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Nuclear Receptor and Cofactor Expression in Female Reproductive Tissues



ACADEMIC DISSERTATION

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To My Parents

ABSTRACT

In the female reproductive tissues the nuclear receptors (NR) have a crucial role in regulating differentiation and proliferation. NRs are transcription factors which bind to specific DNA sequences of target genes in order to regulate their transcription. Transcriptional activity of many NRs also requires ligand binding. Ligands of NRs include hormones and vitamins. Some NRs, for example progesterone receptor (PR), are expressed in two isoforms differing in their transcriptional activities and having distinct physiological roles. In addition to receptor expression, cofactors are crucial in determining NR activity. These include coactivators enhancing the transcriptional activity and corepressors mediating transcriptional silencing.

The main aim of the present study was to characterise the NR expression and regulation of it by estrogens and progestins in the female reproductive tissues. The induction of PR isoform expression by estradiol was studied in two well-defined models: chicken oviduct and breast cancer cell lines. Expression was differentially regulated by estradiol in the chicken oviduct. The preferential PR-B expression in immature oviduct was altered to PR-A dominance after estradiol-induced differentiation. In breast cancer cell lines, E2 regulated the PR isoform expression in a distinctive manner depending on the cell line. Furthermore, breast cancer cell lines were found to differ in the levels of expression of NR mRNAs and regulation of NR levels by estradiol and progestin. NR expression during the menstrual cycle was characterised in human endometrium and myometrium. Expressions of androgen receptor (AR), estrogen receptor α (ER α), ER β , glucocorticoid receptor, PR, retinoic acid receptors (RAR) and vitamin D receptor mRNAs were detected. In the endometrium the AR, ER α , ER β , PR and RAR α mRNA levels were higher in the proliferative phase when compared to secretory phase samples. In the myometrium menstrual cycle-dependent regulation was less apparent.

Cofactor mRNA expression seemed not to be regulated by estradiol and progestin in breast cancer cell lines or during the menstrual cycle in human endometrium and myometrium. The myometrium expressed NR and cofactor mRNAs similarly to the endometrium. However, individual differences were found in the expression levels of cofactors similarly to those found in the case of NRs.

The findings suggest that the expression levels of PR isoforms, NRs and cofactors vary in breast cancer and in the uterus. In addition, variation exists in the hormonal regulation of NR expression in breast cancer cell lines. Due to these variations these tissues may respond in an individual fashion to endocrine treatment, a circumstance to be considered in developing novel therapeutic ligands.

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ABBREVIATIONS

| | |
|------------|---|
| aa | amino acids |
| AF | activating function |
| AIB1 | amplified in breast cancer 1 |
| AP-1 | activator protein 1 |
| AR | androgen receptor |
| ATG | initiation codon |
| bp | base pair |
| cAMP | cyclic 3',5'-adenosine monophosphate |
| CBP | cAMP-response element-binding protein |
| cDNA | complementary deoxyribonucleic acid |
| C-terminal | carboxyl terminal |
| CP | crossing point |
| cPR | chicken progesterone receptor |
| DBD | DNA binding domain |
| DNA | deoxyribonucleic acid |
| E2 | 17 β -estradiol |
| ER | estrogen receptor |
| ERE | estrogen response element |
| GR | glucocorticoid receptor |
| HAT | histone acetyltransferase |
| HDAC | histone deacetylase |
| HRE | hormone response element |
| HRT | hormone replacement therapy |
| Hsp | heat shock protein |
| IGF-1 | insulin-like growth factor-1 |
| IgG | immunoglobulin G |
| kb | kilobase |
| kDA | kilodalton |
| LBD | ligand binding domain |
| mRNA | messenger ribonucleic acid |
| N-CoR | nuclear receptor corepressor |
| NLS | nuclear localisation signal |
| NR | nuclear receptor |
| N-terminal | amino terminal |
| p300 | E1A binding protein p300 |
| PBS | phosphate buffered saline |
| pCAF | p300/CBP-associated factor |
| PCR | polymerase chain reaction |
| PR | progesterone receptor |
| PR-A | A-form of progesterone receptor |
| PR-B | B-form of progesterone receptor |
| R5020 | promegestone |
| RAR | retinoic acid receptor |
| RNA | ribonucleic acid |
| RT | room temperature |
| RT-PCR | reverse transcriptase polymerase chain reaction |
| RXR | retinoid X receptor |

| | |
|-------|---|
| SDS | sodium dodecyl sulphate |
| SERM | selective estrogen receptor modulator |
| SMRT | silencing mediator of repressed transcription |
| SRC-1 | steroid receptor coactivator 1 |
| TIF2 | transcriptional intermediary factor 2 |
| TR | thyroid hormone receptor |
| VDR | vitamin D receptor |

LIST OF ORIGINAL COMMUNICATIONS

The thesis is based on the following articles, referred to in the text by their Roman numerals:

I Syvala H, Vienonen A, Ylikomi T, Bläuer M, Zhuang YH and Tuohimaa P (1997): Expression of the chicken progesterone receptor forms A and B is differentially regulated by estrogen *in vivo*. *Biochemical and Biophysical Research Communications* 231:573-576.

II Vienonen A, Syvala H, Miettinen S, Tuohimaa P and Ylikomi T (2002): Expression of progesterone receptor isoforms A and B is differentially regulated by estrogen in different breast cancer cell lines. *Journal of Steroid Biochemistry and Molecular Biology* 80:307-313.

III Vienonen A, Miettinen S, Manninen T, Altucci L, Wilhelm E and Ylikomi T (2003): Regulation of nuclear receptor and cofactor expression in breast cancer cell lines. *European Journal of Endocrinology* 148:469-479.

IV Vienonen A, Miettinen S, Bläuer M, Martikainen PM, Tomás E, Heinonen PK, Ylikomi T. (2004): Expression of nuclear receptors and cofactors in human endometrium and myometrium. *Journal of the Society for Gynecologic Investigation* 11:104-112.

INTRODUCTION

In the female reproductive tissues nuclear receptors (NR) have a crucial role in regulating differentiation and proliferation during embryogenesis, puberty and reproductive years and even after the menopause. NRs are transcription factors which bind to regulatory regions of their target genes' DNA and control the transcription. The transcriptional activity of some NRs requires binding of specific ligand. Ligands of NRs include hormones and vitamins. The ligand-dependent activity of NRs provides possibilities for the pharmaceutical industry to develop therapeutic substances. For example, synthetic agonists or antagonists of estrogen receptor (ER) and progesterone receptor (PR) have been used for decades in contraception, cancer therapy and hormone replacement therapy (HRT).

In addition to ER and PR, several other NRs are involved in the regulation of cellular events such as apoptosis, differentiation and proliferation in the female reproductive tissues. Some NRs, for example PR, are expressed in two isoforms differing in their transcriptional activities and having different physiological roles. The cellular levels of cognate receptors are essential in determining target tissue response to a specific NR ligand. The regulation of NR expression occurs generally by its own ligands or by other NR ligands. For example, estrogen increases and progesterone reduces the expression of PR.

Besides receptor expression, cofactors, which consist of coactivators and corepressors, are critical in determining the ligand response. NRs form large complexes with coactivators and other transcription factors upon agonist binding, and activate transcription. Antagonist binding may lead to the recruitment of corepressors and repression of transcription. Altered expression levels of coactivators and corepressors may even change the agonist or antagonist properties of ligands. Although ER and PR expression have been widely studied in female reproductive tissues and tumors, knowledge of other NRs and cofactors is limited. The present work was undertaken to characterise the expression of several NRs and cofactors and hormonal regulation of their expression in the female reproductive tissues.

REVIEW OF THE LITERATURE

1. NUCLEAR RECEPTOR SUPERFAMILY

Members of the nuclear receptor (NR) superfamily comprise structurally-related transcription factors, which participate in the regulation of large variety of physiological, developmental and metabolic events. The NR superfamily consists of 48 members in humans (Maglich et al. 2001), divisible into three different types (reviewed in Whitfield et al. 1999, Laudet and Gronemeyer 2002, McKenna and O'Malley 2002). Type I receptors are classical steroid receptors, which upon ligand binding generally form homodimers and bind to hormone response elements (HRE) which are so-called inverted repeats or symmetrical palindromes. Type II receptors, for example thyroid and retinoic acid receptors (TR and RAR), form heterodimers with retinoic X receptor (RXR). HREs of type II receptors are so-called direct repeats. The majority of the superfamily members are type III receptors, which are “orphan” NRs, found in the late 1990s based on their sequence homology to the conserved NR sequence. The ligands of these “orphan” NRs are mostly unknown and have functions as yet unidentified. Some of these NRs may regulate transcription ligand-independently.

1.1. Structure of nuclear receptors

A typical NR consists of five to six functional domains (Figure 1). Of these the N-terminal A/B is the most variable. It participates in transcriptional activation and can contain an activation function 1 region (AF-1), which is considered constitutively active. The length of the A/B domain may be isoform-specific due to alternative splicing or differential promoter usage as described for RAR α and PR (Kastner et al. 1990, Leroy et al. 1991). The A/B domain may be phosphorylated from several serine and threonine sites mediated by different signalling pathways (reviewed in Shao and Lazar 1999, Rochette-Egly 2003). For example, growth factors induce phosphorylation of AF-1 of ER α through a mitogen-activated protein kinase (MAPK) pathway (Kato et al. 1995). The A/B domain participates in interaction with coactivators, thus affecting NR activity (Onate et al. 1998, Webb et al. 1998). These interactions may also be regulated by phosphorylation, as shown for the interaction of ER β with steroid receptor coactivator 1 (SRC-1) (Tremblay et al. 1999).

The C domain or the DNA-binding domain (DBD) is responsible for sequence specific DNA binding and is the most fully conserved structural domain throughout the NR family (reviewed in Freedman 1992). It contains N-terminal and C-terminal zinc-finger DNA-binding motifs. Both motifs contain four cysteine residues which chelate one Zn²⁺ ion. The N-terminal zinc finger contains a region called the P-box, which is involved in identifying the HREs. The C-terminal zinc finger contains a region called D-box which corresponds to the DBD dimerisation interface. DBD binds directly to HREs of target genes, which consist of two half motifs comprising six conserved nucleic acids. Mutations, extensions and duplications have created a great diversity to this conserved core sequence. Greater complexity to the response elements is usually brought by a 1-5 bp-long spacer, which separates the two core sequences. The core sequences can be oriented either as direct repeats, palindromes or everted repeats.

The D domain is called the hinge domain. It allows the DBD and the ligand-binding domain (LBD) to adopt several possible conformations, thus creating different dimerisation interfaces and allowing some receptors to bind to different type of HREs. The hinge domain is involved in binding of corepressors (Horlein et al. 1995). In addition, this domain contains a nuclear localisation signal (NLS) (Ylikomi et al. 1992).

The E domain is a multifunctional domain. It binds to receptor-specific ligands, participates in dimerisation and forms interactions with multiple proteins. In addition, LBD encloses the ligand-dependent AF-2 region, located in the C-terminal part of LBD. Crystal structures of both apo and holo LBDs of several receptors have revealed major conformational changes upon ligand binding, shifting the structure to a more compact complex (reviewed in Bourguet et al. 2000a). The LBD consists of 12 conserved α helical regions and one β turn situated in between helices H5 and H6. Binding of the ligand induces particularly repositioning of C-terminal helices and thus the formation of a ligand-binding pocket, which provides a hydrophobic cavity for the hydrophobic ligands. The conformational structure of LBD after binding either agonist or antagonist determines the binding of coactivators and corepressors to LBD (Brzozowski et al. 1997, Shiau et al. 1998, Xu et al. 2002). The LBD contributes as a major domain of dimerisation. For example, depending on the ligand TR and vitamin D receptor (VDR) can form either homodimers or heterodimerise with RXR *in vitro* (Cheski and Freedman 1994, Collingwood et al. 1997, Kakizawa et al. 1997). The activity of LBD domain may be modulated by phosphorylation (reviewed in Shao and Lazar 1999, Rochette-Egly 2003).

The optional F domain located in the C-terminus of receptors is variable in both length and sequence. Of steroid receptors only ER α and ER β acquire this domain. There are suggestions of its role as a recruiter of cofactors for the LBD domain (Montano et al. 1995, Kim et al. 2003).

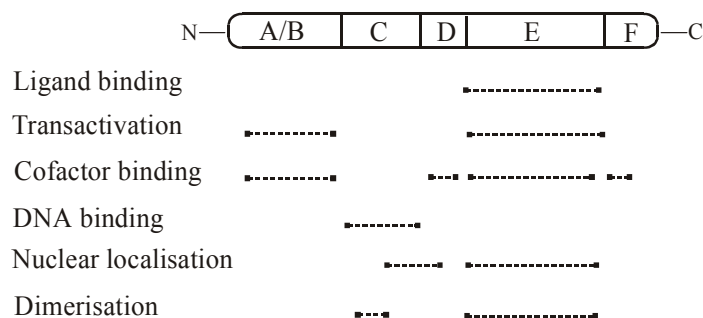


Figure 1. Structural and functional organisation of NRs. A typical NR consist of a variable N-terminal A/B domain, a conserved DNA-binding domain (C), a hinge region (D), a ligand-binding domain (E) and an optional C-terminal domain (F).

1.2. Nuclear receptors as transcription factors

Studies using green fluorescence proteins tagged to NRs have validated the conception of subcellular localisation of NRs. Most NRs partially shuttle between cytoplasm and nucleus and upon hormone binding translocate to the nucleus although, variations exist in whether the major portion of the receptor is located in the nucleus or in the cytoplasm (Georget et al. 1997, Lim et al. 1999, Racz and Barsony 1999, Poukka et al. 2000b, Tyagi et al. 2000, Maruvada et al. 2003). For example, the trafficking of PR between cytoplasm and nucleus is mediated via several NLSs located in the C, D and E domains of the receptor (Ylikomi et al. 1992). Receptor export from nucleus to cytoplasm has been suggested to involve part of the C domain and NLS (Guiochon-Mantel et al. 1994, Tyagi et al. 1998, Black et al. 2001, Saporita et al. 2003). Without ligand some of the steroid receptors form protein complexes consisting of heat shock proteins (Hsp) and associated proteins (see for review Cheung and Smith 2000, DeFranco 2002, Pratt and Toft 2003). These complexes participate in the proper folding of the receptor and participate in receptor shuttling between cytoplasm and nucleus. However, whether *in vivo* steroid receptors bind to Hsp complexes in the nucleus remains ambiguous (reviewed in Ylikomi et al. 1998).

TR and RAR α are capable of gene repression by binding corepressors, while steroid receptors do not repress gene transcription in the absence of hormones (Chen and Evans 1995, Horlein et al. 1995, Farboud et al. 2003, Hauksdottir et al. 2003). Upon ligand binding corepressors dissociate from the receptor due to repositioning of helix 12 (reviewed in Hu and Lazar 2000). This is crucial for ligand response, since patients evincing thyroid hormone resistance have mutations in TR rendering the receptor incapable of dissociating from the corepressor in the presence of thyroid hormone (Yoh et al. 1997). Agonist binding changes the conformation of the ligand binding pocket in such a way that an interaction surface for coactivators is formed. Ligand-bound receptor constitutes a more compact structure than unliganded receptor, a model called mousetrap. This conformation is ligand-dependent, as has been shown for ER α and RAR α (Brzozowski et al. 1997, Shiau et al. 1998, Bourguet et al. 2000b).

The first event in the initiation of transcription by NR is the formation of homo- or heterodimers and binding of liganded NR to the gene regulatory region. This is followed by cofactor recruitment, histone acetylation and chromatin remodelling (Li et al. 1999a, Dilworth et al. 2000, Shang et al. 2000, Aranda and Pascual 2001, Huang et al. 2003). Weak interaction of unliganded RAR/RXR heterodimers to cognate HREs followed by chromatin remodelling has been held to precede the ligand binding and tighter interaction with HREs (Dilworth et al. 2000). Ligand-bound NR associates directly with SRC family coactivators. This complex further recruits the coactivators cAMP-response element-binding protein (CBP), E1A binding protein p300 (p300) or p300/CBP-associated factor (pCAF), which possess histone acetyltransferase (HAT) activity. A recent model proposed by Huang and colleagues (2003) suggests that histone acetylation facilitates the recruitment of SWI/SNF and Mediator complexes. ATPase-containing SWI/SNF is involved in chromatin remodelling while Mediator may be associated with other cofactors and transcription factors. These initial steps are required for the extensive preinitiation complex to bind to the promoter area comprising general transcription factors, TFIID complexes and RNA polymerase II (reviewed in Belandia and Parker 2003).

When antagonists or partial antagonists are bound to NR, the ligand binding pocket acquires a different conformation affecting the cofactor binding (Bourguet et al. 2000a). For example,

when ER α is bound to 4-hydroxytamoxifen, helix 12 creates a conformation which inhibits coactivator binding (Shiau et al. 1998). Partially antagonist-bound to PR-B, androgen receptor (AR) and ER recruit the nuclear receptor corepressor (N-CoR) and the silencing mediator of repressed transcription (SMRT) (Jackson et al. 1997, Zhang et al. 1998, Shang et al. 2000, Shang et al. 2002). Reduced levels of N-CoR may alter the effects of tamoxifen as an antagonist towards agonist action (Lavinsky et al. 1998). Likewise the SRC-1/SMRT ratio determines the agonist/antagonist activity of RU486 for PR (Liu et al. 2002). In addition to different ligands different estrogen response elements (ERE) modulate the conformational structure of ER α or ER β , thus affecting recruitment of coactivators and hence transcriptional activation (Loven et al. 2001, Wood et al. 2001, Hall et al. 2002, Yi et al. 2002).

