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Research Article

# Structural analysis of estrogen receptors: interaction between estrogen receptors and cav-1 within the caveolae<sup>†</sup>

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## Abstract

Pregnancy is a physiologic state of substantially elevated estrogen biosynthesis that maintains vasodilator production by uterine artery endothelial cells (P-UAECs) and thus uterine perfusion. Estrogen receptors (ER- $\alpha$  and ER- $\beta$ ; ESR1 and ESR2) stimulate nongenomic rapid vasodilatory responses partly through activation of endothelial nitric oxide synthase (eNOS). Rapid estrogenic responses are initiated by the ~4% ESRs localized to the plasmalemma of endothelial cells. Caveolin-1 (Cav-1) interactions within the caveolae are theorized to influence estrogenic effects mediated by both ESRs. **Hypothesis:** Both ESR1 and ESR2 display similar spatial partitioning between the plasmalemma and nucleus of UAECs and have similar interactions with Cav-1 at the plasmalemma. Using transmission electron microscopy, we observed numerous caveolae structures in UAECs, while immunogold labeling and subcellular fractionations identified ESR1 and ESR2 in three subcellular locations: membrane, cytosol, and nucleus. Bioinformatics approaches to analyze ESR1 and ESR2 transmembrane domains identified no regions that facilitate ESR interaction with plasmalemma. However, sucrose density centrifugation and Cav-1 immunoisolation columns uniquely demonstrated very high protein–protein association only between ESR1, but not ESR2, with Cav-1. These data demonstrate (1) both ESRs localize to the plasmalemma, cytosol and nucleus; (2) neither ESR1 nor ESR2 contain a classic region that crosses the plasmalemma to facilitate attachment; and (3) ESR1, but not ESR2, can be detected in the caveolar subcellular domain demonstrating ESR1 is the only ESR bound in close proximity to Cav-1 and eNOS within this microdomain. Lack of protein–protein interaction between Cav-1 and ESR2 demonstrates a novel independent association of these proteins at the plasmalemma.

## Summary Sentence

Since ESR1 and ESR2 plasma membrane location are respectively affiliated with Cav-1-dependent and Cav-1-independent mechanisms, a novel difference of ER regulation in endothelial cells derived from the uterine vasculature was identified.

**Keywords:** estrogen receptors, ESR1, ESR2, ER- $\alpha$ , ER- $\beta$ , Caveolae, pregnancy, nitric oxide, eNOS, uterine vasculature, endothelium.

## Introduction

Normal pregnancy is characterized by a multitude of systemic and even more dramatic uterine vascular adaptations [1–6]. Specifically, uterine blood flow (UBF) increases from 1 to 2% of cardiac output during the nonpregnant state and reaches 15–25% of the elevated total cardiac output by term [1, 4, 7], which is necessary for the appropriate delivery of nutrient and oxygen to the placenta and thus the developing fetus [3, 4, 7]. Maladaptation of the uterine vasculature that occurs during gestation is biologically and clinically significant as insufficient elevations of UBF are seen in pathological pregnancies (i.e. preeclampsia) [8, 9] which depending on the severity of the preeclampsia globally reduces levels of estrogens [10]. Insufficient UBF leads to diminished nutrient delivery, which is associated with fetal intrauterine growth restriction, higher prenatal and neonatal morbidity, and sometimes in severe cases leads to maternal and perinatal mortality, which are reported to occur in 6–14 per 1000 live births in the USA [7, 9, 11, 12].

In vivo ovine models have demonstrated that the increases in UBF are temporally associated with rises in the local and/or systemic endogenous estrogen levels during the follicular phase and normal pregnancy [2, 4, 7, 13–15]. Furthermore, reductions in local UBF were observed when unilateral intrauterine artery infusion of ICI 182780, a nonspecific estrogen receptor (ESR) antagonist, was performed in three chronically instrumented ovine models of endogenous and exogenous estrogen-induced increases in UBF [2]. Thus, in vivo models implicate ESRs in the regulation of UBF [2, 13]. We have previously reported the ex vivo relative change in ESR1 and ESR2 (ER- $\alpha$  and ER- $\beta$ , respectively) protein expression levels in several reproductive and nonreproductive endothelia under different hormonal milieu (luteal, follicular, and pregnant physiologic states) [15, 16]. Compared to the luteal phase, ESR1 protein levels increased in the uterine (not systemic) artery endothelium during the follicular phase and pregnancy [15, 16], whereas ESR2 protein levels were higher in uterine, mammary, and placental endothelia only during pregnancy, thus inferring a broader role for ESR2-mediated pathways in all reproductive rather than systemic vasculature studied especially during gestation [15, 16].

