

University of Calabria

Ph.D. in Molecular Bio-pathology

Molecular mechanisms determining aromatase overexpression and inducing rat tumor Leydig cell proliferation: involvement of IGF-I and COX-2

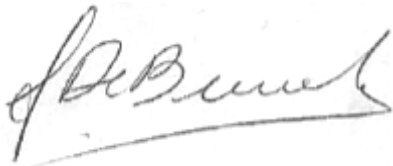
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Scientific Publications

IGF-I regulating aromatase expression through SF-1, supports estrogen dependent tumor Leydig cell proliferation.

Summary

Several studies on both humans and rodents indicate that prenatal or postnatal exposure to estrogens might have a central role in the mechanism leading to male reproductive tract malformations as well as testicular tumors (1;2). While the effects of estrogen on mammary gland tumorigenesis is well known, the role of aromatase overexpression and *in situ* estrogen production in testicular tumorigenesis is not clearly defined. In this study we have investigated the molecular mechanisms causing aromatase overexpression and the effect of estradiol (E2) overproduction on Leydig cell tumor proliferation. Our hypothesis is that constitutive E2 production stimulates Leydig tumor cell proliferation acting on cell cycle regulators. Moreover, among several potential factors inducing aromatase, we investigated the role of IGF-I, produced locally in the testis, and of COX-2 overexpressed in other estrogen-dependent tumors. We used rat R2C Leydig tumor cells and testicular samples from Fischer rats with a developed Leydig tumor (FRTT). Both experimental models express high levels of aromatase and Estrogen Receptor alpha ($ER\alpha$). Treatment with exogenous E2 induced proliferation of R2C cells and upregulation of cell cycle regulators cyclin D1 and E, that were blocked by addition of antiestrogens. These observations led us to suppose an E2/ $ER\alpha$ dependent mechanism for Leydig cell tumor proliferation.

Aromatase expression in rat Leydig cells is driven by the PII promoter regulated mainly by three CRE sites and one SF1 site. Determining the molecular mechanism responsible for aromatase overexpression, we found that total and phosphorylated levels of transcription factors CREB and SF-1 were higher in tumor samples. Moreover, we found that R2C cells produce also high levels of IGF-I that increased aromatase mRNA, protein and activity as a consequence of increased total and phosphorylated SF-1 levels. Binding of IGF-I to its receptor causes receptor autophosphorylation and the activation of an intrinsic tyrosine kinase that acts on various substrates, leading to activation of multiple signaling pathways including the PI3K/AKT and MAPK cascades. In addition, it has been shown that IGF-I

can activate the PLC/PKC pathway (3). Specific inhibitors for IGF-I receptor, Protein Kinase C and Phosphoinositol-3-kinase determined a reduction in SF1 and consequently in aromatase expression and activity. The same inhibitors were also able to inhibit the IGF-1 dependent-SF-1 recruitment to the aromatase PII promoter. These results indicate that in Leydig tumor cells one of mechanism determining aromatase overexpression is an enhanced IGF-I signaling potentiating SF-1 action.

Determining the molecular mechanism responsible for constitutive CREB phosphorylation, we investigate the role of COX-2 (cyclooxygenase-2) an enzyme involved in prostaglandins (PGs) synthesis that has not been detected in the human normal testis, but it is expressed in testicular biopsies of men with cancer. We show that COX-2 is expressed in rat Leydig tumor samples while is not detectable in normal testis. COX-2 specific inhibitor NS398 (5-50 uM) is able to reduce dose-dependently aromatase mRNA, protein expression, activity and tumor Leydig cell proliferation. NS398 significantly decreases CREB activation reproducing the same effect of H89 (a PKA inhibitor) on both aromatase and CREB. The drop in estrogen production determines a decrease in tumor Leydig cell proliferation. Moreover, the addition of increasing amounts of PGE2 were able to increase phosphorylation but not synthesis of CREB which consequently increased aromatase expression. Next, in order to evaluate PGE2 receptor (EP) subtype(s) responsible for induction of aromatase expression and activity, we used the selective inhibitors: SC19220, AH6809, AH23848 for EP1, EP2/EP4 and EP4 respectively. Our data demonstrate that only the AH23848 was able to determine a decrease in CREB phosphorylation and again in aromatase expression. These findings led us to suppose that, in tumor Leydig cells, COX-2-derived PGE2, through an autocrine mechanism, activates PKA which is responsible of CREB activation.

In summary, our results give a contribution to clarify two molecular mechanisms determining aromatase overexpression in Leydig cell tumor. The first one involves some of pathways (PI3-K and PKC) activated the IGF-I determining SF-1 production and enhanced P450 mRNA transcription. The other one involves the production of PGE2 (induced by COX-2 overexpression), which is responsible of PKA activation and CREB

phosphorylation. It remains to elucidate the molecular mechanisms determining IGF-I and COX-2 overexpression in tumoral Leydig cells.

However, the observations that COX-2 and IGF-I pathway inhibitors are able to decrease E2 production and to block Leydig cell tumor proliferation, open new perspectives on therapeutic approach of Leydigoma in the human.

Introduction

1. Endocrinology of the male reproductive system

1.1 The testis: general structure

The human male reproductive system includes the hypothalamic-pituitary-gonadals axis, the epididymis, vas deferens, seminal vesicles, prostate and the urethra. The testis is composed primarily of seminiferous tubules packed closely together and interstitial cells (4). The seminiferous tubules are composed by Sertoli cells that support germ cells during their maturation into spermatozoa. Sertoli cells create a blood-testis barrier, and separate the germinal epithelium into basal and adluminal compartments. They are responsible for the physical support of the germ cells, in addition to providing nutrients and growth factors. The major cell in the interstitial space outside the seminiferous tubule is the Leydig cell, which produces testosterone, a necessary component for germ cell maturation. Male fertility requires the production by the testes of large numbers of normal spermatozoa through a complex process of spermatogenesis. The germ cells are sequentially organised into several layers signifying the respective mitotic or meiotic processes and spermatid development. Each seminiferous tubule is surrounded by mesenchymal cells. Among these are the peritubular myoid cells whose contractile elements generate peristaltic waves along the tubules, but do not present a tight diffusion barrier. Vascular smooth muscle cells, macrophages and endothelial cell types are also located in the interstitial space of the testis. The physiological role of macrophages has long been underestimated. In the rat, the number of macrophages is one quarter of the number of Leydig cells and the presence of macrophages is crucial for (re)population of Leydig cells during development and after experimental depletion (5;6). Immune cells, known to secrete a number of growth factors and cytokines, are part of the intratesticular communication pathways (7).

1.2 Testicular function and its regulation

Testes are components of both the reproductive system (being gonads) and the endocrine system (being endocrine glands). The respective functions of the testicles are:

1. producing sperm (spermatozoa);
2. producing male sex hormones.

These two functions occur in separate compartments within the testis: 1. the seminiferous tubules produce sperm and 2. the interstitial cells (i.e., Leydig cells) synthesize androgens (**Fig. 1**).

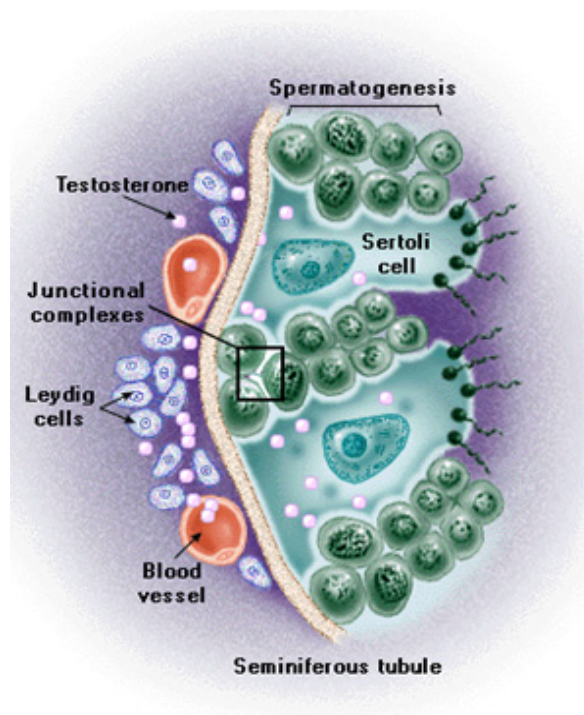


Figure 1. Schematic representation of functions of the testis.

Both functions of the testis, sperm-forming and endocrine, are under control of gonadotropic hormones produced by the anterior pituitary: luteinizing hormone (LH) and follicle-stimulating hormone (FSH). Synthesis and release of both FSH and LH is

regulated by a single gonadotropin releasing hormone (GnRH) also referred to as LHRH, a decapeptide produced by specialized neurons in the hypothalamus. Pulsatile GnRH production signals gonadotroph cells in the anterior pituitary to produce follicle-stimulating hormone (FSH) and luteinizing hormone (LH) that then act on the testis to regulate spermatogenic potential. LH binds to receptors on the surface of Leydig cells in the testis and stimulates the production of testosterone, a steroid hormone that diffuses into the seminiferous tubules. Within the seminiferous tubules only Sertoli cells possess receptors for testosterone and FSH and thus these cells are the major targets of the ultimate hormonal signals that regulate spermatogenesis.

Serum testosterone and inhibin (Sertoli-cell product) downregulate LH and FSH secretion via negative feedback loop. Testosterone also decreases the responsiveness of the pituitary to GnRH (**Fig. 2**).

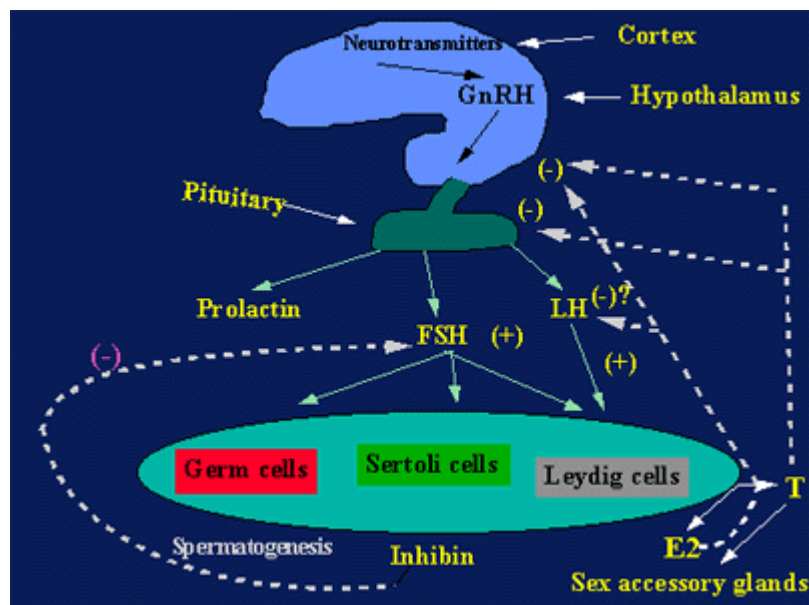


Figure 2. Hypothalamic-Pituitary-Testicular axis.

LH, through specific receptors found on the surface of Leydig cells, controls the production and secretion of testosterone (8;9).

Thus, pituitary gonadotropins are the chief regulators of testicular function. LH stimulates androgen production by Leydig cells after binding to LHR and FSH acts through its receptors in Sertoli cells (FSHR) to regulate spermatogenesis (**Fig. 3**).

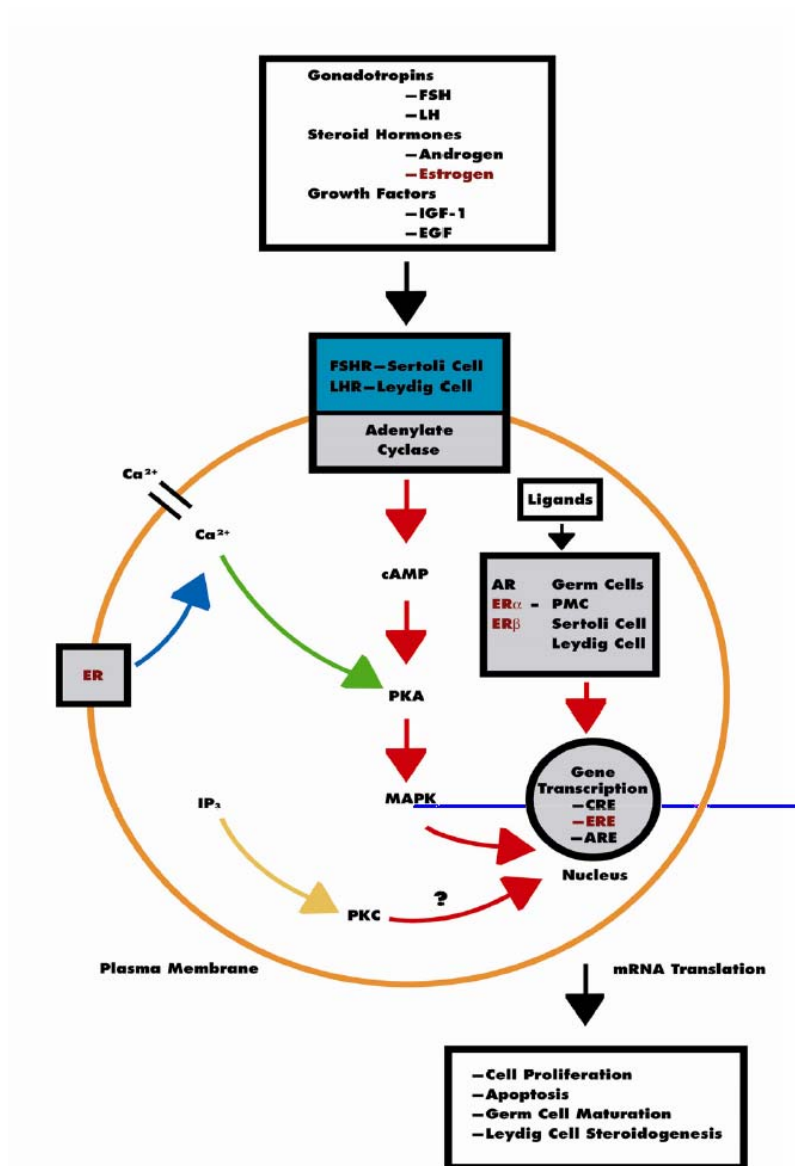


Figure 3. Endocrine regulation of the testis. PMC, peritubular myoid cell; CRE, cAMP responsive elements, ARE, androgen-responsive elements; ERE, estrogen-responsive elements; (by Akingbemi BT 2005).

The interaction of LH with its receptor initiates signalling through GTP binding proteins determining the cyclic AMP production (10). Signal transduction occurs through the protein kinase A pathway as its principal signal transduction mechanism. Some data suggests that intracellular calcium concentration can be induced by the action of LH by activating phospholipases in the lipoxygenase pathway (11). In addition, the changes in calcium can also regulate adenylate cyclase through the protein kinase C pathway.

Within the seminiferous tubules only Sertoli cells possess receptors for testosterone and FSH and thus these cells are the major targets of the ultimate hormonal signals that regulate spermatogenesis. FSH binding to its receptor is known to activate at least 5 signaling pathways in Sertoli cells: cAMP-PKA pathway, MAP kinase pathway, Phosphatidylinositol 3-kinase (PI3-K) pathway, Calcium pathway, Phospholipase A2 (PLA2) pathway. Initially FSH binding to the FSH receptor causes receptor coupled G proteins to activate adenylate cyclase (AC) and increase intracellular cAMP levels. Multiple factors can be activated by cAMP in Sertoli cells including PKA that can phosphorylate a number of proteins in the cell and also regulate the expression and activity of numerous transcription factors including CREB. During puberty, FSH activates the MAP kinase cascade and ERK kinase in Sertoli cells most likely via cAMP interactions with guanine nucleotide exchange factors (GEFs) and activation of Ras-like G proteins. ERK is capable of activating transcription factors including SRF, c-jun and CREB. In granulosa cells, FSH also activates the p38 MAP kinase. FSH and cAMP also likely act through GEFs to activate PI3-K and then phosphoinositide dependant protein kinase (PDK1) and PKB in Sertoli cells. Studies of granulosa cells identified Forkhead transcription factor (Forkhead), SGK (glucocorticoid-induced kinase) and GSK-3 (glycogen synthase kinase-3) as additional downstream targets of the PI3-K pathway. FSH also mediates the induction of PLA2 and the subsequent release of arachadonic acid (AA) and the activation of eicosanoids such as PGE2 that may act as intracellular or extracellular signaling agents (12). However, gonadal steroids, i.e., androgen and estrogen, and other agents that bind or prevent binding to steroid hormone receptors (androgen receptor AR, ER α , and ER β), which are present in Sertoli cells, germ cells and Leydig cells also regulate

testicular function (9). The pathway mediated by adenosine-3',5'-cyclic monophosphate (cAMP) appears to be the primary intracellular signaling pathway in all testicular cells. However, several growth factors e.g., insulin like growth factor-1 (IGF-1) and epidermal growth factor (EGF), acting via their receptors, IGF-1R and EGF-R, possibly modulate AR and ER-mediated pathways. Thus, testicular function is regulated by interactions between several signaling pathways, some acting locally, e.g., AR and ER-mediated pathways, and others indirectly by modulating hypothalamus-pituitary function. Hormonal activation of transcriptional gene activity results in changes in cell differentiation and function.

1.3 Steroid production

Testosterone is the major androgen secreted by the testis from its site of production within the Leydig cells. In addition to testosterone, through the actions of the enzyme 5 α -reductase, dihydrotestosterone is produced by the testis in smaller amounts. The testis also contributes approximately 25% of the total daily production of 17 β -estradiol through the local action of the enzyme aromatase which converts androgenic substrates to this estrogen (13). The remainder of the circulating estradiol is produced by the adrenal and peripheral tissues through the actions of aromatase. Cholesterol represents the major substrate for androgen production by the Leydig cells and is derived by an uptake mechanism involving the binding of circulating low density lipoprotein to specific receptors on Leydig cells which, following internalisation provides a significant source of cholesterol (14). In addition, the Leydig cells are able to undertake de novo synthesis of cholesterol from acetate and relative contributions of these two sources is partly dependent on species and the state of stimulation of the Leydig cells.

The conversion of cholesterol to testosterone involves a number of steps that are catalyzed by enzymes, predominantly belonging to cytochrome P450 family. The mobilization of cellular sources of cholesterol is achieved through the action of cholesterol ester hydrolase and subsequently, this is converted to pregnenolone by the enzyme cholesterol side-chain cleavage termed cytochrome P450SCC (15) (**Fig. 4**).

The conversion of cholesterol to pregnenolone is a key step at which regulation of androgen production within the Leydig cells occurs. Availability of cholesterol substrate can be rate-limiting and the intracellular trafficking of cholesterol across mitochondrial membranes is dependent on the steroidogenic acute regulatory protein (STAR) (16-18).

The role of this protein has been well demonstrated in patients with mutations in the gene encoding STAR in the disorder termed congenital lipid adrenal hyperplasia wherein the mitochondria from the adrenals and gonads of these patients are unable to convert cholesterol to pregnenolone (19). Further, the results of studies involving targeted disruption of the mouse gene encoding STAR support the data derived from human studies (20). Pregnenolone may progress to testosterone production through two pathways. It can be converted to progesterone through the enzyme 3β hydroxysteroid dehydrogenase (the D4 pathway) or can be hydroxylated at the 17α position by the enzyme 17- α hydroxylase to form 17α -hydroxypregnenolone (the D5 pathway). The relative importance of these two pathways vary with the species and the physiological status of the male (21). The further conversion of 17α -hydroxypregnenolone through the D5 pathway involves the formation of the C19 steroid dehydroepiandrosterone catalyzed by the enzyme 17,20 lyase and both steps appear to be catalyzed by a single microsomal enzyme cytochrome P450 c17 encoded by a single copy gene on chromosome 10 (22;23). The conversion of dehydroepiandrosterone to androstenediol is mediated by a microsomal enzyme 17β -hydroxysteroid dehydrogenase encoded by a single gene (24;25). The conversion of substrates from the D5 to the D4 pathway are catalyzed by the enzyme 3β -hydroxysteroid dehydrogenase (26). In the D4 pathway 17α -hydroxyprogesterone proceeds through the action of cytochrome P450 c17 to androstenedione and testosterone. Testosterone can be converted to a dihydrotestosterone by the enzyme 5α -reductase (27) or can be metabolised to 17β -estradiol by the enzyme aromatase (13;28).

2. Estrogen regulation of testicular function

Evidence supporting a role for estrogen in male reproductive tract development and function has been collected from rodents and humans. These studies fall into three categories: i) localization of aromatase and the target protein for estrogen (ER-alpha and ER-beta) in tissues of the reproductive tract; ii) analysis of testicular phenotypes in transgenic mice deficient in aromatase, ER-alpha and/ or ER-beta gene; and, iii) investigation of the effects of environmental chemicals on male reproduction. Estrogen is thought to have a regulatory role in the testis because estrogen biosynthesis occurs in testicular cells and the absence of ERs caused adverse effects on spermatogenesis and steroidogenesis (29). All of these topics will be individually discussed in this section of the introduction. In males, estrogens derive from circulating androgens. Aromatization of the C19 androgens, testosterone and androstenedione, to form estradiol and estrone, respectively, is the key step in estrogen biosynthesis, which is under the control of the aromatase enzyme (**Fig. 5**).

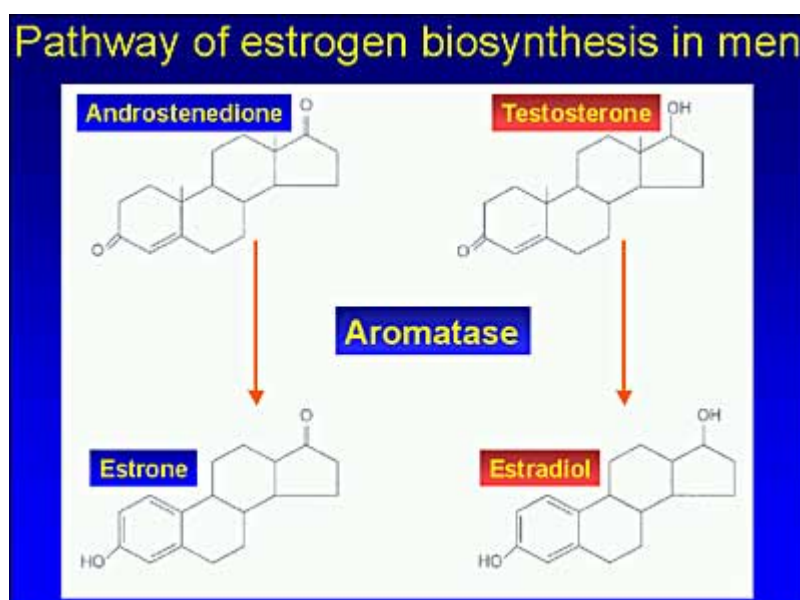


Figure 5. Biochemical pathway of testosterone conversion into estrogens.

2.1 The aromatase gene: structure and regulation

Aromatase is composed of two proteins: a ubiquitous NADPH-cytochrome P450 reductase and a cytochrome P450 aromatase (P450arom), which contains the heme and the steroid-binding pocket. In humans, P450arom is the product of a single gene located in region q21.1 of chromosome 15 and called *cyp19*, which belongs to the cytochrome P450 gene family. The *cyp19* gene is more than 123 kb in length with a coding region of 9 exons (II-X) and 9 nontranslated exons I (30) (**Fig. 6**).

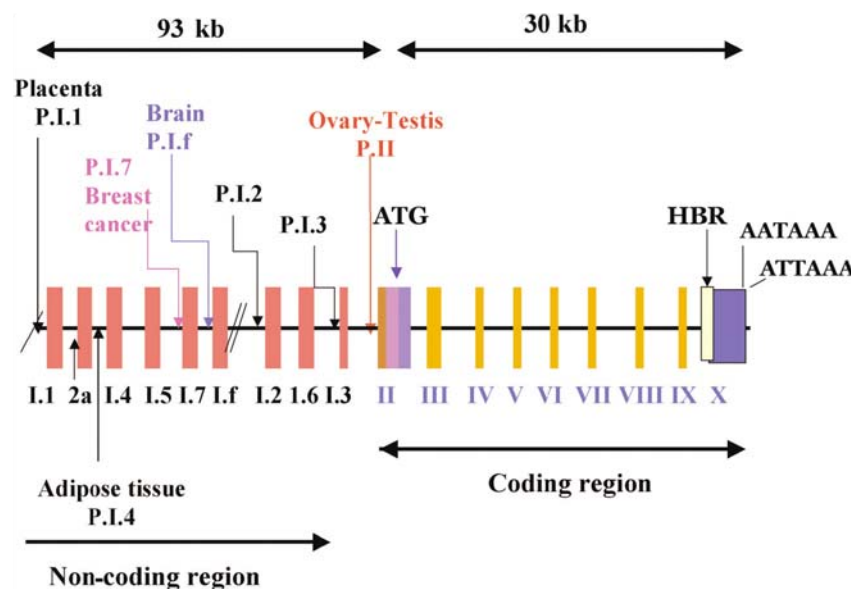


Figure 6. Schematic presentation of the human aromatase gene. P = promoter; (by Carreau S 2007).

Expression of the *cyp19* gene is regulated by tissue-specific promoters producing alternate 5'-untranslated exons I that are then spliced onto a common 3'- splice acceptor site in exon II, upstream of the translation starting site (31-33). Therefore, there is generation of *cyp19* variants with different 5'untranslated regions giving rise to different mRNAs; however, the coding sequences are identical and give rise in humans to a single protein composed of 503 amino acids with a molecular mass of 55 kDa. It is of note that P450arom is encoded by a single *cyp19* gene in most species except for pigs in which three distinct genes encode

three aromatase isoenzymes (34) and for fish in which two *cyp19* genes (specifically expressed in the brain and gonads) have been identified (35). Different mechanisms of regulation of Cyp19 gene expression have been described for various tissues. The synthesis of different aromatase isoforms between species and tissues may involve distinct aromatase genes and/or the function of different promoter elements (36). In human adipose tissue, the primary promoter I.4 lies about 15 kb upstream of the start site of translation (37;38) and is a TATA-less promoter driven by glucocorticoids and class I cytokines e.g. IL-6 and TNF α (33). The region of PII proximal to the translation start site regulates P450arom expression in mammalian gonads (37;39) as well as in Leydig cell tumors (40). Numerous functional motifs have been identified in P.II (33) (**Fig. 7**).

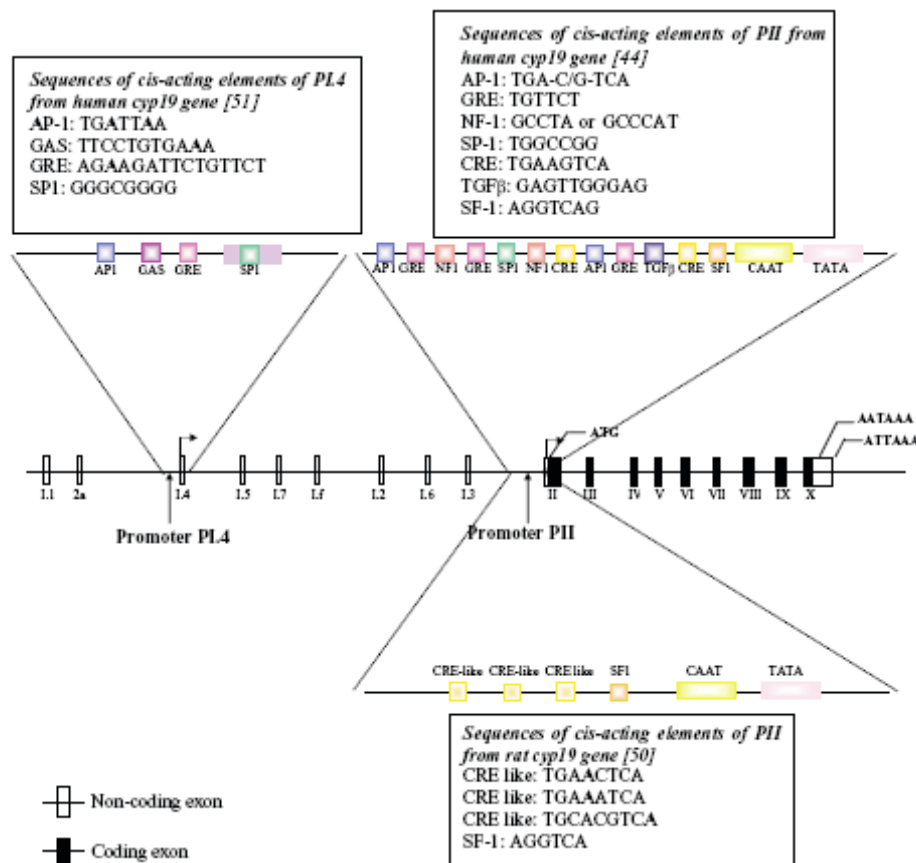


Figure 7. Structure of the human Cyp19 gene showing the various untranslated first exons and their corresponding promoters. The region around promoter PI.4 and PII from human and PII from rat are expanded to show the identified response elements. Sequences of these are shown in boxes; (by Carreau S 2004).

In the testis, FSH and LH act by increasing concentrations of intracellular cyclic AMP to induce expression of P450arom. Promoter PII activity is therefore regulated by cyclic AMP and requires the transcription factors cAMP response element binding protein (CREB), cAMP response element modulator (CREM) and steroidogenic factor-1 (SF-1). SF-1 belongs to the nuclear orphan receptor superfamily and regulates steroidogenic gene transcription (e.g. P450arom via its interaction with numerous coactivators including CREB binding protein, DAX-1, SOX-9, WT1).

It has been shown that the level of P450arom mRNA is increased in Leydig cells of mice deficient for DAX-1 (41). In addition, it is shown that liver receptor homologue-1 (LRH-1), an SF-1 homologue, which is present in Leydig cells and germ cells, but not in Sertoli cells, increases the P450arom gene expression in a mouse Leydig cell line (42).

Moreover, it is now clear that not only P.II drives the aromatase gene in rat testis but two additional promoters, P.I.f (brain promoter) and a new one that we called P.I.Tr (testis rat; (43), are involved. It is also demonstrated that the nutritional status of fetuses (44) and aging (Hamden K, Silandre D, Delalande C, El Feki A, Carreau S, unpublished results) can modulate aromatase gene expression in male rats.

2.2 The Estrogen Receptors (ERs)

Estrogen actions are mediated by binding to specific nuclear estrogen receptors (ERs), which are ligand-inducible transcription factors regulating the expression of target genes after hormone binding. Two subtypes of ERs have been described: estrogen receptor α (ER α) and the more recently discovered estrogen receptor β (ER β). The human gene encoding for ER α is located on the long arm of chromosome 6, while the gene encoding for ER β is located on band q22-24 of chromosome 14.

The two ER (α and β) proteins have a high degree of homology at the amino acid level (Fig. 8).

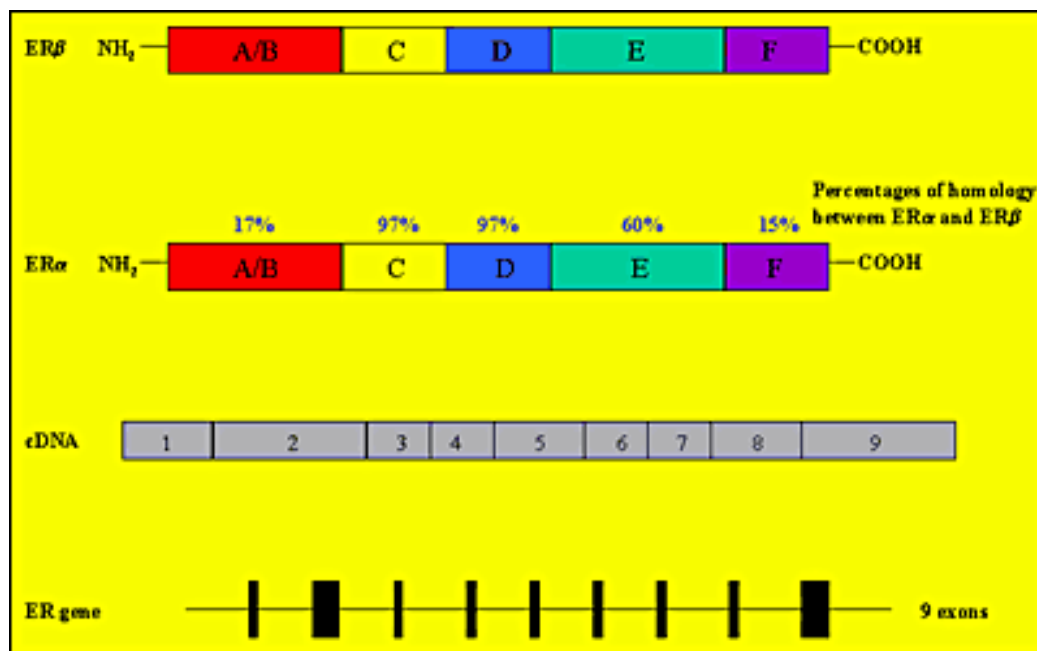


Figure 8. ERs gene and its products (by Akingbemi BT 2005) .

While it is clear that estrogens regulate transcription via a nuclear interaction after binding their receptors, a non-genomic action of estrogens has been recently demonstrated, suggesting a different molecular mechanism accounts for some estrogen actions. In vitro studies showed a very short latency time between the administration of estrogens and the appearance of biological effects. These actions are thought to be mediated through cell-surface receptors, which are not believed to act via a transcriptional mechanism (45). The different types of estrogen action are summarized in Table 1.

Table 1. Estrogen actions and related biomolecular pathways and mechanisms.				
Estrogen Actions	Receptors	Mechanism	Final effect	Features
Genomic (nuclear actions)	ER α	Transcriptional: nuclear interaction with estrogen-responsive elements	Modulation of estrogen target gene expression.	Slow effects (minutes or hours)
	ER β	Transcriptional: nuclear interaction with estrogen-responsive elements	Modulation of estrogen target gene expression.	Slow effects (minutes or hours)
Non Genomic (cell membranes actions)	Estrogen receptors on cells membrane	Cells membrane changes	Changes in ionic transport through cell surface.	Rapid effects (seconds)

ERs are members of the steroid/thyroid hormone super family of nuclear receptors, which share a common structural architecture, and consist of three independent but interacting functional domains: the N-terminal or A/B domains, the C or DNA-binding domain, and the D/E/F or ligand-binding domain (**Fig. 8**). Binding of a ligand to the ER causes a series of downstream events, including receptor dimerization, receptor-DNA interactions mediated by EREs present in the promoter region of target genes, recruitment of and interaction with transcription factors, and the formation of a preinitiation complex.