The transcriptional activity of the receptors is affected by post-transcriptional modifications such as phosphorylation, acetylation, sumoylation and ubiquitination. Multiple signalling pathways participate in the phosphorylation of NRs, subsequently regulating both ligand-dependent and -independent activity, DNA binding and cofactor binding (reviewed in Shao and Lazar 1999, Rochette-Egly 2003). Acetylation, in addition to chromatin modification, may affect NR activity directly (Wang et al. 2001a, Fu et al. 2002). AR has been shown to be acetylated by p300 and pCAF in the D domain of the receptor (Fu et al. 2000). This acetylation may be required for proper release of corepressors and subsequent coactivator binding, whereas acetylation of ER diminishes ligand-dependent activation (Wang et al. 2001a, Fu et al. 2002). Sumoylation, which is a process of covalent linkage of small ubiquitin-related modifiers, modulates the transcriptional activities of at least androgen receptor (AR) and glucocorticoid receptor (GR) (Poukka et al. 2000a, Tian et al. 2002). Ligand-dependent ubiquitination of NRs targets the proteins to proteosomal degradation (Syväälä et al. 1998, Li et al. 1999b, Nawaz et al. 1999a).

1.3. Alternative signalling pathways

In addition to binding to HREs of target genes, NR can cross-talk with other signalling pathways. Several NRs have been shown to repress or initiate activating protein-1 (AP-1) mediated transcription, which is involved in the regulation of cell proliferation and anti-inflammation (reviewed in Laudet and Gronemeyer 2002). Likewise NRs modulate other signalling pathways by interacting with DNA-bound transcription factors such as SP-1 and NF- κ B. A crucial role of these signalling pathways in mediating GR and ER α effects has been suggested by recent studies using mutated receptors unable to bind to their cognate HREs (Reichardt et al. 1998, Jakacka et al. 2002). Female mice heterozygous for mutated DBD of ER α are infertile, while heterozygous ER α knock-out mice are fertile (Lubahn et al. 1993, Dupont et al. 2000, Jakacka et al. 2002). This may be due to an imbalance of classical (HRE binding) and alternative signalling pathways or to an inhibitory effect of this mutated ER α on some other signalling pathways (Jakacka et al. 2002). GR knock-out mice usually die immediately after birth due to underdeveloped lungs, while mice carrying a point mutation causing inability to form GR homodimers and bind to glucocorticoid REs are viable (Cole et al. 1995, Reichardt et al. 1998). These findings emphasise that other signalling pathways are important mediators of NR effects in addition to the classical DNA binding-dependent transcriptional regulation.

The rapid non-genomic actions of NRs include regulation of cell membrane ion channels, G-protein coupled receptors and protein kinase signalling pathways. For example, the effects of

steroids on the cardiovascular system and in the central nervous system are partly mediated via rapid non-genomic mechanisms (reviewed in Simoncini and Genazzani 2003). It is still largely unknown whether these rapid effects occur through specific membrane receptors or through regular receptors located at the cell membrane.

2. COFACTORS AFFECTING NUCLEAR RECEPTOR ACTIVITY

Cofactors or coregulators comprise a large group of molecules including coactivators, cointegrators, corepressors or chromatin remodelling complexes. Over 50 different cofactors have been shown to be associated with the NR transcription complexes (reviewed in Laudet and Gronemeyer 2002). Apart from corepressors, cofactors assist in the assembly of the pre-initiation complex leading to transcriptional activation. Numerous different cofactors and transcription factors form large holocomplexes with NRs. The formation of a holocomplex depends on the receptor, ligand, cell and promoter as well as on multiple cell signalling pathways. Like NRs, cofactors are regulated via posttranslational modifications, for example via acetylation, phosphorylation and ubiquitination (Chen et al. 1999, Font de Mora and Brown 2000, Hong and Privalsky 2000, Rowan et al. 2000, Lopez et al. 2001, Zhou et al. 2001, Yan et al. 2003).

Functions of cofactors include modification and remodelling of chromatin, recruitment and stabilisation of the pre-initiation complex and recruitment of RNA polymerase II (reviewed in Aranda and Pascual 2001, Laudet and Gronemeyer 2002, Belandia and Parker 2003). In addition, cofactors may affect the cellular location of receptors, as shown for the small nuclear RING finger protein (SNURF), which interacts with the AR NLS region and assists AR nuclear localisation (Poukka et al. 2000b). Alternatively, cofactors may affect receptor proteasome degradation pathways, since a ubiquitin protein ligase E6-associated protein (E6-AP) enhances the transcriptional activity of steroid receptors (Nawaz et al. 1999b).

2.1. SRC/p160 family

One of the best-characterised groups of coactivators interacting with NRs is the SRC/p160 family. SRC-1 was the first cloned member of the SRC/p160 coactivator family (Onate et al. 1995). Although cloned as a ligand-dependent enhancer of PR-mediated transcriptional activity it also enhances the transcriptional activity mediated by other NRs such as AR, ER, GR TR, retinoid X receptor (RXR) (Onate et al. 1995, Alen et al. 1999, Bevan et al. 1999, Ma et al. 1999). It is expressed in two isoforms, SRC-1a and SRC-1e, which differ in the C-terminus (Kalkhoven et al. 1998). SRC-1e acts as a more potent enhancer of ER transcriptional activation than SRC-1a. Voegel and colleagues (1996) cloned the second member of the SRC/p160 family called transcriptional intermediary factor 2 (TIF2), and within a short period of time several groups cloned the third member, amplified in breast cancer 1 (AIB1, also known as p/CIP, ACTR, RAC3, TRAM-1) (Anzick et al. 1997, Chen et al. 1997, Li et al. 1997, Takeshita et al. 1997, Torchia et al. 1997).

SRC/p160 family coactivators function as bridging factors recruiting other cofactors such as CBP and p300 to the ligand-bound receptor. In addition, they are able to engage with another HAT pCAF and link it to the complex (Chen et al. 1997, Spencer et al. 1997). Furthermore,

they may bind directly to basal transcription machinery (Takeshita et al. 1996, Ikeda et al. 1999). Themselves SRC-1 and AIB1 have been shown to have moderate HAT activity and they may be acetylated by CBP/p300 (Chen et al. 1997, Spencer et al. 1997, Chen et al. 1999). This acetylation interrupts the interaction of the coactivator with the receptor, thus regulating hormonal response.

In addition to participating in transcriptional activation SRC/p160 family members may participate in the steroid hormone-dependent repression of transcription, as has been shown for agonist- but not antagonist-bound GR- and ER-mediated repression (An et al. 1999, Rogatsky et al. 2001). Besides regulating NR transcriptional activity SRC/p160 family members participate in a variety of other intracellular signalling pathways (reviewed in Leo and Chen 2000).

Observations on mice having null mutants for different SRC/p160 family members confirm that these coactivators are crucial in mediating steroid hormone effects and that they have distinct physiological roles despite their high level of sequence homology. SRC-1 knock-out mice are fertile but suffer from steroid hormone resistance, which may be partially compensated through increased TIF2 expression (Xu et al. 1998). AIB1 knock-out mice have decreased levels of systemic estrogens, probably due to the reduced sensitivity of granulosa cells in the ovary to follicle-stimulating hormone (Xu et al. 2000). Lack of AIB1 delays puberty, reduces fertility and diminishes mammary ductal branching and alveolar formation in response to estrogen and progesterone. In TIF2 null mutant mice the reduced fertility is due to poor development of the chorioallantoic placenta (Gehin et al. 2002).

SRC-1, TIF2 and AIB1 mRNAs are expressed in the normal human mammary gland (Anzick et al. 1997, Berns et al. 1998, Kurebayashi et al. 2000). In breast tumors AIB1 is frequently overexpressed (Anzick et al. 1997, Bouras et al. 2001). TIF2 mRNA levels seem to be upregulated and SRC-1 expression slightly downregulated in breast tumors (Berns et al. 1998, Kurebayashi et al. 2000). In the human endometrium expression of SRC-1, TIF1 and AIB1 has been reported; however, somewhat conflicting results are on record as to whether the expression levels are regulated during the menstrual cycle (Gregory et al. 2002, Wieser et al. 2002, Shiozawa et al. 2003). Women suffering from polycystic ovarian syndrome who evinced increased expression levels of ER α had elevated expression levels of both TIF2 and AIB1 (Gregory et al. 2002).

2.2. Cointegrators

CBP was first identified as a protein binding to the cAMP-response element-binding protein (CREB) (Chrivia et al. 1993). Its protein homologue p300 was found as an adenoviral E1A binding protein (Eckner et al. 1994). CBP and p300 extensively influence the proliferation, differentiation and apoptosis (reviewed in Chan and La Thangue 2001). Mutations of CBP and p300 have been found in many cancer types, suggesting that these proteins have tumor-suppressor-like activity.

They act as bridging molecules connecting other coactivators to the basal transcription machinery, or they can act as scaffold proteins enabling the other coactivators and HAT molecules to assemble in large multiprotein complexes in the transcription initiation environment. Themselves CBP and p300 have strong HAT activity and at least *in vitro* can

acetylate all four core histones (Bannister and Kouzarides 1996, Ogryzko et al. 1996). In addition they have been shown to acetylate a variety of non-chromosomal proteins (reviewed in Chan and La Thangue 2001). NRs recruit p300 and CBP more likely through interaction with SRC-1/p160 proteins, although direct interactions with NRs have also been shown (Chakravarti et al. 1996, Kamei et al. 1996, McInerney et al. 1998, Westin et al. 1998, Kraus et al. 1999, Li et al. 2000a, Sheppard et al. 2001, Shang et al. 2002).

Although CBP and p300 have strong sequence similarity and overlapping functions, the role of these proteins may be not totally overlapping (reviewed in Chan and La Thangue 2001). For example experiments with mice have revealed that CBP is required for normal hematopoietic differentiation while p300 expression is not crucial (Kung et al. 2000). Null mutant mice lacking either CBP or p300 are not viable, suggesting that these proteins cannot fully compensate each other's lost expression (Tanaka et al. 1997, Yao et al. 1998).

Cointegrator pCAF has been found to be able to bind to CBP and p300. It also possesses intrinsic HAT activity (Yang et al. 1996). It binds in ligand-dependent manner to DBD of NR and enhances transcription (Blanco et al. 1998, Korzus et al. 1998). It also interacts with SRC/p160 family members (Chen et al. 1997, Spencer et al. 1997).

CBP and p/CAF mRNAs are expressed in normal mammary glands (Kurebayashi et al. 2000). The expression of CBP is increased in intraductal carcinomas compared to normal mammary glands in correlation with increased ER α expression (Kurebayashi et al. 2000). CBP/p300 expression has been shown in human endometrial glandular and stromal cells, using antibody recognising both CBP and p300 (Shiozawa et al. 2003). The expression was slightly higher in the proliferative than in the secretory phase of the menstrual cycle.

2.3. Corepressors

Corepressors N-CoR and SMRT have been found to be associated with unliganded TR and RAR α and to mediate the transcriptional silencing of TR and RAR (Chen and Evans 1995, Horlein et al. 1995, Jackson et al. 1997, Ordentlich et al. 1999, Park et al. 1999). Corepressors recruit corepressor mSin3 (mammalian Sin3) and histone deacetylases (HDAC) to histone deacetylase chromatin structures, thus causing the chromatin to adopt more a compact repressive state (Heinzel et al. 1997, Nagy et al. 1997, Li et al. 2000b). Although not binding to unliganded steroid receptors, the corepressors may bind to antagonist-bound receptors like ER and PR (Jackson et al. 1997, Smith et al. 1997, Lavinsky et al. 1998). In addition to transcriptional repression N-CoR may promote transcriptional activation, since the retinoic acid-dependent transcriptional activation of a certain type of retinoic acid response element requires N-CoR and HDAC (Jepsen et al. 2000).

Expression of N-CoR and SMRT mRNA has been shown in human mammary glands (Kurebayashi et al. 2000). Their mRNA levels were slightly upregulated in intraductal carcinomas compared to normal mammary glands concomitant with increased ER α expression. Furthermore, N-CoR levels were significantly reduced in intraductal carcinomas compared to invasive ductal carcinomas, again in correlation with increased ER α expression, which would imply that corepressor levels are altered in the course of breast tumorigenesis. Low expression of both SMRT and N-CoR has been reported in the human endometrium

(Wieser et al. 2002, Shiozawa et al. 2003). The levels of N-CoR are expressed most abundantly during menstruation (Wieser et al. 2002).

2.4. Chromatin remodeling complexes

One important function of cofactors is to participate in chromatin remodelling. At least four ATP-dependent chromatin remodeling complexes exist (reviewed in Belandia and Parker 2003). These include the human homologue of yeast SWI/SNF, which enhances ER-, RAR- and GR-mediated transcriptional activity, and the WINAC complex, which mediates recruitment of unliganded VDR to VDR target sites (Muchardt and Yaniv 1993, Chiba et al. 1994, Kitagawa et al. 2003). The recruitment of SWI/SNF by NR is probably not direct but mediated through CBP/p300 (Huang et al. 2003).

The coactivator complex Mediator (also called as VDR-interacting proteins (DRIP), TR-associated proteins (TRAP), activator recruited cofactor (ARC) or the Srb/Mediator coactivator complex (SMCC)) functions as a general transcription activation-associated protein complex (reviewed in Leo and Chen 2000). The Mediator complex consists of more than a dozen proteins. It lacks HAT activity and is not specific solely for NR signalling. It binds to the AF-2 site of NRs through its LxxLL motifs or may bind NR indirectly via association with CBP/p300 (Rachez et al. 2000, Huang et al. 2003). The precise function of the Mediator is still rather speculative (Leo and Chen 2000). This large complex may supplementarily remodel the chromatin structure after initial chromatin acetylation by SRC-1 and CBP. This may be followed by the recruitment of the pre-initiation complex or other transcription factors, or the Mediator complex may target RNA polymerase II to the promoter region.

3. NUCLEAR RECEPTOR EXPRESSION AND FUNCTION IN FEMALE REPRODUCTIVE TISSUES

3.1. Estrogen receptor α

Estrogens have a major role in inducing proliferation and stimulating blood flow and water retention in the reproductive tissues. It was long thought that one receptor mediates the actions of estrogens, even though, disruption of this gene expression in a mouse model proved less crucial than expected (Green et al. 1986, Greene et al. 1986, Lubahn et al. 1993, Curtis et al. 1999). Soon after cloning of ER β it became evident that the actions of estrogens are mostly results of the interplay of both ER α and ER β (Kuiper et al. 1996).

ER α in the mammary gland

In both the normal and malignant breast epithelium estrogens are thought to promote cell proliferation. Approximately 7-15 % of luminal epithelial cells of the normal mammary gland are positive for ER α staining, but these cells are rarely proliferative, which would imply that estrogens stimulate proliferation indirectly (Clarke et al. 1997b, Russo et al. 1999, Shoker et al. 1999a). The highest expression of ER α can be found in the undifferentiated lobules and once the level of differentiation increases ER α is expressed the less (Russo et al. 1999).

During the menstrual cycle, ER α expression is higher in the follicular phase epithelial cells compared to the luteal phase cells (Soderqvist et al. 1993). In the human mammary gland only epithelial cells express ER α , while in rodents both epithelial and stromal cells express ER α (Cunha et al. 1997, Zhuang et al. 2003). ER α expression is critical for the proper development of the mammary glands, since in ER α knock-out mice only undeveloped ducts are present at the nipples (Korach 1994).

Numerous studies have elucidated the role of ERs in breast tumorigenesis, since increased exposure to circulating estrogens may augment the breast cancer risk (reviewed in Hilakivi-Clarke et al. 2002). Moreover, data from breast cancer prevention trials suggest that treatment with antiestrogens reduces the incidence of ER-positive breast cancers (reviewed in Cuzick et al. 2003). One key step towards malignancy may be the increased expression of ER α (Khan et al. 1994, Shoker et al. 1999b, Iwao et al. 2000a). The amount of proliferating cells also expressing ER α increases with age in the normal breast and during the development of malignant breast neoplasia (Clarke et al. 1997b, Shoker et al. 1999a). These findings suggest that the disruption of the hierarchical organisation in the breast, that is, ER α -positive cells regulating by paracrine factors the proliferation of ER α -negative cells is an early event in the development of malignancy.

Approximately one-third of breast cancers lack ER α (reviewed in Lapidus et al. 1998). These tumors are often of more aggressive type than ER-positive and they seldom respond to endocrine treatment. The mutations of the ER α gene are rather uncommon and may not explain all ER-negative tumors (reviewed in Dowsett et al. 1997, Lapidus et al. 1998). Another mechanism underlying the loss of ER α expression is methylation of ER α gene promoter, this resulting in a decreased expression of ER α (Yoshida et al. 2000). Histone deacetylase inhibitors re-induce the transcriptional activation of methylated ER α in human breast cancer cells, suggesting a novel therapeutic possibility (Yang et al. 2000). Abnormal ER α expression may be due to variant mRNA expression. Several ER α variants have been detected by RT-PCR in both normal and malignant tissue, but the expression at protein level is unknown (Dowsett et al. 1997, Hirata et al. 2003). Based on RT-PCR assays the clinical relevance of these variants for the progression of breast cancer has been thought to be small (Anandappa et al. 2000, Chappell et al. 2000).