Both ESR1 and ESR2 orchestrate rapid nongenomic and long-term genomic estrogenic effects on the endothelium [15, 17–20]. Rapid estrogen effects were observed to induce complex signaling mechanisms in numerous endothelial cell types and vascular beds [10, 15, 21–25]. Moreover, the very rapid uterine vasodilator responses to estrogen via ESR1 and/or ESR2 have to a great extent been attributed to be endothelial-mediated responses [24, 26–28]. These complex signaling mechanisms contributed to the increased nitric oxide (NO) production that leads to increases in UBF [23, 28–35]. In endothelial cells, ESRs are known to localize to different intracellular locations [28, 36–38], including potentially a small population to the plasma membrane which, in turn, serves to direct the rapid estrogenic responses, such as biosynthetic vasodilator responses, i.e. NO and prostacyclin (PGI<sub>2</sub>) production [10, 39–41]. Moreover,

studies by Acconcia et al. [42] clearly identified that the ESR1 requires palmitoylation as a post-translational modification to target the receptor to the plasma membrane of HeLa cells. Others have verified these findings in CHO cells [43] and in vivo studies of ovarian and uterine responses to estrogen [44]. Our previous studies, using the pregnant uterine artery endothelial cells (P-UAECs) model that maintains a pregnancy-specific signaling and vasodilator phenotype, revealed the existence of membrane ESRs that increase NO with the membrane-impermeable estradiol-17 $\beta$  conjugate [39]. More recently, we demonstrated that ESR1 and ESR2 are both responsible for these rapid NO effects in UAECs independently of each other [41]. Membrane-bound ESR1 is known to co-localize to specialized, dynamic plasma membrane domains called caveolae. The caveolae compartmentalize many receptors and signaling molecules, including endothelial nitric oxide synthase (eNOS) [36, 38, 45–50]. Caveolae maintain their  $\bar{\sigma}$ -shaped plasma membrane invagination via high levels of cholesterol and its main resident scaffolding protein, caveolin-1 (Cav-1) [38, 51–54]. In endothelium, the enzyme responsible for the de novo production of NO, eNOS, co-localizes with and is thought to be negatively regulated by Cav-1 [38, 46, 53, 55]. Several studies have been focused on understanding the protein–protein interaction between ESR1, Cav-1, and signaling molecules that ultimately activate eNOS located in the caveolae [36, 53, 55]. However, as compared to the extensive data for ESR1, less is known regarding ESR2 subcellular location to the plasma membrane caveolar structures, its interaction with Cav-1, or its mechanism to increase NO bioavailability. This is important based on our recent observations that both ESR1 and ESR2 very rapidly stimulate P-UAEC NO biosynthesis in culture [41]. Consistent with our recent data, Corcoran et al. [24] also showed that in ex vivo pre-contracted human myometrial arteries agonists to both ESR1 (PPT) and ESR2 (DNP) induce partial relaxation in an endothelial and NO-dependent manner.

Therefore, we hypothesize that ESR1 and ESR2 display similar spatial partitioning between the plasma membrane, the cytosol, and the nucleus and have similar interactions with Cav-1 protein at the plasma membrane in P-UAECs. The objectives of this study therefore were to (1) identify the location of ESR1, ESR2, and Cav-1 relative to specific regions of the plasma membrane in P-UAECs; (2) identify regions within ESR1 and ESR2 that can potentially interact with the plasma membrane by utilizing two bioinformatic prediction algorithms; and (3) identify the specific protein–protein interactions between Cav-1 with either ESR1 or ESR2 using both sucrose density centrifugation and a column-based immunoisolation technique in tandem with western blot analysis.

## Materials and methods

### Cell preparation and culture

The University of Wisconsin-Madison research animal care committees of the Medical School and the College of Agriculture and

Life Sciences approved all procedures and protocols for animal handling and experiments, which follow the recommended American Veterinary Medicine Association guidelines for humane treatment and euthanasia of laboratory farm animals. Uterine arteries were obtained from mixed Western breed pregnant ewes at 120–130 days' gestation during nonsurvival surgery as previously described [33, 56, 57]. Uterine arteries were dissected free of connective tissue, fat, and veins. Arteries were rinsed free of blood using medium 199 before tying off arterial branches, clamping off the larger diameter end, and inflating with medium 199 containing 5 mg/ml collagenase B (Roche Molecular Biochemicals) and 0.5% BSA through a three-way stop cock tap. Digestion was allowed to proceed at 37°C for 55 min before flushing the collagenase solution and endothelial cell sheets from the inner surface of the vessel and FACS sorted with Alexa 488 acetylated LDL (Invitrogen, L-23380). The isolated and validated UAECs were cultured in growth media HyClone Minimal Essential Medium with Earle's (MEM/EBSS) with 20% FBS, 100 mg/ml penicillin, and 100 mg/ml streptomycin and propagated [56]. For experiments, passage 3, P-UAECs were plated in T75 flasks containing phenol free endothelial basal medium (Lonza, Walkersville, MD) supplemented with 20% FBS and 1% penicillin-streptomycin.

### Transmission electron microscopy and immunogold labeling

At passage 4 and ~90% confluence, endothelial cells were transferred to poly-L lysine cellware 12 mm round coverslips for preparation for transmission electron microscopy (TEM) and immunogold labeling [50, 58, 59]. Samples were sectioned parallel or perpendicular to the coverslip surface for TEM using a Reichert-Jung Ultracut-E Ultramicrotome and contrasted with Reynolds lead citrate and 8% uranyl acetate in 50% EtOH. Ultrathin sections were observed with a Philips CM120 electron microscope, and images were captured with a Mega View II side-mounted digital camera. See supplement for detailed methods of this technique.