Ligand- receptor interactions ultimately cause changes in target gene expression (46). The N-terminal domain of nuclear receptors encodes an activation function called AF-1, which mediates protein-protein interactions to induce transcriptional activity. It is thought that this domain is highly active in ER α -mediated stimulation of reporter gene expression from a variety of ERE-constructs but its activity in the ER β is limited (47). On the other hand, the C-terminal or ligand-binding domain contains the AF-2 interacting surface that mediates ligand binding and receptor dimerization to stimulate transcriptional activity (48).

Thus, AF-1 and AF-2 are both involved in mediating the transcriptional activation functions of ERs. Although there is a high degree of homology in the DNA-binding domains of ER α and ER β (about 95%), only a partial homology exists in the ligand-binding domain (~60%) (49). Differences in ligand binding, in association with other factors, have the effect of altering the pattern of ER-mediated transcriptional activity. For example, some agonists bind both ER subtypes with the same affinity while others preferentially bind to ER α or ER β (50-52). There is general agreement that ERs function as dimers, and co-expression of ER α and ER β in the same cell causes the formation of homodimers (ER α /ER α and ER β /ER β) or heterodimers (ER α /ER β), which affect ligand-specificity. The interactions between ERs and EREs are complicated by other factors, including the ability of ER β to modulate ER α transcriptional activity and recruitment of several protein co-activators and repressors by both ER subtypes. Therefore, the relative amounts of ER α and ER β in a given tissue are key determinants of cellular responses to estrogen and other ER agonists and antagonists (53). Moreover, ER and other steroid receptors have the ability to mediate biological effects through non-transcriptional mechanisms mediated by protein-protein interactions occurring between ERs and growth factors e.g., IGF-1 and EGF (54). Furthermore, there is growing evidence for the presence of a small pool of ERs localized to the plasma membrane. For example, BSA-conjugated E2, which is unable to gain entry into the cytosol and acts at the plasma membrane, decreased testicular androgen production *in vitro* (55). Membrane ER is thought to signal mainly by coupling to GTP-activating proteins and through pathways involving second messengers (e.g., calcium) and kinase cascades (56). The integration of several pathways implies that estrogen action in any particular tissue and organ is the result of activities mediated by genomic and non-genomic pathways although the physiological significance of specific pathways in the testis remains to be elucidated (57).

2.3 Distribution of ERs and aromatase in the male reproductive system

ERs and the aromatase enzyme are widely expressed in the male reproductive tract in both animals and humans, implying that estrogen biosynthesis occurs in the male reproductive

tract and that both locally produced and circulating estrogens may interact with ERs in an intracrine/paracrine and/or endocrine fashion (45). The concept of a key estrogen action in the male reproductive tract is strongly supported by the fact that male reproductive structures are able to produce and respond to estrogens (58).

2.3.1 ERs and aromatase in rodent testis

Aromatase and ERs are found at a very early stage of development in the rodent testis, thus suggesting a role for estrogens in influencing testicular development (59-61). ER α is expressed by Leydig cells in the rodent fetal testis at a developmental stage in which the androgen receptor is not yet expressed. The developing efferent ductules and epididymis also express ER α in the fetal rodent. By contrast, it is unclear whether ER α is present within the seminiferous tubules of the fetal testis, with variable results having been reported (60). ER α is abundant in the developing efferent ductules, which are the first male reproductive structures to express ERs during fetal development (62). ER β is also found early in testis development in the gonocytes, Sertoli cells and Leydig cells, with the gonocytes showing the highest expression suggesting a role for estrogens in their maturation. In addition, ER β is expressed by rat Wolffian ducts, the structures from which the efferent ductules and epididymis arise (60). Aromatase is expressed in both Leydig and Sertoli cells in the rodent fetal testis, but not in gonocytes and immature structures of seminal tract. ERs and aromatase distribution in the fetal testes is summarized in Table 2.

Table 2. ERs and Aromatase distribution in the rodent fetal testis.			
	ERα	ERβ	Aromatase
Leydig cells	++	++	+
Sertoli cells	-	++	++
Gonocytes	-	+++	-
Seminiferous tubules	+/-	+	+
Ducts	+	+	-

The finding of both aromatase and ERs in the developing fetal testis imply a possible involvement of estrogens in the process of differentiation and maturation of developing rodent testis from an early stage of morphogenesis (59;63). In the postnatal immature rodent testis ER α expression does not occur in the seminiferous epithelium, remaining confined to the Leydig cells, rete testis, efferent ductules and epididymis (Table 3). In the neonatal rodent testis, ER β is widely expressed by the rat seminiferous epithelium (Sertoli cells and germ cells) as well as by Leydig cells, efferent ductules and epididymis. At this stage ER β seems to be the only ER in germ cells and is found in pachytene spermatocytes, round spermatids, and perhaps in elongated spermatids of rats and humans (58) (Table 3).

Table 3. ERs and Aromatase distribution in postnatal immature rodent testis.			
	ERα	ERβ	Aromatase
Leydig cells	+	+	+
Sertoli cells	-	+	+++
Gonocytes	-	+	-
Seminiferous tubules	-	+	+
Ducts	+	++	(?)

Aromatase is expressed by the dividing Sertoli cells and is stimulated by FSH, with the levels of aromatase declining with age. Fetal Leydig cells also have the ability to produce estrogens in response to LH, but aromatase in this cell type is expressed to a lesser degree than during neonatal life. Interestingly the neonatal testis continues to show a greater degree of aromatase expression in the Sertoli cells than in the Leydig cells (the latter only express aromatase to a greater extent in the adult rat testis when they become one of the major sources of estrogens under the influence of LH) (Table 3). Germ cells in immature rats do not yet express aromatase. ER α is expressed in the Leydig cells of both adult rats and mice (64) but not in Sertoli cells. ER α expression in adult rodent germ cells remains to

be confirmed, with its presence in pachytene spermatocytes and round spermatids being suggested by one study yet its absence demonstrated by others such that the prevailing view is that ER α is absent in germ cells. Studies on the precise cellular localization of ERs expression, however, are mainly based on immunocytochemistry, using different antibodies, and led to contradictory results. Whereas, it is generally agreed that both subtypes are expressed by the epithelial cells of the efferent ductules and epididymis, data concerning testicular expression differ between species, possibly due to different specificity characteristics of the antisera used. Knowledge of the distribution of ER α is of great importance in understanding estrogen action on the male reproductive tract. ER α is highly expressed in the proximal reproductive ducts (rete testis, efferent ductules, proximal epididymis) and its expression progressively decreases distally (corpus and cauda of the epididymis, vas deferens). The highest degree of ER α expression is seen in the efferent ductules of the rat (65) and accounts for one of the most well-documented estrogenic actions on male reproductive system, that of fluid reabsorption from the efferent ductules. It has to be remarked that the concentration of ER α in the male reproductive tract is opposite to that of ER β , which is more concentrated in the distal tract (Table 4).

Table 4. ERs and Aromatase distribution in the adult rodent testis.

	ER α	ER β	Aromatase
Leydig cells	+/-	+/-	+++
Sertoli cells	-	+	+
Germ cells	+/-	++	++++
Spermatogonia	- (?)	+	+ (?)
Pachytene Spermatocytes	-/+	+	+
Round Spermatids	-/+	+	++
Spermatozoa	+ (?)	+ (?)	+
Efferent ductules	++++	+	- (?)

ER β is expressed in Leydig, Sertoli and germ cells in adult rodents (66;67) and has also been detected in primate germ cells (68). There is now considerable evidence that germ cells contain both ER β and aromatase (68). It should be noted that there are some controversies in terms of ER β localization, with immunohistochemical studies showing some discrepancies, possibly due to methodological differences. It seems that the regulation of gonocyte multiplication, which is under the influence of growth factors and estradiol, may occur through the involvement of ER β (69). By adulthood, rodent Leydig cells show higher aromatase activity compared to every other age and in comparison to Sertoli cells (70). Aromatase is also expressed at high levels in germ cells throughout all stages of maturation, and its expression appears to increase as the germ cell becomes a mature spermatid (Fig. 9).

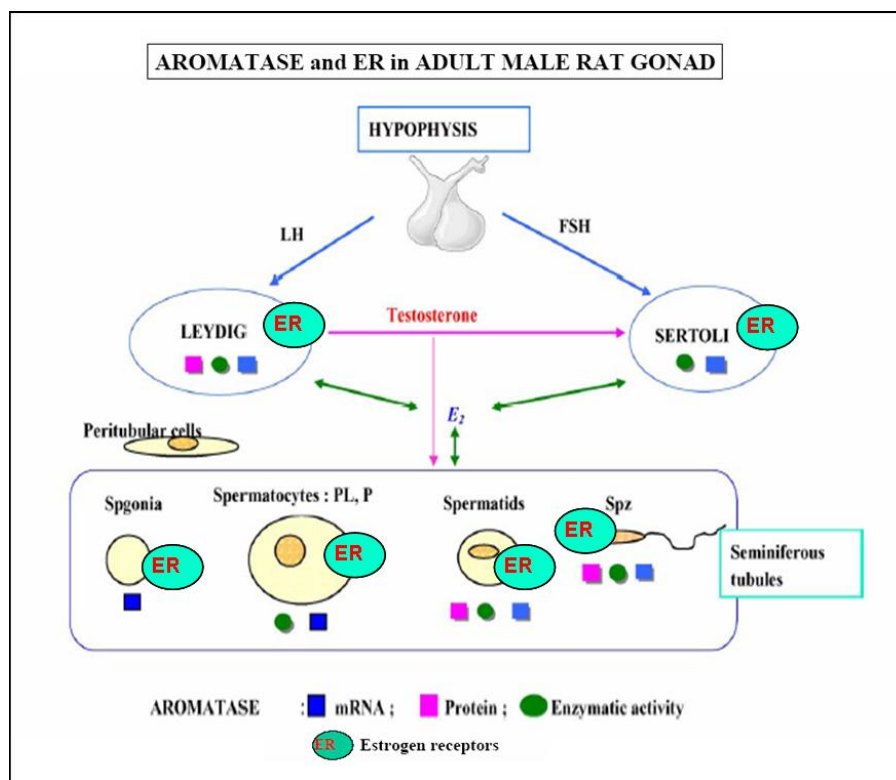


Figure 9. Aromatase and estrogen receptors (ER) in adult male rat gonad. Aromatase has been demonstrated in terms of mRNA (RT-PCR), protein (Western blots) and enzyme activity (measurements of estradiol output in culture media) in the various testicular cells. ER: estrogen receptors localization; (by Carreau S 2003, 2005).

Aromatase mRNA and activity, in fact, are found in germ cells from the pachytene spermatocyte stage in both rats and mice, and during their subsequent maturation into round spermatids(61;70;71). Aromatase seems to be present in higher levels in mature spermatids of the rat than in earlier germ cells (61;71;72). It is of interest that aromatase mRNA expression and enzyme activity is higher in germ cells when compared with Leydig cells, suggesting that germ cells may be a major source of estrogen in adult rodents. When fully developed spermatids are released from the epithelium, aromatase remaining in the residual body is subsequently phagocyted by the Sertoli cell. Some aromatase activity remains in the cytoplasmic droplet that remains attached to the flagellum as the sperm make its way through the epididymis, suggesting that mature spermatozoa are able to synthesize their own estrogen as they traverse the efferent ducts (73;74). The ability to synthesize estrogen gradually decreases as the droplet slowly moves to the end of the tail during epididymal transit until it's finally lost. The demonstration of aromatase in sperm is important as it suggests that the sperm itself could control the levels of estrogen present in the luminal fluid, directly modulating functions such as the reabsorption of fluid from the efferent ductules (65).

2.3.2 ERs and aromatase in the human testis

Both ERs have been found in human testis and reproductive tract. In the male fetus ER β expression is higher than ER α , the latter being absent or expressed at very low levels. In the human fetus ER β immunoreactivity has been shown in the seminiferous epithelium (Sertoli cells and a few germ cells) and in the epididymis suggesting a role for ER β in the prenatal development and function of male reproductive structures (75). In adult men ER α was expressed only in Leydig cells, while ER β has been documented in both Leydig and Sertoli cells and in the efferent ducts (76). The presence of ERs in the human epididymis is still debated, even though recently ER α has been detected in the nuclei of epithelial cells of the caput of the epididymis (77). Both ER α and β have been detected in human pachytene spermatocytes and round spermatids with in situ hybridization (78-80). These latter studies have been contradicted by more recent studies showing strong expression of ER β in human

testis but failing to find evidence for ER α using immunohistochemistry (81) and RT PCR (82), suggesting that ER β is the primary mediator of estrogen action in the human testis. Of particular interest is the demonstration of differential expression of wild type ER β (ER β 1) and a novel human variant form of ER β , arising from alternate splicing (ER β cx, or ER β 2), in the human testis (83). ER β 2, which may act as a dominant negative inhibitor of ER action, was highest in spermatogonia and Sertoli cells in adult men, suggesting that these cells may be "protected" from estrogen action by the expression of this variant. However wild type ER β 1 was highest in pachytene spermatocytes and round spermatids, which have been proposed to be estrogen sensitive, yet was low in less mature germ cells (81). As previously suggested by Durkee et al. (84), ERs are present in human sperm. In particular it has recently been documented by Luconi et al. (85) that the sperm membrane contains an estrogen receptor-related protein able to bind steroid hormones that may act through a calcium-calmodulin dependent pathway and thus perhaps accounts for a well documented rapid non-genomic action. Aromatase expression in the human testis is present in both somatic and germ cells from pachytene spermatocytes through elongated spermatids (80;86). Aromatase is also expressed in both human Leydig and Sertoli cells (71). Recently, the presence of aromatase has been demonstrated not only in immature germ cells, but also in mature human spermatozoa (87). In contrast to rodents, aromatase expression in human gametes is not lost during transit through the genital tracts since P450 aromatase was demonstrated in ejaculated human spermatozoa at three different functional levels: mRNA expression, protein and activity (87). Thus ejaculated human spermatozoa continue to express P450 aromatase and contain active aromatase, and thus sperm have to be considered a potential site of estrogen biosynthesis. These evidences support the concept that human spermatozoa should be considered a mobile endocrine unit since they are able to synthesize and to respond to estrogens. Again, the presence of functionally aromatase in human spermatozoa permits the conversion of androgens into estrogens throughout the whole transit of reproductive tract, an event that constantly provides free estrogens in the seminal fluid able to act on the cells of the reproductive ducts.

2.4 Role of estrogens in animal male reproduction

In animals, a previously unsuspected physiological role of estrogens in testicular function was revealed by the creation of the ER α knockout (α ERKO) mouse. Adult, sexually mature, male α ERKO mice are infertile even though the development of the male reproductive tract is largely unaffected (69). Adult testicular histology shows an atrophic and degenerating seminiferous epithelium, together with dilated tubules and a dilation of the rete testis (88). The disruption of spermatogenesis is progressive as the testicular histology is normal at ten days of age but starts to degenerate at twenty-thirty days. By about 40-60 days the tubules are markedly dilated with a corresponding significant increase in testicular volume while the seminiferous epithelium becomes atrophic. A severe impairment in tubule fluid absorption in the efferent ducts was demonstrated to be the cause of infertility in α ERKO male mice, and this defect is partially mimicked also by the administration of an anti-estrogen in wild-type mice (65). In the male genital tract the highest concentration of ER α is found in the efferent ducts (89) and the estrogen-dependent fluid reabsorption in this site probably results from estrogen interaction with the ER α that seems regulate the expression of the Na(+)/H(+) exchanger-3 (NHE3). In fact, the disruption of ER α or the use of antiestrogens result in decreased expression of NHE3 mRNA, as well as in a decrease of other proteins involved in water reabsorption, such as aquaporin I (90;91). The lack of fluid reabsorption in the efferent ductules of α ERKO male mice and the consequent dilatation of these ductules induces a retroactive progressive swelling of the seminiferous tubules. The seminiferous tubule damage results from the increased fluid pressure and severely impaired spermatogenesis coupled with testicular atrophy as seen at the age of 150 days (65). In addition, reproductive hormones profiles are abnormal in α ERKO male mice as serum LH is significantly increased with a consequent elevated serum testosterone and Leydig cells hyperplasia, but FSH remains in the normal range (69). It is also worth noting that detailed investigations into the development of efferent ductules in α ERKO male mice suggest that a congenital absence of ER α leads to developmental abnormalities in this tissue (92). The recent production of both aromatase

knockout (ArKO) (93) and ER β knockout (β ERKO) (94) mice supports the idea that in mice estrogen actions on the male reproductive tract are more complex than previously suggested on the basis of the α ERKO mice. In fact, unlike α ERKO mice, male ArKO mice are initially fully fertile (93), but fertility decreases with advancing age (95), and, conversely, β ERKO mice are fully fertile and apparently reproductively normal in adulthood (94). From seven months of age male ArKO mice are not able to sire any litters. Again histology of the testes of one-year-old ArKO mice shows a disruption of spermatogenesis at the early spermatid without significant (95). The late onset of the altered phenotype in male ArKO mice is attributable to estrogenic substance present in their diet and which are capable of agonistic effect on spermatogenesis (96). Despite the phenotype of α ERKO male mice, the mechanism involved in the development of infertility is different in ArKO male mice, since the early arrest of spermatogenesis suggests a failure of germ cell differentiation probably caused by the lack of estrogen action at the level of the seminiferous epithelium rather than a problem referable to impaired fluid reabsorption (59). Recent findings from studies in which human germ cells were treated with estrogen in vitro suggest that estradiol may serve as a survival factor for round spermatids and that lack of estradiol may promote apoptosis with a resulting failure in elongated spermatid differentiation (79). Recently studies in mice deficient in both ER α and β ($\alpha\beta$ ERKO mice) showed a male phenotype very close to that of α ERKO mice with infertility and dilated seminiferous tubules (69). These findings, together with the observation that β ERKO male mice are fully fertile (94), lead to the hypothesis that estrogen activity in the male reproductive tract differs with regard to both the type of estrogen receptor involved in the pathway of estrogenic action and the site of action through the male reproductive tract. Importantly, results from mice lacking functional ERs or aromatase point to an important role for estrogen in the maintenance of mating behaviour in male mice, and that infertility in α ERKO, $\alpha\beta$ ERKO and ArKO mice are at least in part due to reductions in various aspects of mating behavior from an early age. The above studies support the concept that a functional ER α , but not ER β , is needed for the development and maintenance of a normal fertility in male mice (69). Clearly, further studies are needed to fully understand the

precise role of estrogens and their receptors in the establishment and maintenance of male fertility, and the importance of intracrine and paracrine pathways for these effects.

2.5 Role of estrogens in human male reproduction

The demonstration of abundant ERs in human efferent ducts and aromatase activity in human sperm, speaks in favor of the involvement of estrogens in male reproductive function. On the other hand, data from human subjects with congenital estrogen deficiency have provided conflicting and somewhat confusing results. The only man with estrogen resistance discovered up till now, a human equivalent of the ERKO mouse, had normal testicular volumes and a normal sperm count but with slightly reduced motility (97). The four adult men affected by congenital aromatase deficiency showed a variable degree of impaired spermatogenesis (98-101). The patient described by Carani et al., showed both a severely reduced sperm count and an impairment of sperm viability with germ cell arrest at the level of primary spermatocytes (63). A more recent patient had complete germ cell arrest on testicular biopsy but a semen analysis was not performed according to patient's religious views (98;99). Data concerning the patient described by Morishima et al. are lacking since sperm counts were not analyzed (100). It should be remarked that a clear cause-effect relationship between infertility and aromatase deficiency is not demonstrable in the patient studied by Carani et al., since one of his brothers was infertile despite the absence of mutations in the aromatase gene, suggesting an alternate common cause for their infertility (102). Recently a new patient with aromatase deficiency has been described to have impaired fertility (101), confirming a possible association between congenital estrogen deficiency and infertility. The variable degree of fertility impairment in men with congenital deficiency of estrogen action or synthesis deficiency does not permit a firm conclusion about whether these features are a consequence of a lack of estrogen action or are only epiphenomena, even though a possible role of estrogen on human spermatogenesis is suggested by rodent studies. Recently, the administration of aromatase inhibitors to infertile men with an impaired testosterone to estradiol ratio resulted in an improvement of fertility rate (103), although in the absence of a placebo or control group, these findings

need to be interpreted with great caution. Clearly our knowledge of a role for estrogen in human male reproduction is far from complete. The exposure to the excess of environmental estrogens has been proposed as a possible cause of impaired fertility.

2.6 Effects of excess estrogen on male reproduction

2.6.1 Exposure to excess estrogens in animals

In order to evaluate the effect of estrogen excess on the reproductive tract, several studies have been performed in various animal species treated with diethylstilbestrol, a synthetic estrogenic compound. In male mice, the critical period for Müllerian duct formation is day 13 post-coitus. Prenatal exposure of fetal male mice to DES caused a delay in Müllerian duct formation by approximately two days as well as incomplete Müllerian duct regression with a female-like differentiation of the non-regressed caudal part (104). An increase in the expression of anti-Müllerian-Hormone (AMH) mRNA in male mice fetuses exposed to DES has also been demonstrated. This increase was not accompanied by a regression of the ducts. This data was interpreted to suggest that the asynchrony in the timing of Müllerian duct formation, with respect to the critical period of Müllerian duct regression, led to the persistence of Müllerian duct remnants at birth in male mice. Moreover DES exposure did not impair embryonal genetic development, but increased ERs number, and slightly prolonged the gestation time (cesarean sections were performed to rescue the litter and revealed no difference in size of fetuses from control and DES treated mothers). The timing of DES exposure is crucial to the induction of abnormalities of Müllerian duct development and regression (104). Many studies in rodents suggest that inappropriate exposure to estrogen in utero and during the neonatal period impairs testicular descent, efferent ductule function, the hypothalamic-pituitary-gonadal axis, and testicular function (58). The latter effect can be a direct consequence of exposure to excess estrogen, as well as a secondary effect due to perturbations in circulating hormones or the ability of the efferent ductules to reabsorb fluid. Some studies show that low dose estrogenic substances given during puberty can actually stimulate the onset of spermatogenesis, likely due to

stimulatory effects on FSH (105), highlighting the fact that the effects of excess estrogen on male fertility are often complex. The effects of excess estrogen in the neonatal period can impact upon the testis into adulthood, with permanent changes in testis function and spermatogenesis evident (106).

2.6.2 Aromatase over-expression in rodents

Recently a transgenic line of mice overexpressing aromatase enzyme (AROM+) has been developed (107;108). These mice show highly elevated serum estradiol concentrations, with a reciprocal decrease in testosterone concentrations. The AROM+ males display several of the changes observed in males perinatally exposed to estrogens, such as undescended testes, testicular interstitial cell hyperplasia, hypoandrogenism, and growth inhibition of accessory sex glands. A disruption of spermatogenesis has also been observed which could be a consequence of multiple factors, including cryptorchidism, abnormal Leydig cell function, hypoandrogenemia or hyperestrogenemia. Estrogens are thought to inhibit Leydig cell development, growth and function, resulting in the suppression of androgen production (58). The observation of numerous degenerating germ cells and the absence of spermatids within the seminiferous tubules of AROM+ mice suggest that germ cells development was arrested at the pachytene spermatocyte stage in the cryptorchid testes. Interestingly, the spermatogenic arrest occurred at a stage where P450arom is typically expressed. The spermatogenic arrest found in the AROM+ mice could be explained, at least partially, by the suppression of FSH action. The reduced serum FSH levels in AROM+ males are further evidence of the inhibiting actions of estrogens on FSH secretion in males. No significant differences in the LH concentrations were seen in AROM+ and wild type mice (107;108).

2.6.3 Exposure to excess estrogens in humans

The clinical use of diethylstilbestrol (DES) by pregnant women in order to prevent miscarriage resulted in an increased incidence of genital malformations in their sons (109). In these individuals the presence of Müllerian ducts remnants was found indicating that fetal exposure to DES may have an effect on sex differentiation in men, as is the case in rodents (104). Moreover a large number of structural and functional abnormalities were found, the most frequent being: epididymal cysts, meatal stenosis, hypospadias, cryptorchidism and microphallus (109). The frequency of abnormalities was dependent on the timing of estrogen exposure: in fact, men who were exposed to DES before 11th week of gestation (i.e. the time of Müllerian ducts formation) had a two fold higher rate of abnormalities than those who were exposed only later (109). This data supports the previously discussed hypothesis that the asynchrony between formation and regression of embryonal reproductive structures is determined by estrogen exposure. Various reports have demonstrated that semen quality of men exposed to DES in utero is significantly worse than in unexposed controls (110;111). However, the sperm concentrations of most of the DES exposed men were well above the limit at which subfertility occurs, and it is therefore not surprising that the fertility of these men was reported to be normal (112). The risk of testicular cancer among men exposed to DES in utero has been a controversial issue and several meta-analyses showed no increased risk (113). However more direct evidence will be necessary in order to fully understand this issue. While various studies suggest that environmental estrogens affect male fertility in animal models, the implications for human spermatogenesis are less clear (114). It has been demonstrated that male mice whose mothers have consumed a 29 ng/g dose of bisphenol A for seven days during pregnancy had a 20% lower sperm production as compared to control males (115). Various abnormalities in reproductive organs have also been described in males exposed to bisphenols (i.e. a significant decrease in the size of the epididymis and seminal vesicles and an increase in prostate gland volume), suggesting that bisphenols interfere with the normal development of the Wolffian ducts in a dose-related fashion. Exogenous estrogens

could interfere with the development of the genital structures if administered during early organogenesis, by leading to both an impairment of gonadotropin secretion and by creating an imbalance in the androgen to estrogen ratio, which may account for impaired androgen receptor stimulation or inhibition according to the dose, the cell type and age (1;116;117). An excess of environmental estrogens has been suggested as a possible cause of impaired fertility in humans (118). A progressive decline in sperm count has been reported in some Western countries during the past 50 years, suggesting a possible negative effect of environmental contaminants on male reproductive function (119). Data concerning the role of estrogens in male reproductive structure development remains conflicting. Animal studies suggest that exposure to estrogen excess may negatively affect the development of reproductive male organs. These effects, however, are considered to be the result of an impaired hypothalamic-pituitary function as a consequence of estrogen excess and of the concomitant androgen deficiency (1;117). Much of the knowledge on excess estrogen exposure and human fertility depends upon animal data and the validity of these concepts to humans has not been established.

2.6.4 Aromatase over-expression in humans

In 1996 a boy with aromatase excess syndrome was reported (120). His condition was presumably inherited in an autosomal dominant fashion with sex-limited expression as his father had a history of peripubertal gynecomastia, elevated serum estrogen levels and increased aromatase activity in vitro. The father was fertile and had a normal libido despite a small testicular volume (15 mL bilaterally), and a reduced testosterone level of 234 ng/dL (120). In the son, mild suppression of testicular growth and Leydig cell function probably reflected direct estrogen negative feedback on pituitary gonadotropin secretion. In general, the inhibitory effects of estrogen on reproductive function appear to be milder in males with aromatase excess syndrome than in patients receiving exogenous estrogens or with estrogen-secreting tumors, probably because serum estradiol and/or estrone levels are lower in the former (120).

3. Testicular cancer

3.1 Introduction

Although cancer of the testes is rare, accounting for only about 1 percent of all cancers in men of all ages and about 5 percent of all male genitourinary system cancers, it is the most common cancer in men between the ages of 15 and 35, and the second most common malignancy in men ages 35 to 39 (121-124).

Because the incidence of testicular cancer has risen markedly in the past 20 years, numerous studies are being conducted to explore possible environmental causes, including the mother's diet during her pregnancy as well as her use of diethylstilbestrol (DES) to prevent miscarriage. Researchers are also looking at the increasing presence of estrogen-mimicking pollutants in the environment. The most consistent occupational association has been the elevated rate among men in professional and white-collar occupation, which may be linked to an increased risk observed with lower levels of exercise. Other possible causes include hereditary factors, genetic anomalies, congenital defects involving the reproductive tract, testicular injury, and atrophy of the testes. Viral infections such as mumps, which cause inflammation of the testes, have not been proven to cause cancer.

Testicular cancer comprises a number of different diseases. Nearly all of the main cell types in the testis can undergo neoplastic transformation, but germ cell-derived tumors constitute the vast majority of cases of testicular neoplasms. Ninety-five percent of testicular cancers arise from sperm-forming, or germ cells and are called germinal tumors. The remaining 5 percent are nongerminal tumors. About 40 percent of germinal tumors are categorized as seminomas. Several other types of germinal tumors are referred to collectively as non-seminomas. Somatic cell tumors, known as sex cord-stromal neoplasms and Leydig cell tumors are relatively rare. However, being derived from endocrine active cells, they have endocrine manifestations.

3.2 Leydig cell hyperplasia and tumors

Although Leydig cells in adult men are considered to be a terminally differentiated and mitotically quiescent cell type, in various disorders of testicular function, focal or diffuse Leydig cell hyperplasia is very common. Micronodules of Leydig cells are frequently seen in certain conditions associated with severe decrease of spermatogenesis or germinal aplasia, such as the so-called Sertoli-cell-only syndrome (Del Castillo syndrome), cryptorchidism, or Klinefelter's syndrome (125). A term "Leydig cell adenoma" is used when the size of a nodule exceeds several fold the diameter of a seminiferous tubule. It is unknown whether Leydig cell adenomas can progress further to form overt Leydig cell tumors, but even if it was the case, it is exceedingly rare. Morphological heterogeneity of hyperplastic Leydig cells is noticeable in some cases.

The mechanism of Leydig cell hyperplasia in the human male is still poorly understood. The disruption of hypothalamo-pituitary-testicular axis leading to an excessive stimulation of Leydig cells by LH can play a central role (125). However, molecular pathways remain largely unknown in the vast majority of cases. In a small subset of cases structural changes of the LH receptor (126;127) and G proteins (128;129) were detected. Constitutively activating mutations of LH receptor cause early Leydig cell hyperplasia and precocious puberty (126;130). Similarly, constitutively activating mutations of Gs-protein in Leydig cells lead into hyperplasia and endocrine hyperactivity (129;131). However, Leydig cell hyperplasia is distinct from tumors that are usually solitary, and the role of the LH receptor and G protein mutations in the tumorigenesis may be limited to few cases (127;129). Leydig cell hyperplasia and adenomas can be easily induced in rodents by administration of estrogens, gonadotropins and a wide range of chemical compounds. Whether or not humans would be similarly susceptible to environmental effects remains to be elucidated.

Leydig cell tumors account for one to three percent of testicular neoplasms and occur in all age groups (131-133). Approximately 20 % are found before the age of 10, most often between five and ten years of age. Precocious puberty is the presenting symptom in these cases. Tumors produce androgens, mainly testosterone in a gonadotropin independent

manner, and therefore LH and FSH remain low in spite of external signs of puberty. Approximately 10 % of the boys also have gynecomastia that is caused by estrogens produced in excess due to aromatase activity. In adults, gynecomastia is found in approximately 30 % of patients (133). The excessive androgen secretion rarely causes notable effects in adults.

Leydig cell tumors are always benign in children and can be treated with surgical enucleation when the tumor is encapsulated (123), whereas in adults malignant tumors have been found in 10-15 % of patients, and inguinal orchidectomy remains the treatment of choice (132). The presence of cytologic atypia, necrosis, angiolymphatic invasion, increased mitotic activity, atypical mitotic figures, infiltrative margins, extension beyond testicular parenchyma, and DNA aneuploidy are associated with metastatic behavior in Leydig cell tumors (133;134). Malignant tumors are hormonally active only in exceptional cases. Benign tumors can be treated by orchidectomy, whereas an additional retroperitoneal lymphadenectomy should be considered when the gross or histological features suggest malignancy (134). Malignant tumors have not responded favorably to conventional chemotherapy and irradiation (134). Survival time has ranged from 2 months to 17 years (median, 2 years), and metastases have been detected as late as nine years after the diagnosis (133;134). Therefore follow-up of patients with malignant Leydig cell tumors has to be life-long. The remaining testis may be irreversibly damaged by longstanding high estrogen levels, resulting in both permanent infertility and hypoandrogenism(133-135).

The most frequently encountered testicular neoplasm of the mouse and rat is the Leydig cell adenoma. Incidence rates vary in different strains with the Sprague-Dawley SD rat ranging from 1 to 5% and the F-344 rat reaching nearly, 100% (136). Early neoplasm are common in 1 yr old F-344 rats and become increasingly more frequent with age (137). Testicular neoplasia is less frequently observed in all strains of mice with incidence ranging from 1 to 2,5%. Leydig cell tumors in rodents generally occur in older animals, but in human can arise in any age, the majority between 20 and 60 yr (138). The estimated incidence in man is 0.1-3 per million. The proliferative lesions in Leydig cells in rodents are similar and are observed as a continuous spectrum starting with smaller nodular foci of

hyperplasia leading to large Leydig cell adenomas that can eventually replace the entire testis. The distinction between hyperplasia and adenoma is not always clear, with size being the major factor in the diagnostic criteria, with some debate over when focal hyperplasia becomes early neoplasia and there can be little morphological difference between a hyperplastic nodule and a small Leydig cell adenoma. The major difference between the testicular tumors observed in human and rodents (particularly the rat) are the high incidence of germ cell tumors in human and their occurrence in relatively young men. In rats, germ cell tumors are extremely rare, but Leydig cell tumors can be almost 100% in incidence in certain strains (e.g., Fisher F-344) and occur most frequently in older animals.

3.3 Relationship between estrogens and Leydig tumors

The biological significance of estrogen-induced testicular tumorigenesis has been suggested by the *in vivo* model overexpressing aromatase transgenic mice (139). Half of these males were infertile and some of them showed larger than normal testis and Leydig cell hyperplasia/Leydig cell tumor. Furthermore, aromatase was markedly immunolocalized in the cytoplasm of interstitial cells, and its immunoreactivity appeared to be strongest in the testes with more advanced stages of neoplasia. The same transgenic animals exhibited estrogen circulating levels at least twice higher than those of control animals and the levels of aromatase mRNA in their testicular tissues were fourfold higher when compared with controls. It is worth to mention how ER α protein in testicular tissue of aromatase transgenic animals was very high with respect to the undetectable levels of control animals. So the authors suggest how an enhanced synthesis of estrogens in tumoral tissues led to an upregulation of ER α expression. Human Leydig cell tumor is a rare testicular neoplasm where estrogen involvement in tumorigenesis process has scarcely been investigated. Recently, a strong aromatase expression in tumoral tissues was revealed by immunostaining and western blotting (140). This finding agrees with a single previous report (141) showing the aromatase immunolocalization in Leydig cell tumors. Furthermore, aromatase expression in control human testicular tissue confirmed Turner's

report in normal testes (142). The enhanced endogenous synthesis of estrogens by Leydig cell tumor was reflected in both patients by a dramatic increase of estrogen circulating levels, resulting more than twofold higher than those of adult normal male, and by the low testosterone levels (at the lower limit of normal range) (140). Moreover, the ratio between the free fraction levels of the two steroids is furthermore increased in the target tissues. The diminished sperm count and motility of both patients may not only be related to altered testicular tropism, parenchymal compression, and increased local temperature ipsilateral to the tumor (143) but also to the detrimental effects of high circulating estrogen levels on the counter-lateral gonad activity. In the adult normal male, 80% of the plasma estradiol originates from aromatization of testosterone and androstenedione in fat, striated muscle, and other tissues including bone and brain, while 20% in the circulation is secreted by the testis. So, it is reasonable to argue how the excessive increase of estradiol circulating levels, observed in the two patients with Leydig cell tumor, is the consequence of an enhanced rate of testicular secretion. This is confirmed by the evidence that estradiol, as well as E2/T ratio circulating levels, drops dramatically following surgical treatment, while for one of the two patients the persistence of a conspicuous bilateral gynecomastia led to bilateral mastectomy (140). Following orchidectomy, the two patients exhibited a moderate increase of sperm count and a remarkable augment of sperm motility (140). The latter event may be reconducted to the restored testosterone circulating levels likely affecting the entire male genital tract. The expression of ER isoforms in Leydig cell tumor is, to date, unknown. In fact, only a single work showed the ER immunolocalization in cryostat sections of Leydig cell tumor (24); recently, immunohistochemical and western blot analysis of tumoral tissues revealed the expression of ER α and of the two ER β isoforms, ER β 1 and ER β 2, in neoplastic Leydig cells of both patients. So, the pattern of ERs expression in tumoral cells appears different from that of control Leydig cells, exhibiting only ER β 1 and ER β 2 as previously reported (81;83) .