ER α in the uterus

ER α knock-out mice have a hypoplastic uterus which does not respond to estrogen treatment (Lubahn et al. 1993, Couse et al. 1995). In the mouse uterus, the effects of estrogens are mediated via a paracrine mechanism, since estrogen-induced proliferation of epithelial cells and down-regulation of epithelial cell PR expression requires stromal ER α expression (Cooke et al. 1997, Kurita et al. 2000). In the human uterus, ER α protein expression is regulated concomitant with the menstrual cycle. In the proliferative phase, estrogen increases the expression of ER α in epithelial and stromal cells of the endometrium, reaching maximal levels in the mid to late proliferative phase, whereas the expression is decreased in the secretory phase (Garcia et al. 1988, Lessey et al. 1988, Snijders et al. 1992, Coppens et al. 1993, Fung et al. 1994, Noe et al. 1999). Lecce and colleagues (2001) have also reported cyclically regulated ER α expression in smooth muscle cells of the vascular wall and sporadic expression in endothelial cells. In the myometrium, ER α expression is cyclically regulated in the subendometrial part whereas the expression in the outer portion of the myometrium is not regulated (Noe et al. 1999). In myomas, ER α mRNA is expressed more abundantly than in

the surrounding myometrium (Wang et al. 2001b). During pregnancy, ER α expression in endometrium and myometrium is relatively low; however, ER α expression is increased in the labouring myometrium and this is linked to the expression of contraction-associated genes (Perrot-Appianat et al. 1994, Mesiano et al. 2002).

Endometrial cancers are often associated with hyperestrogenism. ER α expression has been reported to be associated positively with disease-free survival and tumor grade (Lindahl et al. 1992, Creasman 1993, Fukuda et al. 1998, Gehrig et al. 1999). Stage I tumors, which are ER α -negative, are more likely to relapse (Gehrig et al. 1999). In endometrial cancers as in breast cancer, methylation of the CpG island of ER α at least partly contributes to decreased ER α expression (Maeda et al. 2002, Shiozawa et al. 2002).

ER α in the other reproductive tissues

In the ovaries of ER α knock-out mice, follicle maturation arrests prior to formation of mature follicles, possibly in consequence of increased LH levels (Lubahn et al. 1993, Korach 1994, Schomberg et al. 1999, Dupont et al. 2000). Immunohistochemical results on ER α expression in the human ovaries are somewhat inconsistent. Granulosa cells of secondary follicles express ER α while primordial and primary follicles do not (Iwai et al. 1990, Suzuki et al. 1994). The expression is increased in granulosa cells of the dominant mature follicle prior to the luteinising hormone surge and decreased in samples taken at the time of the surge (Iwai et al. 1990). Furthermore, the theca interna, corpora lutea and stroma are negative for ER α expression (Iwai et al. 1990, Suzuki et al. 1994). However, Pelletier and El-Alfy have reported that granulosa cells and corpora lutea show no expression of ER α while germinal epithelial cells and theca internal cells are positive for ER α immunostaining (Pelletier and El-Alfy 2000). Some ovarian cancers express ER α , but whether the expression is of clinical relevance remains unsettled (reviewed in Perez-Gracia and Carrasco 2002). Overexpression of ER α relative to ER β may be a marker of ovarian carcinogenesis (Pujol et al. 1998). Interestingly, only ER α and not ER β has been seen expressed in metastatic tumors (Rutherford et al. 2000). Epithelial, stromal and muscle cells of the human oviduct express ER α and the expression is regulated during the menstrual cycle (Amso et al. 1994).

Menstrual cycle-dependent changes also occur both in the vaginal tissue and in the cervix. These tissues have been reported to evince higher ER α expression during the proliferative phase compared to secretory phase samples (Sjöberg et al. 1989, Cano et al. 1990). Both ER α and ER β may participate in the regulation of cervical ripening during term pregnancy, since the regulation of expression occurs during term pregnancy or after parturition (Stjernholm et al. 1996, Wang et al. 2001c).

3.2. Estrogen receptor β

Cloning of rat ER β has revealed that some estrogenic effects might be mediated through ER β (Kuiper et al. 1996). Human ER β has 97 % identity with the DBD of ER α and 59 % identity with the LBD sequence (Mosselman et al. 1996, Enmark et al. 1997). It binds 17 β -estradiol in a comparable affinity to ER α , although ligand-binding differences also exist (Kuiper et al. 1997). In female mice most abundant ER β expression can be found in the ovaries. ER β knockout mice have reduced ovarian efficiency and reduced fertility (Krege et al. 1998). ER β possibly mediates a stimulatory effect of estrogens on granulosa cell proliferation (Dupont et

al. 2000). In the uterus, ER β modulates the effects of ER α and mediates the estrogen-induced down-regulation of PR expression in the luminal epithelium (Weihua et al. 2000). ER β knockout mice show normal mammary gland development and lactate normally (Krege et al. 1998). However, when lactating these mice evince morphological differences compared to wild-type mice, revealing that ER β is required for terminal differentiation of the mammary gland (Forster et al. 2002).

Several studies in addition to those made with knock-out mice have suggested that the expression of ER β modulates the activity of ER α . ER β forms heterodimers with ER α , diminishes the sensitivity of ER α -expressing cells to estradiol, increases the antagonist activity of tamoxifen and enhances the agonist activity of genistein (Cowley et al. 1997, Hall and McDonnell 1999, Pettersson et al. 2000, Lindberg et al. 2003).

ER β in the mammary gland

ER β is expressed in both normal and malignant human breast cells (Enmark et al. 1997, Fuqua et al. 1999, Järvinen et al. 2000). This expression is not regulated in relation to menstrual cycle phase (Shaw et al. 2002). Expression of ER β in breast tumors is associated with well-differentiated and slowly proliferating tumors and with better disease-free survival rates (Järvinen et al. 2000, Omoto et al. 2001). Findings of decreased ER β mRNA levels during breast carcinogenesis support the conception that ER β acts as an inhibitor of cell proliferation (Leygue et al. 1999a, Iwao et al. 2000a, Iwao et al. 2000b, Roger et al. 2001). ER β expression may be of significance in tamoxifen sensitivity, since increased expression of ER β mRNA has been found in tamoxifen-resistant breast tumors (Speirs et al. 1999). Likewise, the expression of ER β mRNA is higher in tamoxifen-resistant breast cancer cell lines compared to tamoxifen-sensitive lines (Speirs et al. 1999).

ER β in the uterus

Numerous studies suggest higher expression of ER α compared to ER β in the human endometrium, however, comparison of different RT-PCR reactions or different antibodies is problematic (Matsuzaki et al. 1999, Matsuzaki et al. 2000, Lecce et al. 2001, Fujimoto et al. 2002). In the human endometrium, expression of ER β is regulated during the menstrual cycle in a manner similar to ER α . Immunohistochemical staining of ER β has been stronger in glandular epithelial cells of the proliferative phase than in the secretory phase (Critchley et al. 2001, Lecce et al. 2001). Weak staining in the stromal cells has remained unchanged during the cycle or slightly increased in the secretory phase (Critchley et al. 2001, Lecce et al. 2001). Cell-specific expression of ERs has also been found. Critchley and colleagues (2001) reported ER β but not ER α expression in vascular endothelial cells of the human endometrium and this expression was not regulated in the course of the menstrual cycle, although both ER α and ER β are expressed in perivascular cells. Likewise only ER β is expressed in the uterine-specific leukocytes called uterine natural killer cells (Henderson et al. 2003). In endometrial cancers, ER α has usually been found expressed more than ER β . However, related to poor patient prognosis some lymph node metastasis-positive cases have had higher ratios of ER β /ER α than the corresponding primary lesion (Fujimoto et al. 2002). Furthermore, increased ER β expression is related to myometrial invasion (Takama et al. 2001).

ER β in the other reproductive tissues

In the human ovaries, ER β is expressed in granulosa cells of the growing follicles and in the germinal epithelium (Pelletier and El-Alfy 2000, Taylor and Al-Azzawi 2000). Contradictory

results of ER β immunostaining in thecal cells and corpora lutea have been reported (Pelletier and El-Alfy 2000, Taylor and Al-Azzawi 2000). In ovarian cancer, a decreased expression of ER β mRNA has been reported and loss of ER β protein expression was linked to metastatic tumors (Brandenberger et al. 1998, Rutherford et al. 2000). In the oviduct, ER β immunostaining is mostly located in epithelial cells (Taylor and Al-Azzawi 2000).

In the case of human vaginal tissue, conflicting results of ER β expression have been reported (Pelletier and El-Alfy 2000, Taylor and Al-Azzawi 2000). In the human cervix, ER β is expressed in epithelium and stroma and the levels are regulated concomitant with cervical ripening during pregnancy and parturition (Wang et al. 2001c). Furthermore, ER β but not ER α expression was found in the stromal neutrophils, suggesting a potential role of ER β in the cervical ripening process.

Isoforms of ER β

Moore and colleagues (1998) have cloned 5 isoforms of human ER β , called ER β 1-5 which differ at the C-terminal LBD domain. At the same time, Ogawa and colleagues (1998) cloned the ER β 2 and named it ER β cx. These isoforms have a tissue-specific expression pattern (Moore et al. 1998). The expression of these isoforms may have significance in gynecological disorders and breast cancer, since they can form heterodimers with ER α (Moore et al. 1998). For example, ER β cx, which does not possess ligand binding ability, functions as a dominant repressor of ER α (Ogawa et al. 1998). Expression of ER β cx linked with low PR expression in breast tumors correlates with poor response to tamoxifen therapy (Saji et al. 2002). Although expression of several ER β isoforms at mRNA and protein level has been detected in breast cancer data concerning the clinical significance of ER β expression are as yet rather limited (Leygue et al. 1999a, Tong et al. 2002, Chi et al. 2003). Expression of ER β cx has been detected in normal endometrial tissue and the expression was to some extent regulated with the menstrual cycle in the glands of the functional layer (Critchley et al. 2002).

3.3. Progesterone receptor

The PR-A and PR-B isoforms are generally considered to mediate the tissue-specific effects of progesterone. However, the third functional isoform, PR-C, has been suggested to be present in breast cancer cell lines (Wei and Miner 1994, Wei et al. 1996). PR-A and the 164-amino-acid-longer PR-B are most likely translated from different mRNA transcripts of the same gene due to alternative promoter usage (Kastner et al. 1990). Although *in vivo* PR-A and PR-B are expressed within the same cells, they participate partly in different physiological events (Mote et al. 1999). PR-A is crucial for normal ovarian and uterine responses while PR-B is needed for proper mammary gland morphogenesis in mice (Mulac-Jericevic et al. 2000, Mulac-Jericevic et al. 2003). Transfection assays have revealed cell and promoter type-dependent differences in the transcriptional activities of human PR-A and PR-B. PR-B is a stronger transcriptional activator than PR-A, although depending on cell and promoter context PR-A can also function as an activator. PR-A can repress the transcriptional activity of PR-B and other NRs such as AR and GR (Vegeto et al. 1993, McDonnell et al. 1994). Both receptors can repress the activity of ER (Chalbos and Galtier 1994, Kraus et al. 1995). The variations in transcriptional activity are related to the structural difference of the two isoforms. Both receptors have AF-1 and AF-2 in their N-terminus and in the LBD respectively (Meyer et al. 1990). The N-terminal sequence unique to the PR-B isoform

contains a third AF (AF3) (Sartorius et al. 1994). The first 140 amino acids of PR-A contain an inhibitory function which in PR-B is masked by the PR-B-specific N-terminal sequence (Giangrande et al. 1997, Hovland et al. 1998). Giangrande and colleagues (2000) have demonstrated that PR-A and PR-B differ in their ability to bind coactivators. Furthermore, PR-A was more efficient in binding corepressor SMRT.

PR in the mammary gland

In the mammary gland, progesterone regulates lateral ductal branching and lobular alveolar development and suppresses milk protein synthesis during pregnancy. It may be responsible for proliferation of the mammary gland during the luteal phase of the menstrual cycle, when progesterone levels are high (reviewed in Graham and Clarke 1997). PR expression has been located in the ductal and lobular epithelial cells of the human mammary gland and these cells are mainly non-proliferating (Press and Greene 1988, Clarke et al. 1997a). The expression of PR is not regulated during the menstrual cycle and both PR isoforms are expressed at similar levels within the same cells of the mammary gland (Soderqvist et al. 1993, Clarke et al. 1997a, Mote et al. 2002).

In breast cancer, PR expression has been regarded as a good predictive factor; PR-positive tumors are smaller in size and better differentiated (Stonelake et al. 1994, Osborne 1998). When the clinical outcomes in two large databases were evaluated, ER-positive/PR-positive breast tumors had better prognosis with or without endocrine therapy (Bardou et al. 2003). However, Lydon and associates have shown that murine mammary gland carcinogenesis requires PR expression (Lydon et al. 1999). Furthermore, clinical data suggest that progestins have undesirable outcomes in the breast. In postmenopausal women combined estrogen and progesterone treatment is a more potent risk for breast cancer than estrogen treatment alone (Ross et al. 2000, Schairer et al. 2000, Santen et al. 2001, Rossouw et al. 2002, Beral 2003, Li et al. 2003). Results showing that estrogen and progesterone therapy is linked to greater breast epithelial cell proliferation and greater breast epithelial cell density or to mammographic density support these findings (Greendale et al. 1999, Hofseth et al. 1999). In addition, studies using animal models support the conception that progestins can intensify estrogen-induced proliferation in the mammary gland (Said et al. 1997, Cline et al. 1998).

Transfection experiments showing PR isoform-specific transcriptional activities have elucidated many theories regarding their role in carcinogenesis. Noteworthy is that PR-A knockout mice seem to have normal mammary gland development whereas PR-B knock-out mice exhibit reduced pregnancy-associated ductal and alveolar morphogenesis (Mulac-Jericevic et al. 2000, Mulac-Jericevic et al. 2003). Mice over-expressing PR-A have abnormal features in their mammary glands and are associated more often with neoplasia (Shyamala et al. 1998). Tumors which preferentially express PR-A are less well differentiated than those expressing more PR-B than PR-A (Bamberger et al. 2000). PR-A-over-expressing breast cancer cells detach from monolayer cultures after progesterone treatment, suggesting that PR-A-over-expressing tumors might be more invasive (McGowan and Clarke 1999). Mote and group (2002) have suggested that loss of control of PR isoform expression might be an early step in breast carcinogenesis. They found a predominance of one of the isoforms, more often PR-A in ductal carcinoma *in situ* and in invasive breast lesions. In addition they reported increased inter-cell heterogeneity of PR-A and PR-B expression in association with breast lesion progression to malignancy. PR isoform expression may influence the response to tamoxifen treatment, since growth of T-47D cells solely expressing PR-A and implanted in mice as xenografts was inhibited by tamoxifen, whereas the growth of PR-B-expressing tumors was unchanged (Sartorius et al. 2003).

PR in the uterus

Progesterone with estrogen has a crucial role in the uterus during the menstrual cycle and pregnancy. Progesterone stimulates glandular epithelial secretory activity and decidual transformation of stromal fibroblasts in the luteal phase of the cycle. The expression of PR has been studied mainly using antibodies identifying both receptor isoforms. During the menstrual cycle PR expression in epithelial cells is induced by estrogen in the proliferative phase and reduced by progesterone in the secretory phase (Garcia et al. 1988, Lessey et al. 1988, Press et al. 1988, Snijders et al. 1992, Amso et al. 1994). The expression in the stromal cells is not regulated or is less markedly regulated than in the epithelial cells. Development of PR-A- and PR-B-specific antibodies has made it possible to compare the expression patterns of the two isoforms even within the same cell using the dual immunofluorescent staining method (Mote et al. 1999). In the proliferative phase, the expressions of both isoforms were increased in the glandular epithelial cells. In the stromal cells the PR-A was the predominant form, although the expression levels of both isoforms were increased. In the glandular epithelium, the expression of PR-A was decreased constantly during the secretory phase while the regulation of PR-B expression level was more complicated. PR-B expression decreased in the early secretory phase, increased again in the mid secretory phase and decreased towards the late secretory phase, causing fluctuation in the relative PR-A and PR-B expression ratio in the glandular epithelium. Throughout the secretory phase the PR-A was the predominant isoform in stromal cells. In the myometrium, like ER α expression, PR levels were regulated with the menstrual cycle in the subendometrial part but remained fairly constant in the outer part of the myometrium (Noe et al. 1999).

During pregnancy, progesterone facilitates implantation and maintains pregnancy by quieting the myometrium. The onset of labor requires progesterone withdrawal and estrogen activation. In humans this may be achieved by the modulation of PR-A and PR-B expression (Pieber et al. 2001). Although the mRNAs levels of both isoforms are increased in the laboring compared to nonlaboring myometrium, the increase in PR-A mRNA is more dramatic, suggesting that the withdrawal of progesterone action is due to the suppressive action of PR-A on PR-B (Mesiano et al. 2002). Myomas have higher PR protein levels than the adjacent myometrium. This however, was not found at mRNA level, suggesting posttranslational control (Viville et al. 1997, Englund et al. 1998).