### Prediction of transmembrane domains within proteins

The *Ovis aries*-derived protein sequence for Caveolin-1 (Accession NP.001009477; 178aa), ER- $\alpha$  (Accession No. AAK52104; 431 amino acids), and ER- $\beta$  (Accession No. NP.001009737; 527 amino acids), eNOS (Accession: NP.001123373; 1205aa—the accession number for the same database for all DNA sequences)—were input into the online Biology Workbench 3.2 database, <http://workbench.sdsc.edu/>. These software applications were used to predict ternary structures in the protein sequence studied. These sequences were input into the TMAP algorithm that uses Kyte-Doolittle hydrophathy profile to identify hydrophobic residues that could potentially be membrane-spanning domains [60]. The sequences were also input into the TMHMM algorithm, which uses the Hidden Markov Model to predict transmembrane alpha helices or the location of an intervening loop region [61].

### Protein extraction and western immunoblotting analysis

The total cell extracts were collected using a disposable cell scraper, vortexed, and clarified by centrifugation (13,000  $\times$  g, 5 min). The protein content of the samples was measured by a Bio-Rad

procedure using BSA as the standard. Aliquots of the extracts were frozen at  $-80^{\circ}\text{C}$  until western blot analysis could be performed. Equal amounts of total cell lysates were heated to denatured ( $95^{\circ}\text{C}$ , 10 min) in Laemmli buffer, separated on precasted 4–20% SDS-PAGE, and electrically (100 V, 55 min) transferred to PVDF membranes [15, 16, 54, 56, 57]. Membranes were used to identify ER- $\alpha$  and ER- $\beta$  detected using rabbit anti-ESR1 (HC-20; sc-543 [1:500]; Santa Cruz Biotechnology Inc.), rabbit anti-ESR2 (H-150; sc-8974 [1:500]; Santa Cruz Biotechnology Inc.), and rabbit anti-Cav-1 (No. 3238 [1:10,000]; Cell Signaling Technology). The corresponding secondary antibody was used at a dilution factor of 1:1000 (ESR1 and ESR2), 1:10,000 (Cav-1), and anti- $\beta$ -actin dilution factor of 1:3000. In addition, cell fractionation studies also included the verification of correct fractionation by utilizing western immunoblotting analysis using Plasma Membrane Fraction Western Blot Cocktail (Abcam—ab139413). Anti-mouse secondary antibody was used as 1:1500 dilution. These particular ESR1 and ESR2 antibodies and dilutions were chosen since they showed optimal data that were very consistent with our numerous previous ESR1 and ESR2 studies [15, 16, 40, 57].

### Subcellular protein fractionation

Fractionation was achieved by using the Subcellular Protein Fraction Kit for Cultured Cells (Thermo Scientific No. 78840). The manufacturer's protocol was followed and the samples analyzed using western immunoblotting with the ESR1 and ESR2 antibodies described above. Purity of the fraction was validated for plasma membrane ( $\text{Na}^+/\text{K}^+$ ATPase), cytosol (GAPDH), and Chromatin (Histone H3) using antibodies to standard markers.

### Caveolae isolation

Caveolae isolation was performed as described previously [50, 54, 62]. Briefly, passage 3 P-UAECs were grown to approximately 90% confluence in a T75 flask and then split (passage 4) into 10 T75s for each cell line; five T75s were used as control the others for estrogen treatment. Following treatment, for each cell line, cells were collected in 0.5 mL sodium carbonate buffer (pH = 11) containing phosphatase and protease inhibitors. The proteins from the respective five T75s were pooled and then caveolar isolation was performed using discontinuous sucrose density gradient centrifugation. A light scattering band confined to the 5–35% sucrose interface was enriched with caveolar membranes. Fifteen 1-ml fractions were collected and analyzed using western immunoblotting for ESR1, ESR2, and Cav-1 proteins.

### Immunoisolation Cav-1 columns

P-UAEC lysates were loaded with beads (Carbolink Immobilization kit, Pierce, Rockford, IL) covalently coupled to customized ordered anti-cav-1 antibody (Cell Signaling Tech. Inc.). The cav-1 bound fraction was subsequently eluted according to the manufacturer's instructions and this fraction was analyzed using western immunoblotting and scanning densitometry, as previously performed and described [54]. Indeed, the same protein eluates used in this previous study were utilized in the current study. See supplement for detailed methods of this technique.

## Materials

Electron Microscope: FEI, Tecnai T-12

Antibody Name	Lot number	References	RRID
ESR1	sc-543	PMID:28028198, PMID:28323976, PMID:28475868, PMID:28938408	AB_631471
ESR2	sc-8974	PMID:28962900	AB_2102246
Caveolin-1	3238	PMID:28017794,	AB_2072166

## Statistical analysis

Data are representative of  $n = 3$  or  $n = 4$  separate experiments and presented as means  $\pm$  SEM. P-UAECs each isolated from different experimental animals. ANOVA followed by the Bonferroni multiple comparison test was performed as post hoc analysis or Student's *t*-test was used to determine differences between treatments and controls. Significant was established a priori at  $P < 0.05$ . Statistical analyses were performed with GraphPad Prism 5.0b software.