There is a growing body of evidence that ER α and ER β can be expressed together in the same cell type and independently expressed in another. Therefore, homodimers (ER α -ER α /ER β -ER β) or heterodimers (ER α -ER β) can be formed (28). The binding affinity of

ER α -ER α / ER α -ER β dimers for a consensus DNA estrogen response element is reported to be higher than that of the ER β -ER β homodimer (29). Thus, the presence of ER α could reinforce the estradiol-induced tumor cell proliferation. Finally, it has been demonstrated that neoplastic Leydig cells are potential estrogen biosynthesis sites and display a modified ER expression pattern. Therefore, it appears reasonable to suggest that the high estrogen levels, measured in the two patients, could play a role in the neoplastic transformation of Leydig cells, while the exclusive presence of ER α in tumoral cells could amplify E2 signaling contributing to the tumor cell growth and progression.

4. The IGF system

4.1 Introduction

The insulin-like growth factor (IGF) signalling axis involves the coordinated function of two ligands, IGF-I and IGF-II, three cell surface receptors, at least six high affinity binding proteins and binding protein proteases). This signalling axis plays a pivotal role in normal growth and development (144), and is also implicated in mediating many aspects of the malignant phenotype in a variety of human malignancies (145-147).

IGF-I and -II are growth-promoting peptides, members of a superfamily of related insulin-like hormones that includes insulin and relaxin in the vertebrates and bombyxin, locusta insulin-related peptide, and molluscan insulin-like peptide in invertebrates (148-153). However, insulin and IGFs are the most closely related in terms of primary sequence and biological activity. The IGFs are major growth factors, whereas insulin predominantly regulates glucose uptake and cellular metabolism. They both are secreted as prohormones and undergo through a proteolytic process to produce the active peptide.

Structurally, they consist of A, B, C, and D domains (**Fig. 10**).

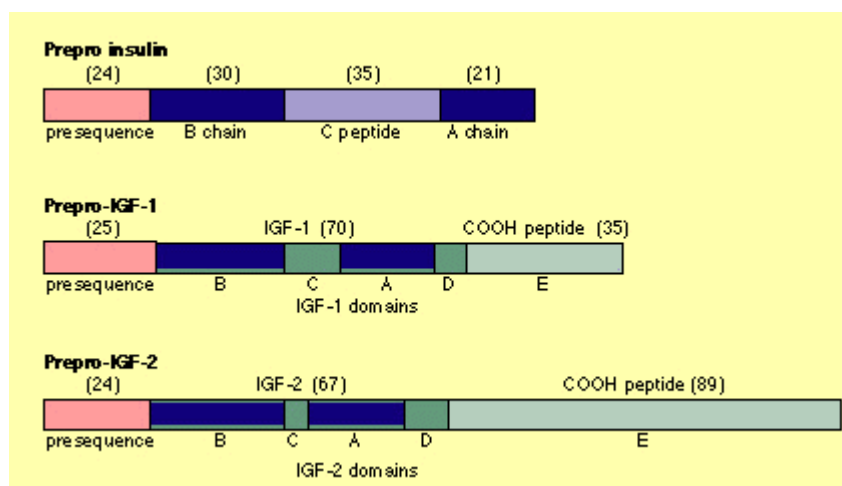


Figure 10. Protein domains in IGFs and Insulin. Regions showing homologies with insulin are indicated by dark blue rectangles. The lengths of individual fragments (in amino acids) are indicated in brackets.

Large parts of the sequences within the A and B domains are homologous to the α - and β -chain of the human proinsulin. This sequence homology is 43% for IGF-I and 41% for IGF-II. No sequence homology exists between the C domains of IGFs and the C peptide region of human proinsulin. The gene encoding IGF-I is highly conserved (154) such that 57 of 70 residues of the mature protein are identical among mammals, birds, and amphibians (155-157). Expression of the IGF-I gene is affected at many levels including gene transcription, splicing, translation, and secretion. IGF-I expression is also influenced by hormonal (GH) (158), nutritional (159), tissue-specific and developmental factors (160). The biological actions of the IGFs are mediated by the type I IGF receptor (IGF-IR), a glycoprotein on the cell surface that transmits IGF binding to a highly integrated intracellular signaling system (161). Binding of IGF-I to its receptor causes receptor autophosphorylation and the activation of an intrinsic tyrosine kinase that acts on various substrates, leading to activation of multiple signaling pathways including the PI3K/AKT and MAPK cascades. In addition, it has been shown that IGF-I can activate the PLC/PKC pathway (3). IGF-II also binds to the IGF-IR both with lower affinity (161). Expression of the IGF-IR gene (162) has been detected in many tissues and is constitutively expressed in most cells (163;164); its promoter is regulated in vitro and in vivo by transcription factors such as Sp1 and the transcription factor p53 (165). Various IGF-I receptor subtypes that present distinct structures or binding properties have also been described. Two of these subtypes, namely hybrid and atypical IGF-I receptors, have been particularly investigated in a variety of cell types (166). The atypical IGF receptors are characterized by their ability to bind insulin as well as IGFs with relatively high affinity (167). Hybrid insulin/IGF-I receptors have been reported in cells expressing both IGF-I and insulin receptors (168); however, the physiological significance of hybrid and atypical IGF receptors is unclear. The IGF-II ligand has greatest affinity for a distinct receptor, the type-II or IGF-II receptor (169). This single chain polypeptide with a short cytoplasmic domain lacking tyrosine kinase activity is identical to the cation-independent mannose-6 phosphate (M6P) receptor (170). The IGF-II/M6P receptor binds two general classes of ligands: 1) non-M6P-containing ligands, the best characterized of which is IGF-II; and 2) M6P-containing

ligands, including lysosomal enzymes. The multifunctional role of the receptor is evidenced by its function in the mediation of lysosomal enzyme trafficking, endocytosis, and lysosomal degradation of extracellular ligands, regulation of apoptotic/mitogenic effects, and possible intracellular signal transduction (171;172). More recently, high-affinity binding of IGF-II to an insulin receptor isoform (IR-A) has also been reported (173), thus suggesting that IGF-II might also signal via the insulin receptor. However, this insulin receptor isoform (IR-A), lacking the alternative spliced exon 11, is preferentially expressed in fetal and cancer cells (174).

A family of six high-affinity IGF-binding proteins (IGFBP-1 through IGFBP-6) coordinate and regulate the biological activity of IGF in several ways: 1) transport IGF in plasma and control its diffusion and efflux from the vascular space; 2) increase the half-life and regulate clearance of the IGFs; 3) provide specific binding sites for the IGFs in the extracellular and pericellular space; and 4) modulate, inhibit, or facilitate interaction of IGFs with their receptors (175;176). IGFBP biological activity is regulated by posttranslational modifications such as glycosylation and phosphorylation and/or differential localization of the IGFBPs in the pericellular and extracellular space (175;176). It is therefore hypothesized that IGFBPs, in addition to stabilizing and regulating levels of diffusible IGFs, might regulate IGF-I cellular responses by facilitating receptor targeting of IGF-I or modulating IGF-I bioavailability in the pericellular space. The effects of the IGFBPs are further regulated by the presence of specific IGFBP proteases, which cleave the binding proteins, generating fragments with reduced or no binding affinity for the IGFs (177). Some IGFBPs, including IGFBP-2 and -3, can induce direct cellular effects independent of the IGFs (176;178). IGFBP-3, similar to IGFBP-5, contains sequences with the potential for nuclear localization (179) and detection of IGFBP-3 in the nuclei of dividing cells, as reported by several investigators (180), strongly suggesting a role for IGFBP-3 in gene regulation. More recently, perinuclear or nuclear localization has also been reported for IGFBP-2 (181); however, the role of IGFBP-2 in this cellular compartment is yet to be determined.

4.2 Effect of Insulin-Like Growth Factor I on testicular function

Although it is well established that testicular function is mainly controlled by the gonadotropins LH and FSH, there is now considerable evidence indicating that local factors are extremely important in regulating the functions of the testis (182). For example, higher insulin levels in testicular fluid have suggested a role for this factor in Leydig cell development and function (183). Another factor, insulin-like growth factor I (IGF-I), is believed to be a potent para/autocrine stimulator of Leydig cell function (184). Several laboratories have demonstrated IGF-I immunoreactivity (185;186) and IGF-I messenger RNA (mRNA) (187) in the adult rat testis. Immunostainable IGF-I has been found in adult human testes (188). Cultures of Sertoli and Leydig cells from adult rats and immature pigs secrete immunoreactive IGF-I into the medium, and this secretion is enhanced by FSH (Sertoli cells) or LH (Leydig cells) (189;190). Type I receptors for IGF-I have been found on human, pig, and rat Leydig cells (191;192), and IGF-I enhances the differentiated functions of Leydig cells (193). IGF-I stimulates the hCG-supported production of cAMP and testosterone by cultures of rat (194) and pig (195) Leydig cells. The response to cAMP analogs is also enhanced (195), suggesting that IGF-I potentiates the action of LH/hCG at sites both proximal and distal to cAMP generation. IGF-I increases the number of LH/hCG receptors (192) and the amount of LH/hCG receptor mRNA (196) as well as the activities of several steroidogenic enzymes and the amounts of mRNAs encoding them (197-199). The role of IGF-I has been demonstrated in testicular growth and development, control of Leydig cell numbers, and in the onset of steroidogenesis and spermatogenesis (184;200). Lastly, the crucial role of IGF-I in the development and function of Leydig cells was obtained in studies of IGF-I gene knock-out mice(201). The testes of these animals were reduced in size and had fewer and smaller Leydig cells than normal, and the plasma testosterone levels were markedly reduced. It has recently been demonstrated that IGF-I null mice have decreased levels of serum testosterone and steroidogenic acute regulatory (StAR) protein (202). StAR has been demonstrated to play an essential role in regulating steroid biosynthesis by mediating the transfer of cholesterol from the outer to the inner

mitochondrial membrane where it is converted to pregnenolone (203). Transcriptional and/or translational inhibition of StAR expression results in a dramatic decrease in steroid biosynthesis whereas approximately 10–15% of steroid synthesis appears to be mediated through StAR-independent mechanisms (204). Recent findings indicate that IGF-I is capable of increasing expression of StAR protein and steroid synthesis in mouse Leydig cells (3).

4.3 IGF system and tumorigenesis

IGF-I is a peptide hormone that is involved in controlling proliferation and differentiation. Although most of the IGF present in circulation is protein bound, a small fraction of IGF-I is "free"; this component may be more bioavailable, but assays specific for free ligand are controversial. The IGF binding proteins IGFBP-3 and IGFBP-1 both affect IGF-I bioavailability and, in addition, seem to exert independent effects on the growth control of malignant cells (205) as part of a comprehensive regulation system of cell survival and death. Several reports indicate that high circulating levels of IGF-I are associated with increased risk of developing breast, colorectal, prostate and skin cancer. In fact, a positive association between circulating levels of IGF-I generally and breast cancer risk was observed in premenopausal women (206). However, results from observational studies have not been consistent (206;207) and considerable uncertainty remains regarding the true association between IGF-I and premenopausal breast cancer risk. Furthermore, the association between IGFBP-3 and breast cancer risk is also inconsistent. In part, these inconsistencies may be attributed to technical variation in performance of assays for IGFs, particularly IGFBP-3, the primary IGF-I binding protein. Other potential explanations for inconsistencies in results include differing blood sampling and storage methods, different definitions of cancer "cases," differences in age at blood sampling, and the possibility of differences between populations in factors that may influence the IGF-I risk relation.

Several studies suggest that IGF-I and IGF-II are important in the pathophysiology of colorectal carcinoma. IGF receptors are found in human colon cancers (208), and full-

length messenger RNAs for IGFs have been detected in human tumor cells (209). Exogenous IGF-I and -II stimulate proliferation of human colorectal cancer cells (210), whereas blockade of the IGF-I receptor inhibits tumor cell growth (211). Individuals with acromegaly, a disease of somatic growth caused by increased growth hormone and IGF-I, have an increased incidence of colonic cancer (212). IGF-binding protein-3 (IGFBP-3) binds more than 95% of the IGF in serum and influences cell proliferation by modulating access of IGFs to the IGF receptors (213). IGFBP-3 also apparently inhibits growth and induces apoptosis through IGF-independent mechanisms (214). Most circulating IGF-I and IGFBP-3 are synthesized in the liver, where expression of each is increased by growth hormone. There is considerable between-person variability in blood levels of IGF-I, IGF-II, and IGFBP-3 (215). Tissue IGF bioactivity is influenced by circulating IGF levels and by local expression of IGFs, IGFBPs, and IGFBP proteases (175). Some factors that regulate determinants of local IGF bioactivity may regulate circulating IGF-I levels in a parallel fashion (216).

5. The cyclooxygenase enzymes (COX)

5.1 Structure, function and regulation of COX

The prostaglandin endoperoxide H synthase (also COX) is a rate-limiting enzyme involved in the conversion of arachidonic acid to prostaglandin H₂, the precursor of various molecules including prostaglandins, prostacyclin, and thromboxanes (**Fig 11**).

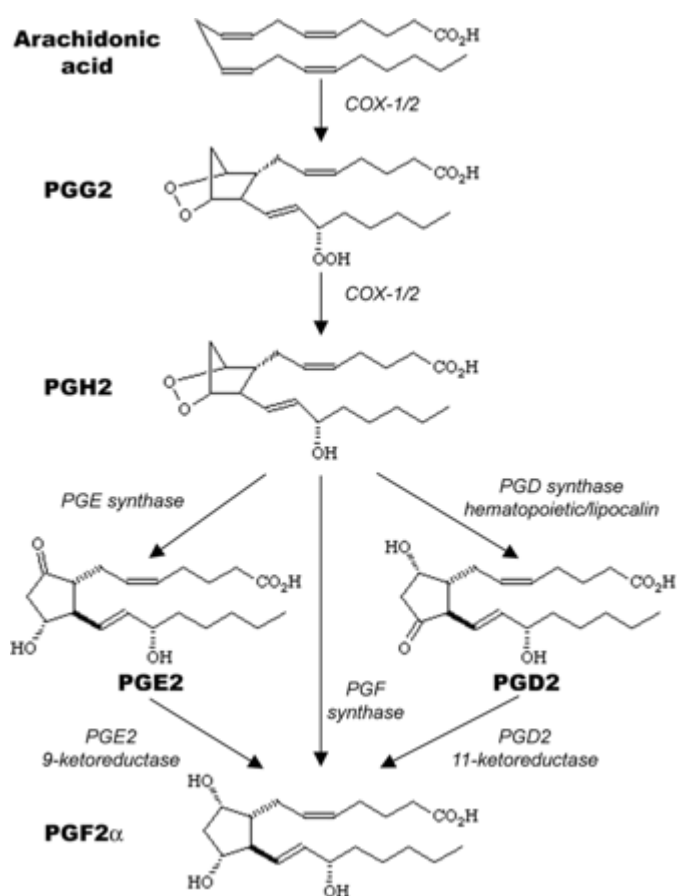


Figure 11. Schematic representation of the COX pathway illustrating the synthesis of the major PGs. This process is initiated when COX-1 and COX-2 catalyze both a reaction in which arachidonic acid is converted to PGG₂ and a subsequent peroxidase reaction in which PGG₂ is reduced to PGH₂, which serves as the common precursor for all of the terminal PGs.

Two COX genes, *COX-1* and *COX-2*, which share over 60% identity at the amino acid level have been identified (217). The gene contains 10 exons is 7.5 kb in length and located at chromosome 1. The transcriptional start site was mapped at 134 bases upstream from the ATG start codon. Nucleotide sequence of 1.8 kb promoter region contains a TATA box and a number of potential regulatory elements including CRE, NF-kappa B, Sp1 and AP2 sites. The linear sequence and three-dimensional structure of the two isoforms are very similar. Even the active site of the isoforms differs minimally (valine/isoleucine substitutions) at only two positions. Nevertheless, inhibitors with high and clinically demonstrable selectivity for the isoforms are available (218-220). COX-1 is constitutively expressed in most cells, thus regarded as a housekeeping molecule, and is responsible for various physiological functions including cytoprotection of the stomach, vasodilatation in the kidney, and production of a proaggregatory prostanoid, thromboxane, by the platelets. On the other hand, the expression of COX-2 is inducible and remains undetectable in most mammalian tissues under basal conditions. Exposure of several types of cells including fibroblasts, endothelial cells and monocytes to bacterial endotoxins, cytokines, hormones or growth factors induces its expression within 2–6 h. Historically, gram (–) bacterial LPS was the first inducer of COX-2 expression to be identified in macrophages (221). It is now known that most pro-inflammatory mediators induce the expression of COX-2. More specifically, LPS and other TLR ligands bind to MyD88-associated receptors and via MEK/ERK induce the transcription factor activator protein 1 (AP1). LPS also activates the TRAF6/NIK/Tpl2/IKK/NFkB pathway, which also leads to induction of COX-2 transcription. Tpl2 signals also lead to ERK1/2 activation, which in turn activates p90RSK and MSK1, which phosphorylate CREB, a central regulator of COX-2 transcription (222). LPS activates C/EBP β and C/EBP δ via p38MAPK and ERK1/2. It should be noted that C/EBP β and CREB play a major role during the initial stage of COX-2 transcriptional activation while C/EBP δ maintains an already induced transcription (223). The transcription complex at the COX-2 promoter requires the transcriptional co-activator p300. It now appears that p300 binds on CREB, AP1, C/EBP and NFkB, controlling the initiation of transcription (224). Nitric oxide (NO) affects COX-2 directly by increasing its

catalytic activity and indirectly by triggering several signalling cascades that affect transcription. Thus, NO reacts acutely with superoxide anions to form peroxynitrite anions (ONOO⁻), which enhance COX-2 catalytic activity in a direct manner (225). It should be noted here that NO may affect carcinogenesis in two parallel ways: first, via activation of COX-2 catalytic activity and secondly in synergy to COX-2 by inducing VEGF production (226). NO and reactive oxygen species (ROs) induce COX-2 mRNA expression (227) via the beta catenin/TCF pathway leading to activation of the polyoma enhancer activator 3 (PEA3) transcription factor (228). Moreover, NO utilizes cAMP/PKA/CREB and JNK/Jun/ATF2 signalling cascades affecting COX-2 transcription (228).

Several pro-inflammatory cytokines such as IL-1 or IFN- γ induce COX-2 expression. The major signalling pathway involved is a cAMP- and PKA-dependent activation of CREB. It is of interest that among the MAPK pathways, p38MAPK appears to be involved while ERK1/2 appears not to participate (229). On the contrary, TNF- α -induced COX-2 expression depends heavily on activation of ERK1/2 and NF κ B. COX-2 expression is induced by several growth factors including IGF, TGF α and EGF. Growth factor-induced COX-2 expression takes place in both normal as well as cancer cells. The IGF-induced signals are mediated by PI3Kinase and Src/ERK but not by p38MAPK while the effect of TGF and EGF is mediated by p38MAPK, ERK1/2 and PI3K (230). UVB induces COX-2 mRNA expression in cancer cells. UVB activates the transcription factors CREB and ATF1 via a cAMP-dependent pathway. Induction of p38MAPK and PI3K but not NF κ B appears to be essential for UVB-induced COX-2 expression (231). Fine-tuning of COX-2 expression levels can occur by extracellular signals such as G-protein coupled receptor (GPCR) binding proteins. The stress neuropeptides corticotropin releasing factor (CRF) and urocortins augment LPS-induced COX-2 expression via cAMP/PKA/CREB activation (232). Accumulation in the cytoplasm of this sphingosine-based lipid-signalling molecule appears to regulate COX-2 expression resulting in inflammation and tumorigenesis. It has been also implicated in the aging process. More specifically, it has been shown that ceramide is the mediator of TNF- α -induced COX-2 expression in fibroblasts and of cannabinoid-induced COX-2 expression in neuroglioma cells (233). It should be noted that

the induction of COX-2 expression by ceramide involves NF κ B but not AP1 or CREB (234). Glycogen synthase kinase 3 (GSK3) phosphorylates/inactivates β -catenin leading to inhibition of the transcription factor TCF4 which regulates COX-2 transcription. Moreover, GSK3 acts through PKC δ to inactivate ERK1/2 and suppress COX-2 expression (235). Another negative regulator of COX-2 expression is the glucocorticoids. Indeed, they may represent the most important negative regulator of COX-2 transcription. They achieve this effect via inhibition of NF κ B. Protein levels of COX-2 are also regulated at a post-transcriptional level via modulation of the stability of its mRNA. COX-2 mRNA contains an ARE element at the 3' end responsible for its stability. HuR binds on COX-2 ARE increasing its half life (236). Signals from cytokines such as IL-1 β , TNF- α or TLR ligands affect COX-2 mRNA stability. The major signalling molecule mediating this process appears to be the p38MAPK. Hypoxia represents another regulator of COX-2 mRNA; it increases its stability most likely via induction of TNF- α . As mentioned above, COX-2 activity is directly regulated by NO. A recent report introduced an additional step in the regulation of COX-2 action; iNOs directly binds to COX-2 and s-nitrosylates it, thus enhancing its enzymatic activity (237) (**Fig. 12**).

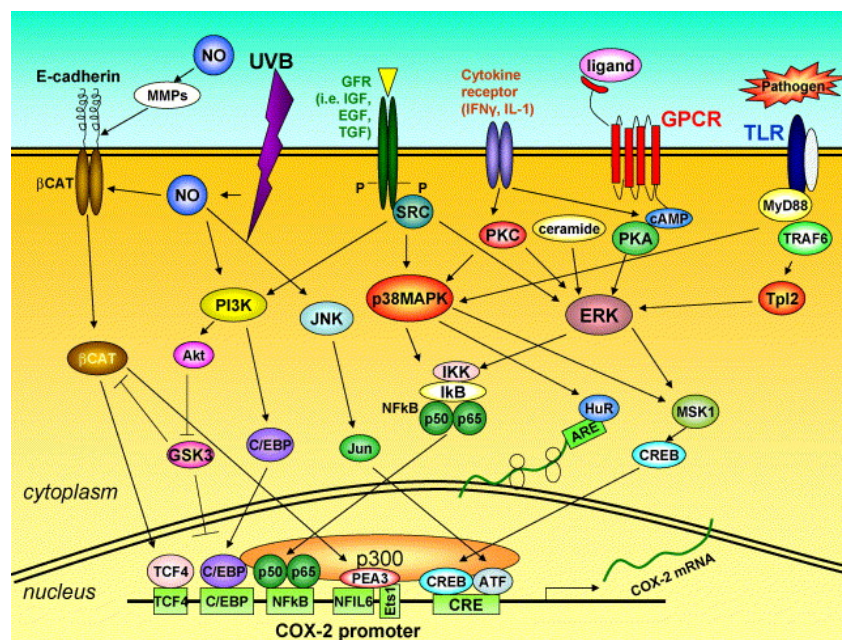


Figure 12. Signalling pathways involved in the regulation of COX-2 expression.

5.2 The cyclooxygenase-2 in diseases and cancer

COX-2 is known to be over-expressed in the synovia of patients with rheumatoid arthritis, osteoarthritis and in the colonic epithelium in ulcerative colitis. Atherosclerosis is now considered a chronic inflammatory disease, a consequence of a pathological interaction between vascular endothelial and immune cells. COX-2 is upregulated in stimulated macrophages during exposure to high levels of oxLDL and in oxLDL-induced foam cell formation (238). Selective inhibition of COX-2 expression reduces early atherogenesis in LDLR (-/-) and APO-E (-/-) mice (239). These studies suggest that COX-2 in macrophages promotes early atherosclerotic lesions through the monocyte chemotactic protein-1 (MCP1) which affects recruitment of monocytes. MCP1 is a member of the small inducible gene (SIG) family and plays a crucial role in the recruitment of monocytes to sites of injury and infection. Interestingly, lack of TLR4 reduces atherosclerosis in APO-E (-/-) mice and is associated to reduced COX-2 and MCP-1 expression in these lesions (240). COX-2 and PGE2 have been shown to promote the release and activation of MMP-2 and MMP-9 (241) which are implicated in macrophage migration and contribute to plaque rupture. Epidemiological studies suggest that anti-inflammatory drugs, especially NSAIDs, may reduce the risk for the development of Alzheimer's disease or at least delay its onset (242). It should be reminded here that the neuropathology of Alzheimer's disease is mainly characterized by deposits of amyloid beta peptides and neurofibrillary tangles as well as by a concomitant chronic inflammation which may be associated, at least in part, to the accumulation of these deposits. Thus, the beneficial effect of NSAIDs may be explained by their anti-inflammatory effects, since COX-2 expressing inflammatory cells are located around the amyloid-plaques.

Recent studies have also highlighted the relevance of COX-2 in human carcinogenesis. In fact, selective COX-2 inhibitors prevent tumorigenesis in experimental animals, and that these compounds induce apoptosis and inhibit growth in several types of cancer cells (243-246). Increased levels of COX-2 has been reported in carcinomas of the colon (247), stomach (248), esophagus (249), lung (250), liver (251), and pancreas (252). COX-2 is not

detected in normal human testes, but it is present in testicular biopsies of men with impaired spermatogenesis (253) or in testicular cancer (254).

There is increasing evidence that dysregulated expression of the COX-2 enzyme is an important pathophysiological step in breast cancer evolution, with numerous studies demonstrating increased levels of COX-2 mRNA and protein in mammary malignant tissue (255). In fact, expression of COX-2 is associated with poor prognostic features, and adverse clinical outcome (256). In human breast cancer, correlations are known to exist between COX-2 levels and expression of angiogenic factors such as vascular endothelial growth factor (257) and then development of distant metastases (258).

Moreover, it has been shown a correlation between COX-2 and aromatase expression (259). Furthermore, COX-2 inhibitors decrease aromatase mRNA and activity in breast cancer cells (260) and the use of combined COX-2 and aromatase inhibitor appear to be more effective than the single agents used alone in decreasing aromatase activity and consequently estradiol production (261).

COX-2 is considered to mediate its deleterious effects via PG synthesis. These molecules have extremely short half-lives, so direct correlation between COX-2 activity and PG presence is difficult to demonstrate experimentally. It is clear, however, that PGs stimulate cell proliferation (262), induce mitogenesis of mammary epithelial cells (263), suppress proliferation of immune cells (264). PG production is also higher in lesions associated with the presence of cancer cells in tumor lymphatics, blood vessels, and axillary nodes, and levels are greater in sites of nodal metastases compared to primary tumor areas (265).

In particular, PGE₂ has been observed in high levels in breast tumor cells and is synthesized by several human breast cancer cell lines (266).

PGE₂ has been found to be the most potent factor stimulating aromatase expression via promoter II (267). A correlation between COX-2 and CYP19 mRNA levels has been demonstrated in human breast cancer specimens using semi-quantitative RT-PCR (259). Furthermore, it was demonstrated that PGE₂ is produced by breast tumors stimulating local estrogen biosynthesis in the surrounding adipose tissue (268;269). Local estrogen production by breast tumors is considered to be an important mechanism by which tumors

develop, evolve, and possible metastasize (268). PGs, produced through COX, exert their actions binding to specific transmembrane G-protein coupled receptors termed Prostanoid (P) receptors, present as different splice variants (270) Specifically, PGE₂ receptors, EP₁ (271), EP₂ (272), EP₃ (273) and EP₄ (274), are transduced through modulation of the activity of either adenylyl cyclase or inositol phospholipid hydrolysis and calcium mobilization (270;275). In particular, EP₁ activates PKC, EP₂ and EP₄ are coupled to PKA, EP₃ can either couple negatively to adenylyl cyclase through binding a G_i protein or associate to inositol phospholipid hydrolysis and calcium mobilization. Importantly, PGE₂ was shown to increase aromatase expression, while on the contrary EP₁ and EP₂ selective antagonists decreased the enzyme activity (276), suggesting that both PKA and PKC pathways are required for activation of promoter PII and aromatase optimal expression.

Specific aim

Several studies on both humans and rodents indicate that prenatal or postnatal exposure to estrogens might have a central role in the mechanism leading to male reproductive tract malformations as well as testicular tumors (1;2). While the effects of estrogen on mammary gland tumorigenesis is well known, the role of aromatase overexpression and *in situ* estrogen production in testicular tumorigenesis is not clearly defined.

In this study we have investigated the molecular mechanisms causing aromatase overexpression and the effect of estradiol (E2) overproduction on Leydig cell tumor proliferation. Our hypothesis is that constitutive E2 production stimulates Leydig tumor cell proliferation acting on cell cycle regulators. Moreover, among several potential factors inducing aromatase, we investigated the role of IGF-I, produced locally in the testis, and of COX-2 overexpressed in other estrogen-dependent tumors.

We believe that an enhanced IGF-I production is responsible for the activation of signalling pathways determining an excess in SF-1 synthesis. This transcription factor, together with CREB, is the most important regulator of aromatase expression. On the other hand, we hypothesize an involvement of COX-2 in the molecular mechanism determining the constitutive activation of CREB in Leydigoma.

Materials and Methods

Cell cultures and animals

TM3 cells (immature mouse Leydig cell line) were cultured in DMEM/F-12 medium supplemented with 5% horse serum (HS), 2.5% fetal bovine serum (FBS) and antibiotics (Invitrogen, S.R.L., San Giuliano Milanese, Italy); R2C cells (rat Leydig tumor cell line) were cultured in Ham/F-10 medium supplemented with 15% HS, 2.5% FBS and antibiotics (Invitrogen, S.R.L., San Giuliano Milanese, Italy). Male Fischer 344 rats (a generous gift of Sigma-Tau Pomezia, Italy), 6 (FRN) and 24 (FRT) months of age, were used for studies. Twenty-four-month-old animals presented spontaneously developed Leydig cell tumors, which were absent in younger animals. Testes of all animals were surgically removed by qualified, specialized animal care staff in accordance with the Guide for Care and Use of Laboratory Animals (National Institutes of Health) and used for experiments.

Aromatase activity assay

The aromatase activity in subconfluent R2C cell culture medium was measured by tritiated water-release assay using 0.5 μM [1β - $^3\text{H}(\text{N})$]androst-4-ene-3,17-dione (DuPont NEN, Boston, MA, USA) as a substrate (277). Incubations were performed at 37 °C for 2 h under a 95%:5% air/CO₂ atmosphere. Obtained results were expressed as picomoles (pmol/h) and normalized to milligrams of protein (pmol/h/mg protein). The protein content was determined by Bradford method (278).

Radioimmunoassay (RIA)

Before the experiments, TM3 cells were maintained overnight in DMEM/F-12 and R2C cells in Ham/F-10 (medium only). The estradiol content of medium recovered from each well was determined against standards prepared in low-serum medium using a RIA kit (DSL 43100; Diagnostic System Laboratories, Webster, TX, USA). Results of the assay were normalized to the cellular protein content per well and expressed as picomoles per

milligram of cell protein. To measure IGF-I concentration in testicular extracts, testes were weighed, homogenated in 500 μ L of 0.05 mol/L Tris/HCl (pH 7.6) plus protease inhibitors, and then submitted to ultrasonication followed by centrifugation, as previously published (279). IGF-I content in testicular extracts and in medium recovered from each well of R2C and TM3 cells was determined following extraction and assay protocols provided with the mouse/rat IGF-I RIA kit (DSL 2900; Diagnostic System Laboratories, Webster, TX, USA).

Chromatin immunoprecipitation (ChIP)

This assay was done using the chromatin immunoprecipitation assay kit from Upstate (Upstate Technology, Lake Placid, NY) with minor modifications in the protocol. R2C cells were grown in 100-mm plates. Confluent cultures (90%) were treated for 24 h with AG1024 (Sigma, St Louis, MO, USA), PD98059 (Calbiochem, VWR International S.R.L. Milano), LY294002 (Calbiochem, VWR International S.R.L. Milano), GF109203X (Calbiochem, VWR International S.R.L. Milano), NS398 (Sigma St Louis, MO, USA), H89 (Sigma St Louis, MO, USA) or for increasing times with 100 ng/mL IGF-I (Sigma St Louis, MO, USA), or left untreated. Following treatment, DNA/protein complexes were cross-linked with 1% formaldehyde at 37°C for 10 min. Next, cells were collected and resuspended in 400 μ L of SDS lysis buffer (Upstate Technology, Lake Placid, NY) and left on ice for 10 min. Then, cells were sonicated four times for 10 s at 30% of maximal power and collected by centrifugation at 4°C for 10 min at 14,000 rpm. Ten microliters of the supernatants were kept as input (starting material, to normalize results) whereas 100 μ L were diluted 1:10 in 900 μ L of chromatin immunoprecipitation dilution buffer (Upstate Technology, Lake Placid, NY) and immunocleared with 80 μ L of sonicated salmon sperm DNA/protein A agarose (Upstate Technology, Lake Placid, NY) for 6 h at 4°C. Immunocomplex was formed using 1 μ L of 1:5 dilution of specific anti-SF-1 antibody (provided by Prof. Ken-ichirou Morohashi, Division for Sex Differentiation, National Institute for Basic Biology, National Institutes of Natural Sciences, Myodaiji-cho, Okazaki,

Japan) or using 2 μ l of specific antibody anti-CREB or anti-pCREB (Cell Signaling, Celbio, Milano, Italy) overnight at 4°C. Immunoprecipitation with salmon sperm DNA/protein A agarose was continued at 4°C until the following day. DNA/protein complexes were reverse cross-linked overnight at 65°C. Extracted DNA was resuspended in 20 μ L of Tris-EDTA buffer. In order to examine the binding of SF-1 and CREB, 3 μ l volume of each sample and input were used for PCR using CYP19 promoter II specific primers: forward, 5'-TCAAGGGTAGGAATTGGGAC-3'; reverse, 5'-GGTGCTGGAATGGACAGATG-3'. PCR reactions were performed in the iCycler iQ Detection System (BioRad Hercules, CA, USA), using 0.1 μ M of each primer, in a total volume of 50 μ L reaction mixture following the manufacturer's recommendations. SYBR Green Universal PCR Master Mix (BioRad Hercules, CA, USA) with the dissociation protocol was used for gene amplification, negative controls contained water instead of DNA. Final results were calculated using the $\Delta\Delta$ Ct method as explained above, using input Ct values instead of the 18S, calibrator was basal (untreated) sample. Amplification products were analyzed on a 1% agarose gel and visualized by ethidium bromide staining. In control samples, nonimmune rabbit immunoglobulin G was used instead of specific antibodies.