In endometrial cancer, PR expression correlates positively with tumor grade, with the depth of myometrial tumor invasion and disease-free survival (Fukuda et al. 1998). Compared to the normal endometrium, endometrial cancer frequently evinces decreased PR expression, which is due to loss of expression of one of the isoforms (Arnett-Mansfield et al. 2001). Tumors expressing either isoform have been associated with higher grades, whereas those expressing both isoforms have been found only in lower grade tumors. One conceivable mechanism underlying the loss of PR-B expression in endometrial cancer may be the methylation of CpG islands, causing gene inactivation (Sasaki et al. 2001). Several cell culture studies suggest that the PR-B isoform mediates the growth-inhibitory effects of progestins in endometrial cancer cells, and cells expressing PR-B are more clearly differentiated and less invasive than PR-A-expressing cells (Kumar et al. 1998, Dai et al. 2002, Smid-Koopman et al. 2003).

PR in the other reproductive tissues

Epithelial and stromal cells of the human vagina and cervix express PR and the expression seems not to be regulated in the course of the menstrual cycle (Cano et al. 1990, Wolf et al.

1991). PR may have a role in cervical ripening, since PR levels are decreased during term pregnancy (Stjernholm et al. 1996).

PR-A expression is necessary and sufficient for the production of oocytes in mice (Mulac-Jericevic et al. 2000, Mulac-Jericevic et al. 2003). In the corpus luteum of the rhesus monkey, PR-B is the predominant isoform through the luteal phase (Duffy et al. 1997). Although the levels of both isoforms were decreased from the early to the very late luteal phase the levels of PR-A were decreased more dramatically, thus altering the PR-A/PR-B ratios. In the human ovary, PR immunostaining has been reported in germinal epithelium, stroma, theca internal cells and the luteinised granulosa cells (Press and Greene 1988, Iwai et al. 1990, Suzuki et al. 1994). The PR expression in the ovary is regulated during the menstrual cycle. In the human oviduct, epithelial and stromal cells express PR and the expression is higher in the follicular than in the luteal phase (Amso et al. 1994). Somewhat inconsistent results have been reported regarding the PR status as a prognostic factor in ovarian cancers (reviewed in Perez-Gracia and Carrasco 2002). A recent finding of Akahira and colleagues (2000) was that PR-B is the predominant isoform in epithelial ovarian carcinoma and PR-B expression may be a prognostic factor for overall survival.

3.4. Androgen receptor

Major physiological ligands for AR are the male hormone testosterone and its metabolite 5 α -dihydrotestosterone. AR was found to be expressed in human genital skin fibroblasts in two isoforms, AR-B and its N-terminally truncated AR-A isoform (Wilson and McPhaul 1994).

AR in the mammary gland

The normal mammary gland expresses AR at low levels in both epithelial and stromal cells (Zhuang et al. 2003). In breast cancers, AR is commonly expressed and a considerable number of poorly differentiated ER-negative and PR-negative cancers are AR-positive (Kuenen-Boumeester et al. 1992, Isola 1993, Brys et al. 2002, Moinfar et al. 2003). Postmenopausal women carry an elevated risk of breast cancer if they have high estrogen levels but also if they have high testosterone levels (for a review see Liao and Dickson 2002).

AR in the uterus

AR expression has been detected in the human endometrium in epithelial and stromal cells (Horie et al. 1992, Mertens et al. 1996). More intense immunohistological staining has been observed during the proliferative than the late secretory phase (Slayden et al. 2001, Ito et al. 2002). Little staining has been observed in the myometrium (Horie et al. 1992). Estrogen treatment increases AR levels in the human endometrium (Fujimoto et al. 1994). Women suffering from polycystic ovarian syndrome and thus having high androgen levels have increased levels of AR in the endometrium (Apparao et al. 2002). Expression of AR has also been detected in adenomyosis, endometriosis and endometrial carcinoma (Horie et al. 1992, Ito et al. 2002).

AR in the other reproductive tissues

In the human ovary, Suzuki and colleagues (1994) have studied AR expression in detail. AR was expressed in stromal cells while granulosa cells of primordial and primary follicles were negatively stained. AR expression was detected in granulosa cells and some theca internal cells of maturing follicles. A majority of epithelial ovarian tumors have been reported to be

AR-positive (Kuhnel et al. 1987). AR expression is related to longer patient survival and lower tumor stage (Slotman et al. 1990). AR expression in the human vaginal mucosa correlated negatively with age and was lower in postmenopausal women than premenopausal, whereas expression levels did not differ in the vaginal submucosa (Berman et al. 2003).

3.5. Glucocorticoid receptor

The natural ligand for human GR is cortisol, which participates in the regulation of a variety of physiological actions such as metabolism and inflammation. GR is expressed in two C-terminally different isoforms, GR α and GR β (Hollenberg et al. 1985, Weinberger et al. 1985). GR β does not bind glucocorticoids and is transcriptionally inactive (Bamberger et al. 1995). However, it is expressed widely in human tissues and may act as a repressor of GR α and thus a potential modulator of glucocorticoid responses. Furthermore, both C-terminally different isoforms have N-terminally truncated slicing variants (reviewed in Yudit and Cidlowski 2002).

GR in the mammary gland

Glucocorticoids and prolactin act synergistically in mammary epithelial cells to activate milk protein gene expression. In virgin mice, fully active GR is required for proper ductal development of the mammary gland, whereas DNA-binding ability of GR is not crucial for the formation of alveoli during pregnancy and for normal lactation (Reichardt et al. 2001). In breast cancer, higher expression of GR mRNA has been found in grade 3 tumors than in benign breast and grades 1 and 2 tumors (Smith et al. 2003). Evidence that 17 β -estradiol (E2) decreases GR expression has been obtained in MCF-7 breast cancer cells, suggesting that estrogens may affect glucocorticoid responses in some cellular context (Krishnan et al. 2001).

GR in the uterus

In the human uterus, GR is expressed in stromal and endothelial cells of the endometrium, while it is not expressed in epithelial cells (Bamberger et al. 2001). Furthermore, GR has been localised in the decidua and in ER- and PR-negative uterine natural killer cells (Henderson et al. 2003).

3.7. Vitamin D receptor

1,25-Dihydroxyvitamin D₃ is the biologically active form of vitamin D and was originally identified as a regulator of calcium and bone homeostasis. In addition it participates in the control of cell proliferation, differentiation and apoptosis. 1,25-Dihydroxyvitamin D₃ binds to VDR, which was cloned first from a chicken intestinal cDNA library (McDonnell et al. 1987) and later from human intestine and T-47D cell cDNA libraries (Baker et al. 1988). VDR forms heterodimers with RXR or forms homodimers (Carlberg et al. 1993, reviewed in Issa et al. 1998). VDR null mutant mice have impaired folliculogenesis and uterine development (Yoshizawa et al. 1997). This is due to estrogen insufficiency caused by decreased P450 aromatase activity (Kinuta et al. 2000).

VDR in the mammary gland

Vitamin D controls proliferation, differentiation and apoptosis in mammary epithelial cells (reviewed in Narvaez et al. 2001). Mammary glands of VDR null mutant mice have evinced increased growth and branching morphogenesis (Welsh et al. 2002). Furthermore, glandular

involution, a process including epithelial cell apoptosis, was delayed in VDR null mutant mice. Vitamin D and its synthetic analogues inhibit the growth of breast cancer cells and induce apoptosis (reviewed in Narvaez et al. 2001, Colston and Hansen 2002). In breast cancer VDR-positive patients have had longer disease-free survival than VDR-negative patients (Colston et al. 1989). Friedrich and colleagues (1998) found increased expression of VDR in breast tumors compared to normal breast tissue.

VDR in the other reproductive tissues

Expression of VDR has also been studied in gynecological carcinomas. Expression of VDR at protein level was observed more often in cervical carcinomas than in normal cervical tissues (Reichrath et al. 1998, Friedrich et al. 2002). VDR expression has been shown in endometrial adenocarcinomas and ovarian tumors (Saunders et al. 1992, Yabushita et al. 1996).

3.8. Retinoic acid receptors α , β and γ

The physiological ligands for RAR α , β and γ are all-*trans* retinoic acid and 9-*cis* retinoic acid, which have important roles in the maintenance of epithelial differentiation, a characteristic utilised in chemotherapy (reviewed in Hansen et al. 2000). RAR α and RAR γ are expressed in two major isoforms, while RAR β has four major isoforms (for review see Leid et al. 1992). RAR may form either homodimers or heterodimers with RXR depending on the HREs (reviewed in (Laudet and Gronemeyer 2002). One of the target genes of RARs is RAR β itself and its expression has been suggested to be critical in the development of several types of cancer, for example breast cancer and cervical carcinoma (Geisen et al. 1997, Widschwendter et al. 1997, Xu et al. 1997).

RAR in the mammary gland

RAR α , RAR β and RAR γ are expressed in the normal mammary gland (Widschwendter et al. 1997). Retinoids induce apoptosis of breast cancer cells and this apoptotic effect may be mediated via RAR β (Pellegrini et al. 1995, Liu et al. 1996, Toma et al. 1997). Such a conception is supported by findings that loss of RAR β 2 expression may be an important event in breast carcinogenesis (Widschwendter et al. 1997, Xu et al. 1997). This loss may be partly due to methylation of RAR β gene (Bovenzi et al. 1999, Sirchia et al. 2000, Widschwendter et al. 2000).

RAR in the uterus

RAR α , RAR β and RAR γ are expressed in epithelial and stromal cells of the human endometrium and the expression is decreased in the secretory compared to the proliferative phase of the menstrual cycle (Kumarendran et al. 1996, Fukunaka et al. 2001, Ito et al. 2001). RAR α , RAR β and RAR γ are also expressed in the human myometrium and at similar levels in leiomyoma (Tsibris et al. 1999). In cervical intraepithelial neoplasia RAR α , β and γ levels are decreased, which may affect retinoid-induced growth inhibition of cervical neoplasia (Behbakht et al. 1996, Xu et al. 1999).

3.9. Retinoid X receptors α , β and γ

The physiological ligand of RXR is 9-*cis* retinoic acid. RXR participates in the regulation a large variety of NR signalling pathways, since RXRs are able to form heterodimers with several NRs, for example with RARs, VDR and thyroid hormone receptors (reviewed in Laudet and Gronemeyer 2002). In addition, it may form homodimers. Several N-terminal isoforms of RXR α , RXR β and RXR γ exist although the function of these variant forms is still unclear (for review see Laudet and Gronemeyer 2002).

RXR in the mammary gland

RXR α , RXR β and RXR γ are expressed in the normal mammary gland (Lawrence et al. 1998). Increased expression of RXR α , but not of RXR β or RXR γ , is linked to an increased risk of the development of invasive breast cancer (Lawrence et al. 1998).

RXR in the uterus

Both epithelial and stromal cells of the human endometrium express RXR α , RXR β and RXR γ and the expression appears to be higher in the proliferative phase than during the late secretory phase (Fukunaka et al. 2001). RXR α expression levels are increased in human leiomyomata compared to the normal myometrium (Tsibris et al. 1999).

4. SELECTIVE STEROID RECEPTOR MODULATORS

The ability of NRs to regulate cell growth and differentiation has drawn attention to their potential as therapeutic targets. Ligands of NRs are currently used in cancer therapy, in cancer prevention and in differentiation therapy. As noted above, multiplicity is the recurrent theme in NR signalling pathways. The activity of a given ligand at some cellular level is determined not only by the receptor, available cofactors and the target gene promoters but also by factors modifying the activity of these molecules, e.g. phosphorylation, ubiquitination etc. A compound is considered a selective NR modulator if it exerts agonist or antagonist effects selectively depending on target tissues. The basis for the concept selective estrogen receptor modulator (SERM) was generated according to the results obtained from studies with the antiestrogen tamoxifen. Clinical use of tamoxifen in the treatment of breast cancer commenced in the 1970s. Tamoxifen has antiestrogenic effects in the breast and breast cancer. In the uterus, in contrast, it acts as an agonist and increases the incidence of uterine cancer (Gottardis et al. 1988, Fornander et al. 1989). In addition to SERMs, all NR are potential targets of new tissue-selective NR modulators. The understanding of the molecular mechanism behind the tissue specificity is essential when designing new synthetic compounds having desired functions in target tissues.

Although originally thought of as reproductive hormones, estrogens cooperate in bone, cardiovascular system and central nervous system. Data derived from clinical studies suggested that long-term HRT usage might be regarded as preventive treatment for osteoporosis, heart diseases and dementia (Paganini-Hill and Henderson 1994, Ettinger et al. 1996, Grodstein et al. 1997, Torgerson and Bell-Syer 2001). Undesirable side effects of estrogen-only HRT comprise an increased risk of endometrial cancer, which may be overcome by progestin (Grady et al. 1995, 1996). Recent large HRT studies, although raising several controversial issues, suggest that combined progestin and estrogen HRT have side

effects which may offset the benefits of these therapies (Rossouw et al. 2002, Beral 2003). These studies further supported previous findings indicating that combined HRT increases the risks of breast cancer (Ross et al. 2000, Schairer et al. 2000, Chen et al. 2002, Rossouw et al. 2002, Beral 2003, Li et al. 2003). A somewhat unexpected finding in the Women's Health Initiative trial was that combined HRT slightly increased the risks of coronary heart disease and probable dementia (Rossouw et al. 2002, Shumaker et al. 2003). Beneficial outcomes of combined HRT usage were a reduced risk of colorectal cancers and hip fractures (Rossouw et al. 2002). Although this trial has been criticised for its limitations in respect of study population and regimens used, the current HRT does not answer the needs which optimal HRT would ensure, namely beneficial effects of estrogens in bone, cardiovascular system and central nervous system while antagonising the effects of estrogen in breast and uterus. Novel selective ER modulators (SERM) have been extensively developed, but only few are yet available. In spring 2003, FDA had approved three SERMS for clinical use; tamoxifen for the prevention and treatment of breast cancer, toremifene for the treatment of advanced breast cancer and raloxifene for the prevention and treatment of osteoporosis. Furthermore, several clinical trials are testing new potential SERMS.

The molecular mechanisms behind the agonist/antagonist profile of SERMs have been most intensively studied. Some of the regulation levels are briefly discussed here as examples of possible mechanisms elucidating the agonist/antagonist profile of selective NR modulators.

The tissue-specific effects of SERMs may be due to differences in ER α and ER β expression. Some cell types express only either ER α or ER β (Taylor and Al-Azzawi 2000). Raloxifen and tamoxifen bind to both ER α and ER β ; thus whether they exert agonist or antagonist effects depends partially on whether they bind to ER α or ER β homodimers or to ER α /ER β heterodimers (Cowley et al. 1997, Pace et al. 1997, Hall and McDonnell 1999). ER α works mostly as an activator whereas ER β can repress the activity of ER α through ERE sites (Cowley et al. 1997, Hall and McDonnell 1999, Lindberg et al. 2003). Structural differences in the AF-1 and AF-2 domains of ER α and ER β contribute partially to the different activities of these receptors. ER α has AF-1 and AF-2 (Bocquel et al. 1989, Tora et al. 1989). ER β has a weak AF-1, which can repress the activity of the C-terminal AF-2 domain (Hall and McDonnell 1999).

Whether the ligand acts as an agonist or antagonist is also dependent on the target gene regulatory region, since receptor- and cell type-specific differences have also been shown in the activation of transcription through AP-1 response elements. Table 1 summarises the differential activities of E2 and tamoxifen depending on the receptor and target gene (Webster et al. 1988, Philips et al. 1993, Tzukerman et al. 1994, Umayahara et al. 1994, Webb et al. 1995, Paech et al. 1997). Mice which are heterozygous for mutation in the DBD of ER α exhibit hyperplasia in the uterus and hypoplasia in the mammary gland (Jakacka et al. 2002). This resembles the outcome of tamoxifen treatment, suggesting that the alternative signalling pathways such as the AP-1-mediated may have a crucial role in determining the SERM-specific responses.

Table 1. Different responses of E2 and tamoxifen or 4-hydroxytamoxifen depend on the receptor and the target gene regulatory region.

| Ligand | ER α | | ER β | |
|-----------|-------------|------|------------|-----------|
| | ERE | AP-1 | ERE | AP-1 |
| E2 | ↑ | ↑ | ↑ | no change |
| Tamoxifen | ↓↑ | ↓ | ↓ | ↑ |

↑ increased or ↓ decreased transcriptional activity

Another level regulating the SERM response is due to the conformational differences which the LBD of ER α and ER β assume after ligand binding (Brzozowski et al. 1997, Shiau et al. 1998, Paige et al. 1999, Pike et al. 1999). When bound to E2, ER α is able to bind coactivators, while bound to 4-hydroxytamoxifen or raloxifen helix 12 of the ER α LBD adopts a position which inhibits binding of coactivators thus blocking AF-2 activity (Brzozowski et al. 1997, Shiau et al. 1998, Wong et al. 2001). In contrast, tamoxifen or raloxifen binding promotes corepressor interaction through helices H3 and H5 of the ER α LBD and this interaction is SERM-specific (Yamamoto et al. 2001, Webb et al. 2003). It is also dependent on the ligand which coactivators will be recruited by the receptor. E2 was shown to promote the interaction of ER α and ER β with the DRIP205, CBP, SRC1 and AIB1 (Wong et al. 2001). Genistein has been shown to enhance the interaction of ER α and ER β with SRC1 and AIB1 while having a minimal effect on interaction with DRIP205 and CBP. The cellular levels of cofactors may affect the SERM response. The estrogenic response of tamoxifen has been shown to require a high level of SRC-1 expression (Shang and Brown 2002).