## Results

### Transmission electron microscopy and immunogold labeling

We first identified the location of the classic  $\bar{\sigma}$ -shaped caveolae invaginations using TEM. We observed numerous caveolae near and at the plasma membrane of P-UAECs. These invaginations were identified in regions near cell-cell attachments (Figure 1A) and the leading edge of the endothelial cell (Figure 1B). TEM and immunogold labeling, depicted as black dots, identified the intracellular location for ESR1 and Cav-1 in P-UAECs (Figure 2). Figure 2A insert illustrates the IgG control sample showing no immunogold staining. ESR1 was found to localize at the plasma membrane, the cytosol, and nucleus (Figure 2B). The antibody for ESR2 did not work for this immunogold staining procedure (not shown). As expected, Cav-1 localized

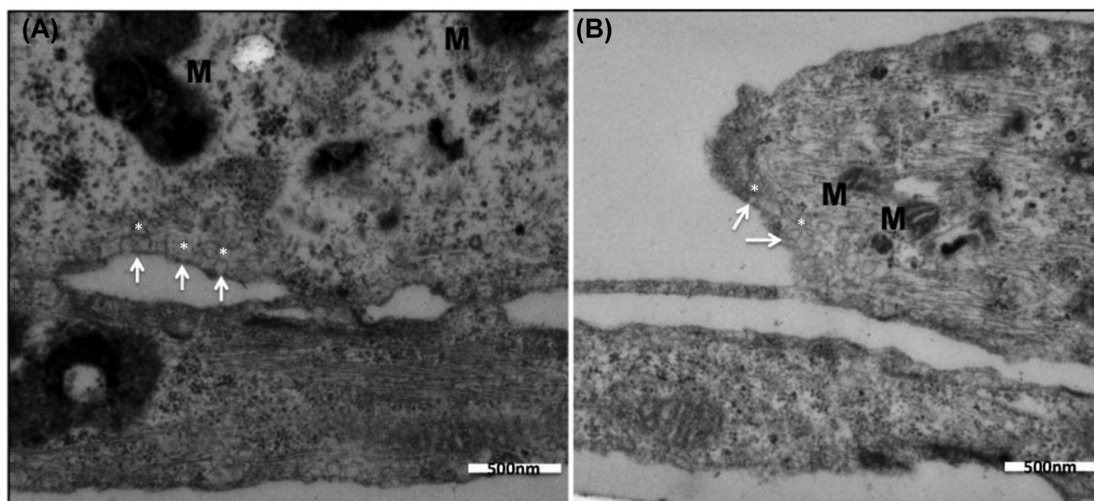
strictly to punctate regions of the plasma membrane without showing the distinct hourglass structure of caveolae that are altered during the harsh fixation process (Figure 2C).

### Subcellular protein fractionation

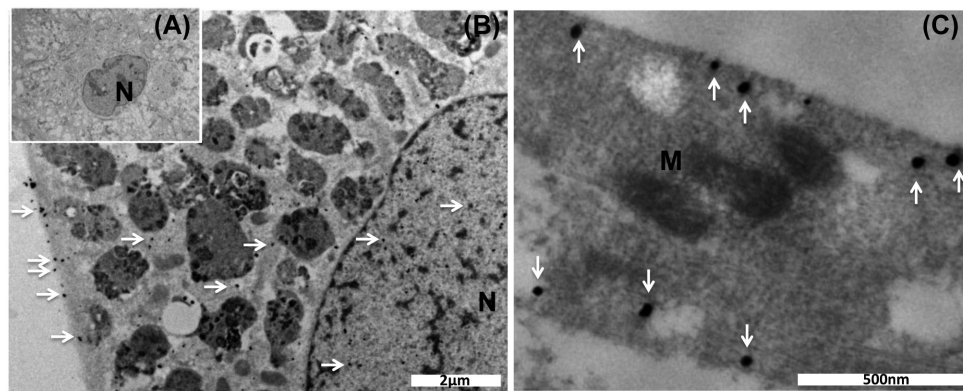
In order to further interrogate cellular localization of the ESRs in UAECs, we also performed subcellular fractionation experiments. Whole cell P-UAEC lysates and brain tissue were used as positive controls. Western immunoblot analyses of ESR1 (Figure 3A) and ESR2 (Figure 3B) proteins were identified within the membranes, cytoplasmic, nuclear, and cytoskeletal fractions. Under these unstimulated conditions, chromatin ESR2, but not ESR1, immunostaining was detected. Although only one antibody each was used in our demonstration of ESR2, but not ESR1, chromatin interaction, this finding is in keeping with the observations that under nonstimulation condition, ESR2 readily interacts with chromatin possibly even without ligand binding. However, the current data do not exclude ESR1 interaction with chromatin under estrogen stimulation [63].

### Prediction of transmembrane domains within protein

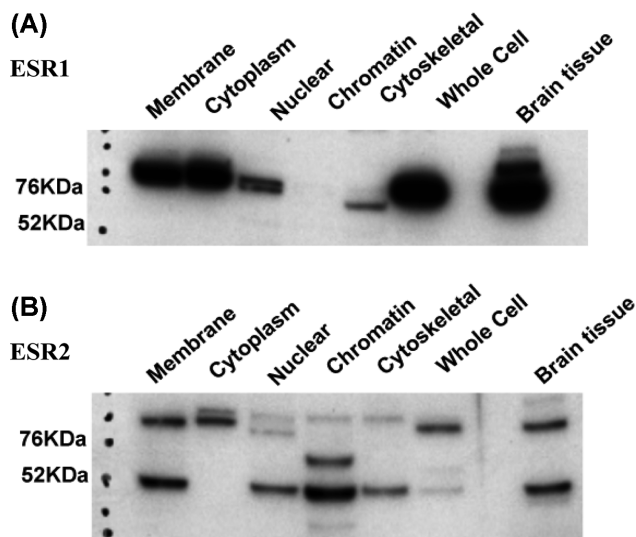
We then utilized two bioinformatic prediction algorithms, TMAP (Supplementary Figure S1) and TMHMM (Figure 4), to identify regions within ESR1 and ESR2 that can potentially facilitate attachment at the plasma membrane [60, 61]. Analysis of ESR1 protein sequence with the TMAP algorithm identified two segments of approximately 20 amino acids (aa). These segments were recognized as regions for ligand binding [62] and co-activator recognition sites [64] (Supplementary Figure S1A). In analyzing ESR2 protein sequence, the TMAP algorithm identified one segment of approximately 15 aa within the protein. This 15 aa segment was recognized as a region for ligand binding and the co-activator recognition site [64] (Supplementary Figure S1B). The analyses of Cav-1 and eNOS using this algorithm predicted sites that could potentially interact with the plasma membrane (data not shown). In the analyses of ESR1 and ESR2 protein sequences using TMHMM, there was zero probability that these proteins would respectively have an alpha helix structure or a location for an intervening loop region that could interact with the plasma membrane (Figure 4A and B). When the Cav-1