Real-time reverse transcription-PCR

Before the experiments, cells were maintained overnight in low-serum medium. Cells were then treated for the indicated times and RNA was extracted from cells using the TRizol RNA isolation system (Invitrogen, S.R.L., San Giuliano Milanese, Italy). TRizol was also used to homogenize total tissue of normal (FRNT) and tumor (FRTT) Fisher rat testes for RNA extraction. Each RNA sample was treated with DNase I (Ambion, Austin, TX), and purity and integrity of the RNA were confirmed spectroscopically and by gel electrophoresis before use. One microgram of total RNA was reverse transcribed in a final volume of 30 μ L using the ImProm-II Reverse transcription system kit (Promega, Promega Italia S.R.L. Milano, Italy); cDNA was diluted 1:3 in nuclease-free water, aliquoted, and

stored at 20°C. Primers for the amplification were based on published sequences for the rat CYP19, rat CREB, and rat SF-1 genes. The nucleotide sequences of the primers for CYP19 were forward, 5'-GAGAACTGGAAGACTGTATGGAT-3', and reverse, 5'-ACTGATTCACGTTCTCCTTTGTCA-3'. For CREB amplification, we used the following primers: forward, 5'-AATATGCACAGACCACTGATGGA-3', and reverse, 5'-TGCTGTGCGAATCTGGTATGTT-3'; for SF-1 amplification, primers have been previously published (42). PCR reactions were done in the iCycler iQ Detection System (BioRad Hercules, CA, USA) using 0.1 µmol/L of each primer, in a total volume of 30 µL reaction mixture following the manufacturer's recommendations. SYBR Green Universal PCR Master Mix (BioRad Hercules, CA, USA) with the dissociation protocol was used for gene amplification; negative controls contained water instead of firststrand cDNA. Each sample was normalized on the basis of its 18S rRNA content. The 18S quantification was done using a TaqMan rRNA Reagent kit (Applied Biosystems, Monza, Milano, Italy) following the method provided in the TaqMan rRNA Control Reagent kit (Applied Biosystems, Monza, Milano, Italy). The relative gene expression levels were normalized to a calibrator that was chosen to be the basal, untreated sample. Final results were expressed as n-fold differences in gene expression relative to 18S rRNA and calibrator, calculated using the $\Delta\Delta C_t$ method, as follows:

$$n\text{-fold} = 2^{-(\Delta C_{t\text{sample}} - \Delta C_{t\text{calibrator}})}$$

where ΔC_t values of the sample and calibrator were determined by subtracting the average C_t value of the 18S rRNA reference gene from the average C_t value of the different genes analyzed.

Western blot analysis

R2C and TM3 cells or total tissue of FRNT and FRTT were lysed in ice-cold radioimmunoprecipitation assay (Ripa) buffer containing protease inhibitors (20 mmol/L Tris, 150 mmol/L NaCl, 1% Igepal, 0.5% sodium deoxycholate, 1 mmol/L EDTA, 0.1% sodium dodecyl sulphate (SDS), 1 mmol/L phenylmethylsulfonyl fluoride (PMSF), 0.15 units/ml aprotinin and 10 μ mol/L leupeptin) for protein extraction. The protein content was determined by Bradford method (278). The proteins were separated on 11% SDS/polyacrylamide gel and then electroblotted onto a nitrocellulose membrane. Blots were incubated overnight at 4 °C with: 1. anti-human P450 aromatase antibody (1:50) (Serotec, Oxford, UK, MCA 2077), 2. anti-ER α (F-10) antibody (1:500) (Santa Cruz Biotechnology, Santa Cruz, CA, USA, sc8002), 3. anti-ER β (H-150) (1:1000) (Santa Cruz Biotechnology, Santa Cruz, CA, USA, sc8974), 4. anti-cyclin D1 (M-20) antibody (1:1000) (Santa Cruz Biotechnology, Santa Cruz, CA, USA, sc718), 5. anti-cyclin E (M-20) antibody (1:1000) (Santa Cruz Biotechnology, Santa Cruz, CA, USA, sc481), 6. anti-CREB antibodies (1:1000) (Cell Signaling Technology, Celbio, Milan, Italy, 48H2) and (1:1000) (Biosource Inc. Camarillo CA USA, AHO0842); 7. anti-pCREB ser133 (1:1000) (Cell Signaling Technology, Celbio, Milan, Italy, 87G3) or anti-pCREB Ser129/133 (1:1000) (Biosource Inc. Camarillo CA USA, 44-297G), 8. anti SF-1 (1:1000) provided by Prof. Ken-ichirou Morohashi, Division for Sex Differentiation, National Institute for Basic Biology, National Institutes of Natural Sciences, Myodaiji-cho, Okazaki, Japan), 9. anti-pSF-1 (1:1000) provided by Dr Holly A. Ingraham Department of Physiology, University of California, San Francisco, San Francisco, California 94143-0444, USA), 10. anti-IGF-I receptor (IGF-IR; 1:800; Santa Cruz Biotechnology Santa Cruz, CA, USA, sc713; 11. anti COX-2 (1:1000) (Cell Signaling Technology, Celbio, Milan, Italy, 4842), 12. anti-actin (C-2) antibody (1:1000) (Santa Cruz Biotechnology, Santa Cruz, CA, USA, sc8432), 13. anti GAPDH (FL-335) (1:3000) (Santa Cruz Biotechnology, Santa Cruz, CA, USA, sc25778). Membranes were incubated with horseradish peroxidase (HRP)-conjugated secondary antibodies (Amersham Pharmacia Biotech, Piscataway, NJ) and

immunoreactive bands were visualized with the ECL western blotting detection system (Amersham Biosciences, Cologno Monzese, Italy). To assure equal loading of proteins membranes were stripped and incubated overnight with β -actin or GAPDH antiserum.

Immunohistochemical analysis

Tumor human testicular tissues were retrieved from biopsy of two male patients with Leydig cell tumour (ages 31 and 33 years). Control human testicular tissues were retrieved from biopsy of two male patients (ages 29 and 35 years) showing testes with a Sarcoidosis-like granulomatous lesion. The archival human cases were provided by the Pathologic Anatomy Unit (Annunziata, Hospital) Italy.

Immunohistochemical experiments were performed on formalin-fixed and paraffin-embedded testis tissues after heat-mediated antigen retrieval (280). Paraffin embedded sections, 5 μ m thick, were mounted on slides precoated with poly-lysine, and then they were deparafinized and dehydrated (7-8 serial sections). Hydrogen peroxide (3% in distillate water) was used, for 30 minutes, to inhibit endogenous peroxidase activity while normal horse serum (10%) was utilised, for 30 minutes, to block the non-specific binding sites.

Immunodetection was carried out using anti-COX2 (1:50), primary antibodies at 4°C overnight. Then, a biotinylated horse universal IgG was applied (1:600) for 1 hour at RT, followed by the avidin-biotin-horseradish peroxidase complex (ABC/HRP) (Vector, Laboratories, CA, USA). Immunoreactivity was visualized by using the diaminobenzidine chromogen (DAB)(Zymed Laboratories, CA, USA). Sections were also counterstained with haematoxylin. The primary antibody was replaced by normal rabbit serum in negative control sections. Absorption controls have utilised primary antibodies preabsorbed with an excess (5nmol/ml) of the purified respective blocking peptides at 4°C for 48 hours (data not show).

Cell proliferation assay

For proliferative analysis a total of 1×10^5 cells were seeded onto 12-well plates in complete medium and let grow for 2 days. Prior to experiments, cells were maintained for 24h in Ham/F-10 medium and the day after treated with ICI 182780 (Astra-Zeneca, Basiglio, Milano, Italy), 4-hydroxytamoxifen (OHT) (Sigma St Louis, MO, USA), Letrozole (Novartis Pharma AG, Basel, Switzerland), NS398 (Sigma, St Louis, MO, USA), H89 (Sigma, St Louis, MO, USA), AH 23848 (Sigma, St Louis, MO, USA), 17β -estradiol (E2) (Sigma St Louis, MO, USA), or treated at the indicated times with IGF-I or PGE2 (Sigma, St Louis, MO, USA), alone or in combination with inhibitors or incubated with an anti IGF-I antibody (Santa Cruz Biotechnology, Santa Cruz, CA, USA, sc1422). Control (basal) cells were treated with the same amount of vehicle alone (DMSO) that never exceeded the concentration of 0.01% (v/v). [^3H]Thymidine incorporation was evaluated after 6 h incubation with 1 μCi [^3H]thymidine (PerkinElmer Life Sciences, Boston, MA, USA) per well. Cells were washed once with 10% trichloroacetic acid (TCA) (Sigma, St Louis, MO, USA), twice with 5% trichloroacetic acid and lysed in 1 ml 0.1 mol/L NaOH at 37°C for 30 min. The total suspension was added to 10 ml optifluor fluid and was counted in a scintillation counter.

Non-radioactive in vitro assay for PKA activity in cell lysates

This assay was performed using the PepTag for non-radioactive detection of cAMP-dependent protein kinase assay kit from Promega (Madison, WI). R2C cells were grown in 100X60mm plates to 100% confluence. After stimulation (4h) cells were washed with phosphate-buffered saline (PBS) (5ml per 100 mm dish) and lysed in cold PKA extraction buffer (0.5 ml/plate) containing 25 mmol/L Tris-HCl pH 7.5, 0,5 mmol/L EDTA, 0,5mol/L EGTA, 10mmol/L beta-mercaptoethanol, 1ug/ml leupeptin, 1ug/ml aprotinin. The lysates were cleared by centrifugation at $14,000 \times g$, 5 min and 5 ul of cleared lysates were subjected to a kinase reaction with the fluorescence-labeled PKA substrate, kemptide,

following the manufacturer's protocol. The reaction was stopped by boiling the samples for 10 min. The samples were separated on 0,8% agarose gel by electrophoresis at 100V for 15 minutes. Phosphorylated peptide migrated toward the anode (+), while non-phosphorylated peptide migrated toward the cathode (-). The gel was photographed on a transilluminator. The quantitative differences in the amount of phosphorylated and non-phosphorylated peptide species were detected by spectrophotometric method reading the absorbance at 570 nM.

RNA interference

COX-2 Sthealth® siRNA and scrambled siRNA were purchased from Invitrogen (Invitrogen, S.R.L., San Giuliano Milanese, Italy). Twenty-four hours after plating cells into 60 mm dishes at 4×10^6 cells, siRNAs were transfected to a final concentration of 50, 100 or 200 nM using Lipofectamine2000 Transfection Reagent (Invitrogen, S.R.L., San Giuliano Milanese, Italy) according to manufacturer's instructions. Two days after transfection cells were used for western analysis or cell proliferation assay.

Data Analysis and Statistical Methods

Pooled results from triplicate experiments were analyzed using one-way ANOVA with Student-Newman-Keuls multiple comparison methods, using SigmaStat version 3.0 (SPSS, Chicago, IL).

Results

Estradiol induces Leydig cell tumor proliferation through an autocrine mechanism

We performed our study utilizing as model system R2C Leydig tumor cells. These cells have been demonstrated to have high aromatase expression and, consequently, activity (40), while we used another Leydig cell line, TM3 cells, as a normal control. We also analyzed testes from older and younger Fischer rats. Aged animals have a high incidence of spontaneous neoplasm of Leydig cells (281;282), a phenomenon not observed in younger animals, allowing us to use them as a good *in vivo* model to confirm results obtained in cell lines. Our first step was to measure estradiol (E2) content in culture medium of R2C and TM3 cells maintained in culture for increasing time. While E2 levels in TM3 medium were extremely low (data not shown) in R2C cells E2 levels after 24 h were 0.5 pmol/mg protein and increased by 7-fold at 96 h (Fig. 1A).

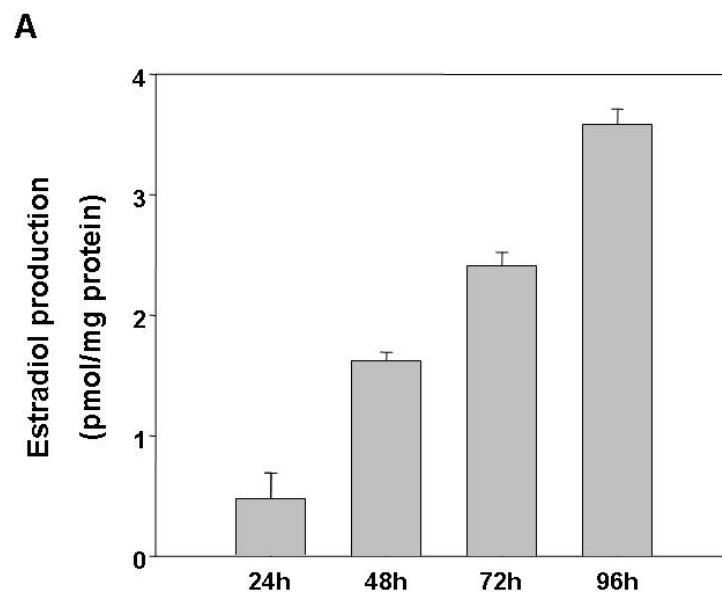


Figure 1 A. E2 production in R2C cells. R2C cells were cultured for the indicated times in serum free medium. E2 content was determined by RIA and normalized to the cell culture well protein content. Data represent the mean \pm SEM of values from three separate cell culture wells expressed as pmol/mg protein.

This production was dependent on high constitutive active aromatase activity, since the presence of aromatase inhibitor Letrozole was able to decrease E2 production at all time points tested (Fig. 1B). E2 levels after 24 h treatment with Letrozole were still detectable, but were completely knock down when we removed the medium after 24 h and renewing the treatment for an additional 24 h. The same effect was maintained for the other two time points investigated (Fig. 1B).

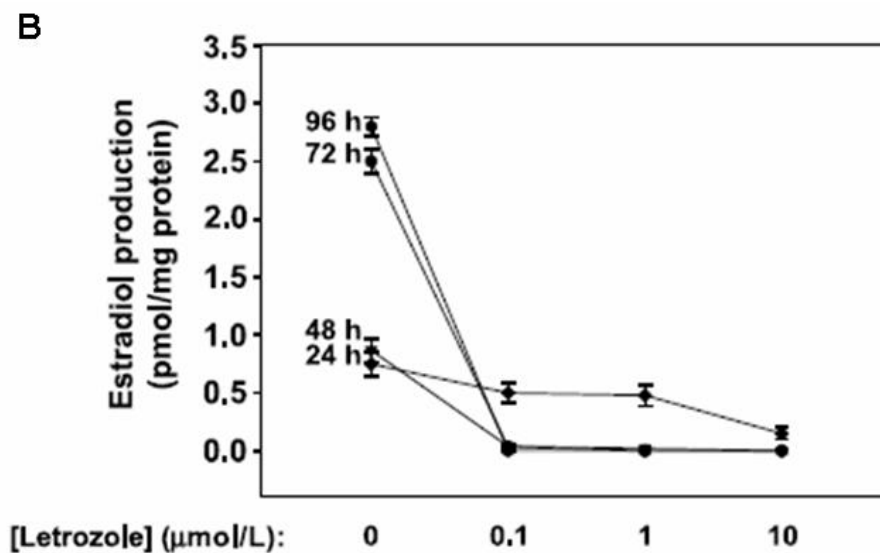


Figure 1 B. E2 production in R2C cells. R2C cells were treated for the indicated times in HAM-F10 in the absence (0) or presence of aromatase inhibitor letrozole (0.1, 1, 10 $\mu\text{mol/L}$). Every 24h, before renewing treatment, cell culture medium was removed and analyzed for steroid content. E2 content was determined by RIA and normalized to the cell culture well protein content. Data represent the mean \pm SEM of values from three separate cell culture wells expressed as pmol/mg protein.

Once estradiol is produced it can exert its actions binding to specific receptors, the estrogen receptors α e β (ER α and ER β). Analysis of the two receptor protein isoforms in our models demonstrated that tumor Leydig cells express both isoform of ERs (Fig. 2). Particularly the α isoform seems to be more expressed in R2C cells respect to TM3 and in FRTT respect to the its control FRNT where ER β is more expressed. Moreover aromatase protein content is extremely high in tumoral samples(139) (Fig. 2).

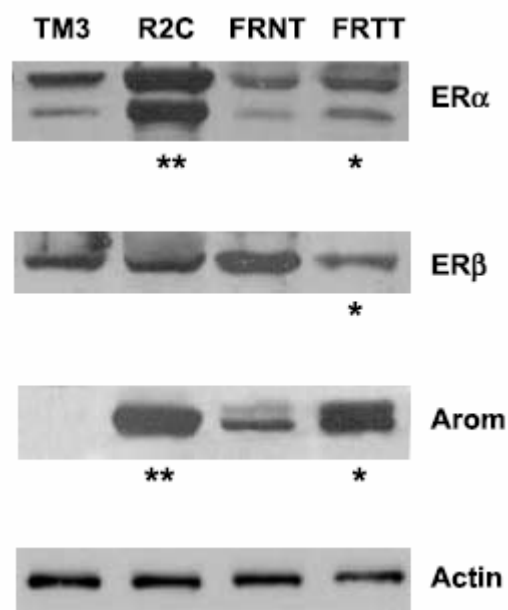


Figure 2. Expression of estrogen receptors (ER) and aromatase in R2C cells. ER α , ER β and aromatase western blot analysis was performed on 50 μ g of total proteins extracted from TM3 and R2C cells or from total tissue of normal (FRNT) and tumor (FRTT) Fisher rat testes. Results are representative of three independent experiments. β -Actin was used as a loading control. Protein expression in each lane was normalized to the β -actin content and expressed as fold over control represented by normal cells. Normalized absorbances were subjected to statistical analysis; statistically significant differences are indicated (*, $P < 0.05$; **, $P < 0.01$, compared with control).

Our next experiments demonstrated that estrogen receptors are required for proliferation through a short autocrine loop maintained by endogenous E2 production in Leydig tumor cells.

For instance, the use of both antiestrogens hydroxytamoxifen (OHT) and ICI 182,760 (ICI) and the use of aromatase inhibitor Letrozole (Letr) determined a dose-dependent inhibition of cell proliferation (Fig. 3A). Among the different doses tested the highest dose of OHT (10 $\mu\text{mol/L}$) was able to inhibit cell proliferation by 90%, ICI (10 $\mu\text{mol/L}$) by 86% and letrozole (10 $\mu\text{mol/L}$) by 70%.

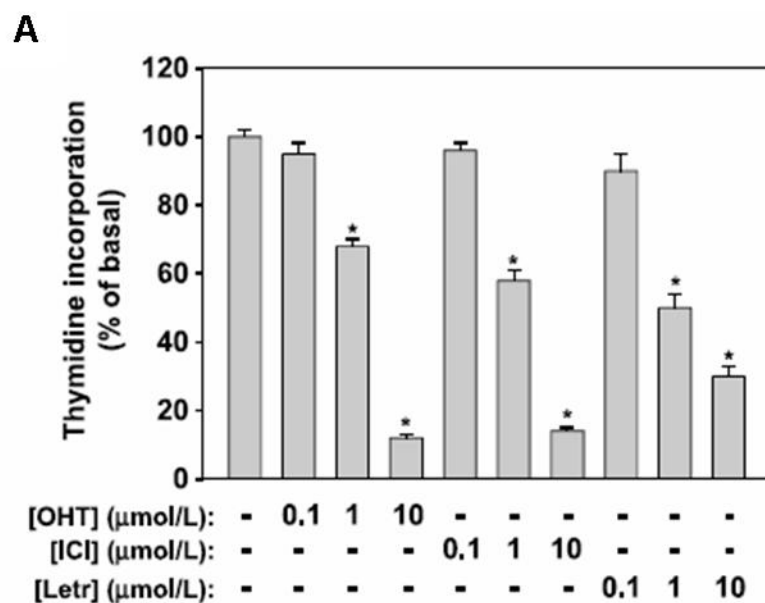


Figure 3 A. Effects of antiestrogens, aromatase inhibitor Letrozole and estradiol on R2C cell proliferation. Cells were treated for 96h in HAM-F10 in the absence (-) or presence of antiestrogens hydroxytamoxifen (OHT) or ICI 182,760 (ICI) or aromatase inhibitor letrozole (Letr) at the indicated concentrations. Proliferation was evaluated by [^3H] Thymidine incorporation analysis. Values expressed as percent of untreated (basal) cells (100%) represent the mean \pm SEM of three independent experiments each performed in triplicate. (* $P < 0.05$ compared with basal condition).

In the same vein, starving cells for prolonged time and changing the medium every day in order to remove local E2 production, we found that addition of 1, 10 and 100 nmol/L E2 stimulated Leydig tumor cell proliferation (Fig. 3B), and partially abrogated the inhibition induced by Letrozole (Fig. 3C).

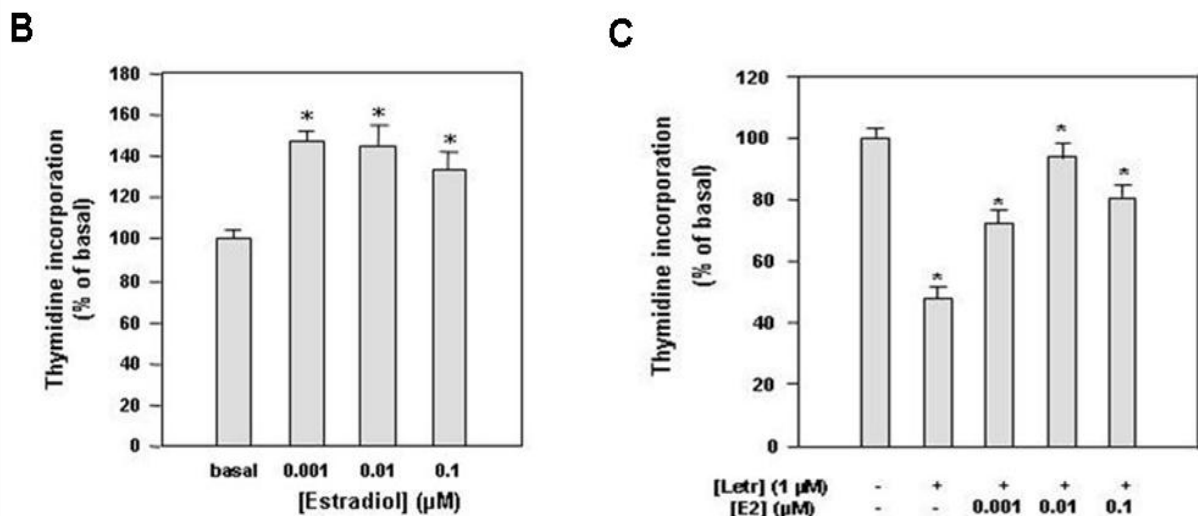


Figure 3 B, C. Effects of antiestrogens, aromatase inhibitor Letrozole and estradiol on R2C cell proliferation. (B) Cells were cultured for 48h in serum-free HAM-F10, every 24 h cell culture medium was removed and renewed. Cells were then treated for 24 h with estradiol at the indicated concentrations. (C) Cells were cultured for 24h in serum-free HAM-F10, cells were then treated for 48 h with letrozole (1μmol/L) changing the culture medium and renewing treatment every 24h. For additional 24h cells were treated with letrozole (Letr) (1μmol/L) in combination with estradiol (E2) at the indicated concentrations. Proliferation was evaluated by [3H] Thymidine incorporation analysis. Values expressed as percent of untreated (basal) cells (100%) represent the mean ± SEM of three independent experiments each performed in triplicate. (*P< 0.05 compared with basal condition).

The stimulatory effect of E2 was concomitant with the increased levels of cell cycle regulator cyclin D1 and E, whose expression was inhibited by pure antiestrogen ICI 182,760 (Fig. 4). All these results address how the classic E2/ER α signalling may control Leydig cell tumor growth and proliferation similarly to what observed in other estrogen-dependent tumors.

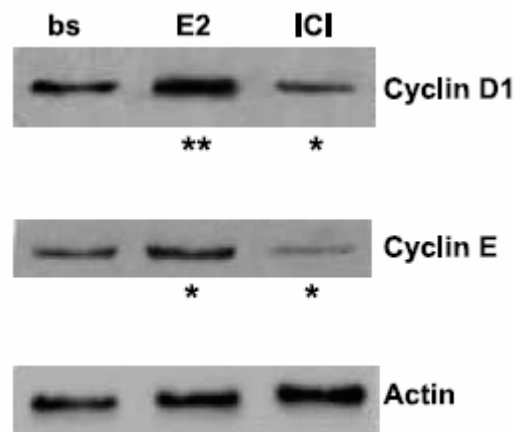


Figure 4. Effects of E2 and ICI 182,760 on cyclin D1 and E protein levels. R2C cells were cultured for 48h in serum-free HAM-F10, every 24 h cell culture medium was removed and renewed. Cells were then treated for 24 h in the absence (bs) or in the presence with estradiol (E2) (1 nmol/L) and ICI 182,760 (ICI) (1 μ mol/L) before extracting total proteins. Western blot analysis of Cyclin D1 and Cyclin E was performed on 50 μ g of total proteins extracted from R2C cells. Blots are representative of three independent experiments with similar results. β -Actin was used as a loading control. Protein expression in each lane was normalized to the β -actin content and expressed as fold over control represented by basal condition. Normalized absorbances were subjected to statistical analysis; statistically significant differences are indicated (*, $P < 0.05$; **, $P < 0.01$, compared with basal condition).

Aromatase overexpression is determined by constitutive activation of transcription factors SF-1 and CREB

Aromatase gene transcription in rat Leydig cells is driven by the PII promoter, which is principally regulated through three CRE-like sites and one NRE site binding SF-1 and LRH-1 (40;42). Constitutive active levels of CREB have been previously demonstrated in R2C cells (283).

Here we confirmed these data and demonstrated high phosphorylated status of CREB together with enhanced phosphorylation of SF-1 in FRTT (Fig. 5). Furthermore we demonstrated the presence of high expression levels of SF-1 with the protein present in a phosphorylated status in R2C but not in TM3.

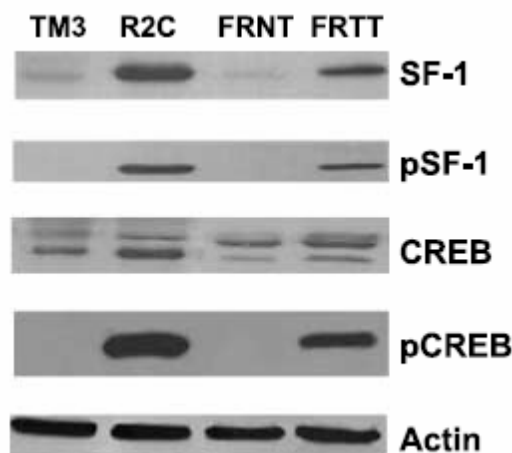


Figure 5. Expression of total and phosphorylated forms of SF-1 and CREB. Western blot analyses of SF-1, pSF-1, CREB, and pCREB were done on 50 μ g of total proteins extracted from TM3 and R2C cells or from total tissue of normal (FRNT) and tumor (FRTT) Fisher rat testes. Blots are representative of three independent experiments with similar results. β -actin was used as loading control.

IGF-I is produced by R2C cells and induces aromatase expression through PI3K- and PKC- mediated activation of SF-1

Starting from previous findings showing the ability of IGF-I to activate SF-1 and CREB, which leads to an increase in StAR transcription and then steroidogenesis (3;284), we investigated the role of this factor in regulating aromatase.

Determination of IGF-I content in TM3 and R2C culture medium by RIA revealed a significant difference in growth factor production, with R2C cells producing 4-fold higher IGF-I amounts (Fig. 6A). Moreover, we measured IGF-I content in testicular tissues, revealing a significant difference between FRTT and FRNT (Fig. 6B).

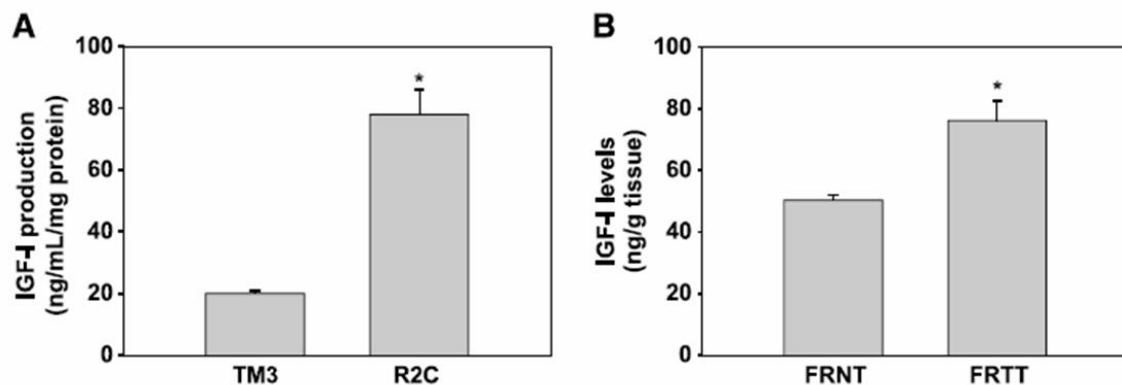


Figure 6 A, B. IGF-I production and autocrine effects in Leydig cells. (A) TM3 and R2C cells were cultured for 24 h in serum-free medium and IGF-I levels in culture medium were determined by RIA. IGF-I levels were normalized to the cell culture well protein content. *Columns*, mean of three independent experiments each done in triplicate; *bars*, SE. (B) Total protein extracts from FRNT and FRTT were assayed for IGF-I content. IGF-I levels were normalized to the tissue weight. *Columns*, mean of three independent samples; *bars*, SE. *, $P < 0.01$, compared with control conditions, represented by TM3 cells or FRNT.

IGF-I exerts its actions by binding to specific receptors (IGF-IR); however, we did not reveal differences in IGF-IR expression between TM3 and R2C cells (Fig. 6C). Upon binding to its receptor, IGF-IR, IGF-I activates three major transductional pathways: Ras/Raf/MAPK, PI3K/AKT, PLC/PKC; to demonstrate involvement of IGF-I transductional pathways in modulating aromatase expression in Leydig cell tumors, we used specific inhibitors: of IGF-I receptor (IGF-IR) [AG1024 (AG)], of ERK1/2 [PD98059 (PD)], of PI3K [LY294002 (LY)] and of PKC [GF109203X (GFX)]. IGF-I receptor inhibitor (AG1024) was able to inhibit aromatase activity in R2C cells by 85%, LY294002 determined 65 % inhibition, PD98059 35 % and GF109203X 61% (Fig. 6D).

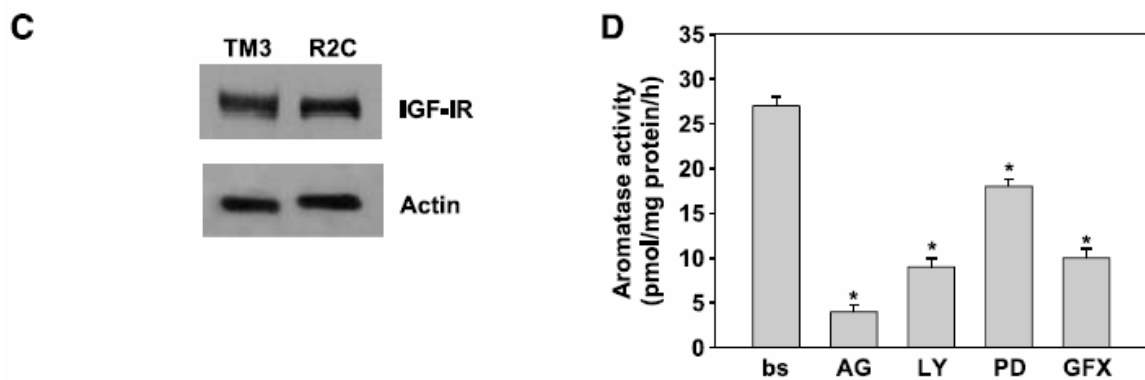


Figure 6 C, D. IGF-I production and autocrine effects in Leydig cells. (C) Western blot analysis of IGF-IR in TM3 and R2C cells. β -Actin was used as a loading control. (D) R2C cells were treated with AG1024 (AG; 20 μ mol/L), LY294002 (LY; 10 μ mol/L), PD98059 (PD; 20 μ mol/L), and GF109203X (GFX; 20 μ mol/L). Aromatase activity was assessed by using the modified tritiated water method. Results obtained are expressed as picomoles of [3 H]H $_2$ O released per hour and normalized to the well protein content (pmol/h/mg protein). *Columns*, mean of three independent experiments each done in triplicate; *bars*, SE. *, $P < 0.01$, compared with basal (bs).

The same inhibitory pattern was observed also on aromatase mRNA (Fig. 7A). Parallely all of the different inhibitors but not PD98059 were able to reduce SF-1 mRNA (Fig. 7 B), while CREB remained unchanged (Fig. 7C). For SF-1 inhibition was 75% with AG1024, 90 % with LY204002 and 80 % with GF109203X (Fig. 7B).