The stability of ER α has also been shown to be ligand-specific (Wijayaratne and McDonnell 2001). E2 promotes degradation of ER α through the ubiquitin proteasome pathway and this is required for efficient transcriptional activity of ER α (Nawaz et al. 1999a, Lonard et al. 2000). The pure antagonist ICI 182,780 also reduces ER α stability while tamoxifen seems to stabilise ER α (Wijayaratne et al. 1999, Wijayaratne and McDonnell 2001).

One level of complexity has been suggested after findings that ER α gene polymorphism may affect response of HRT in bone and cardiovascular effects (Salmen et al. 2000, Herrington et al. 2002a, Herrington et al. 2002b). This may further lead to the identification of other associated genes having significant polymorphism, this indicating a need to chart patients' genetic background before determining the best available treatment.

AIMS OF THE PRESENT STUDY

The present work was undertaken to characterise the expression of several NRs and cofactors and the hormonal regulation of their expression in various female reproductive tissues. Broader knowledge of the receptor and the cofactor expression would help in the understanding of the responses of target tissues during hormonal treatments and when developing new ligands.

Specific aims of the study were:

1. to study the regulation of PR-isoform (PR-A and PR-B) expression by estrogen in the chicken oviduct and in breast cancer cell lines (I, II)
2. to study NR expression and hormonal regulation of expression in different breast cancer cell lines (III)
3. to characterise NR expression in proliferative and secretory phase endometrium and myometrium (IV)
4. to evaluate cofactor expression and its hormonal regulation in different breast cancer cell lines (III)
5. to characterise the expression of cofactors in proliferative and secretory phase endometrium and myometrium (IV)

MATERIALS AND METHODS

1. EXPERIMENTAL ANIMALS (I)

Two-week old White Leghorn chicks (Mäkelän Jalostukanala, Vilppula, Finland) were injected daily with 1 mg of 17 β -estradiol (E2) (1,3,5(10)-estratriene-3,17 β -diol, Sigma, St. Louis, MO, USA) dissolved in propylenglycol for up to 21 days. Immature control animals were not hormone- or vehicle-treated. Magnum parts of the oviducts were dissected out 24 hours after the last injection.

2. CELL CULTURE AND TRANSFECTIONS (II, III, IV)

Human breast cancer cell lines MCF-7, T-47D and ZR-75-1 were maintained in DMEM/F12 medium (Gibco BRL, N.Y., USA) supplemented with 5% fetal bovine serum, penicillin (100 IU/ml), streptomycin (100 μ g/ml), and bovine insulin (10 ng/ml, Sigma). MCF-7 cells were cultured with 1 nM E2 (Sigma). The culturing medium was changed to phenol red-free DMEM/F12 medium (Gibco) containing antibiotics and 5% dextran charcoal-treated serum one week before experimentation. Thereafter the medium was changed every second day. Cells were treated with either E2, R5020 (Schering Aktiengesellschaft, Berlin, Germany), cAMP (8-bromoadenosine 3':5'-cyclic monophosphate, Sigma) or with IGF-1 (insulin-like growth factor-1, human, recombinant, Sigma). After indicated treatments cells were washed with phosphate buffered saline (PBS) and trypsinised. The cell suspension was diluted with PBS and centrifuged for 10 min at 680 x g to collect the cell pellet.

Human promyelocytic cells HL-60 were grown in RPMI medium (Gibco) supplemented with 10% fetal bovine serum, penicillin (100 IU/ml), streptomycin (100 μ g/ml), HEPES (10 mM) and glutamine (2 mM). Before trypsinisation HL-60 cells were treated for 48 h with 200 mM 8CTP-cAMP (Sigma) and 1 mM SR11237 (gift from Dr. H. Gronemeyer, IGBMC, Department of Cell Biology and Signal Transduction, Illkirch, France).

COS cells were cultured in DMEM/F12 medium containing 5% fetal bovine serum, penicillin and streptomycin. The cells were transfected using the Lipofectamine reagent (Gibco) according to the supplier's instructions.

3. UTERINE SAMPLES (IV)

Uterine samples were obtained from 13 premenopausal women ranging in age from 38 to 50 years (mean 43 years) undergoing hysterectomy at Tampere University Hospital. The study was approved by the ethical committee of Tampere University Hospital and each patient had given fully informed consent. The donors were undergoing hysterectomy for various reasons excluding endometrial or myometrial malignancies. They had not used HRT. Instantly after removal of the uterus tissue specimens were taken from a site considered macroscopically to

be representative of the endometrium and myometrium. Endometrial and myometrial tissues were fractionated from the same tissue piece except for two endometrial samples obtained by endometrial biopsy. The samples were frozen and stored at -80°C until determination. Paraffin sections from each specimen were hematoxylin eosin-stained to determine the phase of the menstrual cycle. Histologically, six of the specimens represented the proliferative phase (days 5 to 19), one was from the interval phase (day 16) and six represented the secretory phase (days 17 to 31).

4. RNA ISOLATION

Total RNA was isolated from frozen chicken oviducts and human uterine samples according to Chomczynski and Sacchi (Chomczynski and Sacchi 1987). From breast cancer cells total RNA was isolated using TRIzol reagent (Gibco) according to manufacture's instructions. The amount of RNA was assayed by measuring the optical density of samples at wavelength 260 nm. Gel electrophoresis was used to confirm the integrity of the samples.

5. NORTHERN BLOTTING (I)

RNA samples were run on a 1% agarose gel containing formaldehyde and blotted to nylon filter (Magna, MSI, Westerborough, MA, USA). RNA was fixed on the nylon filter by baking it for 2 hours at 80°C . The filter was hybridised with [^{32}P]-labelled HindIII fragment of chicken PR cDNA (Jeltsch et al. 1990). The hybridisation was continued for 18 hours at 46°C in a solution containing 50 % formamide, 5 X SSPE, 5 % Denhardt's solution, 0.5 % SDS and 100 $\mu\text{g/ml}$ denatured herring sperm DNA. After washing the filter was exposed to autoradiography. To obtain an optimal signal Kodak MS-Biomax (Eastman Kodak Company, CT, USA) was used with an intensifying screen.

6. RIBONUCLEASE PROTECTION ASSAY (RPA) (II, III, IV)

Probes

The probe for detecting PR isoform-specific mRNAs was made by subcloning the cDNA fragment corresponding to nucleotides +618 to +971 according to Kastner and associates to transcription vector pGEM-T Easy (Promega, Madison, WI, USA) (Kastner et al. 1990). The sequence and the orientation were ensured by DNA sequencing. PR probe plasmid was digested with Sall restriction enzyme. The probe for identifying PR mRNAs was so designed that it could hybridise to both PR-A and PR-B specific mRNAs and yield three different lengths of hybrids. The longest hybrid (353 bp), called PR-B, is produced from transcripts which may encode both PR-B and PR-A. Both shorter hybrids, called PR-A/1 (220/210 bp) and PR-A/2 (129 bp), are produced from transcripts initiated after the first ATG site, thus encoding only PR-A-specific mRNAs.

The steroid receptor, VDR/RAR and cofactor probes are listed in Table 2. Probes for detecting GR, AR, PR, ER β , cyclin A, VDR and ER α mRNAs were included in the steroid

receptor set. Probes for detecting VDR, RAR α , RAR β , RAR γ , RXR α , RXR β and RXR γ mRNAs were included in the VDR/RAR set and those for N-CoR, SMRT, pCAF, CBP, TIF2, AIB1, SRC-1 and p300 in the cofactor set. Probes were made by PCR-amplifying the selected area of each gene's cDNA and further inserting the PCR product to the vectors listed in Table 1. TA-cloning was used to insert the PCR fragments to the pGEM-T Easy vector (Promega). BamHI and EcoRI digestion sites, which were included in the PCR primers, were used to subclone the PCR fragments to the pSG5 vector (Stratagene, La Jolla, CA, USA). The orientation and the sequence of the constructs were confirmed by DNA sequencing. The constructs were digested with the restriction enzymes listed in Table 2.

RPA

The RiboQuant *In vitro* transcription kit (Pharmingen, San Diego, CA, USA) was used to produce the antisense [32 P]-uridine triphosphate-labelled probes from linearised plasmids. The MEGAshortscript T7 kit (Ambion, Austin, TX, USA) was used to transcribe a [32 P]-labelled ribosomal 18S probe from plasmid pTRI RNA 18S (Ambion).

When breast cancer cell line samples were analysed, 5 μ g of total RNA was hybridised with 5×10^5 cpm [32 P]-labelled RNA probe (PR probe) or probe set (steroid receptor, VDR/RAR or cofactor set) (specific activity 1.7×10^9 cpm/ μ g) and with 340 ng of [32 P]-labelled 18S RNA probe (specific activity 89000 cpm/ μ g) using an RPA-kit (RPA III, Ambion). When uterine samples were analysed, 7.5 μ g of total RNA was hybridised with 1×10^6 cpm [32 P]-labelled RNA probe set (steroid receptor, VDR/RAR or cofactor set) (specific activity 1.7×10^9 cpm/ μ g) and with 680 ng of [32 P]-labelled 18S RNA probe (specific activity 56000 cpm/ μ g). The length of the synthesised 18S probe was 128 bp and that of the protected hybridised 18S was 80 bp. Yeast RNA was used as a negative control. In addition, either 8 μ g of breast cancer cell line sample RNA or 15 μ g of uterine tissue sample RNA were used to check that probes were in molar excess in hybridisation reactions. Hybridisation was carried on 43°C for at least 16 h. Samples were resolved by running them through 5% polyacrylamide gel containing 8 M urea. Autoradiography was used for visualisation of hybrids. Gels were scanned using the PhosphoImager Storm[®] (Molecular Dynamics, Amersham Biosciences, Buckinghamshire, UK) or films were scanned using a Personal Densitometer SI (Molecular Dynamics). The radioactive intensities of hybrids were calculated with ImageQuant software (versions 5.0 and 5.1, Molecular Dynamics). In order to verify probe specificity each probe of the VDR/RAR and cofactor sets was labelled alone to confirm the specificity. Total RNA from COS cells transfected with the corresponding cDNA was used to verify the appropriate hybrid for ER α , ER β , VDR, RAR α , RAR β and RAR γ . Furthermore, total RNA (4 μ g) from HL-60 cells was hybridised with the 32 P-labelled cofactor set and GAPDH probe using Pharmingen's RPA kit according to the supplier's instructions to demonstrate that the cofactor set identified all the corresponding genes. The intensities of 18S hybrids were used for normalisation of loading between samples. Comparisons were made only with samples run along the same RPA assay and gel. To assess whether insulin, estradiol and progesterin regulated the expression levels, the relative intensity of the hormone-treated sample was divided by the relative intensity of the control.

Table 2. Probes for RPA (AC# symbolises for GeneBank accession number, ¹basepairs)

| Gene | Size ¹ | mRNA region | AC# | Vector | Restriction enzyme |
|--------------|-------------------|----------------|----------|-------------|-----------------------|
| GR | 500 | 1741-2240 | M10901 | pGEM-T Easy | Sall |
| AR | 460 | 2641-3100 | M23263 | pGEM-T Easy | Sall |
| PR | 400 | 3945-4344 | X51730 | pGEM-T Easy | Sall |
| ER β | 316 | 503-818 | X99101 | pGEM-T Easy | Sall |
| Cyclin A | 300 | 598-897 | A32139 | pGEM-T Easy | Sall |
| ER α | 220 | 1846-2065 | M12674 | pGEM-T Easy | Sall |
| VDR | 326 | 1-326 | AF026260 | pSG5 | XbaI |
| RXR α | 290 | 83-372 | X52773 | pSG5 | XbaI |
| RXR β | 259 | 141-399 | M84820 | pSG5 | XhoI |
| RXR γ | 232 | 9-240 | U38480 | pSG5 | XhoI |
| RAR γ | 202 | 404-605 | M24857 | pSG5 | XhoI |
| RAR β | 183 | 333-515 | X07282 | pSG5 | XhoI |
| RAR α | 166 | 309-474 | X06538 | pSG5 | XbaI |
| N-CoR | 361 | 72-432 | AA564930 | pSG5 | HindIII |
| SMRT | 311 | 600-910 | U37146 | pSG5 | HindIII |
| pCAF | 266 | 901-1166 | U57317 | pSG5 | XhoI |
| CBP | 234 | 598-831 | U47741 | pSG5 | XhoI |
| TIF2 | 200 | 3111-3310 | X97674 | pSG5 | XhoI |
| AIB1 | 179 | 2594-2772 | AF010227 | pSG5 | BamHI |
| SRC-1e | 160 | 1421-1580 | U19179 | pSG5 | BamHI |
| SRC-1a | 145 | 4053-4197 | U90661 | pSG5 | BamHI |
| p300 | 130 | 7404-7533 | U01877 | pSG5 | BamHI |

7. RT-PCR (III, IV)

The expression of ER α and VDR mRNAs from breast cancer cell line samples were also analysed using real-time RT-PCR (LightCycler, Roche Diagnostics, Mannheim, Germany). Acidic ribosomal phosphoprotein P0 (RPLP0) was used as an endogenous RNA control and primers for it were selected as described by Bièche and colleagues (2001). All primer pairs were selected in different exons in order to avoid amplification from possible contaminating genomic DNA. Table 3 summarises the sequences of the primers.

Table 3. Primers, product size and reaction conditions applied in real time PCR using LightCycler instrument.

| Primer | Primer sequence | Annealing temp. | Mn(OAc) ₂ concentration | Product size |
|----------------|----------------------------|-----------------|------------------------------------|--------------|
| ER α -F | 5'-CCACTCAACAGCGTGTCTC-3' | 55°C | 2.5 mM | 242 bp |
| ER α -R | 5'-GGCAGATTCCATAGCCATAC-3' | | | |
| VDR-F | 5'-CTGACCCTGGAGACTTTGAC-3' | 55°C | 3.0 mM | 276 bp |
| VDR-R | 5'-TTCCTCTGCACTTCCTCATC-3' | | | |
| RPLP0-F | 5'-GGCGACCTGGAAGTCCAAC-3' | 58°C | 3.25 mM | 149 bp |
| RPLP0-R | 5'-CCATCAGCACACAGCCTTC-3' | | | |

One step RT-PCR was performed using a LightCycler RNA Master SYBR Green I kit (Roche) according to manufacturer's instructions. The total reaction volume was 20 μ l containing 200 ng of total RNA and 0.5 μ M of each primer. The Mn(OAc)₂ concentration varied depending on the assay (listed in Table 3). Reaction conditions in the LightCycler instrument were chosen according to the manufacturer's recommendations. Reverse transcription was performed at 61°C for 20 min followed by denaturation at 95°C for 30 s. PCR cycles consisted of 3 steps; denaturation at 95°C for 1s, annealing at 55°C - 58°C for 5 s and elongation at 72°C for 11 s (ER α), 12 s (VDR) or 7 s (RPLP0). A total of 38 cycles were carried out. Fluorescence was measured at the end of each elongation step at 72°C. However, when amplifying RPLP0 the fluorescence was measured at 81°C to avoid measurement of fluorescence due to an undesired faintly amplified product, which had a T_m lower than 81°C. The specificities of PCR products were verified by a melting curve analysis using the LightCycler instrument. In addition, the lengths of the PCR products were verified by agarose gel electrophoresis. The Fit Points Method determined the crossing point (CP) at which the fluorescence of each sample rose appreciably above the background fluorescence. Relative quantification of the target gene in comparison to the reference gene RPLP0 (ratio) was calculated using the CP and the efficiencies (E) of the PCR reactions.

$$\text{ratio} = (E_{\text{target}})^{\Delta \text{CP}_{\text{target}}(\text{control-sample})} / (E_{\text{RPLP0}})^{\Delta \text{CP}_{\text{RPLP0}}(\text{control-sample})} \text{ (Pfaffl 2001).}$$

Relative quantification of VDR mRNA levels from uterine tissue samples was also done using real time PCR (AbiPrism 7000, Applied Biosystems, Foster City, CA, USA). A High-Capacity cDNA Archive Kit (Applied Biosystems) was used to convert 8 μ g of total RNA to cDNA as described by the manufacturer. RPLP0 was used as an endogenous RNA control. Primers, which are listed in Table 4, were designed using Primer Express 2.0 (Applied Biosystems) and selected in different exons. Real time PCR was done using 20 ng of sample cDNA and SYBR[®] Green PCR Master Mix (Applied Biosystems) according to producer's protocol. As a calibrator we utilised total RNA from epithelial cells isolated from the endometrium basically as described by Laird and associates (Laird et al. 1997) (proliferative

phase, day 7). The results were expressed as N-fold differences in VDR gene expression (N_{VDR}) relative to RPLP0 expression and the calibrator. N_{VDR} (ratio) was calculated using the above equation except that control values were replaced with the calibrator values.