**Figure 1.** Transmission electron micrograph (TEM) identifying distinct caveolae structures in the uterine artery endothelial cell (UAEC) plasma membrane. The caveolae were found to line up along the length of the plasma membrane, (A) the regions close to cell-cell contacts, and (B) the leading edge of the cell. The darker intracellular discs are mitochondria. Arrows point to the  $\bar{\sigma}$ -shaped caveolae invaginations. M = mitochondria.



**Figure 2.** Transmission electron micrograph (TEM) identifying immunogold labeled ESR1 and caveolin-1 proteins in the uterine artery endothelial cells derived from the pregnant state (P-UAEC). (A) IgG control samples were incubated with IgG antibody followed by secondary antibody containing immunogold particles. (B) Immunogold labeling of ESR1 identified the protein localization at the plasma membrane, the cytosol, and the nucleus. (C) Illustrates the location of Cav-1 close to or at the plasma membrane. Immunogold labels are identified by small black dots. M = mitochondria, N = nucleus.



**Figure 3.** Subcellular fractionation to identify the location of ESR1 and ESR2 in uterine artery endothelial cells derived from the pregnant state (P-UAEC). Whole cell lysates were used for subcellular protein fractionation kits for cultured cells (Thermo Scientific) to identify the location of ESR1 and ESR2 in P-UAECs. The fractionations collected were analyzed using western immunoblotting and probed with ESR1 or ESR2 antibodies. (A) ESR1 was detected in the membrane, cytosolic, and at lower levels in the nuclear and cytoskeletal fractions. (B) ESR2 was detected in the membrane, cytosolic, nuclear, chromatin, and cytoskeletal fractions as both a monomer (~55 KDa) and dimer (110 KDa). Whole cell lysates from P-UAECs and brain tissue were used as positive controls. Fractions were defined based on standard markers of plasma membrane (Na<sup>+</sup>/K<sup>+</sup>ATPase), cytosol (GAPDH), and chromatin (Histone H3) markers.

protein sequence was analyzed using TMHMM, a region between amino acids 95–120 demonstrated a 100% probability of being a transmembrane segment (Figure 4C).

### Caveolar isolation

Next we performed sucrose density centrifugation to evaluate if ESR1 and ESR2 are present in caveolae-enriched preparations. In these studies, we combined P-UAECs fractions 4–7 that were identified as Cav-1 highly enriched [54] and observed ESR1 localized to both the caveolar and as expected the noncaveolar (lanes 9–12)

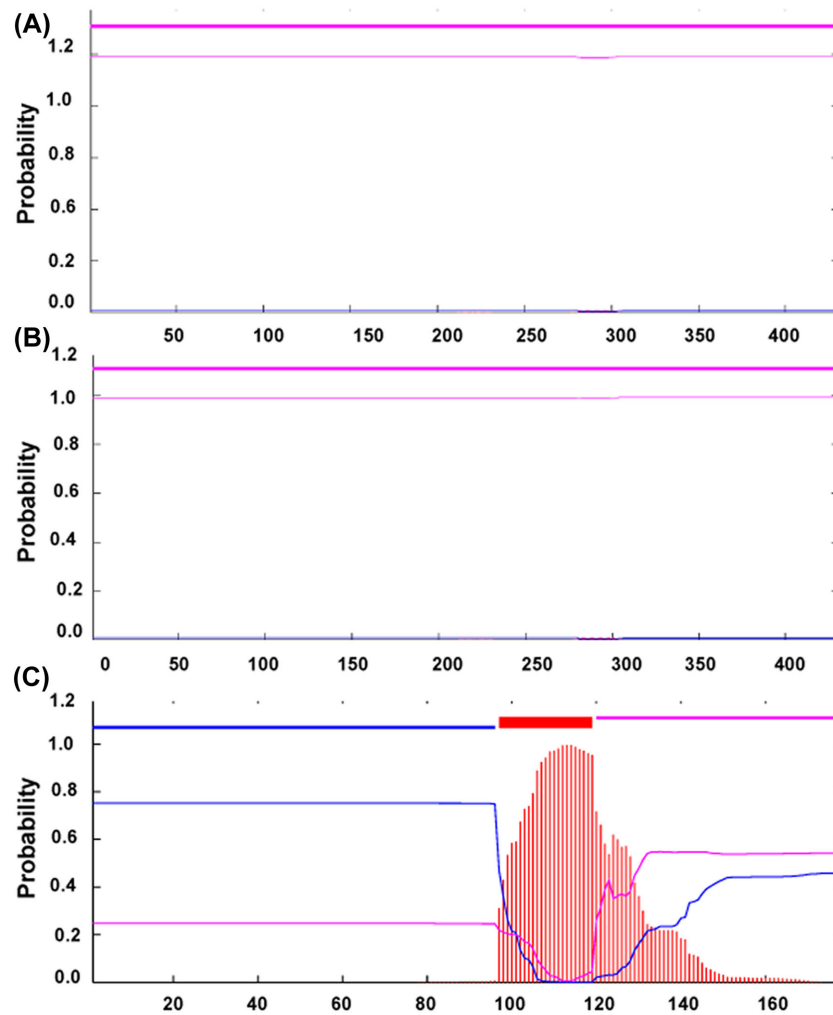
fractions (Figure 5). By contrast, ESR2 was completely undetectable using this antibody within the caveolae fraction, but on the same western blots, ESR2 was strongly detected in the noncaveolar fractions thus also serving as a positive control for the antibody used. Fraction 8 was omitted in the ESR analysis based on Cav-1 immunostaining to clearly differentiate the difference between caveolae and noncaveolae fractions relative to fraction markers.