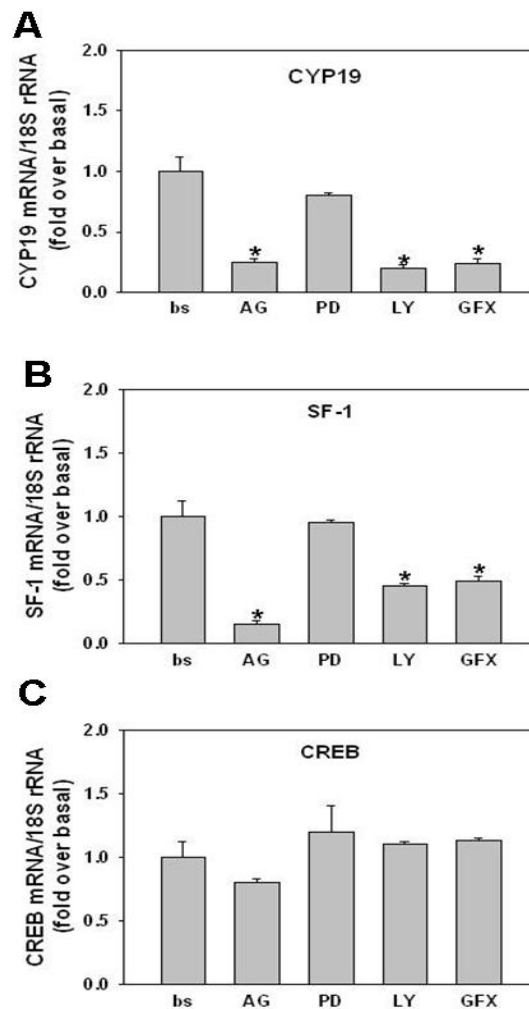


Figure 7. Effects of inhibitors of IGF-I pathways on mRNA expression of CYP19, SF-1 and CREB in R2C cells. Total RNA was extracted from R2C cells untreated (bs) or treated for 24h with AG1024 (AG) (20 μ mol/L), LY294002 (LY) (10 μ mol/L), PD98059 (PD) (20 μ mol/L) and GF109203X (GFX) (20 μ mol/L). Real time RT-PCR was used to analyze mRNA levels of CYP19, SF-1, and CREB. Data represent the mean \pm SEM of values from three separate RNA samples. Each sample was normalized to its 18S ribosomal RNA content. Final results are expressed as n-fold differences of gene expression relative to calibrator (bs) calculated with the $\Delta\Delta C_t$ method. * $P < 0.001$ compared to basal condition (bs).

Analysis of protein levels by western blot confirmed the data on mRNA (Fig. 8). Treatments with increasing doses of AG1024 (Fig. 8A), LY204002 (Fig. 8B) and GF109203X (Fig. 8D) but not PD98059 (Fig. 8C) were able to induce a dose-dependent inhibition of total and phosphorylated levels of SF-1, on the other hand CREB was not affected by the presence of any of the inhibitors (Fig. 8).

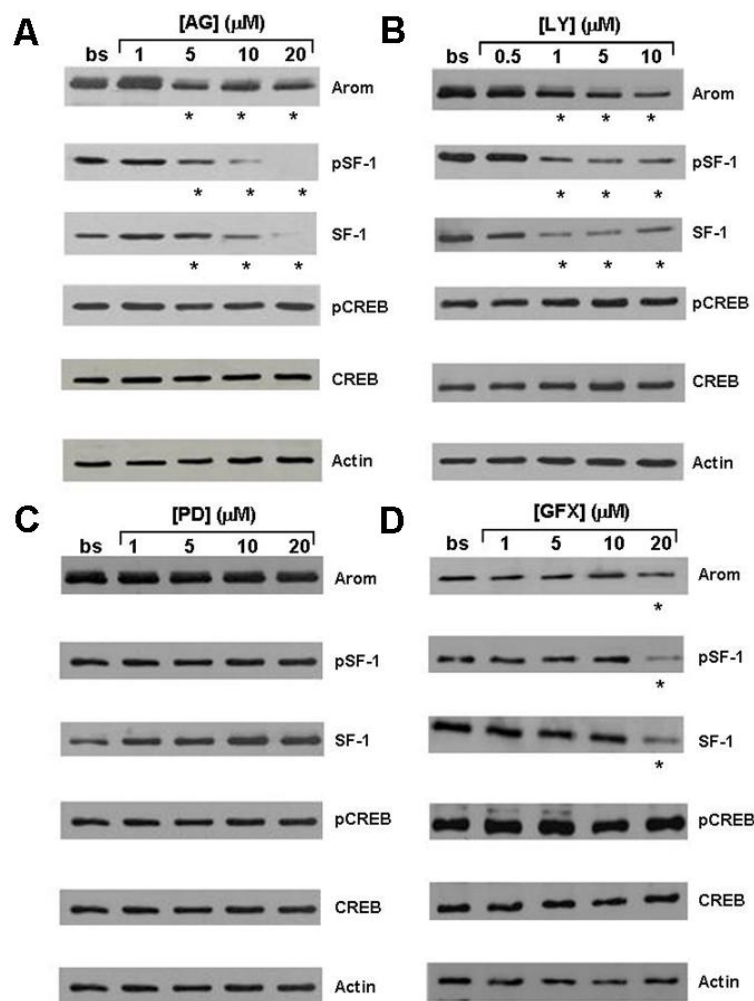


Figure 8. Effects of IGF-I pathway inhibitors on aromatase, SF-1 and CREB expression in R2C cells. A to D, Western blot analyses were done on 50 μg of total proteins extracted from R2C cells untreated (bs) or treated for 24 h with the indicated doses of AG1024 (AG) (A), LY294002 (LY) (B), PD98059 (PD) (C), and GF109203X (GFX) (D). Representative of three independent experiments with similar results. β-Actin was used as a loading control. Normalized absorbances were subjected to statistical analysis; statistically significant differences are indicated (*, P < 0.01, compared with basal).

IGF-I induces aromatase expression and activity in R2C cells

To further demonstrate the prevalent role of SF-1 in IGF-I induced aromatase expression in Leydig cell tumor, we monitored the effect of IGF-I on CYP19 and SF-1 expression. Addition of exogenous amounts of IGF-I were able to induce aromatase activity by 1.8-fold (Fig. 9).

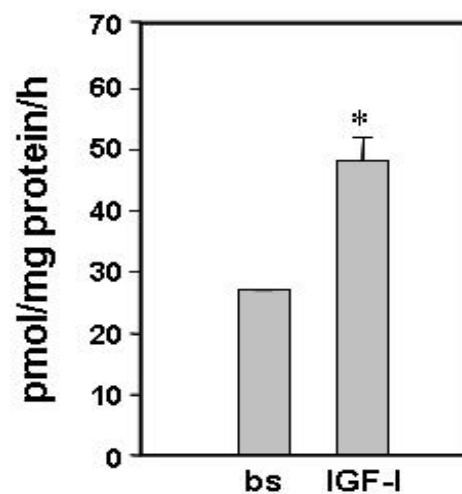


Figure 9. Aromatase activity in R2C cells in response to IGF-I. Cells were treated with IGF-I (100 ng/ml) for 24h. Aromatase activity was assessed by using the modified tritiated water method. Results obtained are expressed as pmoles of [³H]H₂O released per hour and are normalized to the well protein content (pmol/h/mg protein). Values represent the mean ± SEM of three independent experiments each performed with triplicate samples. *P<0.05 compared to basal (bs).

A significant effect of IGF-I treatment was seen also on CYP19 mRNA levels (Fig. 10A). IGF-I was able to induce a significant increase of 2- and 3.8-fold in aromatase mRNA at 12h and 24h, respectively (Fig. 10A). Aromatase protein levels under the same treatments reflected the mRNA data (Fig. 10B). Analysis of expression levels of total and phosphorylated forms of transcription factors SF-1 and CREB showed an increase in SF-1 and pSF-1 in the presence of IGF-I starting at 4 h, whereas no differences were observed for CREB at any of the investigated times (Fig. 10B).

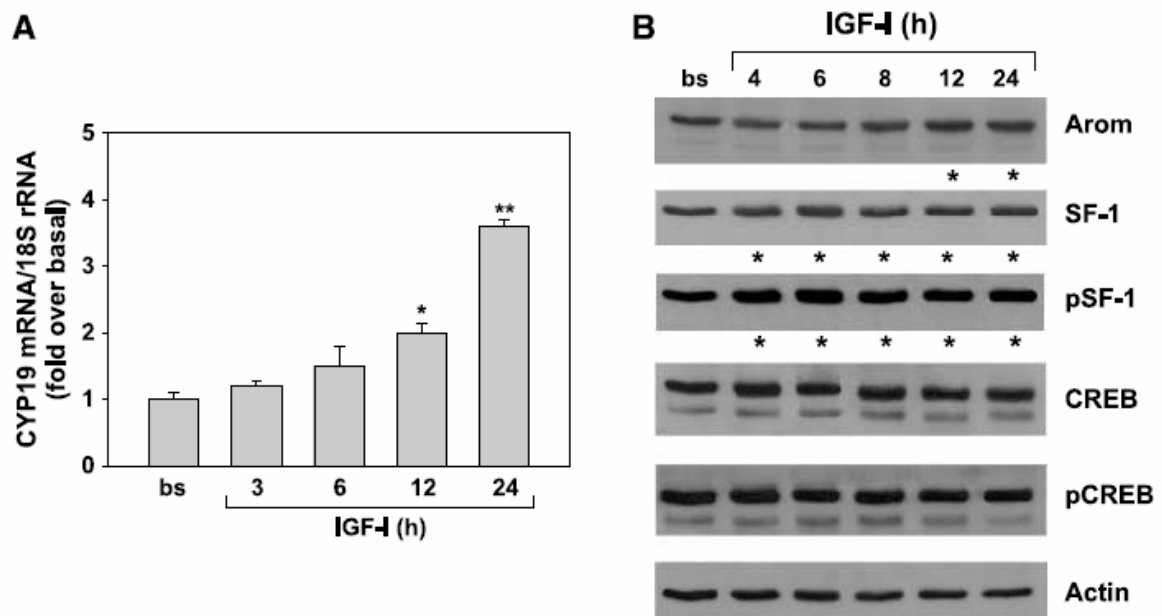


Figure 10 A, B. Effects of IGF-I on aromatase, SF-1 and CREB expression in R2C cells. Cells were treated in serum-free medium for the indicated times with IGF-I (100 ng/mL). (A), Total RNA was extracted from R2C cells untreated or treated as indicated. Real-time reverse transcription-PCR was used to analyze CYP19 mRNA levels. *Columns*, mean of values from three separate RNA samples; *bars*, SE. Each sample was normalized to its 18S rRNA content. *, $P < 0.01$; **, $P < 0.001$, compared with basal. (B), Western blot analyses were done on 50 μg of total proteins extracted from R2C cells untreated (bs) or treated as indicated. Representative of three independent experiments with similar results. β -Actin was used as a loading control. Normalized absorbances were subjected to statistical analysis; statistically significant differences are indicated (*, $P < 0.01$, compared with bs).

AG1024, LY294002, and GF109203X were able to inhibit IGF-I effects on CYP19 mRNA (Fig. 10C) and protein levels (Fig. 10D) as a consequence of a decreased SF-1 expression (Fig. 10D).

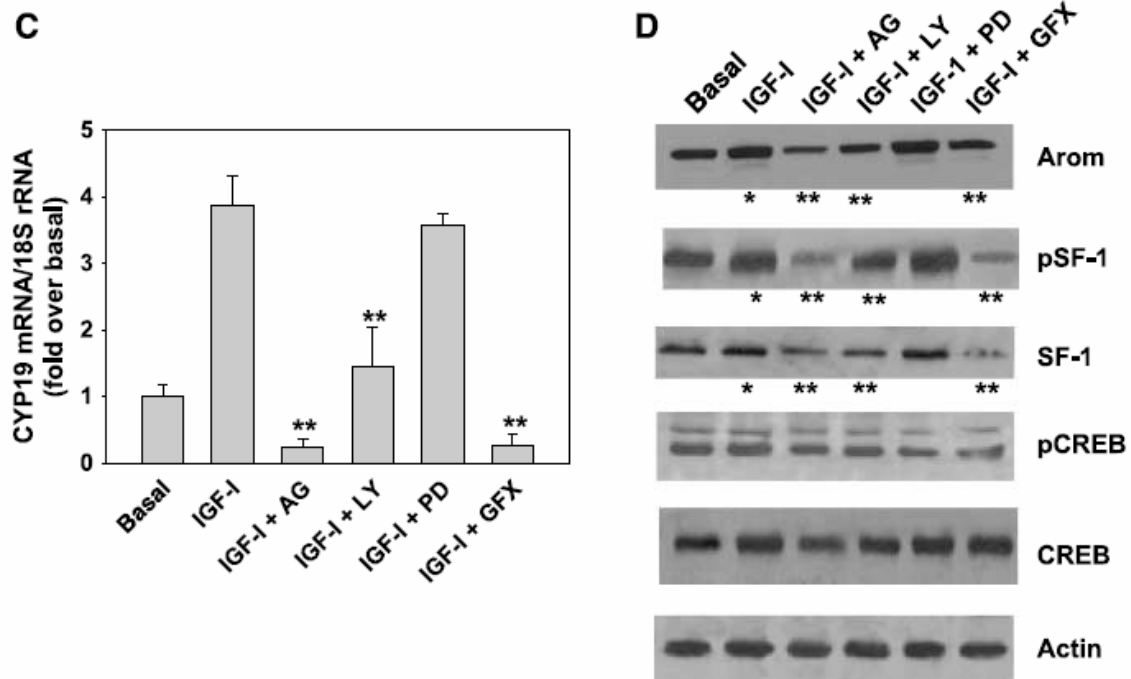


Figure 10 C, D. Effects of IGF-I on aromatase, SF-1 and CREB expression in R2C cells. Cells were treated in serum-free medium for 24 h with AG1024 (AG) (20 μ mol/L), LY294002 (LY) (10 μ mol/L), PD98059 (PD) (20 μ mol/L), and GF109203X (GFX) (20 μ mol/L), alone or in combination with IGF-I (100 ng/mL). **(C)**, Total RNA was extracted from R2C cells untreated or treated as indicated. Real-time reverse transcription-PCR was used to analyze CYP19 mRNA levels. *Columns*, mean of values from three separate RNA samples; *bars*, SE. Each sample was normalized to its 18S rRNA content. **, $P < 0.001$, compared with IGF-I. **(D)**, Western blot analyses were done on 50 μ g of total proteins extracted from R2C cells untreated (basal) or treated as indicated. Representative of three independent experiments with similar results. β -Actin was used as a loading control. Normalized absorbances were subjected to statistical analysis; statistically significant differences are indicated (*, $P < 0.01$, compared with basal; **, $P < 0.01$, compared with IGF-I).

Changes in IGF-I pathway activation status lead to changes in SF-1 binding to the aromatase PII promoter

We also performed CHIP assay to investigate how IGF-I stimulation influence per se binding of transcription factors to the aromatase PII promoter. We evidenced how in basal condition all the different inhibitors but not PD98059 reduced the amount of bound SF-1 reflecting changes in SF-1 protein amount (Fig. 11A). The increase in SF-1 protein content seen under IGF-I treatment (Fig. 10B) reflected an increase in SF-1 binding to the PII promoter (Fig. 11B).

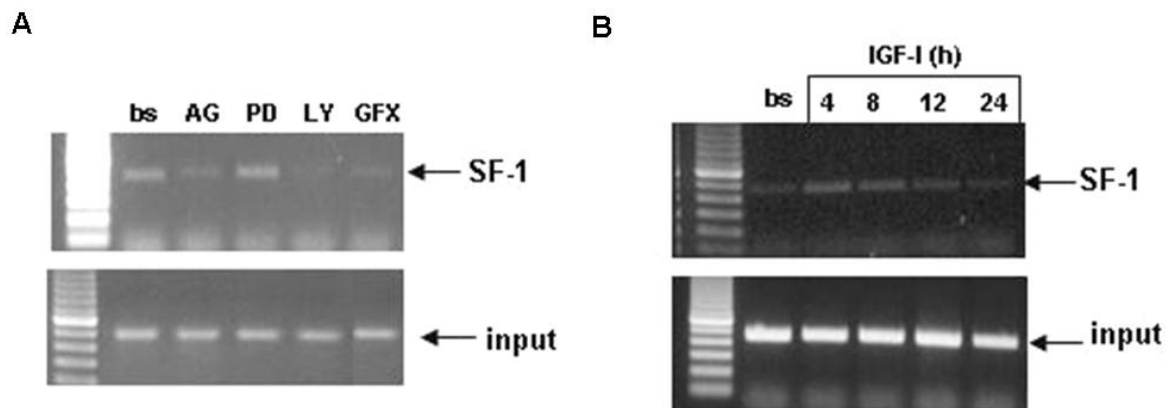


Figure 11. IGF-I increases SF-1 recruitment to the aromatase PII promoter through PI3K and PKC. (A) R2C cells were incubated for 24 h with AG1024 (20 μ mol/L), LY294002 (10 μ mol/L), PD98059 (20 μ mol/L) and G109203FX (20 μ mol/L). Untreated cells (bs) were treated with the same amount of vehicle alone (DMSO) that never exceeded 0.01% (v/v). (B) R2C cells were incubated for the indicated times with IGF-I (100 ng/ml). *In vivo* binding of SF-1 to the aromatase PII promoter was examined using CHIP assay. Immunoprecipitated (SF-1) and total (10% input) DNA were subject to PCR using specific primers. Similar results were obtained in two additional experiments.

IGF-I–induced estradiol production modulates R2C cell proliferation

Treatment with IGF-I induces aromatase activity and estradiol production, which are decreased by AG1024, LY294002, and GF109203X, as well as by PD98059 (Fig. 12A and B).

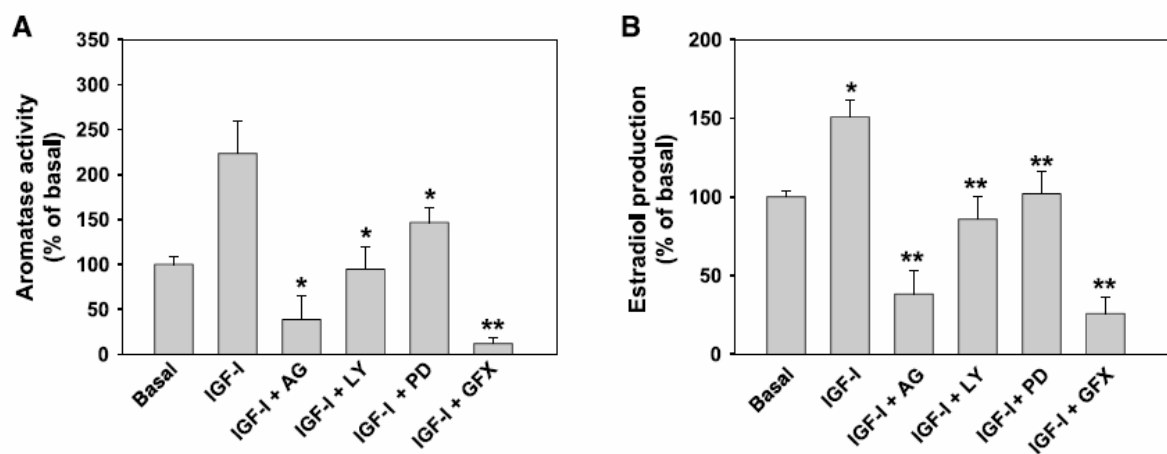


Figure 12 A, B. Effects of IGF-I and IGF-I pathway inhibitors on estradiol production and R2C cell proliferation. Cells were treated in serum-free medium for 24 h with IGF-I (100 ng/mL) alone or in combination with AG1024 (AG) (20 μ mol/L), LY294002 (LY) (10 μ mol/L), PD98059 (PD) (20 μ mol/L), and GF109203X (GFX) (20 μ mol/L). **(A)**, Aromatase activity is expressed as percent of basal. *Columns*, mean of three independent experiments each done in triplicate; *bars*, SE. *, $P < 0.01$; **, $P < 0.001$, compared with IGF-I. **(B)**, R2C cells were maintained for 48 h in serum-free medium, before being treated for 24 h. E2 content in R2C culture medium was determined by RIA and normalized to the cell culture well protein content. *Columns*, mean percent of basal; *bars*, SE. *, $P < 0.05$, compared with basal; **, $P < 0.01$, compared with IGF-I.

The observed changes in estradiol production modified R2C cell proliferative behavior (Fig. 12C). In addition, the use of an anti-IGF-I antibody in immunoneutralization experiments caused a dose-dependent inhibition in tritiated thymidine incorporation (Fig. 12C). The ability of IGF-I to stimulate, and that of the inhibitors to block, cell proliferation was linked to an alteration in cyclin D1 and cyclin E expression (Fig. 12D).

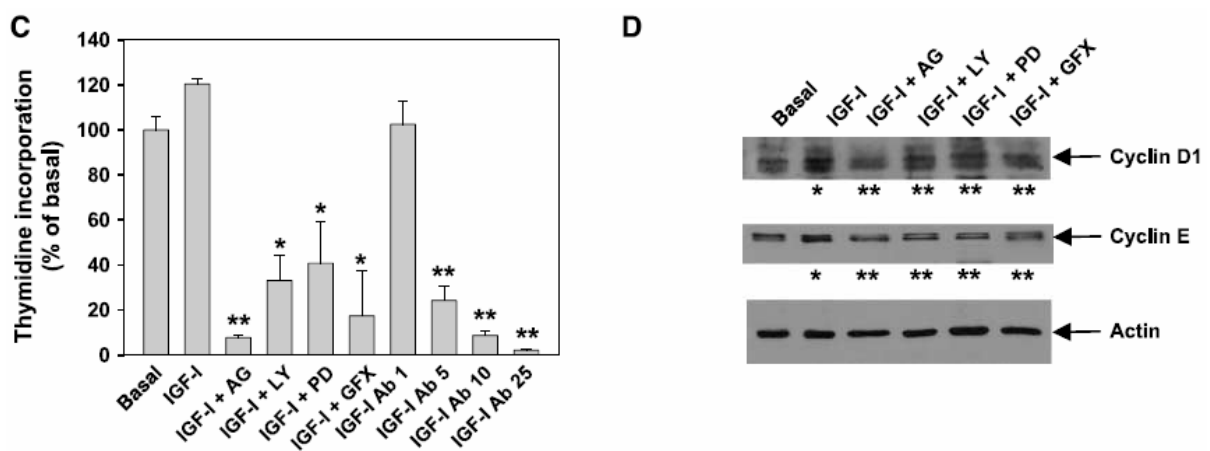


Figure 12 C, D. Effects of IGF-I and IGF-I pathway inhibitors on estradiol production and R2C cell proliferation. Cells were treated in serum-free medium for 24 h with IGF-I (100 ng/mL) alone or in combination with AG1024 (AG) (20 μ mol/L), LY294002 (LY) (10 μ mol/L), PD98059 (PD) (20 μ mol/L), and GF109203X (GFX) (20 μ mol/L). (C), R2C cell proliferation was evaluated by [3 H]thymidine incorporation analysis. Cells were maintained for 24 h in serum-free medium and treated for 24 h as indicated. IGF-I antibody (IGF-I Ab) was added to the medium at 1, 5, 10, and 25 μ g/mL. Columns, mean percent of untreated (basal) cells (100%) from three independent experiments each done in triplicate; bars, SE. *, $P < 0.01$; **, $P < 0.001$, compared with IGF-I. (D), Western blot analyses were done on 50 μ g of total proteins extracted from R2C cells treated as indicated. Representative of three independent experiments with similar results. β -Actin was used as a loading control. Normalized absorbances were subjected to statistical analysis; statistically significant differences are indicated (*, $P < 0.01$, compared with basal; **, $P < 0.01$, compared with IGF-I).

COX-2 is highly expressed in tumor Leydig samples and is necessary for aromatase expression

Using western analysis we investigated COX-2 expression in normal and tumor Leydig samples (Fig. 13A). Both R2C cells in basal condition as well as testes from Fischer rats with a developed tumor (FRTT) express increased COX-2, that is absent in normal controls. Moreover, we found similar results in human samples; the cytoplasm of neoplastic human Leydig cells showed a strong COX2 immunoreactivity, while immunonegative nuclei displayed only the blue counterstaining (Fig. 13B). Control human testes showed immunonegative reaction for COX-2 (Fig 13B).

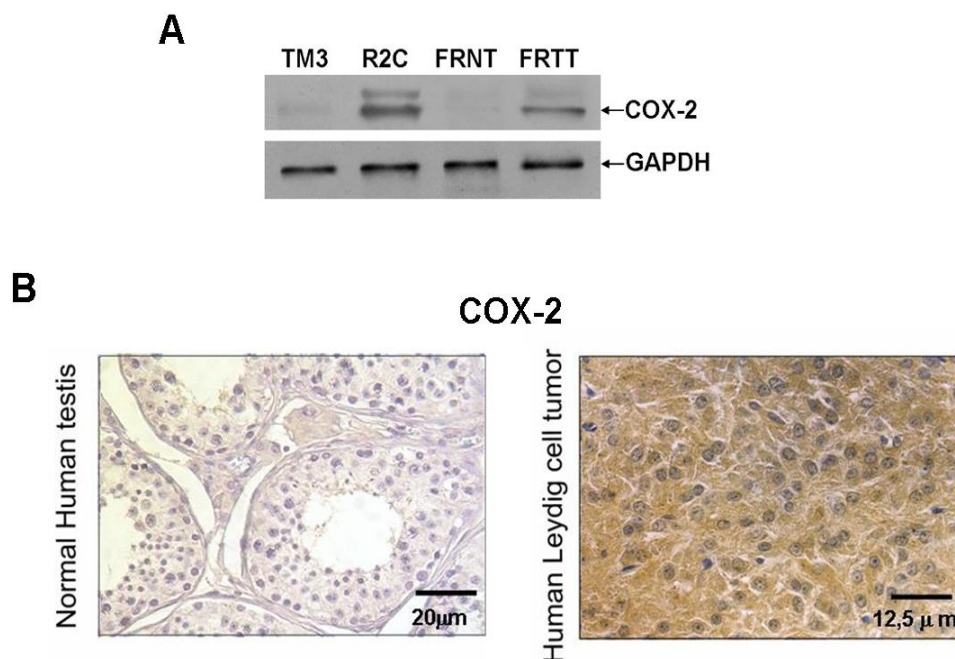


Figure 13. Expression of Cyclooxygenase-2 in tumor Leydig samples. (A) Western blot analysis was performed on 50 µg of total proteins extracted from TM3 and R2C cells or from total tissue of normal (FRNT) and tumor (FRTT) Fischer rat testes. GAPDH was used as a loading control. Results are representative of three independent experiments. (B) Immunolocalization of COX-2 in normal human testis and in testis with a Leydig cell tumor. Scale bars = 20µm (normal human testis); 12,5µm (human Leydig cell tumor). Brown (diaminobenzidine) cytoplasmic staining is indicative of COX-2 immunoreactivity.

Same experiments performed with COX-1 antibodies did not give different levels of expression between rat and human tumoral samples (data not shown). We have previously shown that expression of aromatase, SF-1 and phosphorylated form of CREB are higher in rat tumor Leydig cells. The altered activation of CREB, together with higher SF-1 expression, can explain the increase in aromatase levels observed in tumor Leydig cells. Knock down of COX-2 in R2C cells, using siRNA, caused a significant decrease in aromatase expression together with a decrease in CREB phosphorylation (Fig. 14).

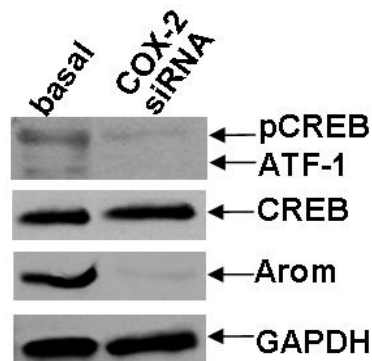


Figure 14. Effects of knocking down COX-2 on CREB and aromatase expression. R2C cells were transfected in serum-free medium with COX-2 (100nM) siRNA. After 48h western blot analysis of pCREB, CREB and aromatase were performed on 50 μ g of total protein extracted from R2C cells transfected with scrambled siRNA (basal) or with COX-2 siRNA (COX-2 siRNA). Blots are representative of three independent experiments with similar results. GAPDH was used as a loading control.

COX-2 inhibitor NS398 decreases pCREB and aromatase expression

To investigate whether COX-2 is involved in the mechanism determining pCREB activation in R2C cells we used a specific COX-2 inhibitor NS398 (NS). Western blot analyses showed that addition of increasing doses of NS (5, 25 and 50 $\mu\text{mol/L}$) caused a decrease in both phosphorylated CREB, as seen using a specific anti pCREB antibody, and aromatase levels (Fig. 15A). A drop in aromatase expression was also reflected by a change in enzymatic activity, that was dramatically reduced with all the investigated NS398 doses (Fig. 15B).

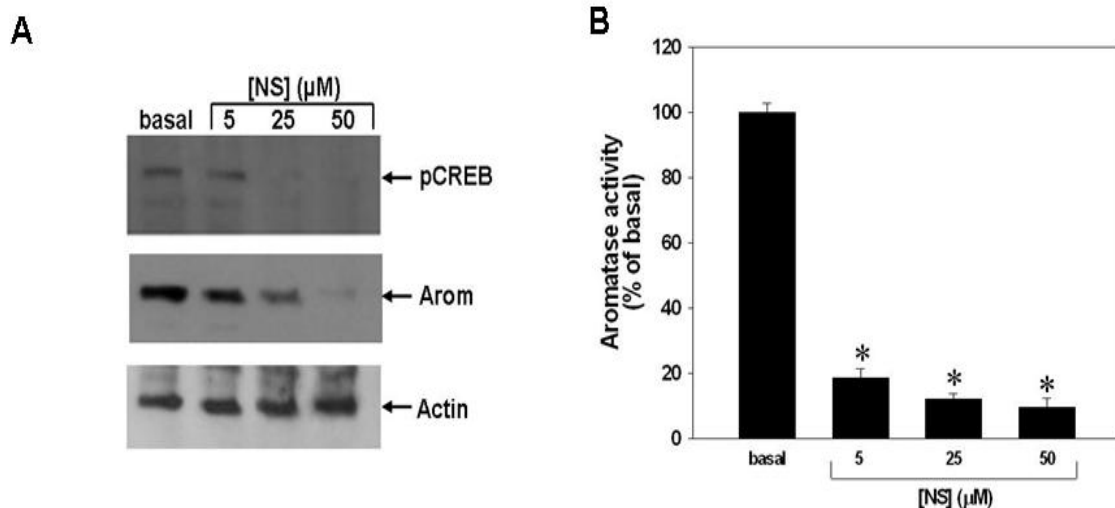


Figure 15 A, B. Effects of COX-2 inhibitor on aromatase expression in R2C cells. (A) Western blot analysis of pCREB and aromatase were performed on 50 μg of total proteins extracted from R2C cells non treated (basal) and treated with NS398 (5, 25, 50 $\mu\text{mol/L}$) for 24h. Blots are representative of three independent experiments with similar results. β -actin was used as a loading control. (B) R2C cells were untreated (basal) or treated for 24h with the increasing amounts of NS398 (5, 25, 50 $\mu\text{mol/L}$). Aromatase activity was assessed by using the modified tritiated water method. Results obtained were calculated as pmoles of $[3\text{H}]\text{H}_2\text{O}$ released per hour normalized to the well protein content (pmol/h/mg protein) and expressed as percent of basal. Columns, mean of three independent experiments each done in triplicate; bars, SE. *, $P < 0.01$, compared with basal.

Being active CREB a transcription factor necessary for aromatase transcription via PII promoter, these observation could potentially reflect changes on the mRNA levels. As seen by real time RT-PCR, addition of the different doses of NS398, determined a decrease in aromatase mRNA (Fig. 15C), without affecting CREB levels (Fig. 15D), indicating a specific effect of COX-2 inhibition on the phosphorylative protein status.

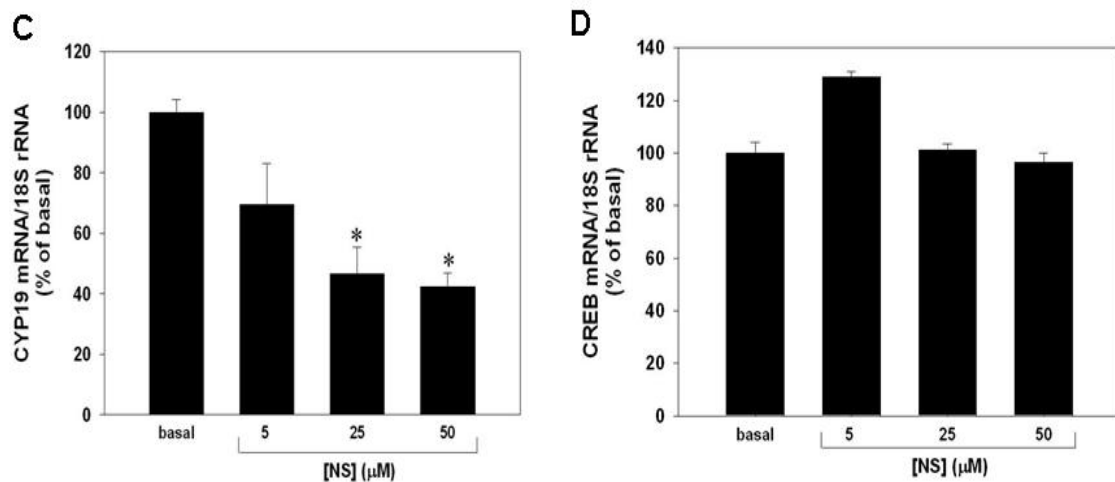


Figure 15 C, D. Effects of COX-2 inhibitor on aromatase expression in R2C cells. Total RNA was extracted from R2C cells untreated (basal) or treated for 24 h with the indicated doses of NS398. Real-time reverse transcription-PCR was used to analyze mRNA levels of CYP19 (C) and CREB (D). Columns, mean of values from three separate RNA samples; bars, SE. Each sample was normalized to its 18S rRNA content. *, P < 0.01 compared with basal.

The effects of NS398 on aromatase expression led us to hypothesize that potentially, there could be a decrease in pCREB binding to the aromatase PII promoter responsible for a decreased gene transcription. With a ChIP assay, we were able to show a specific decrease in pCREB binding (Fig. 16A) without any change in the amount of total CREB protein present on the aromatase PII promoter (Fig. 16B).