Table 4. Primers used in analysing mRNA expression with the AbiPrism instrument.

| Primer | Primer sequence |
|---------|----------------------------|
| VDR-F | 5'-CCTTCACCATGGACGACATG-3' |
| VDR-R | 5'-CGGCTTTGGTCACGTCAC-3' |
| RPLP0-F | 5'-AATCTCCAGGGGCACCATT-3' |
| RPLP0-R | 5'-CGCTGGCTCCCACTTTGT-3' |

8. WESTERN BLOT ANALYSIS (I, II)

Chicken oviducts were homogenised in 3 volumes of homogenisation buffer containing 10 mM Tris-HCl, 1.5 mM EDTA, 12 mM monothioglycerol, 10 mM Na_2MoO_4 , pH 7.4. In addition, the homogenisation buffer contained 0.3- 0.9 mM phenylmethyl-sulphonyl fluoride, 0.1 mM leupeptin, 77 $\mu\text{g/ml}$ aprotinin, 1.5 mM pepstatin and 100 $\mu\text{g/ml}$ bacitracin. Nuclear material was fractionated by centrifuging the homogenate at 800 g for 5 min. The supernatant was further centrifuged at 100 000 g (+4°C) for 1 hour and the consequent supernatant was used as cytosolic extract. The pellet obtained after low-speed centrifugation was washed with homogenisation buffer containing 10 mM Na_2MoO_4 . It was further incubated with buffer containing 10 mM Tris, 1.5 mM EDTA, 12 mM monothioglycerol, 0.4 M KCl, pH 8.0 for 1 hour at +4°C and then centrifuged at 4000 g for 30 min. The resulting supernatant was precipitated at a final volume of 50% saturated ammonium sulphate. Both cytosolic and nuclear fractions were dissolved in 4 volumes of sample buffer (63 mM Tris-HCl, 2% SDS, 10% glycerol, 1.5 mM EDTA, 5% β -mercaptoethanol, 0.05% bromophenol blue, pH 7.4) and boiled for 5 min.

Cell pellets from breast cancer cells were lysed using 4 volumes of sample buffer, which contained 63 mM Tris-HCl, 2% SDS, 10% glycerol, 5% β -mercaptoethanol, 0.025% bromophenol blue. After homogenisation of the cell pellet each sample was drawn several times through a 23 G needle in order to reduce the viscosity of the samples. Before storing the samples at -70°C they were boiled for 5 min.

Western blots were done according to standard procedures (Laemmli 1970). Samples were run through 6.5 % polyacrylamide gels containing 0.1 % SDS followed by electrophoretic transfer to nitrocellulose membranes (Protran, Schleicher & Schuell, Dassel, Germany). The transfer buffer contained 25 mM Tris, 192 mM glycine, 20 % (v/v) methanol. Transfer was done either for 2 hours (I) or overnight (II). Membranes were blocked with 5 % bovine serum albumin or 1% non-fat milk milk TBS (50 mM Tris, 0.9% NaCl, pH 8.0) for 1 hour at +37°C. Membranes were incubated with primary monoclonal antibodies PR22 (I)(Sullivan et al. 1986) and NCL-PGR (II) (Novocastra Laboratories, Newcastle, UK) or with polyclonal IgG-

RB (I) (Tuohimaa et al. 1984) at +4°C overnight. The final concentrations were 1 µg/ml for PR22, 150 ng/ml for NCL-PGR and 5 µg/ml for IgG-RB. After washings with TBS the membranes were incubated with secondary antibodies, peroxidase-conjugated anti-mouse or anti rabbit antibodies (Cappel, West Chester, PA, USA) at RT 1 hour. These antibodies were used in a dilution of 1:10000 (I) or 1:50000 (II). After washings with TBS the peroxidase was visualised using an enhanced chemiluminescence (ECL) detection system according to the instructions of the manufacturer (Amersham International). The intensities of subsequent bands were quantified using either digitalised images of X-ray films or densitometric scanning of X-ray films (Personal Densitometer, Molecular Dynamics).

9. STATISTICAL METHODS (III, IV)

The statistical significance of differences after hormonal treatments of breast cancer cell lines was assessed using the non-parametric Mann-Whitney U test (SPSS 10.1 for Windows). The same test was also used to determine the statistical significance of differences in the expression levels of proliferative and secretory phase endometrium and myometrium samples. Results were considered statistically significant at $p < 0.05$. The difference in expression levels between endometrium and myometrium was assayed using Wilcoxon signed ranks test (SPSS 10.1 for Windows). Results were considered statistically significant at $p < 0.05$. Spearman's bivariate correlation analysis (SPSS 10.1 for Windows) was used to analyse correlations between the ratio of cyclin A endometrium to cyclin A myometrium and the same ratios of steroid receptors, VDR, RARs and cofactors N-CoR, pCAF, AIB1 and p300. Correlation was considered statistically significant at $r > 0.6$ and $p < 0.05$.

RESULTS

1. PR ISOFORM EXPRESSION (I, II)

1.1. Expression and regulation by estrogen in chicken oviduct

The chicken oviduct is a classical model system for study of the hormonal regulation of PR expression, since its differentiation and maturation can be initiated in immature animals by hormonal administration. Chicken PR (cPR) is expressed in two PR isoforms (Gronemeyer et al. 1987, Jeltsch et al. 1990). The molecular weight of cPR-A is 79 kD and of cPR-B is 110 kD. Western blot analysis was used to quantitate the isoform expression at protein level in the immature chicken oviduct as well as after estrogen stimulation. Both cytosolic and nuclear extracts were analysed. PR-B was the preferentially expressed isoform in immature oviducts but PR-A expression was also detected. When estrogen was administered for 3 days to 2-week-old chickens, the preferential expression of PR-B isoform had changed to almost equal expression of both isoforms. Longer estrogen exposure, from 7 up to 21 days, preferentially increased the PR-A isoform expression.

The expression of PR was also studied at mRNA level using Northern blotting. The [³²P]-labelled probe recognised the sequence encoding the C-terminal end of the receptor. Jeltsch and colleagues (1990) have used the same probe and identified three polyadenylation variant mRNA species (sizes 8.2 kb, 4.5 kb and 3.3 kb) and a 5' truncated mRNA (size 4.1 kb). This 5' truncated mRNA does not contain the first ATG codon and thus can only be translated to PR-A protein. In the present study, four PR-specific bands were detected approximately corresponding to the mRNA sizes described by Jeltsch and colleagues (1990). In the immature oviduct, 8.0 kb, 4.4 kb, 3.1 kb mRNAs were strongly expressed while the PR-A-specific 3.9 kb mRNA was barely detected. Estrogen treatment markedly induced the PR-A-specific mRNA. The other 3 mRNA variants were also detected. Notable was that the signal for 8.0 kb mRNA was reduced compared to other mRNA signals.

1.2. Expression and regulation by E2 in breast cancer cell lines

The finding that E2 preferentially increases the expression of PR-A in the chicken oviduct differed from the results reported for breast cancer cell line T-47D. In this cell line estrogen has been shown to preferentially induce PR-B expression (Graham et al. 1995a). We further studied whether estrogen regulates PR isoform expression uniformly in different breast cancer cell lines. Western blot analysis was used to quantitate the relative expression of PR-A (85-94 kDa) and PR-B (116-120 kDa) in three breast cancer cell lines (Clarke and Satyaswaroop 1985, Horwitz et al. 1985). When cultured in phenol red-free medium with 5 % DCC serum, MCF-7, T-47D and ZR-75-1 cells expressed PR isoforms at fairly equal levels. When cells were treated with 10 nM E2 for up to 48 hours differential responses were detected. In T-47D cells both PR isoforms were induced by E2 in a similar way. The PR-A/PR-B ratio of control cells was 1.07 ± 0.35 and when the cells were treated with E2 for 48h the ratio was 1.10 ± 0.45 . In MCF-7 cells E2 induced a preferential increase in the PR-A form and expression of both isoforms reached maximal levels in 24 hours. The PR-A/PR-B ratio of control cells was

1.03 ± 0.06 and changed to 1.71 ± 0.09 after 48 hours' E2 treatment. In ZR-75-1 cells the expression of PR-B was preferentially increased and the maximal expression of PR-B was observed 24 hours after E2 addition. However, PR-A expression increased up to 48 hours. The PR-A/PR-B ratio of ZR-75-1 control cells was 0.90 ± 0.30 and the ratio changed to 0.40 ± 0.03 after 24 hours' E2 treatment.

To test whether this differential regulation of PR isoforms by E2 also occurs at mRNA level, the expression of PR-A and PR-B specific mRNAs was analysed using RPA. Two different hybrids were detected. The longer of them (353 bp) was obtained from transcripts which may encode both isoforms, but are most probably translated to PR-B (Kastner et al. 1990). The shorter hybrid (220/210) was obtained from mRNA which can only be translated to PR-A. The third possible hybrid, also encoding PR-A, was not detected, suggesting either that those transcripts were not expressed or that the expression was too weak to be detected. E2 induced PR mRNA expression in all cell lines in a way similar to that at protein level. In T-47D cells no clear dominance of either hybrid was detected. In MCF-7 cells preferential up-regulation of the 220/210 bp hybrid was detected in three out of four experiments. In ZR-75-1 cells the 353 bp hybrid was induced more in three out of four experiments.

1.3. Regulation by insulin, IGF-1 and cAMP

We further studied whether insulin, IGF-1 or cAMP alter the PR isoform ratio, since these agents have been reported to induce PR expression (Katzenellenbogen and Norman 1990, Cho et al. 1994). All three cell lines were cultured with 5 % DCC serum and treated with 10 nM E2 and insulin (10 ng/ml or 1 µg/ml) or IGF-1 (1 or 100 ng) for 24 hours. Insulin or IGF-1 did not affect the PR protein expression when compared to control cells treated with E2. When cell lines were cultured with 5 % DCC serum and treated with 10 µM 8-bromo-cAMP for 48 hours no changes in expression level could be detected.

2. NUCLEAR RECEPTOR EXPRESSION IN BREAST CANCER CELL LINES (III)

A lot of studies have surveyed the hormonal regulation of ER and PR in breast cancer cell lines. However, much less is known about the expression and regulation of expression of other NRs. In order to provide comparable information the expression levels of NR mRNAs in three commonly used breast cancer cell lines were characterised. The mRNA levels of steroid receptors, VDR, RARs and RXRs were quantitated using RPA. The regulation of expression by insulin, E2 and progesterone was also studied in these cell lines.

2.1. Expression of nuclear receptors

The expression of GR, AR, PR, ERβ, ERα, VDR, RARα, RARβ, RARγ, RXRα, RXRβ and RXRγ mRNAs was analysed in MCF-7, T-47D and ZR-75-1 cells. There were differences in the expression levels, but all cell lines expressed mRNAs for steroid receptors, VDR, RARα, RARγ and RXRα. For example, T-47D cells expressed most abundantly PR and VDR. MCF-

7 cells expressed most abundantly RAR γ . The expression of AR and GR was most abundant in ZR-75-1 cells. No expression of RAR β , RXR β and RXR γ mRNAs was detected.

2.2. Regulation of expression by insulin, E2 or progestin

Regulation of NR expression was analysed using control cells grown without E2 and insulin. Cells were treated with either 1 μ g/ml insulin, 1 nM E2 or a combination of both for 24 hours. In addition, samples treated for one week with 1 nM E2 and 1 μ g/ml insulin were analysed. Regulation of NR expression by progestin was analysed using cells grown for one week with 1 nM E2 and 1 μ g/ml insulin. Cells were treated with either ethanol (control) or 10 nM R5020 for 24 hours. Experiments were repeated 3 to 5 times. The regulation was considered significant if the following criteria were met: the expression was changed 2-fold compared to control and the p values in Mann-Whitney U test were less than 0.05. Table 5 summarises all the statistically significant results. Insulin alone did not significantly regulate the expression of any receptor analysed. Expression of cyclin A was checked for to evaluate that the hormonal treatments had the expected effects on cellular proliferation.

Table 5. Hormonal regulation of NR expression in breast cancer cell lines (mean \pm standard deviation).

| Cell line | mRNA | Estradiol (24h) | Estradiol+insulin (24h) | Estradiol+insulin (1 week) | R5020 (24h) |
|-----------|-------------------------------|----------------------------|---|-------------------------------|------------------------------|
| MCF-7 | PR | \uparrow 5.83 \pm 1.77 | \uparrow 4.37 \pm 2.01 | \uparrow 3.19 \pm 0.91 | \downarrow 0.52 \pm 0.10 |
| | ER β | \uparrow 7.55 \pm 2.89 | \uparrow 5.39 \pm 3.52 ¹ | \uparrow 3.01 \pm 1.78 | \downarrow 0.55 \pm 0.11 |
| | ER α ^{RT-PCR} | | | \downarrow 0.21 \pm 0.14 | |
| | AR | | | \downarrow 0.37 \pm 0.20 | |
| | GR | | | \downarrow 0.48 \pm 0.22 | |
| | VDR ^{RT-PCR} | | | | \uparrow 8.02 \pm 0.99 |
| T-47D | PR | \uparrow 3.01 \pm 0.80 | \uparrow 2.31 \pm 0.93 | \uparrow 3.69 \pm 2.31 | \downarrow 0.53 \pm 0.16 |
| | ER β | \uparrow 3.87 \pm 1.50 | \uparrow 2.43 \pm 0.94 | \uparrow 4.04 \pm 1.95 | \downarrow 0.47 \pm 0.28 |
| | ER α ^{RT-PCR} | \uparrow 2.29 \pm 0.29 | \uparrow 2.20 \pm 0.45 | \uparrow 2.03 \pm 0.90 | \downarrow 0.40 \pm 0.18 |
| | AR | | \downarrow 0.32 \pm 0.29 ² | | |
| | VDR ^{RT-PCR} | | | \downarrow 0.48 \pm 0.08 | \uparrow 4.70 \pm 1.11 |
| | RAR α | | \uparrow 2.07 \pm 0.68 | | \downarrow 0.46 \pm 0.12 |
| ZR-75-1 | PR | \uparrow 4.06 \pm 2.16 | \uparrow 3.14 \pm 1.19 | \uparrow 3.37 \pm 1.18 | \downarrow 0.36 \pm 0.34 |
| | ER β | \uparrow 3.95 \pm 1.93 | \uparrow 3.07 \pm 1.47 | \uparrow 3.05 \pm 1.31 | \downarrow 0.33 \pm 0.39 |
| | ER α ^{RT-PCR} | | \downarrow 0.45 \pm 0.17 | \downarrow 0.43 \pm 0.19 | \downarrow 0.31 \pm 0.19 |
| | RAR α | \uparrow 2.22 \pm 0.50 | \uparrow 2.70 \pm 0.55 | \uparrow 2.31 \pm 0.69 | |
| | RAR γ | | | \uparrow 2.87 \pm 2.40 | |

\uparrow denotes for up-regulation. \downarrow denotes for down-regulation. ^{RT-PCR}Result from quantitative RT-PCR. ¹Mean based on two values, third repeat up-regulated but the intensity of the control sample below detection limit. ²Mean based on two values, not statistically significant.

3. COFACTOR EXPRESSION IN BREAST CANCER CELL LINES (III)

3.1. Expression of cofactors

Large group of cofactors have been shown to affect the transcriptional activity of NRs. The expression levels of some cofactors have been shown to be altered in breast cancer and proposed thus to modulate the response to estrogen (Anzick et al. 1997, Leygue et al. 1999b, Kurebayashi et al. 2000, Murphy et al. 2000, Hudelist et al. 2003). We wanted to compare the mRNA expression levels of cofactors N-CoR, SMRT, pCAF, CBP, TIF2, AIB1, SRC-1a, SRC-1e and p300 mRNAs in MCF-7, T-47D and ZR-75-1 cell lines. The hybrids encoding N-CoR, SMRT, pCAF, CBP, TIF2, AIB1 and p300 were detected. No expressions of SRC-1a and SRC-1e were detected although the probe yielded proper hybrids when hybridised to total RNA from HL-60 cells. The expression of AIB1 varied most; it had highest expression in MCF-7 cells while T-47D and ZR-75-1 cells had much weaker expression.

3.2. Hormonal regulation of cofactor expression

The same samples were analysed as described in section 2.2. Insulin, E2 or a combination of both did not regulate the expression of N-CoR, AIB1, CBP or pCAF. Neither were they regulated after one week E2 and insulin treatment. Likewise, the mRNAs of N-CoR, AIB1, CBP or pCAF were not regulated after 24 hours' R5020 treatment. The expressions of SMRT, TIF2 and p300 were too low to be quantified accurately.

4. NUCLEAR RECEPTOR EXPRESSION IN HUMAN UTERUS (IV)

NR expression was studied in human uterine tissue in addition to breast cancer cell lines since mammary gland and uterus are the most remarkable target tissues of estrogen and progesterone. In addition, the human uterine tissue provides a model to study the physiological hormonal regulation of NR expression. RPA was used to analyse the mRNA expression levels of different steroid receptors, VDR, RARs and RXRs in human endometrium and myometrium from hysterectomy samples. Six of the samples represented the proliferative phase (6 endometrium and 4 myometrium samples), one represented the interval phase and six the secretory phase. The expression of mRNAs encoding for AR, ER α , ER β , GR, PR, RAR α , RAR β , RAR γ and VDR was detected using the RPA. The assay was not sufficiently sensitive to detect RXR α , RXR β and RXR γ mRNAs, although at protein level these receptors have been detected in the human endometrium (Fukunaka et al. 2001).