### Immunoisolation Cav-1 columns

To directly evaluate the protein–protein interactions between Cav-1 and either ESR1 or ESR2 and relative to their location within the caveolae, we developed a column-based immunoisolation method using Cav-1 antibody [54]. These studies were also performed to confirm and validate our observations using sucrose density centrifugation. In Figure 6, we evaluated the relative levels of ESR1 and ESR2 in Cav-1 bound eluates from the immunoisolation columns. Cav-1 and ESR1 protein–protein interactions were clearly detected in the Cav-1 bound fraction whereas ESR2 did not bind to Cav-1 demonstrating a complete absence of physical association between ESR2 and Cav-1 thus validating and confirming those data presented above in Figure 5.

### Discussion

In the current study, we evaluated in P-UAECs the spatial partitioning of ESR1 and ESR2 between the plasma membrane, the cytosol, and the nucleus of UAECs and then directly determined for the first time the differential protein–protein interactions of both ESR1 and ESR2 with Cav-1 protein. The major observations we report herein are as follows: (1) the caveolar structures at the P-UAEC plasma membrane, ESR1, and ESR2 were identified to be present in several subcellular locations including the plasma membranes where their estrogenic effects influence rapid endothelial biological functions; (2) the bioinformatic predictions identified that neither ESR1 nor ESR2 contains a transmembrane region that can cross the plasma membrane; and (3) we were able to identify in caveolae a physical direct association between Cav-1 and ESR1 and contrary to our hypothesis, the complete lack of association between Cav-1 and ESR2, therefore identifying for the first time a novel difference of ESR regulation in P-UAECs. In addition to the difference in association between Cav-1 and the ESRs, we were also able to detect ESR1,



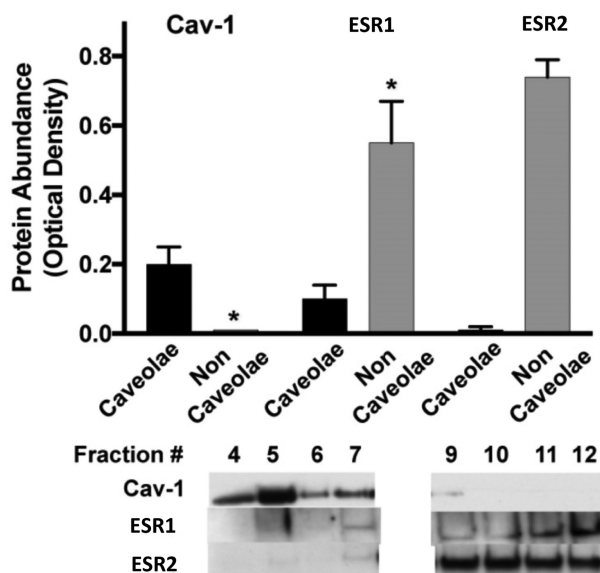
**Figure 4.** The TMHMM algorithm profile for ESR1, ESR2, and Cav-1. TMHMM algorithm provides a probability index for alpha helix or intervening loop regions within a protein sequence and TMHMM revealed that neither (A) ESR1 nor (B) ESR2 contain segment(s) resembling an alpha helix or intervening loop region that may potentially interact and/or anchor the protein within the plasma membrane. (C) The TMHMM algorithm also reveals that Cav-1 contains a segment, with high probability, to contain an alpha helix or intervening loop that can interact with plasma membrane.

but not ESR2, within the caveolae microdomains, supporting the protein–protein interaction observed between Cav-1 and ESR1.