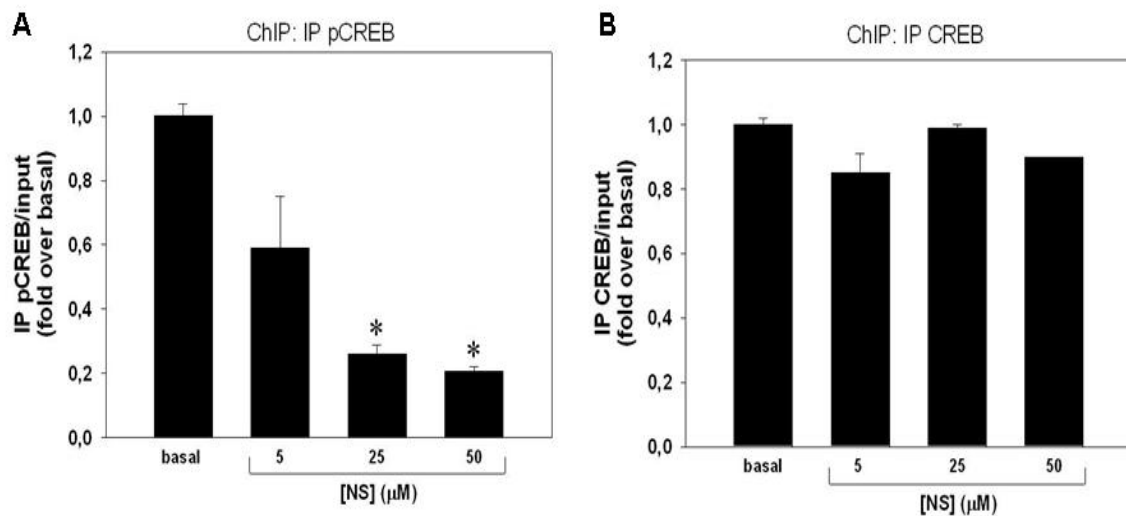


Figure 16. Effects of COX-2 inhibitor on pCREB and CREB binding to aromatase PII promoter in R2C cells. ChIP assays were performed on R2C cells untreated (basal) or treated for 24 h with the indicated doses of NS398. Immunoprecipitated (pCREB and CREB) and total (10% input) DNA were subject to real time PCR using specific primers (**A**, **B**). Untreated cells (basal) were treated with the same amount of vehicle alone (DMSO) that never exceeded 0.01% (v/v). *Columns*, mean of values from three separate experiments; *bars*, SE. Each sample was normalized to the amplified input values. *, P < 0.01 compared with basal.

PGE2 activated pathway regulates aromatase expression

Either isoform of COX is responsible for prostaglandins (PGs) synthesis. Starting from previous findings demonstrating that PGE2 stimulates aromatase expression (267;276) we investigated the role of this factor in the regulation of aromatase in our cell model.

Addition of exogenous amounts of PGE2 to R2C cells were able to increase CREB phosphorylation and consequently aromatase expression (Fig. 17A). Since PGE2 works binding to four different receptor isoforms, named EP, we tested the effect of selective inhibitors (EP1 [SC19220], of EP2/EP4 [AH6809], of EP4 [AH23848]) on pCREB and aromatase levels (Fig. 17B). Among the tested antagonist only the one selective for the EP4, AH23848 was able to produce an effect; specifically, a decrease in pCREB and in aromatase levels.

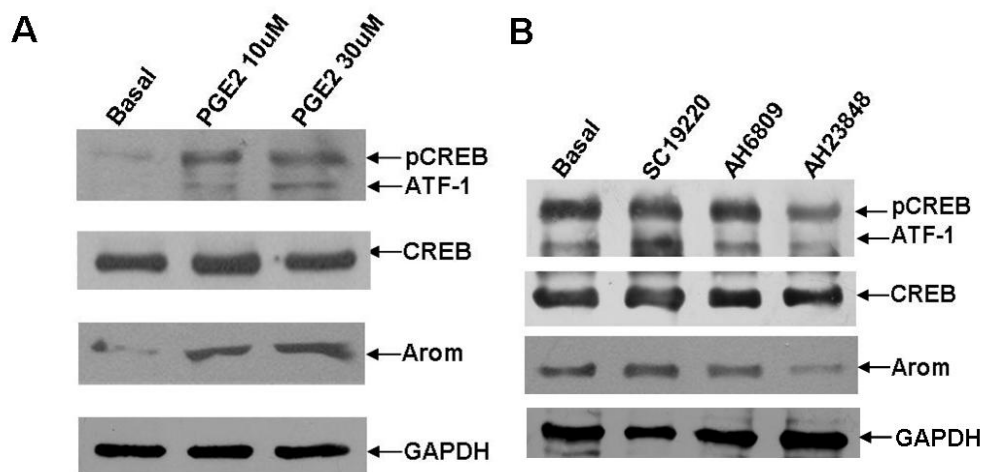


Figure 17. Effects of PGE2 administration and EP inhibitors on CREB and aromatase expression in R2C cells. (A) Western blot analysis of pCREB, CREB and aromatase were performed on 50 μ g of total proteins extracted from R2C cells non treated (basal) and treated with PGE2 (10 and 30 μ mol/L) for 48h. Blots are representative of three independent experiments with similar results. GAPDH was used as a loading control. (B) Western blot analysis of pCREB, CREB and aromatase were performed on 50 μ g of total proteins extracted from R2C cells non treated (basal) and treated with EP inhibitors (SC19220, AH6809, AH23848) (10 μ mol/L) for 48h. Blots are representative of three independent experiments with similar results. GAPDH was used as a loading control.

Moreover, addition of PGE2 abrogated the inhibition on aromatase activity caused by AH23848 (Fig 18).

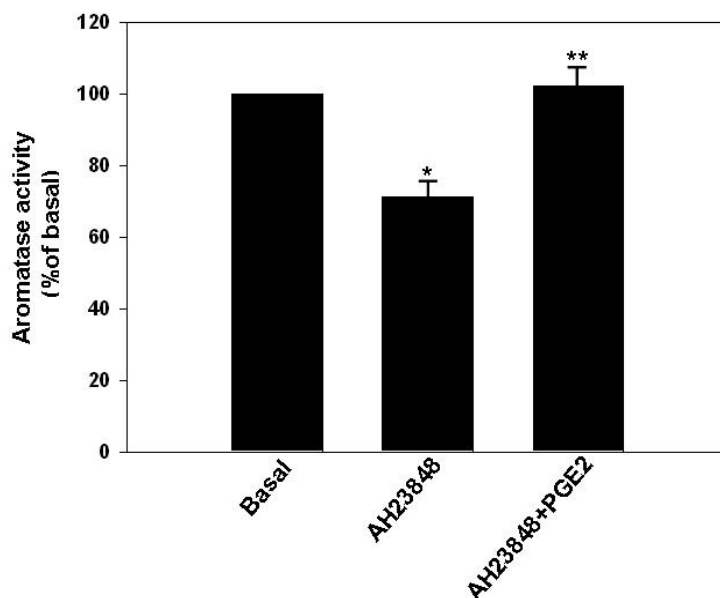


Figure 18. Effects of PGE2 and AH23848 on aromatase activity in R2C cells. Cells were cultured for 24h in serum-free HAM-F10 and then treated for 48 h with AH23848 (10 $\mu\text{mol/L}$). Medium was then removed and replaced with medium only or where indicated with PGE2 (30 $\mu\text{mol/L}$). Aromatase activity was assessed by using the modified tritiated water method. Results obtained were calculated as pmoles of $[3\text{H}]\text{H}_2\text{O}$ released per hour normalized to the well protein content (pmol/h/mg protein) and expressed as percent of basal. *Columns*, mean of three independent experiments each done in triplicate; *bars*, SE. *, $P < 0.01$, compared with basal; **, $P < 0.01$, compared with AH23848.

PKA inhibitor H89 decreases aromatase expression and activity as a consequence of reduced pCREB activation

EP4 transduces its signal activating PKA, and we wanted to test the effect of a specific PKA inhibitor, H89, on aromatase expression. H89 decreased in a dose dependent manner both phosphorylated CREB and aromatase levels (Fig. 19A). A drop in aromatase expression was also reflected by a change in enzymatic activity, that was reduced with all the investigated H89 doses (Fig. 19B).

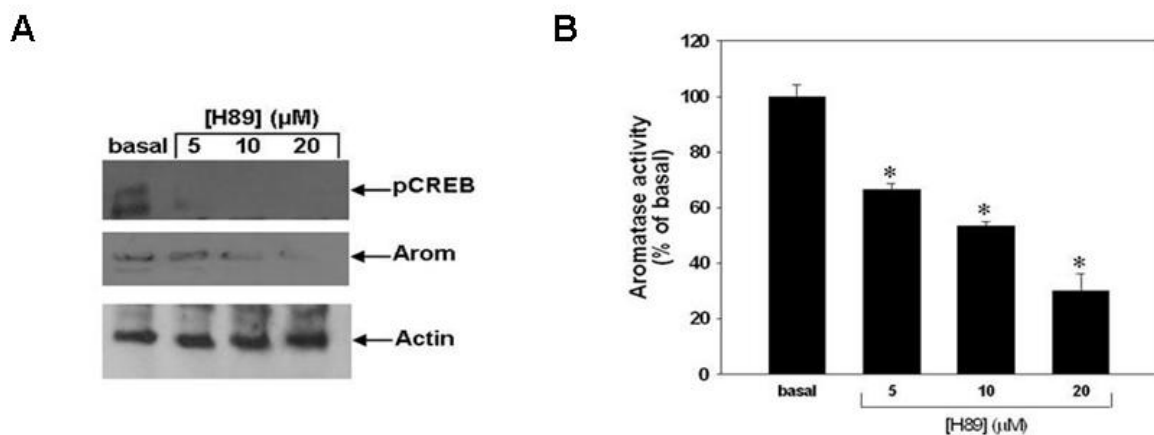


Figure 19 A, B. Effects of PKA inhibitor H89 on aromatase expression in R2C cells. (A) Western blot analysis of pCREB and aromatase were performed on 50 μg of total proteins extracted from R2C cells non treated (basal) and treated with H89 (5, 10, 20 μmol/L) for 24h. Blots are representative of three independent experiments with similar results. β-actin was used as a loading control. (B) R2C cells were untreated (basal) or treated for 24h with the increasing amounts of H89 (5, 10, 20 μmol/L). Aromatase activity was assessed by using the modified tritiated water method. Results obtained were calculated as pmoles of [3H]H₂O released per hour normalized to the well protein content (pmol/h/mg protein) and expressed as percent of basal. *Columns*, mean of three independent experiments each done in triplicate; *bars*, SE. *, P < 0.01, compared with basal.

Similarly, H89 decreased aromatase mRNA (Fig. 19C), but had no effect on CREB mRNA levels (Fig. 19D).

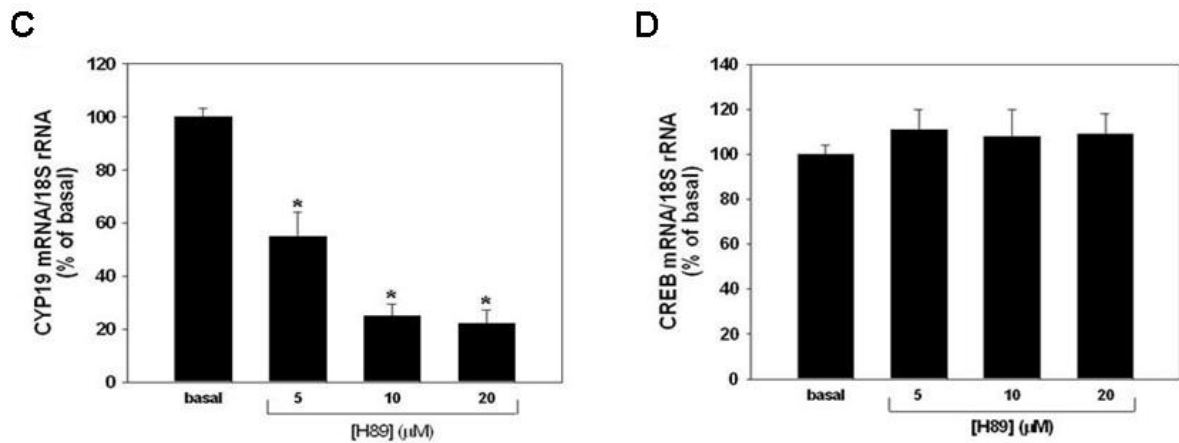


Figure 19 C, D. Effects of PKA inhibitor H89 on aromatase expression in R2C cells. Total RNA was extracted from R2C cells untreated (basal) or treated for 24 h with the indicated doses of H89. Real-time reverse transcription-PCR was used to analyze mRNA levels of CYP19 (C) and CREB (D). Columns, mean of values from three separate RNA samples; bars, SE. Each sample was normalized to its 18S rRNA content. *, P < 0.001 compared with basal.

The decrease in aromatase expression was due to a decrease in pCREB binding to the aromatase PII promoter (Fig. 20A), while the amount of total CREB protein present on the aromatase PII promoter did not change (Fig. 20B).

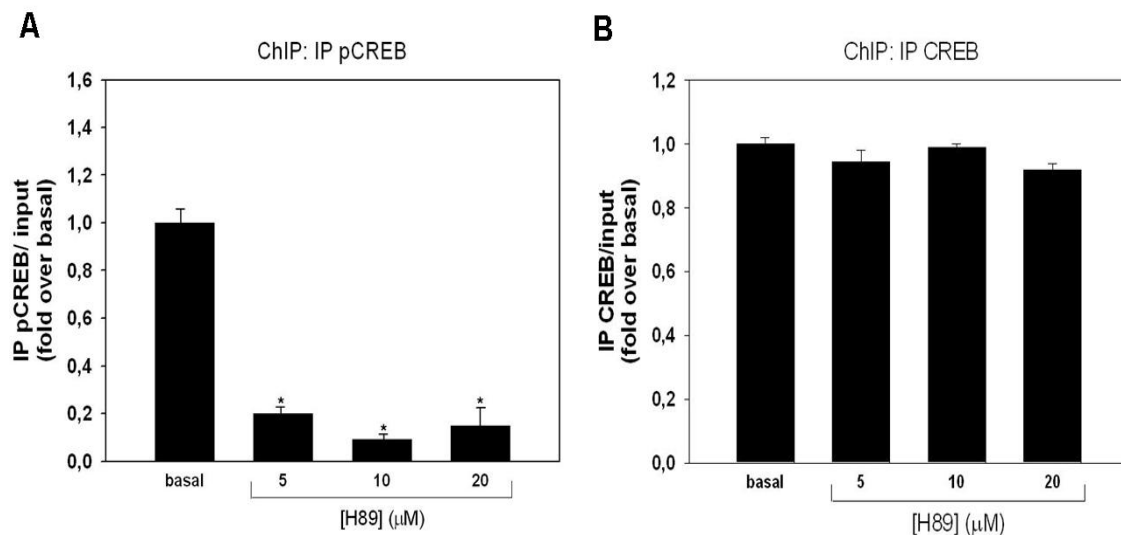


Figure 20. Effects of PKA inhibitor on CREB and pCREB binding to aromatase PII promoter in R2C cells. ChIP assays were performed on R2C cells untreated (basals) or treated as indicated. Untreated cells (basal) were treated with the same amount of vehicle alone (DMSO) that never exceeded 0.01% (v/v). Immunoprecipitated (pCREB and CREB) and total (10% input) DNA were subject to real time PCR using specific primers (**A**, **B**). *Columns*, mean of values from three separate experiments; *bars*, SE. Each sample was normalized to the amplified input values. *, P < 0.01 compared with basal.

A further demonstration of PKA implication in all the observed effects derives from the direct measurement of kinase activity after treatment with the inhibitors (Fig. 21). As expected H89 caused a 58% inhibition of PKA activity after 4h treatment, similarly NS398 and AH23848 determined 33 and 70 % inhibition respectively (Fig. 21).

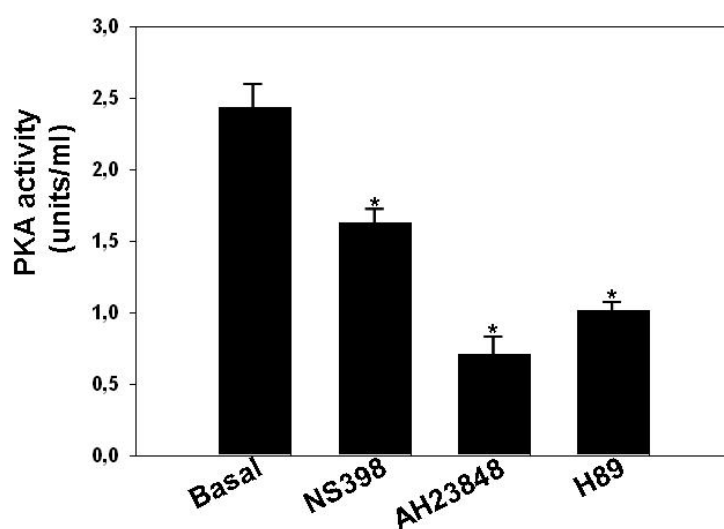


Figure 21. Effect of NS398, AH23848 and H89 on PKA activation. Cell lysates were analyzed for PKA activity by non-radioactive in vitro PKA assay as described in materials and methods. R2C cells were treated for 4h with NS398 (50 $\mu\text{mol/L}$), AH23848 (10 $\mu\text{mol/L}$) and H89 (20 $\mu\text{mol/L}$). Absorbance of phosphorylated peptide was quantified by spectrophotometric method. Results are mean \pm S.D. of three independent experiments. *P < 0.001 compared to basal.

Inhibition of PGE₂ dependent pathway decreases estradiol production and consequently tumor Leydig cell proliferation

The involvement of COX-2 through PGE₂ production and PKA activation in controlling aromatase activity in tumor Leydig cell is further supported by the ability of NS398, AH23848 and H89 to inhibit basal estradiol production (Fig. 22).

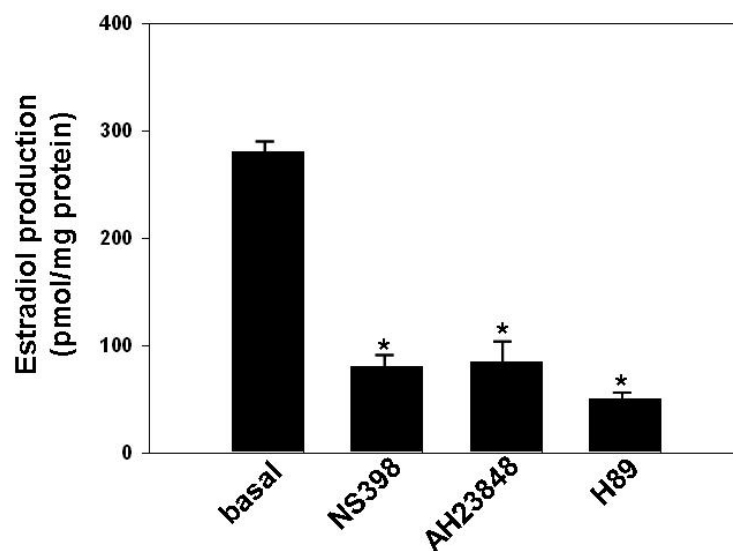


Figure 22. Effects of NS398, AH23848 and H89 on estradiol production. Cells were maintained for 24 h in serum free HAM-F10 medium before being treated for 48 h with NS398 (50 $\mu\text{mol/L}$), AH23848 (10 $\mu\text{mol/L}$) or H89 (10 $\mu\text{mol/L}$) or maintained untreated (basal). E₂ content in culture medium was determined by RIA and normalized to the cell culture well protein content. *Columns*, mean of three independent experiments each done in triplicate; *bars*, SE. *, $P < 0.05$, compared with basal.

As expected, the effect of decreased E2 production was a decrease in cell proliferation, that with the higher doses of both NS398, AH23848 or H89 was 72%, 70% and 82% respectively (Fig. 23 A, B, C).

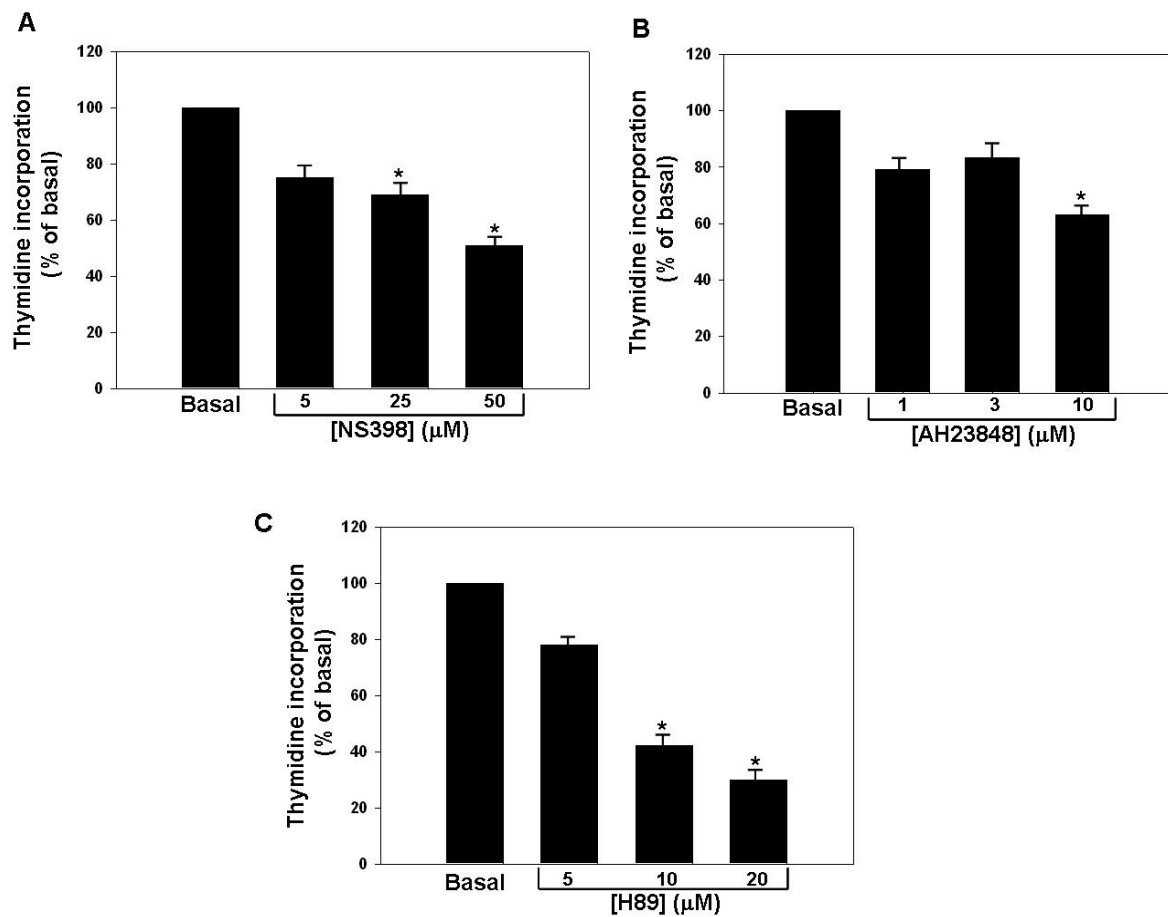


Figure 23. Effects of NS398, AH23848 and H89 on Leydig cell proliferation. (B, C) Cells were treated in serum-free medium in the absence (basal) or presence of NS398 (A), AH23848 (B) or H89 (C) at the indicated concentrations for 72h after 24 h starvation. R2C cell proliferation was evaluated by [^3H] Thymidine incorporation analysis. Values expressed as percent of untreated (basal) cells (100%) represent the mean \pm SEM of three independent experiments each performed in triplicate. (*) $P < 0.05$ compared with basal.

An additional demonstration of the involvement of COX-2 dependent pathway in controlling estradiol production in R2C cells derives from a evaluation of cell proliferation after knocking down COX-2 in these cells with a specific siRNA (Fig. 24). Thymidine incorporation was reduced by all the amounts of transfected COX-2 siRNA.

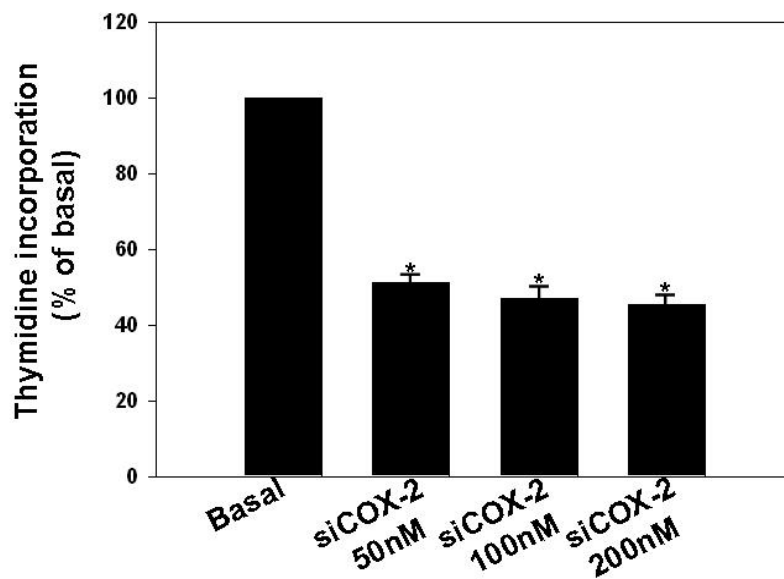


Figure 24. Effects of knocking down COX-2 on Leydig cell proliferation. R2C cells were transfected in serum-free medium with COX-2 siRNA at the indicated concentrations. After 48h cell proliferation was evaluated by [³H] Thymidine incorporation analysis. Values expressed as percent of untreated (basal) cells (100%) represent the mean \pm SEM of three independent experiments each performed in triplicate. (*) $P < 0.05$ compared with basal.

These changes in cell cycle can be explained by the decrease in Cyclin E expression determined by NS398 (Fig. 25A) , AH23848 (Fig. 25B) and H89 (Fig. 25C).

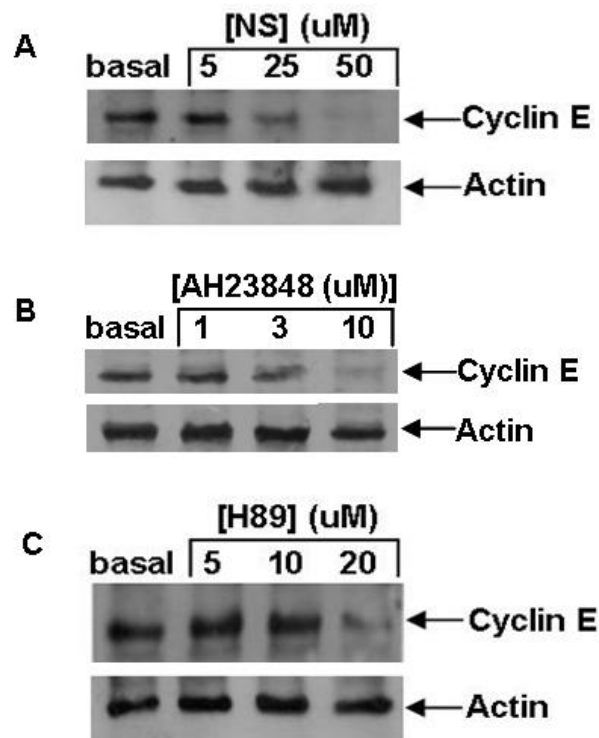


Figure 25. Effects of NS, AH23848 and H89 on cyclin E expression. Western blot analysis of cyclin E was performed on 50 μ g of total protein extracted from R2C cells non treated (basal) and treated with NS398 (5, 25, 50 μ mol/L), AH23848 (1, 3, 10 μ mol/L) and H89 (5, 10, 20 μ mol/L) for 24h. Blots are representative of three independent experiments with similar results. β -actin was used as a loading control.

These findings led us to suppose that in tumor Leydig cells the PGE2 derived from COX-2 overexpression could act through an autocrine mechanism in activating aromatase expression.

Discussion

The current study was aimed to explain the molecular mechanism responsible for aromatase overexpression in tumor Leydig cells with a consequent excess of estradiol *in situ* production sustaining tumor cell growth and proliferation.

Mammalian testis is capable of estrogen synthesis, whose production is regulated by different factors at different ages. In mature animals, aromatization of testosterone to estradiol is enhanced by LH/chorionic gonadotropin (CG) and not by FSH. The site of this synthesis appears to be age-dependent, at least in some species, such as the rat (285). Leydig cells are an elective target site of LH/CG which controls testosterone biosynthesis as well as its conversion to estradiol through aromatase activity. Leydig cell is also known to be the site of estrogen synthesis in several species, including mice (286), humans (287), swine (288), and sheep (289). Alterations in local estrogen synthesis may have significant consequences in malignancy of these cells. In the present study we observed that maintenance of R2C cells in the absence of serum induces a conspicuous release of E2 from cellular storage in a time dependent manner. This synthesis was abrogated by treatment with Letrozole, an aromatase inhibitor, addressing how estrogen production is dependent on high constitutive aromatase activity.

A strongly increased aromatase expression was observed in R2C cells respect to the normal cell line control TM3 as well as in FRTT respect to FRNT. These findings concord with a previous study on human tissues showing that the increase in estrogen synthesis, as a consequence of a more intense aromatase activity, is higher in Leydig cell tumor fraction than in normal tissue surrounding the tumor of the same patient (290).

Mediators of the physiological effects of estrogens are the estrogen receptors (ER), α and β . ER α appears to be confined to Leydig cells in testicular tissue (58), while ER β has been detected immunohistochemically in several rat testicular cell types, including Sertoli cells, germ cells, and peritubular cells (291). An enhanced expression of ER α resulting in an increased ER α /ER β ratio was observed in R2C compared to TM3 cell line as well as in

FRTT respect to FRNT. This is in agreement with previous reports demonstrating that transgenic mice overexpressing aromatase have an enhanced occurrence of breast and Leydig cell tumors together with an enhanced expression of ER α in the tumoral tissue (139). The latter findings address reasonably how an estrogen short autocrine loop may be involved in breast and testicular tumorigenesis in the presence of an excess of locally produced estradiol. Indeed, an arrest of cell growth was observed following abrogation of local E2 production with Letrozole or after addition of ER α inhibitors ICI or OHT. Besides, only after removal of medium every day along with prolonged R2C starvation abolishing local steroid production, we observed how exogenous E2 was able to display proliferative effects.

One mechanism through which estrogens induce cell proliferation is by increasing protein levels of G1 regulatory cyclins A, B1, D1, D3, and E in target cells (292). In our study we showed that the expression of two of the most important regulators of Leydig cell cycle, cyclin D1 and E can be increased by E2 and downregulated by treatment with antiestrogens. These data further confirm that aromatase overexpression and the consequent E2 production may be the cause of altered cell cycle regulation of Leydig tumor cells.

In the attempt to explain the molecular mechanism determining aromatase overexpression in our tumor cell line, we focused our attention on expression levels of transcription factors identified as crucial regulators of aromatase gene expression: CREB and SF-1. In the adult testis SF-1 is predominantly expressed in Leydig cells (293). The increase of total and/or phosphorylated protein can potentiate SF-1 transcriptional activity (294). In R2C cells and in FRTT compared to the normal controls we found higher SF-1 phosphorylated protein levels as a consequence of elevated protein content. Total CREB levels were similar in all samples but highly phosphorylated in tumor samples. Starting from these observations we investigated which pathways could be involved in the activation of these transcription factors.

The most important signal that initiates steroidogenesis in Leydig cells is the binding of LH to the LH receptor (295). It has been demonstrated that LH/LHreceptor signaling

pathway is constitutively active in R2C cells and makes the phenotype of these cells constitutively steroidogenic (296). For instance in the presence of a specific PKA inhibitor, constitutive synthesis of Steroidogenic Acute Regulatory Protein (StAR) mRNA and steroids were significantly inhibited (297). These observations fit well with our findings evidencing how the presence of PKA inhibitor determined a strong decrease in aromatase activity together with a drop in CREB phosphorylation. In the presence of a specific PKC inhibitor no effects were elicited on phosphorylation of CREB, while SF-1 dropped dramatically.

It has been shown that CREB in mouse Leydig cells can be phosphorylated also through the PKC pathway, activated by IGF-I (296). In this study we have revealed that R2C tumor Leydig cells release higher levels of IGF-I in the culture medium respect to TM3 cells. However, the exposure to IGF-I as well as the treatment with inhibitors of IGF-I signalling did not affect CREB phosphorylation status but decreased SF-1 phosphorylation, postulating a separate mechanism controlling CREB and SF-1 activation in modulating aromatase activity.

These findings led us to suppose that the IGF-I derived from tumor Leydig cells could act through an autocrine mechanism in activating aromatase expression.

IGF-I receptors have previously been identified in Leydig cells of several species (188;198;298;299). It has been hypothesized that changes in IGF-RI expression can influence tumor cell progression. However in our cellular models, we did not reveal differences in IGF-RI expression between normal and tumor cells, indicating that IGF-I level may be the determining factor in potentiating IGF-I signalling. A previous study investigating the effects of long term IGF-I treatment on Leydig cells did not reveal alterations in DNA synthesis, indicating that IGF-I may act as a differentiation factor rather than a mitogenic factor (191). In fact, expression levels of all mRNA species associated with testosterone (T) biosynthesis were shown to be lower in the absence of IGF-I, while treatment with IGF-I/insulin has been found to stimulate steroidogenesis and StAR expression in Leydig cells through a process that does not require cAMP signalling (184;299;300).

In the same vein we may reasonable hypothesize that IGF-I could sustain, through an autocrine/paracrine mechanism, the elevated aromatase expression/activity in tumor Leydig cells. To verify this hypothesis we studied the various signalling pathways initiated by IGF-I through IGF-IR. Binding of IGF-I to its receptor causes receptor autophosphorylation and the activation of intrinsic tyrosine kinase that acts on various substrates including the insulin receptor substrate (IRS) and Shc adaptor proteins. These activated proteins recruit other factors, leading to activation of multiple signalling pathways including the phosphatidyl inositol 3-kinase (PI3K)/Akt and the mitogen-activated protein (MAP) kinase cascade. In addition, it has been shown that IGF-I can activate also the phospholipase C (PLC)/protein kinase C (PKC) pathway (3;301).

To demonstrate a role for IGF-I in mediating aromatase activation we used specific inhibitors for IGF-I signaling [AG1024 (AG)], ERK1/2 [PD98059 (PD)], PI3K [LY294002 (LY)] and PKC [GF109203X (GFX)] and showed a reduction of aromatase activity with all of them. Together these data confirm a role for IGF-I in mediating aromatase activation in tumor Leydig cells. All of the different inhibitors but PD were able to produce a similar inhibitory pattern on both aromatase and SF-1 mRNA and protein expression. Furthermore by ChIP assay we evidenced that SF-1 binding to the aromatase promoter II that was reduced by AG, LY, GFX but not by PD indicating a central role of this transcription factor in regulating aromatase gene transcription in tumor Leydig cells. This is the first report of a direct link between SF-1 transcription and IGF-I signalling pathway in regulating aromatase expression.