To characterise the proliferation status of the samples, the cyclin A mRNA levels were quantitated. As expected, cyclin A mRNA levels were higher in the proliferative phase endometrium samples compared to the secretory phase (Mann-Whitney U test: $p=0.010$). Most myometrium samples from the proliferative phase had higher cyclin A expression levels than the secretory phase samples, but this phenomenon was not statistically significant ($p=0.088$).

The expression levels of ER β (Mann-Whitney U test, $p=0.004$), PR ($p=0.004$), AR ($p=0.016$) and RAR α ($p=0.004$) were higher in the proliferative-phase endometrium than in the secretory-phase endometrium. Also the expression of ER α ($p=0.055$) was higher in most of the proliferative-phase endometrial samples than in the secretory phase. Like cyclin A expression, the levels of ER α ($p=0.055$), ER β ($p=0.088$) and PR ($p=0.055$) mRNAs appeared to be higher in most of the proliferative-phase myometrium samples but this trend was not statistically significant. The expression of GR, RAR β and RAR γ mRNAs were not regulated during the menstrual cycle. Since the expression of VDR was hardly detectable the quantitation was confirmed using RT-PCR. All samples expressed VDR, but the expression was not regulated during the menstrual cycle.

The mRNA expression levels of endometrium and myometrium from the same patient were also compared. AR (Wilcoxon, $p=0.013$, AR_{End}/AR_{Myom} mean \pm S.D. 0.66 ± 0.46) and RAR β ($p=0.013$, RAR β _{End}/RAR β _{Myom} 0.77 ± 0.25) mRNAs were expressed more abundantly in the myometrium than in the endometrium. Likewise, GR ($p=0.021$) expression was more abundant in the myometrium than in the endometrium except for two patients from the late secretory phase who had less GR mRNA in the myometrium than in the endometrium (GR_{End}/GR_{Myom} ratios 15.87 and 2.32).

Besides the menstrual cycle-dependent changes, there were substantial individual differences in the expression levels of cyclin A and NRs. Since the expression ratio of cyclin A in the endometrium did not correlate with the expression ratio in the myometrium (Figure 2A) (correlation coefficient $r=0.445$, $p=0.17$), Spearman's bivariate correlation analyses were made in order to establish whether the receptor expression would explain this phenomenon. Patient-to patient variation in the cycA_{End}/cycA_{Myom} ratio was detected which could not be explained by menstrual cycle phase (Figure 2B). CycA_{End}/cycA_{Myom} correlated with the endometrium vs. myometrium ratios of AR ($r=0.809$, $p=0.003$), ER α ($r=0.838$, $p=0.001$), ER β ($r=0.941$, $p<0.001$), PR ($r=0.992$, $p<0.001$) and RAR β ($r=0.627$, $p=0.039$). The correlations with ER α and PR are shown in Figures 2C and D.

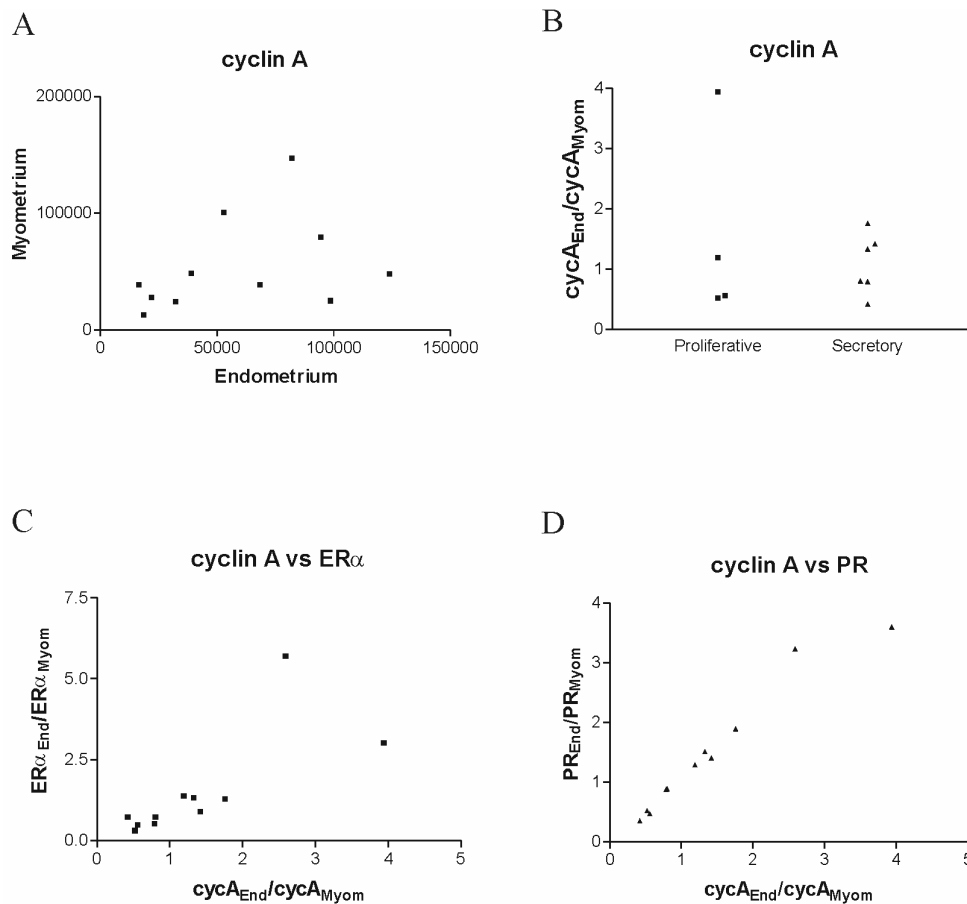


Figure 2. (A) Expression levels of cyclin A in the endometrium did not correlate with the expression levels in the myometrium. (B) $CycA_{End}/cycA_{Myom}$ in the proliferative and secretory phase samples. $CycA_{End}/cycA_{Myom}$ correlated with the same ratios of ER α (C) and PR (D).

5. COFACTOR EXPRESSION IN HUMAN UTERUS (IV)

Due to the essential role of cofactors on the NR transcriptional activity RPA was also used to analyse the mRNA expression levels of different cofactors from the uterine samples. N-CoR, SMRT, pCAF, CBP, TIF2, AIB1 and p300 mRNAs were expressed in all samples in both the endometrium and myometrium. Expression levels of N-CoR, pCAF, AIB1 and p300 did not differ between the proliferative and secretory phases. No statistically significant trends were observed in the endometrium vs. myometrium ratios of N-CoR, pCAF, AIB1 and p300. Due to the detection limit for RPA, the expression levels of SMRT, CBP and TIF2 were not reliably quantified. No expression whatsoever of SRC-1e and SRC-1a mRNAs was detected although SRC-1 expression in the endometrium has been reported (Gregory et al. 2002, Wieser et al. 2002, Shiozawa et al. 2003).

The expression levels of N-CoR, pCAF, AIB1 and p300 appeared to vary between different patients regardless of their menstrual phase. Spearman's bivariate correlation analyses were made in order to test whether the $\text{cycA}_{\text{End}}/\text{cycA}_{\text{Myom}}$ ratio was associated with the expression levels of cofactors. As with steroid receptors, the $\text{cycA}_{\text{End}}/\text{cycA}_{\text{Myom}}$ ratio correlated with the endometrium vs. myometrium ratios of corepressor N-CoR ($r=0.664$, $p=0.026$) and coactivators AIB1 ($r=0.682$, $p=0.021$) and p300 ($r=0.729$, $p=0.011$).

DISCUSSION

1. METHODOLOGICAL CONSIDERATIONS

Three mRNA detection methods were used for the relative quantification of mRNA expression. The expression of cPR-specific mRNAs was analysed using traditional Northern blot analysis, since cPR is expressed as several different transcripts (Gronemeyer et al. 1987, Jeltsch et al. 1990). The benefit of this method is that all transcripts containing the sequence the probe is able to hybridise will be detected according to their size, if expressed abundantly enough. This is beneficial when analysing the expression of genes whose transcription and transcripts have not yet been thoroughly characterised. In addition, Northern blot does not require expensive equipment. The sensitivity of this method is poor in comparison with RT-PCR. However, if carefully designed it is nonetheless suitable for quantitation of mRNA.

The RPA method was chosen to quantify the mRNA expression of human PR isoforms, NRs and cofactors. As a method it is more sensitive than Northern blot, but cannot compete with the sensitivity of RT-PCR. Benefits of RPA include high capacity, since in a single RPA reaction mRNA transcripts of several different genes can be detected simultaneously. In addition, with proper probe designing this method is suitable for characterising transcripts of the same gene which vary in length.

Due to low signal levels ER α and VDR mRNA levels in breast cancer cell lines and VDR mRNA level in uterine samples were also analysed using real-time RT-PCR. This method offers the most sensitive means of analysing mRNA expression. In real-time RT-PCR quantitation is based on measurement of fluorescent dyes after every cycle. The detection method used in all analyses was SYBR Green I. The fluorescence of this dye is enhanced upon binding to the minor groove of double-stranded DNA. Thus the amount of fluorescence increases upon an increase in PCR product. The quantitation is based on a value called the crossing point (CP), which is the point at which the fluorescence of each sample, rises appreciably above the background fluorescence and the reaction enters exponential amplification. The fact that the measurement is made during the early cycles of the assay provides several benefits. For example, none of the reaction components is limiting at this point, the ongoing loss of polymerase activity and accumulation of substances which inhibit the PCR reaction are less marked than at the end of the exponential phase.

2. HORMONAL REGULATION OF PR ISOFORM EXPRESSION

Estrogens commonly increase PR expression in reproductive tissues. Although in the normal mammary gland PR expression is not regulated during the menstrual cycle, it is induced by E2 *in vitro* (Soderqvist et al. 1993, Clarke et al. 1997a, Mote et al. 2002, Zhuang et al. 2003). Whether the expressions of both PR isoforms are similarly regulated is less clear. We elucidated the E2-dependent up-regulation in two well-defined model systems, the chicken oviduct and breast cancer cell lines. Differential regulation of PR isoforms by E2 was found in both these models.

The PR expression in the immature chicken is thought to be constitutive and not induced by estrogen (Tanabe et al. 1979). We demonstrated here that this constitutive expression comprises preferential PR-B expression. Estrogen was found to induce the expression of both isoforms, but the expression of PR-A was preferentially induced. The expression ratio altered after 7 days of estrogen treatment to PR-A predominance. The preferential change was also seen at mRNA level. This may be due to stabilisation of PR-A-specific mRNA, since estrogen has been held to regulate PR expression in the chicken oviduct at post-transcriptional level (Turcotte et al. 1991). Preferential up-regulation of PR-A protein in the chicken oviduct has also been shown in newly-hatched chicks treated with follicle-stimulating hormone or luteinising hormone during embryonic development (Gonzalez-Moran and Camacho-Arroyo 2003). This up-regulation is probably mediated indirectly by induction of estrogen synthesis in the ovary. Estrogen-induced cytodifferentiation is required for the induction of egg white proteins by progesterone (Palmiter and Wrenn 1971, Moen and Palmiter 1980). *In vitro* studies have suggested that the synthesis of egg white protein ovalbumin may be PR-A-mediated or PR-B-repressed (Tora et al. 1988). Differential regulation of PR isoforms by E2 has also been found in the rat forebrain; estrogen induces PR-B mRNA expression in preferentially the preoptic area, PR-A mRNA again, in the hippocampus (Camacho-Arroyo et al. 1998). In the hypothalamus both PR forms were induced similarly. Using dual antibody staining, Mote and colleagues (1999) have studied the isoform-specific regulation of PR expression in the human endometrium during the menstrual cycle. They report that fluctuations in estrogen and progesterone concentrations differentially regulate PR isoform expression in glandular epithelium and stroma. They confirm that cell type-specific regulation of human PR isoform expression occurs in normal physiological conditions.

Preferential PR-B induction by E2 had previously been shown in T-47D cells (Graham et al. 1995a). We further studied whether this phenomenon is characteristic of other PR-positive breast cancer cell lines. We found that E2 induces PR isoform expression in a cell line-specific manner. In MCF-7 cells E2 was found to preferentially induce the expression of PR-A, while in ZR-75-1 cells PR-B was preferentially up-regulated. We could not confirm the result that E2 preferentially stimulates PR-B in T-47D cells. In our cell culture system, E2 induced the expression of both isoforms similarly in T-47D cells. However, these cell lines were not grown under the same selective pressures. Our cells were grown in steroid depleted medium for only one week while Graham and colleagues (1995a) used steroid-depleted medium for several weeks to increase the sensitivity of cells to E2. Like cancer cells in general, the T-47D cell line is genetically unstable and easily forms colonies which differ in their hormonal response (Reddel et al. 1988, Graham et al. 1989). Differential receptor regulation by E2 in breast cancer cell lines has been previously shown for ER α (Saceda et al. 1988, Read et al. 1989, Clayton et al. 1997). In addition to E2, cAMP, insulin and IGF-1 have been shown to induce PR expression in MCF-7 cells under low-serum-containing medium or in serum-free medium (Katzenellenbogen and Norman 1990, Cho et al. 1994). In the present study, no induction of PR was seen in any cell line studied. This may be due to the higher serum concentration (5%) used. Serum may contain factors which repress basal PR expression and suppress the stimulatory effects of cAMP and IGF-1, while E2 induces PR expression more effectively in the presence of a high serum concentration (5%) (Katzenellenbogen and Norman 1990, Cho et al. 1994).

Breast tumors exhibit wide variation in their PR-A/PR-B ratios, while in normal mammary gland the PR isoforms are expressed at similar levels (Graham et al. 1995b, Mote et al. 2002). Adjacent cells of the normal mammary gland express homogeneous PR isoform ratios, while premalignant and malignant lesions evince heterogeneity in this ratio (Mote et al. 2002). The

authors suggest that the loss of co-ordinated expression of PR isoforms is an early event in the development of breast tumors. The dominance of PR-A expression may affect the breast tumor response to endocrine therapy, since PR isoforms differ in their transcriptional activities; for example PR-A may repress the transcriptional activity of PR-B and AR (Vegeto et al. 1993, Chabos and Galtier 1994, McDonnell et al. 1994, Kraus et al. 1995). High PR-A expression compared to PR-B expression may lead to altered gene expression. Indeed T-47D cells engineered to express solely either PR-B or PR-A exhibit differential gene expression profiles (Richer et al. 2002). Based on gene expression profiles the authors propose that three different types of progesterone-responsive genes exist. One group is regulated by PR-A, one by PR-B and one group consists of genes which PR-B induces while PR-A diminishes this induction. Consequently, the PR-A/PR-B ratio of breast tumors may be critical for endocrine therapy. Several studies have reported more frequent preferential expression of PR-A than PR-B in breast tumors (Graham et al. 1995b, Bamberger et al. 2000, Mote et al. 2002). Progesterone induces cancer-associated cytoskeletal changes only in PR-A over-expressing breast cancer cells (McGowan et al. 2003). Moreover, in response to progestin PR-A over-expressing breast cancer cells detach from the monolayer cultures (McGowan and Clarke 1999). Thus preferentially PR-A-expressing tumors may be associated with more invasive phenotypes. In addition to breast cancer, preferential PR-A expression has been found in endometrial cancer (Arnett-Mansfield et al. 2001, Sasaki et al. 2001). Endometrial cell culture models suggest that PR-B has greater influence on progesterone-induced growth inhibition and PR-A expression may be associated with less fully differentiated and more invasive phenotypes (Kumar et al. 1998, Dai et al. 2002, Smid-Koopman et al. 2003). An aberrant PR isoform ratio in general may be linked to higher-grade endometrial tumors (Arnett-Mansfield et al. 2001).

3. DIFFERENTIAL EXPRESSION OF NUCLEAR RECEPTORS

One aspect of cell or tissue-specific responses of estrogen and progesterone is the cross-talk with other NRs. In addition to regulating the expression levels of their own receptors, E2 and progesterone regulate the levels of other NRs. Some ligands may not bind specifically to one receptor but have cross-reactivity with other receptors as well. For example, PR antagonist RU486 may bind to AR, GR, and ER β (Cadepond et al. 1997, Zou et al. 1999). The receptor levels thus may have influence when considering endocrine treatments of breast cancer. Broader knowledge of NR expression would help in the development of new selective NR modulators such as SERMs. RPA analysis was used to compare the mRNA levels of steroid receptors, VDR, RARs and RXRs in different breast cancer cell lines and in uterine samples of different individuals.

The MCF-7, T-47D and ZR-75-1 breast cancer cell lines expressed mRNAs for GR, AR, PR, ER α , ER β , VDR, RAR α , RAR γ and RXR α . Variations in their expression levels were observed when comparing the control samples of each cell line, which would imply that these cell lines may respond to endocrine treatment differently.