In the present study, we sought to identify caveolae structures and the location of ESR1 and ESR2 within P-UAECs and the caveolae. The understanding of the ESRs in the caveolae is significant due to the different rapid nongenomic membrane versus prolonged genomic (nuclear) estrogenic effects on the endothelium. We first used TEM in order to identify caveolar structures within the plasma membrane of UAECs and to for the first time more precisely used immunogold techniques localize ESR1 and ESR2 to the plasma membrane, cytoplasm, and nucleus. The former data are consistent with several others that observed the caveolae structures localize at the plasma membrane of numerous endothelial cells types and that these structures assume the classic  $\bar{v}$ -shaped invaginations [47, 50, 65, 66]. We theorized that respective location of ESR1 and ESR2 would be important for understanding the rapid NO-mediated uterine vasodilatory effects on the endothelium by estrogen that we previously reported in vivo [2, 5, 13, 29, 67, 68] and in vitro [24, 39, 41, 69, 70]. In the present study, ESR1 was detected in the plasma membrane as well as several intracellular locations similar to other reports that

studied the cardiovascular system especially the endothelium and numerous endothelial cell types [40, 47, 65, 71]. We further verified this for the first time using both immunogold labeling and subcellular protein fractionation. Unlike ESR1, the visual identification of ESR2 location using immunogold labeling was unsuccessful due to either the apparent lack of specificity in the available antibodies or the difficulty for these antibodies to access the epitope of the relatively intact protein in a cell. In contrast, our subcellular fractionation data clearly showed that ESR2 is indeed present within the membrane, cytosol, and nuclear fractions, as seen in previously reports [72, 73], none of which tried to explicitly define a caveolar localization of ESR2. Unfortunately, the harsher chemical sample processing required for immunogold labeling of our proteins did not allow for a clear identification of the caveolae structures along with co-localization with ESR1 or ESR2 with gold particles.

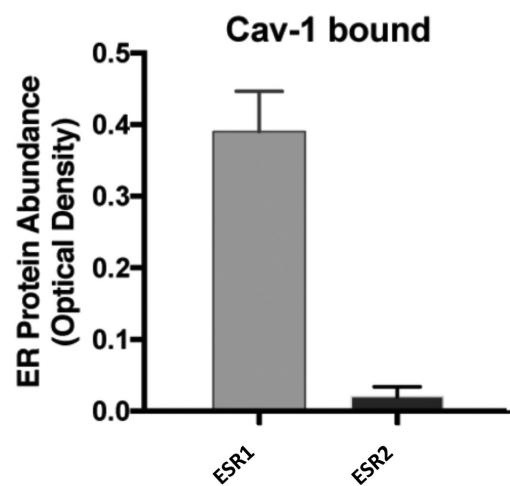
Therefore, to further assess the potential localization of ESR1 and ESR2 to the plasma membrane, we utilized for the first time bioinformatic predictions to identify potential transmembrane regions that could facilitate anchoring of ESR1, ESR2, and/or Cav-1 to the endothelial plasma membrane. The two algorithms that we



**Figure 5.** ESR1 and ESR2 locations within the caveolae in uterine artery endothelial cells derived from the pregnant state (P-UAECs). Caveolae isolation was achieved using whole cell lysates loaded on a sucrose density gradient solution. Immunoblot analysis of caveolae fractions (top row) was defined by cav-1 protein enrichment (lanes 4–7) and noncaveolae fractions devoid of cav-1 (lanes 9–12). Fraction 8 was not used for analysis. ESR1 was detected in both caveolae and noncaveolae fractions (middle row), whereas ESR2 was only detected in the noncaveolae fractions (bottom row). \* $P > 0.05$ .

employed identified no transmembrane regions within either ESR1 or ESR2 that would allow these receptors to be inserted into the plasma membrane [60, 61]. Although TMHMM showed zero probability of the ESRs has an alpha helix structure or a location for an intervening loop region that can interact with the plasma membrane, these findings further validate the use of these algorithms in predicting these types of regions from the protein sequence. However, the lack of these candidate regions within the ESRs secondary structures does not preclude other cellular mechanisms such as post-translational modification from facilitating their targeting to and in close interaction with the membrane. For example, acylation (i.e. N-myristoylation or palmitoylation) is a known post-translational modification that is well documented to be key for eNOS being targeted to the caveolae [74, 75]. TMAP and TMHMM identified a specific region within Cav-1 protein sequence that would allow a direct interaction between the protein and the membrane; this observation is consistent with our current TEM and Cav-1 immunogold data (Figure 1). Cav-1 is also acylated in order to facilitate its interaction with the plasma membrane in addition to the hydrophobic region we were able to identify in this study (Figure 4C). The identified hydrophobic region within Cav-1 protein sequence allows for a direct interaction with the membrane; this observation is consistent with conclusions of other studies that Cav-1 maintains the classical  $\bar{\nu}$ -shaped invaginations at the membrane [66, 76].

Estrogenic effects are known to occur acutely or chronically (nongenomic and genomic); therefore, the regulatory mechanisms that govern these effects are likely dependent on several significant protein–protein interactions [15, 51]. One important known level of regulation may involve the acute interaction between ESR1 and/or ESR2 with Cav-1 [15, 38, 63, 72, 77]. The current sucrose density caveolae isolation demonstrated ESR1 detection within the caveolae fractions. In the current study, we also report for the first time



**Figure 6.** ESR1 and ESR2 protein–protein interaction with Cav-1 in uterine artery endothelial cells derived from the pregnant state (P-UAECs). Whole cell lysate were loaded onto beads (Carbolink Immobilization kit) that were coupled to anti-cav-1 antibody for immunoisolation in order identify protein–protein interactions between Cav-1 and ESR1 or ESR2 and analyzed using western immunoblot analysis. Protein–protein interactions between Cav-1 and ESR1, but not ESR2, were observed; the latter indicating that these proteins do not interact.

