3′UTR suggests that the mechanisms by which E_2 reduces AT_1R expression in the AC primarily involve 5′LS RBPs.

In summary, our results suggest that, in the rat AC, E_2 reduces AT_1Rs and Ang II-induced aldosterone release by a posttranscriptional mechanism in which AT_1R translational efficiency is inhibited. Our results showing that E_2 regulates RBP activity in the 5′LS, but not in the CR or 3′UTR of the AT_1R mRNA, further supports our hypothesis that E_2 reduces AT_1R translation in the AC by inhibiting ribosomal scanning attributable to increased steric hindrance from 5′LS RBPs. In addition to furthering our understanding of the molecular mechanisms underlying estrogen modulation of AT_1Rs and Ang II-induced aldosterone release, our data raise the possibility that dysregulation of this E_2-mediated posttranscriptional mechanism contributes to the increased incidence of cardiovascular disease observed after menopause, deriving from a loss in E_2-mediated attenuation of Ang II-induced aldosterone responses.

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