Furthermore, addition of IGF-I itself was able to increase aromatase activity and expression. These events were due to an increase in the amount of total and phosphorylated SF-1 levels whose binding to the aromatase promoter was shown to be rapidly augmented. So we postulate that an enhanced endogenous IGF-I local production may contribute to maintain an elevated aromatase activity sustained by a direct stimulatory effect of SF-1. For instance the inhibition of IGF-I signalling through inhibition of either PI3K/AKT and PLC/PKC pathways were able to block SF-1 expression and protein phosphorylation. Particularly treatment with AG blocked SF-1 phosphorylation more efficiently than the

separate treatment of PI3K or PKC, addressing how both pathways may synergize in upregulating SF-1 activity. In the presence of PD, SF-1 expression remained unchanged together with unaffected aromatase mRNA and protein levels. Importantly aromatase activity appeared decreased in the presence of PD suggesting a potential stimulatory role of ERK1/2 on the enzyme at a post-transcriptional level. From our findings then emerges a double mechanism inducing enhanced expression of aromatase: 1. a constitutive activation of PKA determining CREB phosphorylation; 2. an enhanced IGF-I signaling potentiating SF-1 action. The enhanced expression of SF-1 may be maintained by the lack of DAX-1 (Dosage-Sensitive Sex Reversal, Adrenal Hypoplasia Congenita, Critical Region on the X Chromosome, Gene-1) in R2C cells (283). DAX-1 is a specific co-repressor of SF-1 and inhibits StAR expression and steroidogenesis by 40-60% when overexpressed in R2C cells (283). The lack of DAX-1 expression in R2C cells may be due to the constitutive active PKA signalling, in fact since in a mouse Leydig cell line was shown a marked decrease of DAX-1 mRNA within 3 h after addition of LH or forskolin (302). Then, the activation of LH/LHr/PKA pathway decreases DAX-1 expression and promotes SF-1 activity, at the same time PKA activation if the cause an higher CREB phosphorylation and consequently activity. The mechanism responsible for PKA constitutive activation in tumor Leydig cells is yet to be defined.

Our hypothesis was that an increase in COX-2 levels and consequent prostaglandin synthesis could be the event responsible for PKA activation. This hypothesis was supported by immunostochemistry showing COX-2 overexpression in human Leydigoma samples and its absence in normal testes. In addition, western analysis for COX-2 on normal and tumor Leydig samples showed that COX-2 is highly expressed in R2C cells and in testicular lysates from Fischer with tumors.

Similarly, COX-2 is expressed in breast cancer (254) and it has been shown a correlation between aromatase and COX-2 expression in this type of tumor (259). Knock down of COX-2 in R2C cells using RNAi was able to decrease aromatase expression and to almost abolish CREB phosphorylation. These events produced by COX-2 knock down were also observed using a COX-2 selective antagonist, NS398. In addition, using ChIP assay, we

were able to show that the amount of pCREB bound to the PII promoter was significantly reduced, this implies that the cause of the observed reduction in aromatase expression could be due to a decrease in PKA-dependent CREB phosphorylation.

Several studies have been performed on aromatase regulation in breast cancer, which represents another estrogen-dependent type of tumor, meaning that it expresses estrogen receptor and requires estrogen for growth (303). Similarly to tumor Leydig cells, breast cancer cells have an increased aromatase expression (304), due to a switch in the promoter region utilized in gene expression. In breast cancer patients is found a switch from promoter I.4 to promoter I.3 and II and I.7 (267;305-307) regulated through cAMP-mediated pathways. In addition, a previous study on adipose stromal cells surrounding breast cancer cells, showed PGE₂ to be a potent activator of aromatase expression via promoter II. Furthermore, it was demonstrated that PGE₂ is produced by breast tumors stimulating local estrogen biosynthesis in the surrounding adipose tissue, suggesting a potential paracrine/autocrine role for prostaglandins (PGs) in regulating aromatase expression in other cell types, including tumor Leydig cells.

Different prostaglandins are produced by the rat testis at different levels; in particular they include PGF₂ α (79,5%), PGE₂ (20.3%) and PGD₂ (0.17%) (308). PGE₂-producing rat testicular cells include Leydig cells, Sertoli cells and spermatogenic cells and it has been implicated in the control of testicular steroidogenesis, spermatogenesis and local immunity (309). In addition, in the mouse there is also a correlation between COX-2 expression and PGE₂ production in male genital organs (310). Even in another species, such as newt, it was observed that PGE₂ increases 17 β -estradiol, cAMP and aromatase activity while decreasing testosterone, probably as a consequence of increased conversion into estrogens (311). Consistent with findings related to COX-2 and tumor, PGE₂ is also known to possess properties that promote malignant growth. For example, PGE₂ stimulates angiogenesis, invasiveness and inhibits immune surveillance (312). PGs, produced through COX, exert their actions binding to specific transmembrane G-protein coupled receptors termed Prostanoid (P) receptors, present as different splice variants (270).

Specifically, PGE₂ receptors, EP₁(271) , EP₂(272), EP₃(273) and EP₄(274), are transduced through modulation of the activity of either adenylyl cyclase or inositol phospholipid hydrolysis and calcium mobilization (270;275). In particular, EP₁ activates PKC, EP₂ and EP₄ are coupled to PKA, EP₃ can either couple negatively to adenylyl cyclase through binding a G_i protein or associate to inositol phospholipid hydrolysis and calcium mobilization. Importantly, PGE₂ was shown to increase aromatase expression, while on the contrary EP₁ and EP₂ selective antagonists decreased the enzyme activity (276), suggesting that both PKA and PKC pathways are required for aromatase optimal expression.

In our experiments using selective antagonists for the different EP subtypes, we found that only AH23848, an EP₄ inhibitor was able to decrease aromatase. EP₄ transduces its signal through PKA, and in fact its block determines a decrease in CREB phosphorylation. These events are opposite to what observed using PGE₂, which allows for increase in aromatase expression and in CREB phosphorylation.

R2C cells are known to have a constitutive active PKA activity (313), we measured kinase activity after treating R2C cells with COX-2 inhibitor NS398, EP₄ inhibitor AH23848 and after treatment with a specific PKA inhibitor H89. All of the tested antagonists were able to decrease enzyme activity. The importance of PKA pathway in regulating aromatase expression in R2C cells can be seen in the experiments with H89, which specifically decreasing CREB phosphorylation determines a decrease in aromatase levels.

As is the case for IGF-I pathways inhibitors, that decrease estrogen production as a consequence of decreased aromatase expression, all of the tested inhibitors working at different levels on the same pathway, directly on either COX-2, EP₄ or PKA determine a drop in the ability of R2C cells to produce estradiol. This event as previously shown causes a decrease in tumor cell proliferation, depending on the decrease of estrogen regulated cyclin such as cyclin E. The importance of COX-2/PGE₂ dependent pathway is further confirmed by knocking down COX-2 expression with siRNA. The absence of this protein in R2C cells causes a decrease in tumor cell progression.

All these data complete our knowledge on the mechanisms involved in aromatase regulation in Leydig cell tumor: COX-2 over-expression inducing PGE2 synthesis activates PKA, which increases CREB phosphorylation; phosphorylated CREB binds CYP19 PII promoter together with SF-1, regulated by IGF-I, and increase aromatase expression. Constitutive active aromatase produces higher estradiol levels which then, increase Leydig cell proliferation (Diagram 1).

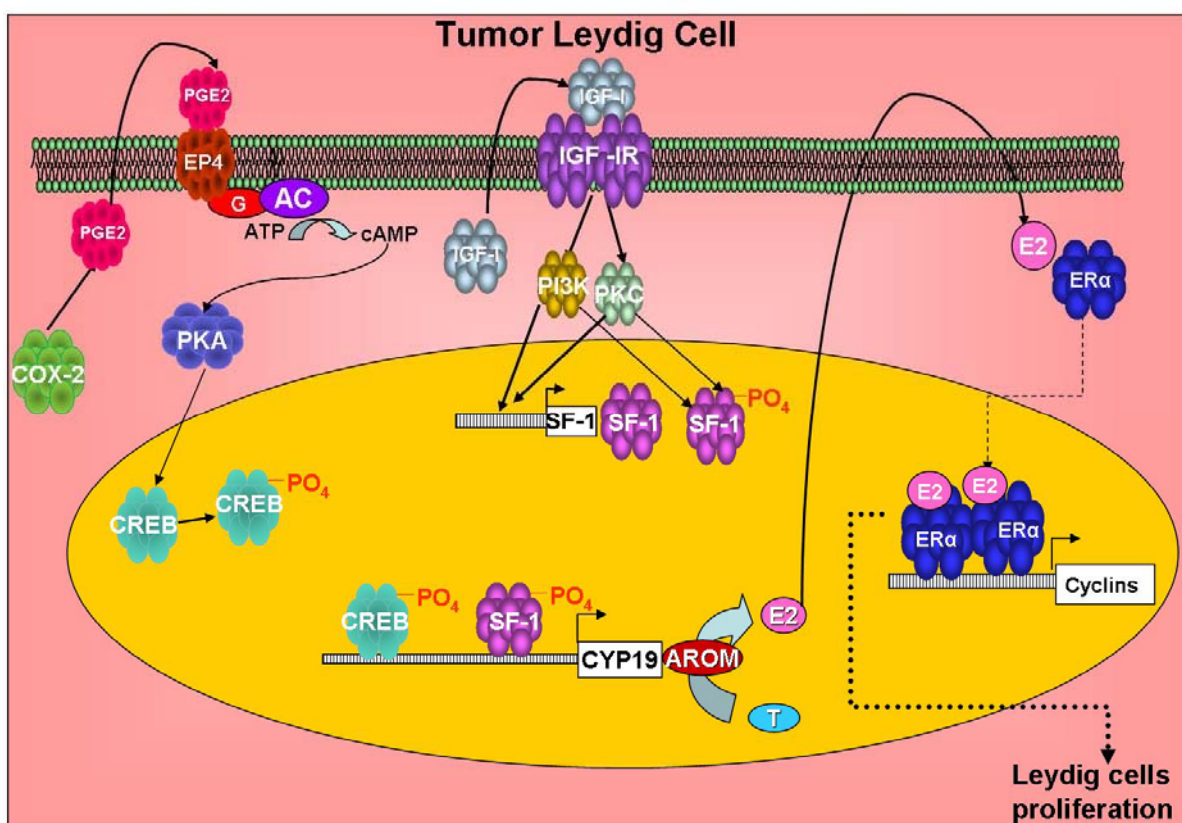


Diagram 1. Schematic model showing the mechanism of tumor Leydig cell proliferation.

Targeted inhibition of COX-2 and/or PGE2 are now regarded as potential strategies to stop completely the occurrence or progress of cancers. Selective COX-2 inhibitors are used for treatment of colorectal polyps in humans (243;314;315) women with high grade cervical dysplasia (316), and experimental studies showed that specific inhibition of COX-2 or PGE2 led to significant *in vivo* tumor reduction in murine lung cancer models (244).

In fact, the observation that antiestrogens and aromatase inhibitors, IGF-I signalling blockers as well as COX-2 inhibitor are able to reduce R2C proliferation opens new perspectives on the adjuvant therapeutic approach of testicular cancer. Remains to explain which molecular mechanism(s) is responsible for the elevated IGF-I production in tumor Leydig cells. In vivo, administration of hCG increases IGF-I mRNA levels in rat Leydig cells (317). LH deprivation determines a decrease in BrdU incorporation as well as a decrease in mRNA levels of IGF-I and IGF-I receptor (318). These observations together with our data showing a decrease in IGF-I basal production after treatment with a PKA inhibitor (data not shown) suggest the possibility that LH can mediate its proliferative effects also by regulating IGF-I and its receptor in Leydig cells and that the altered LH/LHreceptor activated pathway in R2C cells could be the cause of IGF-I overproduction .

The mechanism determining COX-2 expression and if the constitutive activation of LH/LHr/PKA signalling in R2C cells may be involved in upregulation of IGF-I expression remains also to be explored.

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Insulin-Like Growth Factor-I, Regulating Aromatase Expression through Steroidogenic Factor 1, Supports Estrogen-Dependent Tumor Leydig Cell Proliferation

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Abstract

The aim of this study was to investigate the role of estrogens in Leydig cell tumor proliferation. We used R2C rat Leydig tumor cells and testicular samples from Fischer rats with a developed Leydig tumor. Both experimental models express high levels of aromatase and estrogen receptor α (ER α). Treatment with exogenous 17 β -estradiol (E₂) induced proliferation of R2C cells and up-regulation of cell cycle regulators cyclin D1 and cyclin E, the expression of which was blocked by addition of antiestrogens. These observations led us to hypothesize an E₂/ER α -dependent mechanism for Leydig cell tumor proliferation. In determining the molecular mechanism responsible for aromatase overexpression, we found that total and phosphorylated levels of transcription factors cyclic AMP-responsive element binding protein and steroidogenic factor 1 (SF-1) were higher in tumor samples. Moreover, we found that tumor Leydig cells produce high levels of insulin-like growth factor I (IGF-I), which increased aromatase mRNA, protein, and activity as a consequence of increased total and phosphorylated SF-1 levels. Specific inhibitors of IGF-I receptor, protein kinase C, and phosphatidylinositol 3-kinase determined a reduction in SF-1 expression and in IGF-I-dependent SF-1 recruitment to the aromatase PII promoter. The same inhibitors also inhibited aromatase expression and activity and, consequently, R2C cell proliferation. We can conclude that one of the molecular mechanisms determining Leydig cell tumorigenesis is an excessive estrogen production that stimulates a short autocrine loop determining cell proliferation. In addition, cell-produced IGF-I amplifies estrogen signaling through an SF-1-dependent up-regulation of aromatase expression. The identification of this molecular mechanism will be helpful in defining new therapeutic approaches for Leydig cell tumors. [Cancer Res 2007;67(17):8368–77]

Introduction

The etiology and pathogenesis of human testicular tumors are poorly defined. It has been reported that serum estrogen levels are elevated in patients with testicular germ cell cancer as a consequence of increased local estrogen production reflecting higher aromatase activity present in Sertoli and Leydig cells (1).

Ninety-five percent of all human testicular neoplasms arise from germinal cells whereas Leydig cell tumors are the most common tumors of the gonadal stroma (2).

In rodents, reproductive system tumors are uncommon in general, with the few exceptions of Leydig cell and ventral prostatic neoplasms in some rat strains (3) or non-inbred mice (4); however, analogously to the human (5), chronic administration of estrogens induces testicular tumors.

A useful model used to investigate whether excess estrogens might have a central role in the mechanism leading to testicular tumorigenesis are transgenic mice overexpressing aromatase and presenting enhancement of circulating 17 β -estradiol (E₂) levels (6). About half of the male mice are infertile and/or have enlarged testis and show Leydig cell hyperplasia and Leydig cell tumors (6), whereas the female mice reveal mammary gland hyperplasia associated with an altered expression pattern of proteins involved in apoptosis, cell cycle, growth, and tumor suppression (7). Whereas the effects of estrogen on mammary gland tumorigenesis in human and rodents are well known, the role of aromatase overexpression and *in situ* estrogen production in testicular tumorigenesis has not been clearly defined. In this study, we have investigated the molecular mechanisms causing aromatase overexpression and the effect of estradiol (E₂) overproduction on rat Leydig cell tumor proliferation. As an experimental model, we used the R2C rat Leydig tumor cell line; to validate our *in vitro* data in an *in vivo* model, we used Leydig cell tumors from older Fisher rats characterized by an exceptionally high incidence of spontaneous neoplasm with aging (8).

Aromatase activity is regulated primarily at the level of gene expression and is present in testicular somatic cells and along the maturative phases of male germ cells (9, 10). The *CYP19* gene that encodes aromatase has at least eight unique promoters that are used in a tissue-specific manner (11). The proximal promoter II regulates aromatase expression in human fetal and adult testis, R2C and H540 rat Leydig tumor cells, and purified preparations of rat Leydig, Sertoli, and germ cells (12, 13). Specific sequences seem to be mainly involved in aromatase expression: a sequence that contains a half-site binding nuclear receptors (AGGTCA) in position –90 in the rat binding steroidogenic factor 1 (SF-1; ref. 14) and cyclic AMP (cAMP)-responsive element (CRE)-like sequences binding cAMP-responsive element binding protein (CREB)/activating transcription factor protein family members (15, 16) localized upstream at a more distal position, in the rat in positions –169 (TGCACGTCA), –335 (TGAAGTCA), and –231 (TGAAATCA; ref. 17). Similar responsive elements (binding CRE and SF-1) have been reported for the steroidogenic acute regulatory (StAR) protein gene promoter (18) whose expression is regulated by insulin-like growth factor-I (IGF-I) signaling in Leydig cells. Because the StAR protein is involved in the transfer of cholesterol from the outer to the inner

Note: Supplementary data for this article are available at Cancer Research Online (<http://cancerres.aacrjournals.org/>).

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mitochondrial membrane, the rate-limiting and regulated step in steroidogenesis IGF-I plays an important role in the regulation of testicular steroid biosynthesis.

For these reasons, we investigated the role of IGF-I, a peptide also shown to have a role in testicular growth and development and in the control of Leydig cell number (19). IGF-I is produced locally in the testis, in Sertoli, Leydig, and peritubular cells derived from the immature rat testis and cultured *in vitro* (20, 21). The crucial role of IGF-I in the development and function of Leydig cells was highlighted by studies on *IGF-I* gene knockout mice (22, 23). The failure of adult Leydig cells to mature and the reduced capacity for testosterone production are caused by deregulated expression of testosterone biosynthetic and metabolizing enzymes (24). Expression levels of all mRNA species associated with testosterone biosynthesis are lower in the absence of IGF-I. However, this study did not investigate the effect of IGF-I on aromatase expression, although an effect could be supposed.

Starting from these findings, in this study we investigated whether a testicular overproduction of IGF-I could be one of the mechanisms determining aromatase overexpression in rat tumor Leydig cells through the activation of specific transcription factors. The elevated aromatase-dependent E_2 production in Leydig cells, through an autocrine/paracrine mechanism mediated by their own receptors, could contribute to the hormone dependence of testicular tumorigenesis by stimulating Leydig tumor cell proliferation.

Materials and Methods

Cell cultures and animals. TM3 cells (immature mouse Leydig cell line) were cultured in DMEM/F-12 supplemented with 5% horse serum (HS), 2.5% fetal bovine serum (FBS), and antibiotics (Invitrogen S.R.L.); R2C cells (rat Leydig tumor cell line) were cultured in Ham/F-10 supplemented with 15% HS, 2.5% FBS, and antibiotics (Invitrogen). Male Fischer 344 rats (a generous gift of Sigma-Tau), 6 (FRN) and 24 (FRT) months of age, were used for studies. Twenty-four-month-old animals presented spontaneously developed Leydig cell tumors, which were absent in younger animals. Testes of all animals were surgically removed by qualified, specialized animal care staff in accordance with the Guide for Care and Use of Laboratory Animals (NIH) and used for experiments.

Aromatase activity assay. The aromatase activity in subconfluent R2C cell culture medium was measured by tritiated water-release assay using 0.5 $\mu\text{mol/L}$ [1β - $^3\text{H}(\text{N})$]androst-4-ene-3,17-dione (DuPont NEN) as a substrate (25). Incubations were done at 37°C for 2 h under a 95%:5% air/ CO_2 atmosphere. Obtained results were expressed as picomoles per hour (pmol/h) and normalized to milligrams of protein (pmol/h/mg protein).

RIA. Before the experiments, TM3 cells were maintained overnight in DMEM/F-12 and R2C cells in Ham/F-10 (medium only). The estradiol content of medium recovered from each well was determined against standards prepared in low-serum medium using a RIA kit (DSL 43100; Diagnostic System Laboratories). Results of the assay were normalized to the cellular protein content per well and expressed as picomoles per milligram of cell protein.

To measure IGF-I concentration in testicular extracts, testes were weighed, homogenated in 500 μL of 0.05 mol/L Tris/HCl (pH 7.6) plus protease inhibitors, and then submitted to ultrasonication followed by centrifugation, as previously published (26). IGF-I content in testicular extracts and in medium recovered from each well of R2C and TM3 cells was determined following extraction and assay protocols provided with the mouse/rat IGF-I RIA kit (DSL 2900; Diagnostic System Laboratories).

Chromatin immunoprecipitation. This assay was done using the chromatin immunoprecipitation assay kit from Upstate with minor modifications in the protocol. R2C cells were grown in 100-mm plates.

Confluent cultures (90%) were treated for 24 h with AG1024 (Sigma), PD98059 (Calbiochem, VWR International S.R.L.), LY294002 (Calbiochem, VWR International), GF109203X (Calbiochem, VWR International), or for increasing times with 100 ng/mL IGF-I (Sigma), or left untreated. Following treatment, DNA/protein complexes were cross-linked with 1% formaldehyde at 37°C for 10 min. Next, cells were collected and resuspended in 400 μL of SDS lysis buffer (Upstate Technology) and left on ice for 10 min. Then, cells were sonicated four times for 10 s at 30% of maximal power and collected by centrifugation at 4°C for 10 min at 14,000 rpm. Ten microliters of the supernatants were kept as input (starting material, to normalize results) whereas 100 μL were diluted 1:10 in 900 μL of chromatin immunoprecipitation dilution buffer (Upstate Technology) and immunocleared with 80 μL of sonicated salmon sperm DNA/protein A agarose (Upstate) for 6 h at 4°C. Immunocomplex was formed using 1 μL of 1:5 dilution of specific anti-SF-1 antibody (provided by Prof. Ken-ichirou Morohashi, Division for Sex Differentiation, National Institute for Basic Biology, National Institutes of Natural Sciences, Myodaiji-cho, Okazaki, Japan) overnight at 4°C. Immunoprecipitation with salmon sperm DNA/protein A agarose was continued at 4°C until the following day. DNA/protein complexes were reverse cross-linked overnight at 65°C. Extracted DNA was resuspended in 20 μL of Tris-EDTA buffer. A 3- μL volume of each sample and input was used for PCR using CYP19 promoter II-specific primers. The PCR conditions were 1 min at 94°C, 1 min at 50°C, and 2 min at 72°C for 30 cycles using the following primers: forward, 5'-TCAAGGGTAGGAAATTGGGAC-3'; reverse, 5'-GGTGC-TGGAATGGACAGATG-3'. Amplification products were analyzed on a 1% agarose gel and visualized by ethidium bromide staining. In control samples, nonimmune rabbit immunoglobulin G was used instead of specific antibodies.

Real-time reverse transcription-PCR. Before the experiments, cells were maintained overnight in low-serum medium. Cells were then treated for the indicated times and RNA was extracted from cells using the TRizol RNA isolation system (Invitrogen). TRizol was also used to homogenize total tissue of normal (FRNT) and tumor (FRIT) Fisher rat testes for RNA extraction. Each RNA sample was treated with DNase I (Ambion), and purity and integrity of the RNA were confirmed spectroscopically and by gel electrophoresis before use. One microgram of total RNA was reverse transcribed in a final volume of 30 μL using the ImProm-II Reverse transcription system kit (Promega, Promega Italia S.R.L.); cDNA was diluted 1:3 in nuclease-free water, aliquoted, and stored at -20°C. Primers for the amplification were based on published sequences for the rat *CYP19*, rat *CREB*, and rat *SF-1* genes. The nucleotide sequences of the primers for *CYP19* were forward, 5'-GAGAACTGGAAGACTGTATGGAT-3', and reverse, 5'-ACTGATTCACGTTCTCCTTTGTCA-3'. For CREB amplification, we used the following primers: forward, 5'-AATATGCACAGAC-CACTGATGGA-3', and reverse, 5'-TGCTGTGCGAATCTGGTATGTT-3'; for SF-1 amplification, primers have been previously published (27). PCR reactions were done in the iCycler iQ Detection System (Bio-Rad) using 0.1 $\mu\text{mol/L}$ of each primer, in a total volume of 30- μL reaction mixture following the manufacturer's recommendations. SYBR Green Universal PCR Master Mix (Bio-Rad) with the dissociation protocol was used for gene amplification; negative controls contained water instead of first-strand cDNA. Each sample was normalized on the basis of its 18S rRNA content. The 18S quantification was done using a TaqMan rRNA Reagent kit (Applied Biosystems) following the method provided in the TaqMan rRNA Control Reagent kit (Applied Biosystems). The relative gene expression levels were normalized to a calibrator that was chosen to be the basal, untreated sample. Final results were expressed as *n*-fold differences in gene expression relative to 18S rRNA and calibrator, calculated using the $\Delta\Delta C_t$ method as follows:

$$n - \text{fold} = 2^{-(\Delta C_{t\text{sample}} - \Delta C_{t\text{calibrator}})}$$

where ΔC_t values of the sample and calibrator were determined by subtracting the average C_t value of the 18S rRNA reference gene from the average C_t value of the different genes analyzed.

Western blot analysis. R2C and TM3 cells or total tissue of FRNT and FRTT were lysed in ice-cold radioimmunoprecipitation assay buffer containing protease inhibitors (20 mmol/L Tris, 150 mmol/L NaCl, 1% Igepal, 0.5% sodium deoxycholate, 1 mmol/L EDTA, 0.1% SDS, 1 mmol/L phenylmethylsulfonyl fluoride, 0.15 units/mL aprotinin, and 10 μ mol/L leupeptin) for protein extraction. The protein content was determined by the Bradford method. The proteins were separated on 11% SDS-polyacrylamide gel and then electroblotted onto a nitrocellulose membrane. Blots were incubated overnight at 4°C with (a) antihuman P450 aromatase antibody (1:50; Serotec, MCA 2077), (b) anti-ER α (F-10) antibody (1:500; Santa Cruz Biotechnology), (c) anti-ER β (H-150) antibody (1:1,000; Santa Cruz Biotechnology), (d) anti-cyclin D1 (M-20) antibody (1:1,000; Santa Cruz Biotechnology), (e) anti-cyclin E (M-20) antibody (1:1,000; Santa Cruz Biotechnology), (f) anti-CREB antibodies [48H2 (1:1,000; Cell Signaling Technology) and AHO0842 (1:1,000; Biosource, Inc.); (g) anti-pCREB Ser¹³³ (87G3; 1:1,000; Cell Signaling Technology) or anti-pCREB Ser^{129/133} (1:1,000; Biosource, Inc.), (h) anti-SF-1 (1:1,000; provided by Prof. Ken-ichirou Morohashi), (i) anti-pSF-1 (1:1,000; provided by Dr. Holly A. Ingraham, Department of Physiology, University of California, San Francisco, San

Francisco, California), (j) anti-actin (C-2) antibody (1:1,000; Santa Cruz Biotechnology), and (k) anti-IGF-I receptor (IGF-IR; 1:800; Santa Cruz Biotechnology). Membranes were incubated with horseradish peroxidase-conjugated secondary antibodies (Amersham Pharmacia Biotech) and immunoreactive bands were visualized with the enhanced chemiluminescence Western blotting detection system (Amersham Biosciences). To ensure equal loading of proteins, membranes were stripped and incubated overnight with β -actin antiserum.

Cell proliferation assay. For proliferative analysis, a total of 1×10^5 cells were seeded onto 12-well plates in complete medium and allowed to grow for 2 days. Before the experiments, cells were maintained overnight in Ham/F-10 medium and were treated the next day with ICI 182780 (a gift from Astra-Zeneca), 4-hydroxytamoxifen (Sigma), and letrozole (a gift from Novartis Pharma AG) and E₂ (Sigma), or treated for 24 h with IGF-I alone or in combination with inhibitors, or incubated with an anti-IGF-I antibody (Santa Cruz Biotechnology). Control (basal) cells were treated with the same amount of vehicle alone (DMSO) that never exceeded the concentration of 0.01% (v/v). [³H]Thymidine incorporation was evaluated after a 24-h incubation period with 1 μ Ci of [³H]thymidine (Perkin-Elmer

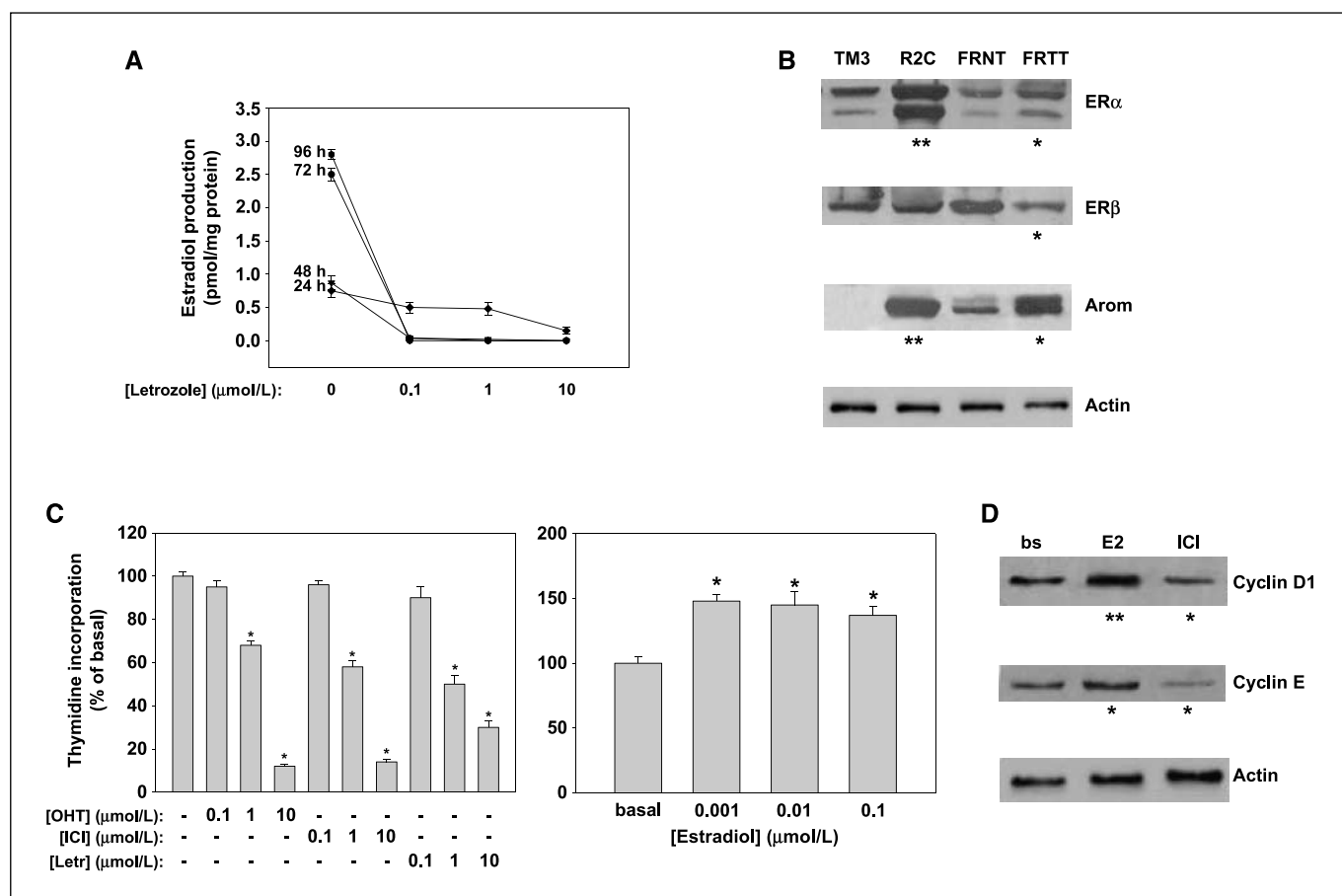


Figure 1. E₂ production and autocrine effects in R2C cells. **A**, cells were treated for the indicated times in HAM-F10 in the absence (0) or presence of aromatase inhibitor letrozole (0.1, 1, and 10 μ mol/L). Every 24 h, before renewing treatment, cell culture medium was removed and analyzed for steroid content. E₂ content in R2C culture medium was determined by RIA and normalized to the cell culture well protein content. Points, mean from three separate cell culture wells; bars, SE. **B**, Western blot analyses of ER α , ER β , and aromatase (*Arom*) were done on 50 μ g of total proteins extracted from TM3 and R2C cells or from tissues of normal (FRNT) and tumor (FRTT) Fisher rat testes. Representative of three independent experiments. β -Actin was used as a loading control. **C**, R2C cell proliferation was evaluated by [³H]thymidine incorporation analysis. Cells were treated for 96 h in HAM-F10 in the absence (–) or presence of antiestrogens hydroxytamoxifen (*OHT*) or ICI 182780 (*ICI*) or aromatase inhibitor letrozole (*Letr*) at the indicated concentrations or treated with estradiol (0.001–0.1 μ mol/L) for 24 h after being cultured for 48 h in serum-free HAM-F10, removing and renewing cell culture medium every 24 h. **D**, R2C cells were cultured for 48 h in serum-free HAM-F10; every 24 h, cell culture medium was removed and renewed. Cells were then treated for 24 h in the absence (basal, *bs*) or presence of estradiol (1 nmol/L) and ICI 182780 (1 μ mol/L) before extracting total proteins. Western blot analysis of cyclin D1 and cyclin E was done on 50 μ g of total proteins extracted from R2C cells. β -Actin was used as a loading control. Protein expression in each lane was normalized to the β -actin content and expressed as fold over control represented by normal cells (**B**) or basal condition (**D**). Normalized absorbances were subjected to statistical analysis; statistically significant differences are indicated (*, $P < 0.05$; **, $P < 0.01$, compared with basal or control).

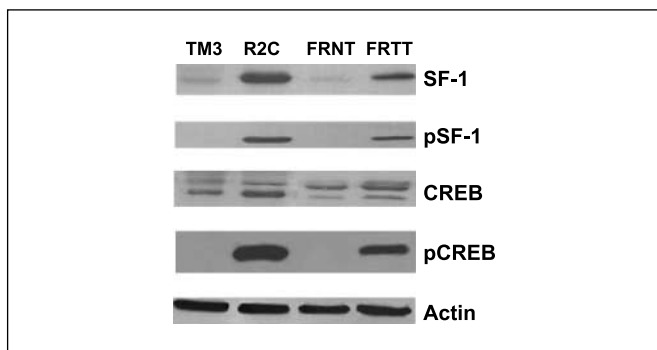


Figure 2. Expression of total and phosphorylated forms of SF-1 and CREB. Western blot analyses of SF-1, pSF-1, CREB, and pCREB were done on 50 µg of total proteins extracted from TM3 and R2C cells or from tissues of normal (FRNT) and tumor (FRTT) Fisher rat testes. Representative of three independent experiments with similar results. β-Actin was used as a loading control. Protein expression in each lane was normalized to the β-actin content.

Life Sciences) per well. Cells were washed once with 10% trichloroacetic acid, twice with 5% trichloroacetic acid, and lysed in 1 mL of 0.1 mol/L NaOH at 37°C for 30 min. The total suspension was added to 10 mL optifluor fluid and was counted in a scintillation counter.

Data analysis and statistical methods. Pooled results from triplicate experiments were analyzed by one-way ANOVA with Student-Newman-Keuls multiple comparison methods, using SigmaStat version 3.0 (SPSS).