that ESR1 column-based immunisolates with Cav-1 antibody [54] demonstrated a very close protein–protein association of these proteins in UAECs. Cav-1 and ESR1 interactions also directly suggest that Cav-1 may help translocate ESR1 to the plasma membrane where it is assembled with other signaling molecules within the caveolae [38, 54]. As we and others have previously described, the caveolae are known to concentrate a plethora of receptors and signaling transducing kinases that rapidly facilitate the response to stimuli that is received by the endothelium [15, 38, 48, 49, 51, 54, 78]. Using sucrose density centrifugation, we present the novel observation that indeed ESR1, but not ESR2, was localized to the caveolar-enriched fractions, whereas as expected both receptors subtypes were present at high levels in the noncaveolar fractions. However, herein we also validated this and report for the first time that there was little to no protein–protein interaction observed between ESR2 and Cav-1. Thus, these data are the first to demonstrate that plasma membrane ESR2, unlike ESR1, is not localized to the caveolae. Pedram et al. [43] reported an elegant study in which they discovered a signature 9 amino acid motif suggesting it as a unifying mechanism for sex steroid receptors to translocate to the plasma membrane. They also directly proved that palmitoylation increases the physical association of ESR1 with the plasma membrane and facilitates Cav-1 association using siRNA for Cav-1 in transfected CHO cells. Their ESR1 Cav-1 conclusions are consistent with many other studies including the current data presented in Figures 5 and 6 [65, 79, 80]. They made similar assumptions for the ESR2; however, they did not show data on IP of ESR2 identifying Cav-1 co-IP using CHO cells and thus did not directly prove localization to the same plasma membrane location by interacting with Cav-1. Our current novel data directly demonstrate that ESR2 utilizes a Cav-1-independent localization in the endothelial plasma membrane which we propose explain some of the differences observed between rapid estrogenic actions of ESR2 versus those of ESR1 in increasing bioavailability of vasodilators, i.e. NO [41] and PGI<sub>2</sub> [10]. Particularly given that our recently reported data demonstrating that activation of



either ESR1 or ESR2 increases NO biosynthesis [41], whereas PGI<sub>2</sub> increased in an ESR1-dependent manner with no ESR2 involvement in P-UAECs [10]. Taken together, these novel data suggest that increased NO bioavailability is driven in a Cav-1-dependent and independent mechanism (ESR1 and ESR2, respectively) while PGI<sub>2</sub> is only regulated via a Cav-1-dependent ESR1 pathway. In future studies, altering the raft compartment to disrupt ESR1 and/or ESR2 association by depleting cholesterol or Cav-1 and determining the effects on NO versus PGI<sub>2</sub> production responses to estrogen treatments will provide functional clues of the individual contributions of these two ESR subtypes relative to caveolae. In addition, in human umbilical vein endothelial cells, a widely used endothelial cell model, only the combined treatment of ESR1 and ESR2-specific agonists was required to mimic the rapid estradiol-17β-induced S-nitrosylation of proteins [63]. However, the role of Cav-1 in protein S-nitrosylation or the signaling pathway activated by the ESRs is unknown.

### Perspectives and significance

Estrogen and its receptors, ESR1 and ESR2, are important contributors in women's cardiovascular health and especially in the reproductive vascular beds (e.g. uterine, ovarian, and mammary). These receptors exert rapid short-term and slow long-term effects on the vasculature and have an important role in uterine vascular adaptations during pregnancy. Our work with P-UAECs identified abundant caveolae structures and the ESRs intracellular locations. We also identified for the first time a key difference in protein-protein interactions between the ESR1 and ESR2 with Cav-1. The closer interaction between ESR1 and Cav-1 points to estrogen/ESR1 rapid effect that is Cav-1 dependent, whereas we report for the first time that ESR2 appears to be regulated at the plasma membrane in a Cav-1-independent manner. Therefore, we identified a novel distinctive interaction between ESR1 and ESR2 with Cav-1, highlighting a potential differential regulatory mechanism in the rapid estrogenic effects in P-UAECs. Delineating mechanisms establishing the role of estrogen and ESRs in the uterine endothelial vasodilatory phenotype of pregnancy provides greater understanding of specific mechanisms functioning abnormally in gestational vascular pathophysiology such as hypertension and preeclampsia. Exploiting such differences in previously unrealized regulatory role of Cav-1 over ESR-mediated signaling may point to a potential therapeutic target to alleviate cardiovascular dysfunction in gestational diseases such as preeclampsia.

### Supplementary data

Supplementary data are available at [BIOLRE](https://doi.org/10.1002/biol.12345) online.

**Supplement Figure 1.** The TMAP algorithm profile for ESR1 and ESR2. TMAP algorithm uses Kyte-Doolittle Hydrophobicity Profile to identify hydrophobic regions. This algorithm analyzed 15aa (solid line) or 4aa (dashed line) to quantify the hydrophobicity within a given sequence. (A) TMAP revealed that ESR1 contains two segment containing highly hydrophobic residues as identified by the solid bar on the top of the graph. These regions are part of the ligand-binding and co-activator binding sites. (B) The TMAP algorithm also reveals that ESR2 contains a segment with highly hydrophobic residues, which also align with the ligand-binding domain. Both Cav-1 and eNOS show no 15aa or 4aa segments with high level of hydrophobicity (data not shown).

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