The expression of NR mRNAs was also studied in the human endometrium and myometrium. AR, ER α , ER β , GR, PR, RAR α , RAR β , RAR γ and VDR mRNAs were expressed in both endometrium and myometrium. Although these two tissues are functionally and structurally

different, NRs transcripts were expressed in similar manner in both except for AR, GR and RAR β mRNA, which in most cases were expressed more abundantly in the myometrium than in the endometrium. A novel finding of this study was also that VDR is expressed in normal human uterine tissue.

Patient-to-patient variations in the expression levels of NRs could be detected when comparing endometrium and myometrium samples within the same cycle phase. Cyclin A expression is related to the proliferation status of the uterine tissue. As expected, cyclin A was clearly regulated in the endometrium samples during the menstrual cycle; higher expression levels were detected in the proliferative than in the secretory phase samples. Patient-to-patient variation was also observed in cyclin A mRNA levels. Noteworthy was that although presumably both endometrium and myometrium are predisposed to the same hormone concentrations, the cyclin A mRNA level in the endometrium did not correlate with the expression level in the corresponding myometrium. When calculating patients' cyclin A endometrium vs. myometrium ratio marked variation prevailed which could not be explained by menstrual cycle phases. This finding was further studied by comparing each patient's $cycA_{End}/cycA_{Myom}$ to the same ratios of NRs. Strong correlations were found between $cycA_{End}/cycA_{Myom}$ and the ratios of AR, ER α , ER β and PR. Interestingly, $cycA_{End}/cycA_{Myom}$ ratio correlated with the same ratio of RAR β , although RAR β was not found to be regulated during the menstrual cycle in the endometrium. Altogether this finding would suggest that the proliferation status of the endometrium and myometrium is associated with the expression level of AR, ER α , ER β , PR and RAR β .

4. HORMONAL REGULATION OF NUCLEAR RECEPTOR EXPRESSION

Mammary gland and uterus are the two most notable target tissues of estrogen and progesterone. Due to difficulties of obtaining samples of normal mammary gland breast cancer cell lines were used as an *in vitro* model system to characterise how estrogen and progesterone regulate the mRNA expression levels of steroid receptors, VDR, RARs and RXRs. The endometrial and myometrial samples from hysterectomies were used as a model of physiological regulation.

As with the PR isoforms, a cell line-specific regulation pattern was also observed for other NRs after E2 treatment. Likewise progestin differently regulated some of the NRs. Such differential regulation has already been reported for ER α expression. The ER α mRNA levels are decreased in MCF-7 cells and increased in T-47D and ZR-75-1 cells after E2 treatment (Saceda et al. 1988, Read et al. 1989, Clayton et al. 1997). In our experimental conditions E2 increased ER α mRNA levels in T-47D cells and a trend towards decreased expression was observed in MCF-7 cells. However, in ZR-75-1 cells E2 reduced the ER α mRNA level, which is contradictory to previous results (Clayton et al. 1997). This may be due to different cell clones, since as noted above, breast cancer cells are genetically somewhat unstable and easily form colonies differing in their hormonal response. Cell line-specific regulation of AR, RAR α , RAR γ and VDR by E2 was also observed. RAR α mRNA levels were decreased only in T-47D cells after progestin treatment, as previously shown (Roman et al. 1992). VDR mRNA levels were increased several-fold by progestin treatment in MCF-7 and T47D cells and a minor increase was observed in ZR-75-1 cells. Thus, in addition to regulating their own receptor levels, estrogens and progestins regulate other NR levels which are involved in

controlling cell proliferation and differentiation. The mechanisms behind the cell line-specific hormonal regulation call for further analysis. However, our results imply that tumors from different individuals or even different clones of the same tumor might respond differentially to endocrine therapy.

In the endometrium AR, ER α , ER β and PR mRNAs were more abundantly expressed in the proliferative than in the secretory phase, as earlier reported (Lau et al. 1996, Matsuzaki et al. 1999, Matsuzaki et al. 2000, Slayden et al. 2001). RAR α was also expressed more abundantly during the proliferative phase. Previously Kumarendran and colleagues (1996) have reported that mRNAs for RARs are not markedly regulated during the menstrual cycle, although Fukunaka and colleagues (2001) have found higher protein expression levels of all RARs during the proliferative compared to the secretory phase. In the myometrium none of the NR mRNAs studied was regulated statistically significantly, although ER α , ER β and PR mRNA levels were higher in most of the proliferative phase samples compared to the secretory phase samples. These results, indicating the myometrium as a more insensitive tissue in response to hormonal fluctuations, are in accord with those of a study by Noe and colleagues (1999). They reported that in the myometrium ER α and PR levels are regulated in the layer adjacent to the endometrium in an endometrial-like pattern during the menstrual cycle, while expression patterns in the outer part of the myometrium are more stable. In the present study the myometrial sample was not separated into different layers and the myometrial samples may contain both the layer reactive for cyclical hormonal fluctuations as well as the hormonally less active part.

When comparing the hormonal regulation of NR mRNA expression in breast cancer cells and in the human endometrium the expected similarities were seen, but also tissue-specific hormonal responses. This comparison cannot be made without keeping in mind that the hormonal regulation of the endometrium is based on physiological changes, thought to be due to increased levels of estrogen in the proliferative phase and increased levels of progesterone and decreasing levels of estrogen in the secretory phase. Thus in general, estrogens seemed to up-regulate and progestins to reduce PR and ER β mRNA expression in both breast cancer cells and the human endometrium. ER α mRNA expression in the endometrium exhibited a trend towards decreased expression in the secretory phase. In breast cancer cells the ER α mRNA levels were either increased or decreased by E2 depending on the cell line. Progestin treatment reduced ER α expression in T-47D cells and in ZR-75-1 cells, while in MCF-7 cells regulation was not observed at all. Increased expression of AR was detected in the proliferative phase endometrium compared to the secretory phase. Progestin treatment or short-term E2 treatment did not regulate AR mRNA levels in any breast cancer cell lines studied, but longer-term E2 treatment reduced the expression in MCF-7 cells. A higher expression level of RAR α mRNA was observed in the proliferative phase endometrium. E2 also seemed to increase RAR α expression in T-47D and ZR-75-1 cells. Long-term E2 treatment induced RAR γ mRNA expression in ZR-75-1 cells, while no regulation was observed in other cell lines or in endometrium samples.

5. COFACTOR EXPRESSION

Cell and tissue type differences exist in the expression levels of cofactors (Misiti et al. 1998, Shang and Brown 2002). In the present work two different types of tissues were used to determine cofactor expression and regulation of expression by estrogen and progesterone. In the breast cancer cell lines, the AIB1 mRNA level varied most when comparing different cell lines. It was expressed most abundantly in MCF-7 cells, previously described as containing AIB1 gene amplification (Anzick et al. 1997). Though no regulation of cofactor expression was noted during the menstrual cycle, individual cofactor mRNA expression levels varied markedly. Since the relative expression levels of cofactors determine whether the ligand acts as agonist or antagonist, the expression levels may affect the individual response to endocrine therapy (Lavinsky et al. 1998, Wagner et al. 1998, Liu et al. 2002, Shang and Brown 2002).

Levels of cofactors seemed not to be regulated either in breast cancer cell lines by estrogens and progestins or in the human uterus during the menstrual cycle. This is in line with other studies reporting fairly stable expression of different cofactors in breast cancer cell lines after estrogen treatment as well as in the human endometrium during the menstrual cycle (Thenot et al. 1999, Gregory et al. 2002, Shiozawa et al. 2003). In contrast, the protein expression levels of cofactors AIB1, SRC-1 and N-CoR may be altered during the cycle in the endometrium, although reports on N-CoR and SRC-1 expression are partly ambiguous (Gregory et al. 2002, Wieser et al. 2002, Shiozawa et al. 2003). A further novel finding in this present study was that also the myometrium expresses cofactors N-CoR, SMRT, pCAF, CBP, TIF2, AIB1 and p300 similarly to the endometrium.

The finding that cofactor levels varied individually was further studied by comparing each patient's $cycA_{End}/cycA_{Myom}$ to the same ratios of cofactors. Interestingly, the $cycA_{End}/cycA_{Myom}$ correlated with the same ratios of N-CoR, AIB1 and p300, although the expression levels of these cofactors were not regulated during the menstrual cycle. This correlation may indicate that the proliferation status of the endometrium and myometrium is associated with the expression levels of N-CoR, AIB1 and p300.

6. CELL-OR TISSUE-SPECIFIC EFFECTS OF NUCLEAR RECEPTOR LIGANDS

The present study consists of three different types of female reproductive tissues. We found that they all had complexities in their hormonal response to E2 and progesterone. These complexities consisted of PR isoform expression, NR and cofactor expression and hormonal regulation of NR expression. These results augment the knowledge about ligand-specific cellular or tissue responses. These responses are dependent on several factors in addition to pharmacokinetic factors such as metabolism and bioavailability (Figure 3).

The activity depends on the target gene regulatory regions. NRs may bind directly to DNA through cognate HREs or bind DNA indirectly through binding of other transcription factors. The activity of SERMs has been shown to vary depending on whether it binds directly to ERE or indirectly to DNA through AP-1 and transcription factor Sp1 (Webb et al. 1995, Paech et al. 1997, Zou et al. 1999).

Furthermore the ligand-specific cellular or tissue response is dependent on the expression of cognate receptors. ER α and ER β bind partly the same ligands and ER β may modulate the activity of ER α (Hall and McDonnell 1999, Weihua et al. 2000). Some ligands exhibit cross-reactivity with several steroid receptors; in particular antagonists of PR may bind to AR, GR and ER β , as shown for RU486 (Cadepond et al. 1997, Zou et al. 1999). The results of the present study imply that levels of NRs in different breast cancer cell lines and in the human uterus of different individuals differ. Due to this variation, breast cancers in different individuals or uterine tissue may respond in a selective fashion to endocrine treatment.

Some of the NRs are expressed in different isoforms. These may differ in their transcriptional activities and may have diverse physiological roles, as shown for PR-A and PR-B (Mulac-Jericevic et al. 2000, Mulac-Jericevic et al. 2003). As noted above, PR isoform expression has been reported to be abnormal in breast and endometrial cancers. The isoform expression may be associated with antiestrogen resistance, since estrogen-dependent human breast xenografts expressing solely PR-A were growth-inhibited by tamoxifen while PR-B-expressing xenografts were unresponsive (Sartorius et al. 2003). The results of the present study suggest that PR isoforms are regulated by E2 differently in different breast cancer cell lines. This selective regulation may be of physiological relevance in the treatment of breast cancer.

A ligand-bound receptor adopts a ligand-specific conformation and recruits cofactors. Which cofactors are recruited depends on the ligand but also the HRE which the receptor binds to affects the conformation and cofactor recruitment (Brzozowski et al. 1997, Shiau et al. 1998, Takeyama et al. 1999, Loven et al. 2001, Wong et al. 2001, Wood et al. 2001, Hall et al. 2002, Yi et al. 2002). The level of cofactors has been thought to regulate the agonist/antagonist activity of selective NR modulators (Lavinsky et al. 1998, Wagner et al. 1998, Liu et al. 2002, Shang and Brown 2002). The results presented here and elsewhere suggest that the expression levels of cofactors in general are not hormonally regulated (Thenot et al. 1999, Nephew et al. 2000, Gregory et al. 2002, Shiozawa et al. 2003). Cofactor expression is cell-type dependent and is probably related to cell differentiation. Altered expression of several cofactors has been proposed in breast cancer (Anzick et al. 1997, Leygue et al. 1999b, Kurebayashi et al. 2000, Murphy et al. 2000, Hudelist et al. 2003). For example, AIB1 expression is increased in human breast carcinomas and the high expression level has been found to be associated with high tumor grade (Bouras et al. 2001, Hudelist et al. 2003). SRC-1 expression may be lower in breast tumors than in the normal breast and the low expression may be associated with tamoxifen resistance (Berns et al. 1998). Our results imply that in breast cancer cell lines and even in normal uterine tissues individual differences prevail in the expression levels of cofactors. This individual variation may bring an additional level of complexity to the biological response to certain selective NR modulators.

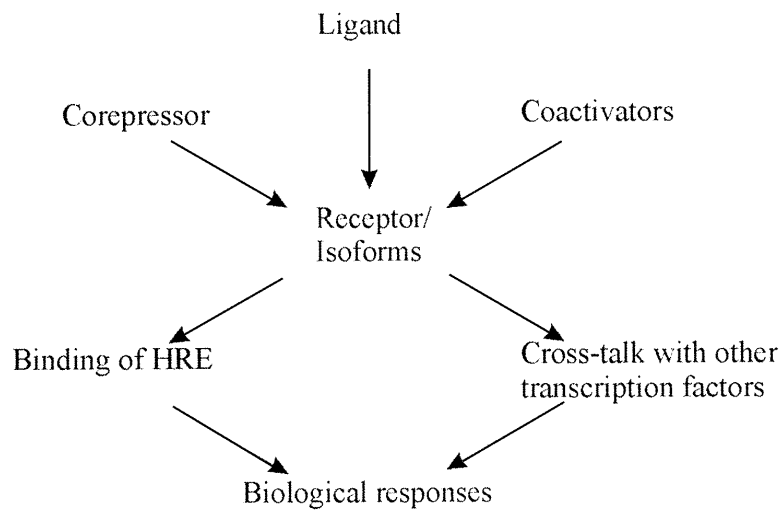


Figure 3. Cell or tissue specific biological responses of NR ligands are dependent on several factors.

SUMMARY AND CONCLUSIONS

The PR isoform expression and regulation by E2 were studied in the chicken oviduct and in breast cancer cell lines at both mRNA and protein level. The expression in the immature chicken oviduct was found to consist in preferential PR-B protein expression, although PR-A was also detected. Estrogen treatment, which is known to induce growth and differentiation in the oviduct, altered the PR isoform ratios by preferentially increasing the expression of PR-A protein as against expression of PR-B. This phenomenon was also noted at mRNA level. Considering the different biological activities of these receptor isoforms the results of this study would suggest that progesterone response in the chicken oviduct is dependent on the hormonal and developmental status of the organ.

In breast cancer cell lines E2 increases the expression of PR. In the present work, the regulation of PR isoform expression by E2 was characterised in three different breast cancer cell lines both at mRNA and at protein level. Differential regulation of PR-A and PR-B was observed when comparing the cell lines. In T-47D cells both isoforms were increased similarly upon E2 treatment, in MCF-7 cells PR-A was preferentially increased, while in ZR-75-1 cells the preferentially increased isoform was PR-B. This regulation was observed at both protein and mRNA level. The results of this study suggest that since E2 regulates PR isoform expression in distinct manner in different breast cancer cell lines, breast tumors in general may evince differential regulation of PR isoform expression and may thus have altered responses to hormonal therapy.

In addition to the differential regulation of PR isoforms, MCF-7, T-47D and ZR-75-1 breast cancer cell lines were found to differ in their expression levels of NR mRNAs and in the regulation of NR mRNA levels by E2 and progestin. These findings further indicate that breast tumors in general might differ in their responses to endocrine therapy.

NR expression during the menstrual cycle was characterised in the human endometrium and myometrium. Expression of AR, ER α , ER β , GR, PR, RAR α , RAR β , RAR γ and VDR mRNAs were detected in both endometrium and myometrium. NR transcripts were expressed in similar manner in both tissue types except for AR, GR and RAR β mRNA, which in most cases were expressed more abundantly in the myometrium than in the endometrium. In the endometrium the AR, ER α , ER β , PR and RAR α mRNA levels were higher in the proliferative phase when compared to secretory phase samples. In the myometrium no statistically significant changes were observed; however, most of the proliferative samples evinced higher expression of ER α , ER β and PR than the secretory phase samples.

An interesting finding was the patient-to-patient variation in the expression levels of cyclin A, NRs and cofactors, which occurred both in the endometrium and in the myometrium. Furthermore, the cyclin A expression level in the endometrium did not correlate with the expression level in the corresponding myometrium. To test which factors could explain differences in proliferation, the endometrium vs. myometrium ratio of cyclin A was compared to the same ratios of NRs and cofactors and the ratios of AR, ER α , ER β , PR, RAR β , N-CoR, AIB1 and p300 was found to correlate with the cyclin A ratio. The expression levels of these receptors and cofactors may thus be associated with the hormone sensitivity of endometrium and myometrium.

Both E2 and progestin treatments appeared not to regulate the expression of AIB1, pCAF, CBP, and N-CoR in breast cancer cell lines. Furthermore, cofactor mRNA expression was evidently not regulated during the menstrual cycle in the human endometrium and myometrium. The myometrium expressed the mRNAs encoding N-CoR, SMRT, pCAF, CBP, TIF2, AIB1 and p300 similarly to the endometrium.

Altogether the present study consists of three different type of female reproductive tissues which all have complexities in their hormonal response to E2 and progesterone. These complexities consist of several aspects, PR isoform expression, NR and cofactor expression and hormonal regulation of NR expression. The results broaden out the knowledge of NR and cofactor expression in these well-studied models. Furthermore, they suggest that individual variation exist in the expression levels of NRs and cofactors. Due to these variations these tissues may respond in an individual fashion to endocrine treatment, a circumstance to be reckoned with in when developing novel therapeutic ligands.

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A handwritten signature in black ink, appearing to read 'Annika Vienonen', with a long horizontal flourish extending to the right.

Annika Vienonen

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