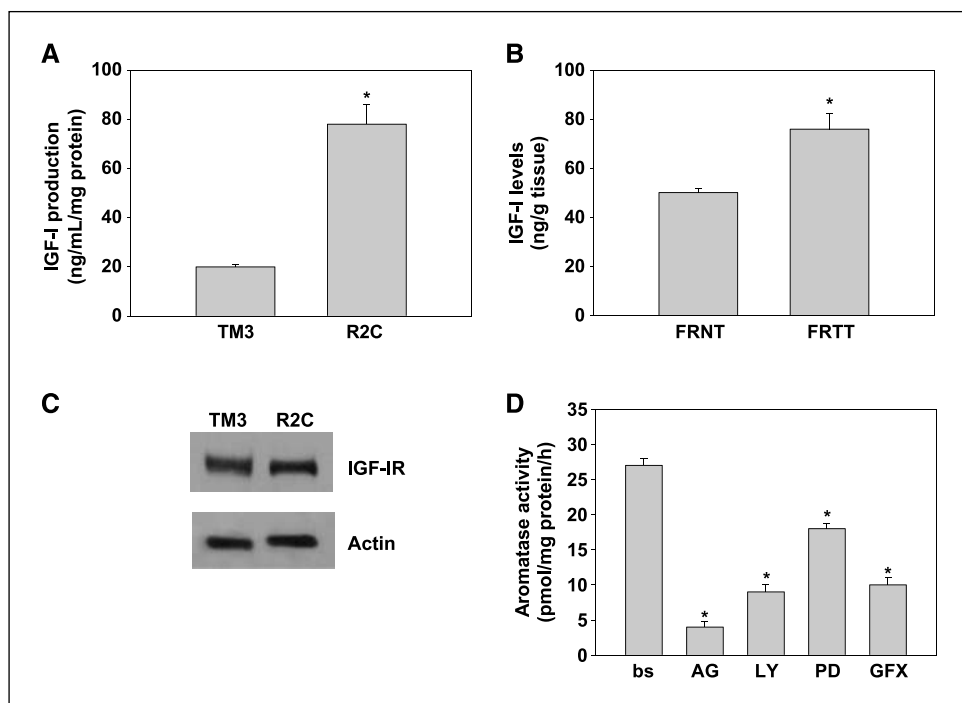
Results

Estradiol induces Leydig cell tumor proliferation through an autocrine mechanism. We carried out our study using R2C Leydig tumor cells as model system. These cells have been shown to have high aromatase expression and activity (14). We also used another Leydig cell line, TM3, as a normal control and analyzed testes from older and younger Fischer rats. Aged animals have a

high incidence of spontaneous Leydig cell neoplasm (8, 28), a phenomenon not observed in younger animals, allowing us to use them as a good *in vivo* model to confirm results obtained in cell lines. Our first step was to measure estradiol content in culture media of R2C and TM3 cells. Whereas E₂ levels in TM3 medium were extremely low (data not shown) in R2C cells, E₂ levels after 24 h were 0.5 pmol/mg protein and increased by 7-fold at 96 h (Fig. 1A). This production was dependent on high constitutive active aromatase activity because the presence of the aromatase inhibitor letrozole was able to decrease E₂ production at all doses and times tested (Fig. 1A). E₂ levels after 24-h treatment with letrozole were still detectable but were completely knocked down when we removed the medium after 24 h and renewed the treatment for an additional 24 h. The same effect was maintained at the other two time points investigated (Fig. 1A). Once estradiol is produced, it can exert its actions by binding to specific receptors, the estrogen receptors α and β (ERα and ERβ). Analysis of the two protein receptor isoforms in our models showed that tumor Leydig cells express both isoforms of ER (Fig. 1B). Particularly, the α isoform seems to be more expressed in R2C cells with respect to TM3 and in FRTT with respect to its control FRNT (Fig. 1B) in which ERβ, instead, is more expressed (Fig. 1B). In R2C as well as in FRTT, an increase in the ERα/ERβ ratio was observed (Supplementary Fig. S1A). Moreover, aromatase protein content is extremely high in tumor samples (Fig. 1B).

Our next experiments showed that ERs are required for proliferation through a short autocrine loop maintained by endogenous E₂ production in Leydig tumor cells. For instance, the use of both antiestrogens 4-hydroxytamoxifen and ICI 182780 and the use of the aromatase inhibitor letrozole determined a dose-dependent inhibition of cell proliferation (Fig. 1C). Among the different doses tested, the highest dose of 4-hydroxytamoxifen (10 µmol/L) was able to inhibit cell proliferation by 90%; 10 µmol/L ICI 182780, by 86%; and 10 µmol/L letrozole, by 70%. Moreover,

Figure 3. IGF-I production and autocrine effects in Leydig cells. A, TM3 and R2C cells were cultured for 24 h in serum-free medium and IGF-I levels in culture medium were determined by RIA. IGF-I levels were normalized to the cell culture well protein content. Columns, mean of three independent experiments each done in triplicate; bars, SE. B, total protein extracts from FRNT and FRTT were assayed for IGF-I content. IGF-I levels were normalized to the tissue weight. Columns, mean of three independent samples; bars, SE. *, P < 0.01, compared with control conditions, represented by TM3 cells or FRNT. C, Western blot analysis of IGF-IR in TM3 and R2C cells. β-Actin was used as a loading control. D, cells were treated with AG1024 (AG; 20 µmol/L), LY294002 (LY; 10 µmol/L), PD98059 (PD; 20 µmol/L), and GF109203X (GFX; 20 µmol/L). Aromatase activity was assessed by using the modified tritiated water method. Results obtained are expressed as picomoles of [³H]H₂O released per hour and normalized to the well protein content (pmol/h/mg protein). Columns, mean of three independent experiments each done in triplicate; bars, SE. *, P < 0.01, compared with basal.



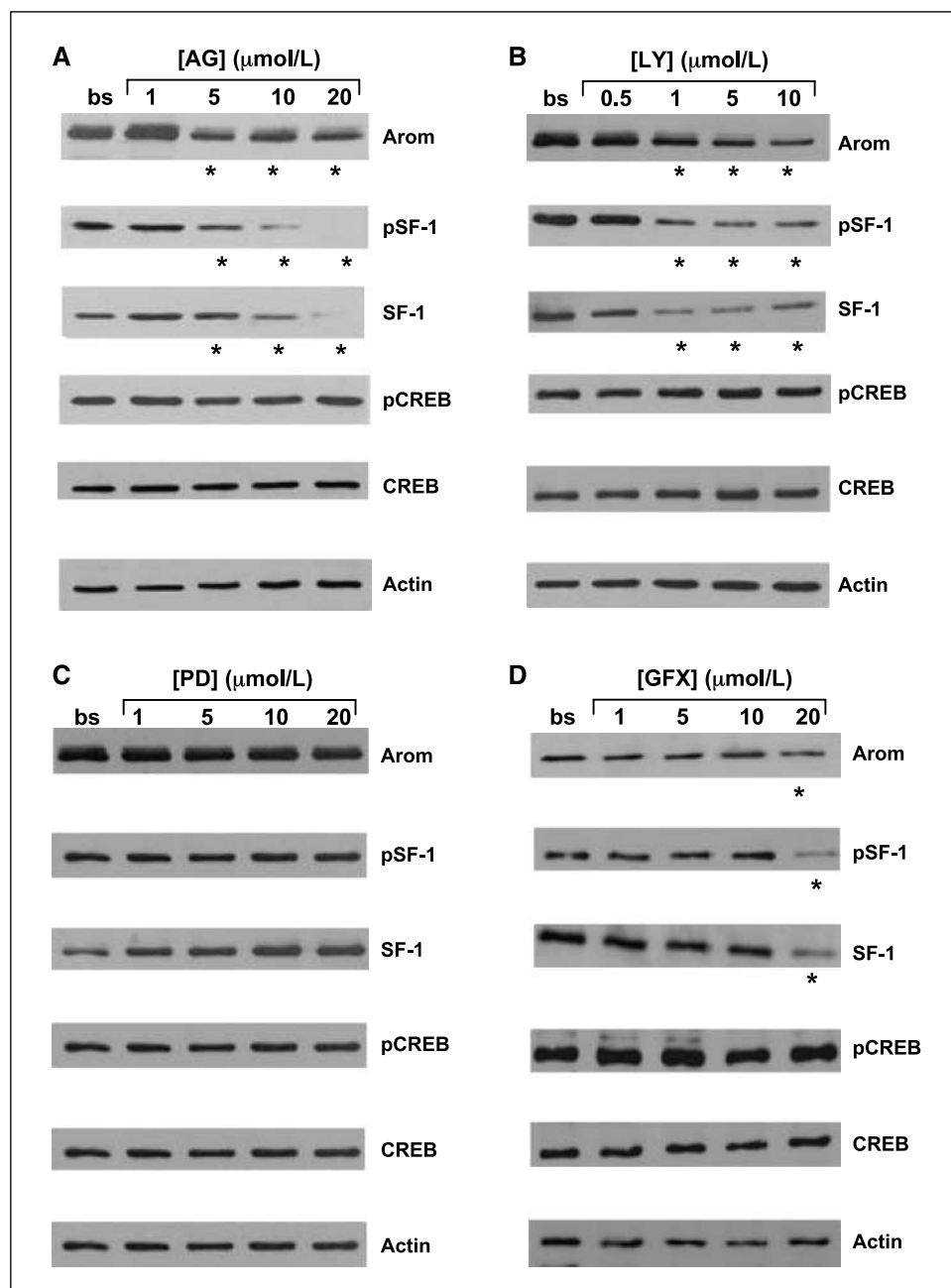


Figure 4. Effects of IGF-I pathway inhibitors on aromatase, SF-1, and CREB expression in R2C cells. *A* to *D*, Western blot analyses were done on 50 μg of total proteins extracted from R2C cells untreated (*bs*) or treated for 24 h with the indicated doses of AG1024 (*A*), LY294002 (*B*), PD98059 (*C*), and GF109203X (*D*). Representative of three independent experiments with similar results. β -Actin was used as a loading control. Normalized absorbances were subjected to statistical analysis; statistically significant differences are indicated (*, $P < 0.01$, compared with basal).

after starving cells for a prolonged time and changing the medium everyday to remove local E_2 production, we found that addition of 1, 10, and 100 nmol/L E_2 stimulated Leydig tumor cell proliferation (Fig. 1C), overcoming the inhibition induced by letrozole (Supplementary Fig. S1B). The stimulatory effect of E_2 was concomitant with increased levels of cell cycle regulators cyclin D1 and cyclin E, whose expression was inhibited by the pure antiestrogen ICI 182780 (Fig. 1D). All these results address how the classic $\text{E}_2/\text{ER}\alpha$ signaling may control Leydig cell tumor growth and proliferation similarly to what was observed in other estrogen-dependent tumors.

Aromatase overexpression is determined by constitutive activation of transcription factors SF-1 and CREB. Aromatase gene transcription in rat Leydig cells is driven by the PII promoter,

which is mainly regulated through three CRE-like sites and one NRE site binding SF-1 and LRH-1 (14, 27). Constitutively active levels of CREB have previously been shown in R2C cells (29). Here, we confirmed these data and showed that FRIT have a high phosphorylated CREB status (Fig. 2), together with enhanced expression and phosphorylation of SF-1, with respect to FRNT (Fig. 2). Furthermore, we showed the presence of high expression levels of SF-1 with the phosphorylated protein present in R2C but not in TM3 cells (Fig. 2).

IGF-I is produced by R2C cells and induces aromatase expression through phosphatidylinositol 3-kinase- and protein kinase C-mediated activation of SF-1. Starting from previous findings showing the ability of IGF-I to activate SF-1 and CREB, which leads to an increase in StAR transcription and then

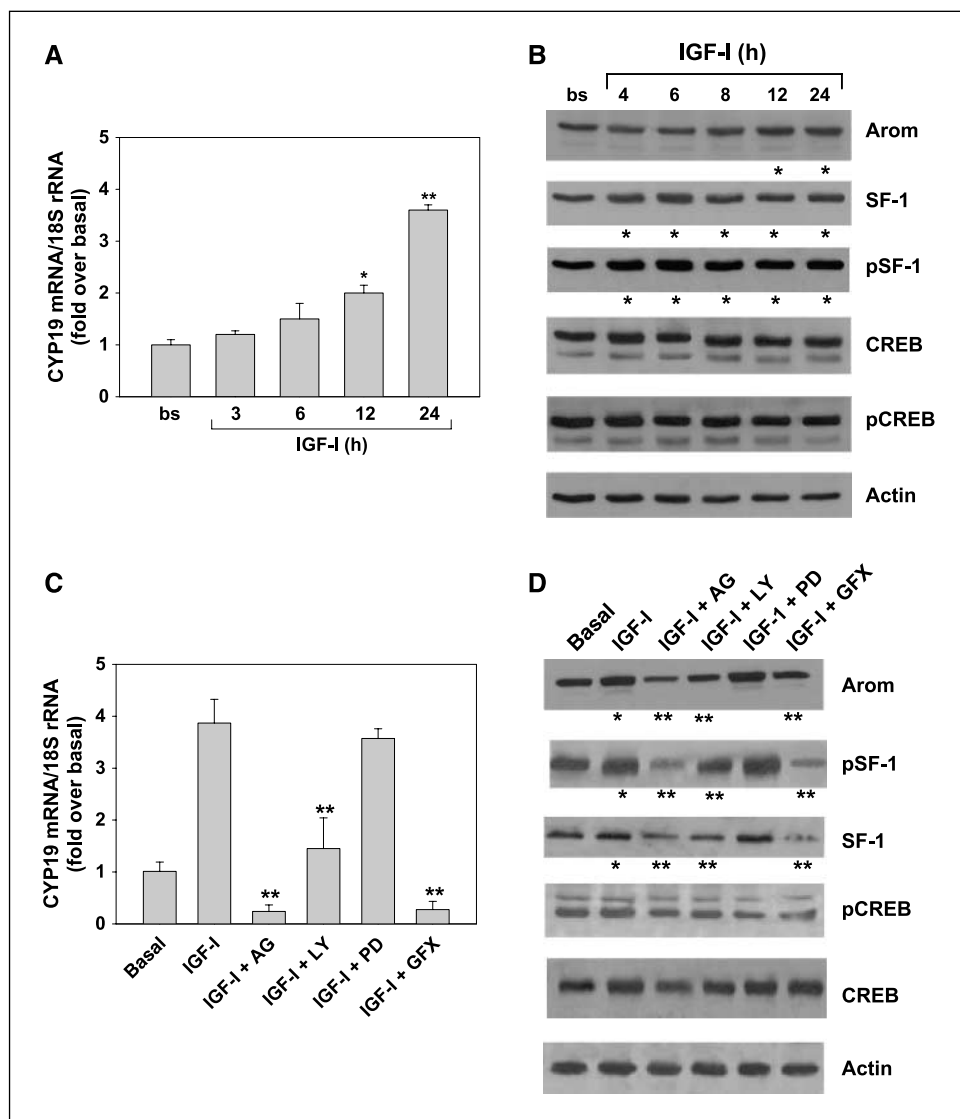
steroidogenesis (18), we investigated the role of this factor in regulating aromatase. Determination of IGF-I content in TM3 and R2C culture medium by RIA revealed a significant difference in growth factor production, with R2C cells producing ~4-fold higher IGF-I amounts (Fig. 3A). Moreover, we measured IGF-I content in testicular tissues, revealing a significant difference between FRIT and FRNT (Fig. 3B). IGF-I exerts its actions by binding to specific receptors (IGF-IR); however, we did not reveal differences in IGF-IR expression between TM3 and R2C cells (Fig. 3C).

On binding to IGF-IR, IGF-I activates three major transductional pathways: Ras/Raf/mitogen-activated protein kinase (MAPK), phosphatidylinositol 3-kinase (PI3K)/AKT, and phospholipase C (PLC)/protein kinase C (PKC). To show the involvement of IGF-I transductional pathways in modulating aromatase expression in Leydig cell tumors, we used specific inhibitors of IGF-IR (AG1024), extracellular signal-regulated kinase (ERK)-1/2 (PD98059), PI3K (LY294002), and PKC (GF109203X). The IGF-IR inhibitor was able to inhibit aromatase activity by 85%; LY294002 determined 65% inhibition; PD98059, 35%; and GF109203X, 61% (Fig. 3D). A similar inhibitory pattern, except for PD98059, was observed also on

aromatase mRNA (Supplementary Fig. S2A) and protein content (Fig. 4A-D). All of the different inhibitors, excluding PD98059, were able to reduce SF-1 mRNA (Supplementary Fig. S2B), whereas CREB remained unchanged (Supplementary Fig. S2C). Analysis of protein levels by Western blot confirmed the data from mRNA (Fig. 4A-D). Treatments with increasing doses of AG1024, LY294002, and GF109203X, but not PD98059, were able to induce a dose-dependent inhibition of total and phosphorylated levels of SF-1 without affecting CREB (Fig. 4A-D).

Addition of exogenous amounts of IGF-I was able to induce a significant increase of 2- and 3.8-fold in aromatase mRNA at 12 and 24 h, respectively (Fig. 5A). Aromatase protein levels under the same treatments reflected the mRNA data (Fig. 5B). Analysis of expression levels of total and phosphorylated forms of transcription factors SF-1 and CREB showed an increase in SF-1 and pSF-1 in the presence of IGF-I starting at 4 h, whereas no differences were observed for CREB at any of the investigated times (Fig. 5B). AG1024, LY294002, and GF109203X were able to inhibit IGF-I effects on CYP19 mRNA and protein levels (Fig. 5C and D) as a consequence of a decreased SF-1 expression (Fig. 5D).

Figure 5. Effects of IGF-I on aromatase, SF-1, and CREB expression in R2C cells. Cells were treated in serum-free medium for the indicated times with IGF-I (100 ng/mL) or for 24 h with AG1024 (20 μmol/L), LY294002 (10 μmol/L), PD98059 (20 μmol/L), and GF109203X (20 μmol/L), alone or in combination with IGF-I (100 ng/mL). *A* and *C*, total RNA was extracted from R2C cells untreated or treated as indicated. Real-time reverse transcription-PCR was used to analyze CYP19 mRNA levels. *Columns*, mean of values from three separate RNA samples; *bars*, SE. Each sample was normalized to its 18S rRNA content. *, *P* < 0.01; **, *P* < 0.001, compared with basal. *B* and *D*, Western blot analyses were done on 50 μg of total proteins extracted from R2C cells untreated (basal) or treated as indicated. Representative of three independent experiments with similar results. β-Actin was used as a loading control. Normalized absorbances were subjected to statistical analysis; statistically significant differences are indicated (*, *P* < 0.01, compared with basal; **, *P* < 0.01, compared with IGF-I).



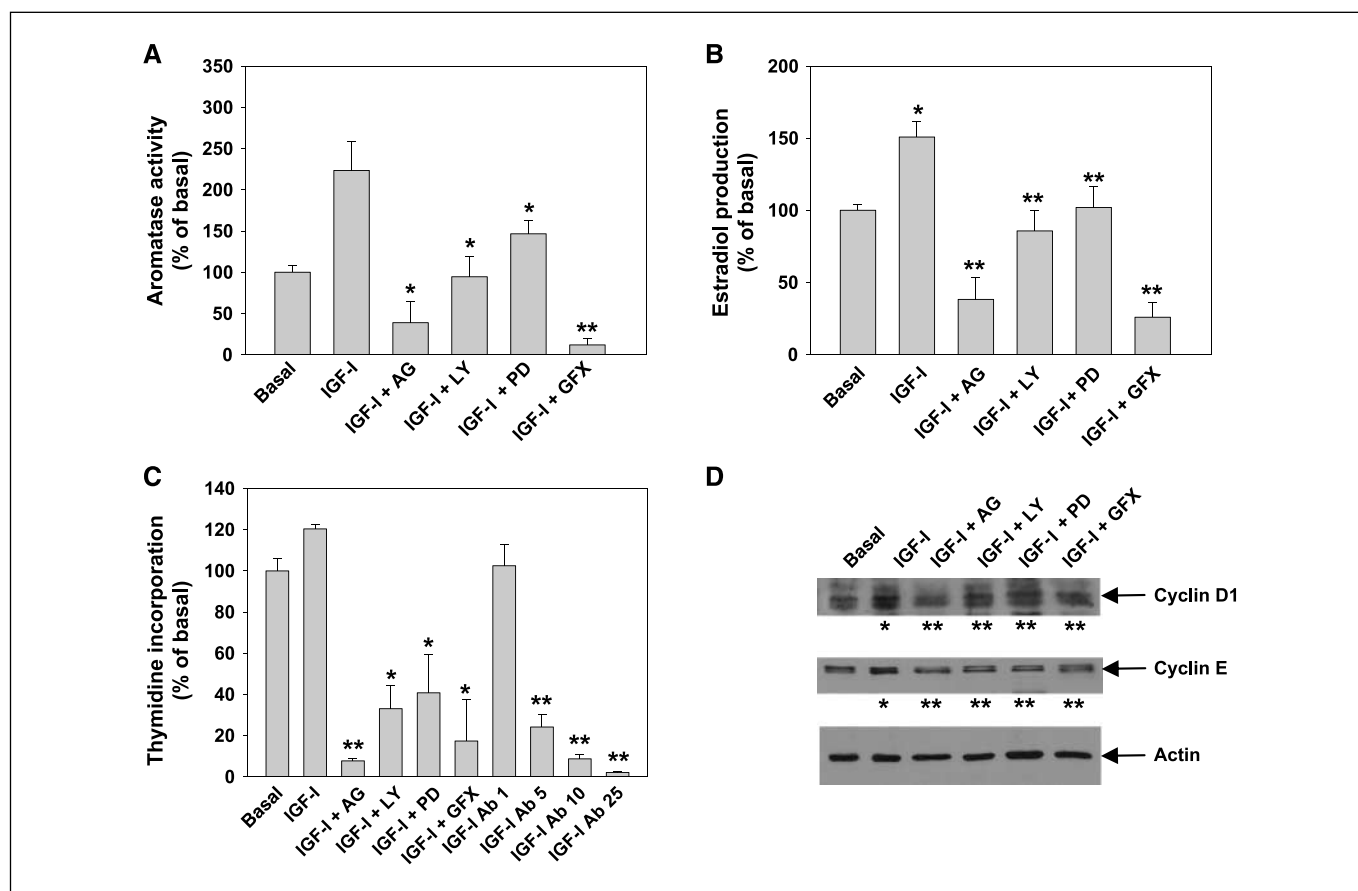


Figure 6. Effects of IGF-I and IGF-I pathway inhibitors on estradiol production and R2C cell proliferation. Cells were treated in serum-free medium for 24 h with IGF-I (100 ng/mL) alone or in combination with AG1024 (20 μ M), LY294002 (10 μ M), PD98059 (20 μ M), and GF109203X (20 μ M). **A**, aromatase activity is expressed as percent of basal. **Columns**, mean of three independent experiments each done in triplicate; **bars**, SE. *, $P < 0.01$; **, $P < 0.001$, compared with IGF-I. **B**, R2C cells were maintained for 48 h in serum-free medium, before being treated for 24 h. E_2 content in R2C culture medium was determined by RIA and normalized to the cell culture well protein content. **Columns**, mean percent of untreated (basal) cells (100%) from three independent experiments each done in triplicate; **bars**, SE. *, $P < 0.05$, compared with basal; **, $P < 0.01$, compared with IGF-I. **C**, R2C cell proliferation was evaluated by [3 H]thymidine incorporation analysis. Cells were maintained for 24 h in serum-free medium and treated for 24 h as indicated. IGF-I antibody (IGF-I Ab) was added to the medium at 1, 5, 10, and 25 μ g/mL. **Columns**, mean percent of untreated (basal) cells (100%) from three independent experiments each done in triplicate; **bars**, SE. *, $P < 0.01$; **, $P < 0.001$, compared with IGF-I. **D**, Western blot analyses were done on 50 μ g of total proteins extracted from R2C cells treated as indicated. Representative of three independent experiments with similar results. β -Actin was used as a loading control. Normalized absorbances were subjected to statistical analysis; statistically significant differences are indicated (*, $P < 0.01$, compared with basal; **, $P < 0.01$, compared with IGF-I).

We also carried out chromatin immunoprecipitation assays to investigate how IGF-I influences binding of transcription factors to the aromatase PII promoter. The increase in SF-1 protein content that was seen under IGF-I treatment reflected an increase in SF-1 binding to the PII promoter (Supplementary Fig. S3A). Moreover, we evidenced how in basal conditions (Supplementary Fig. S3B), as well as after IGF-I treatment (Supplementary Fig. S3C), all the different inhibitors, but not PD98059, reduced SF-1 binding.

IGF-I-induced estradiol production modulates R2C cell proliferation. Treatment with IGF-I induces aromatase activity and estradiol production, which are decreased by AG1024, LY294002, and GF109203X, as well as by PD98059 (Fig. 6A and B). The observed changes in estradiol production modified R2C cell proliferative behavior (Fig. 6C). In addition, the use of an anti-IGF-I antibody in immunoneutralization experiments caused a dose-dependent inhibition in tritiated thymidine incorporation (Fig. 6C). The ability of IGF-I to stimulate, and that of the inhibitors to block, cell proliferation was linked to an alteration in cyclin D1 and cyclin E expression (Fig. 6D).

Discussion

The current study aimed to explain the molecular mechanism responsible for aromatase overexpression in tumor Leydig cells leading to a consequent excess of *in situ* estradiol production that sustains tumor cell growth and proliferation.

The mammalian testis is capable of estrogen synthesis, which is regulated by different factors at different ages. In mature animals, aromatization of testosterone to estradiol is enhanced by luteinizing hormone (LH)/chorionic gonadotropin (CG) and not by follicle-stimulating hormone. The site of this synthesis seems to be age dependent, at least in some species such as the rat (30). Leydig cells are an elective target site of LH/CG that controls testosterone biosynthesis as well as its conversion to estradiol through aromatase activity. Alterations in local estrogen synthesis may have significant consequences in malignancy of these cells. In the present study, we observed that R2C cells release a conspicuous amount of E_2 from cellular storage in a time-dependent manner. In this condition, E_2 production ($1,300 \pm 230$ pg/ 10^6 cells/24 h) is significantly higher compared with E_2 levels produced by TM3 cells and by primary rat Leydig cell cultures (246 pg/ 10^6

3 β -hydroxysteroid dehydrogenase-positive cells/24 h; ref. 31). E₂ synthesis by R2C cells was abrogated by treatment with letrozole, addressing how steroid production is dependent on high constitutive aromatase activity. A strong increase in aromatase expression was observed in R2C cells compared with the normal cell line TM3 control, as well as in FRTT compared with FRNT. These findings agree with a previous study on human tissues showing that the increase in estrogen synthesis, as a consequence of a more intense aromatase activity, is higher in the Leydig cell tumor fraction than in normal tissues surrounding the tumor of the same patient (32).

Mediators of the physiologic effects of estrogens are ER α and ER β . An enhanced expression of ER α , resulting in an increased ER α /ER β ratio, was observed in R2C compared with TM3 cell line, as well as in FRTT compared with FRNT. This is in agreement with previous reports showing that transgenic mice overexpressing aromatase have an enhanced occurrence of breast and Leydig cell tumors together with an enhanced expression of ER α in the tumor tissue (6). The latter findings reasonably address how a short estrogen autocrine loop may be involved in breast and testicular tumorigenesis in the presence of an excess of locally produced estradiol. Indeed, an arrest of cell growth was observed following abrogation of local E₂ production with letrozole or after addition of ER α inhibitors ICI 182780 or 4-hydroxytamoxifen. Besides, only after changing the medium everyday along with prolonged R2C starvation, abolishing local steroid production, did we observe how exogenous E₂ was able to display proliferative effects.

One mechanism through which estrogens induce cell proliferation is by increasing protein levels of G₁ regulatory cyclins A, B1, D1, D3, and E in target cells (33). In our study, we showed that the expression of two of the most important regulators of Leydig cell cycle, cyclin D1 and cyclin E, can be increased by E₂ and down-regulated by treatment with antiestrogens. These data further confirm that aromatase overexpression and the consequent E₂ production may be the cause of altered cell cycle regulation of Leydig tumor cells.

In an attempt to explain the molecular mechanism determining aromatase overexpression in our tumor cell line, we focused our attention on the expression levels of transcription factors identified as crucial regulators of aromatase gene expression, CREB and SF-1. In the adult testis, SF-1 is predominantly expressed in Leydig cells (34). The increase of total and/or phosphorylated protein can potentiate SF-1 transcriptional activity (35). In R2C cells and in FRTT, compared with the normal controls, we found higher phosphorylated SF-1 protein levels as a consequence of elevated protein content. Total CREB levels were similar in all samples but highly phosphorylated in tumor samples. Starting from these observations, we investigated which pathways might be involved in the activation of these transcription factors.

The most important signal regulating Leydig cell function is the binding of LH to the LH receptor (LHR; ref. 36). Several observations indicate that constitutively active mutants of LHRs could be involved in Leydig cell transformation (37). It has been shown that the LH/LHR signaling pathway is constitutively active in the R2C tumor Leydig cell line and makes the phenotype of these cells constitutively steroidogenic (38). For instance, in the presence of a specific protein kinase A (PKA) inhibitor, constitutive syntheses of *Star* mRNA and steroids were significantly inhibited (39). These observations fit well with our findings indicating how the presence of PKA inhibitor determined a strong decrease in

aromatase activity, together with a drop in CREB phosphorylation (data not shown). Here, we show that the presence of a specific PKC inhibitor had no effects on CREB phosphorylation while SF-1 dropped dramatically.

It has been shown that CREB in mouse Leydig cells can be phosphorylated also through the PKC pathway activated by IGF-I (38). In this work, we have revealed that R2C tumor Leydig cells release higher levels of IGF-I in the culture medium with respect to TM3 cells, and the concentration of IGF-I in FRTT is increased with respect to FRNT. However, the exposure to IGF-I as well as to the treatment with inhibitors of IGF-I signaling did not affect the CREB phosphorylation status but decreased SF-1 phosphorylation, postulating separate mechanisms that control CREB and SF-1 activation in modulating aromatase activity.

It has been suggested that IGF-I can influence Leydig cell survival and proliferation (40, 41). Moreover, it has been shown that IGF-I up-regulates aromatase expression in primary cultures of rat Leydig cells through a cAMP-independent mechanism (42). Our findings led us to suppose that the elevated IGF-I levels derived from tumor Leydig cells *in vivo* and *in vitro* contribute to enhance aromatase expression through an autocrine mechanism activating SF-1. The important role played by IGF-I in Leydig cell tumorigenesis is further supported by the substantially unchanged IGF-IR expression level between TM3 and R2C cells. Binding of IGF-I to its receptor causes receptor autophosphorylation and the activation of an intrinsic tyrosine kinase that acts on various substrates, leading to activation of multiple signaling pathways including the PI3K/AKT and MAPK cascades. In addition, it has been shown that IGF-I can activate the PLC/PKC pathway (18). We treated R2C cells with specific inhibitors of IGF-I signaling (AG1024), ERK1/2 (PD98059), PI3K (LY294002), and PKC (GF109203X) in the presence or absence of IGF-I and revealed that addition of IGF-I itself was able to increase aromatase expression, activity, and estradiol production, whereas all the inhibitors determined a reduction of enzyme activity and estradiol release.

For instance, the inhibition of IGF-I signaling through inhibition of either the PI3K/AKT or PLC/PKC pathway was able to block SF-1 expression and protein phosphorylation. In particular, treatment with AG1024 blocked SF-1 phosphorylation more efficiently than the separate treatment with PI3K or PKC alone, addressing how both pathways may synergize in up-regulating SF-1 activity. In the presence of PD98059, SF-1 expression remained unchanged as did aromatase mRNA and protein levels. Importantly, aromatase activity and estradiol production seemed to be decreased in the presence of PD98059, suggesting a potential stimulatory role of ERK1/2 on the enzyme at a posttranscriptional level. Furthermore, we observed that SF-1 binding to the aromatase promoter II is enhanced by IGF-I and reduced by AG1024, LY294002, and GF109203X, but not by PD98059, indicating the central role of this transcription factor in regulating aromatase gene transcription in tumor Leydig cells. This is the first report of a direct link between SF-1 transcription and the IGF-I signaling pathway in regulating aromatase expression.

The observed changes in estradiol production due to IGF-I determined an effect on R2C cell proliferative behavior. In fact, inhibitors of IGF-I signaling or the use of an anti-IGF-I antibody in immunoneutralization experiments blocked thymidine incorporation. Moreover, IGF-I up-regulates cyclins D1 and E whereas IGF-I signaling inhibitors decrease the same factors, analogously to the antiestrogen ICI 182780.

From our findings emerges a double mechanism inducing enhanced expression of aromatase: (a) constitutive activation of the LH/cAMP/PKA pathway, which determines CREB activation; (b) enhanced IGF-I signaling potentiating SF-1 action. The enhanced activity of SF-1 in inducing aromatase expression may be maintained by the lack of DAX-1 (dosage-sensitive sex reversal, adrenal hypoplasia congenita, critical region on the X chromosome, gene 1) expression in R2C cells (29). DAX-1 is a specific corepressor of SF-1 (43, 44) and inhibits StAR expression and steroidogenesis by 40% to 60% when overexpressed in R2C cells (29). The lack of DAX-1 expression in R2C cells may be due to constitutively active PKA signaling because in a mouse Leydig cell line, a marked decrease of DAX-1 mRNA occurred within 3 h after addition of LH and forskolin (45). Then, the activation of LH/LHR/PKA pathway at the same time decreases DAX-1 expression and promotes SF-1 activity. A further demonstration of the role of DAX-1 in regulating P450 aromatase expression comes from the observations that in TM3 cells, IGF-I induces SF-1 expression but is unable to induce aromatase expression because DAX-1 is highly expressed (data not shown). Finally, the finding that in DAX-1 knockout mice aromatase is overexpressed selectively in Leydig cells (46) underscores the importance of this type of transcription factor in local testicular estrogen production *in vivo*.

It remains to be explained which molecular mechanism(s) is responsible for the elevated IGF-I production in Leydig tumor cells. *In vivo*, the administration of human CG increases IGF-I mRNA levels in rat Leydig cells (47). LH deprivation determines a decrease in bromodeoxyuridine incorporation as well as a decrease in IGF-I and IGF-IR mRNA levels (48). These observations suggest the possibility that LH can mediate its proliferative effects also by regulating IGF-I and its receptor in Leydig cells and that the altered LH/LHR-activated pathway in R2C cells could be the cause of IGF-I overproduction. Moreover, the observation that in murine Leydig cells IGF-I is able to increase LHR mRNA stability (49), together with data showing that the presence of an anti-IGF-I antibody

reduces the steroidogenic responsiveness to LH/human CG (50), also suggests the possibility of IGF-I action in sustaining LH/LHR signaling. Aromatase overexpression seems to be induced by the combined enhancement of LH/LHR and IGF-I signaling. Particularly, LH/LHR signaling determines a constitutive active CREB phosphorylation on aromatase gene promoter whereas IGF-I overproduction stimulates SF-1 binding on the same promoter through an autocrine mechanism. In other words, from this study, it emerges that the reproducibility of data between our *in vivo* and *in vitro* models is linked to an enhanced PKA activity, together with increased E₂/ER α and IGF-I signaling.

In conclusion, in this study we showed that in Leydig tumor cells, aromatase overexpression determines an excessive local estradiol production that is able to stimulate the expression of genes involved in cell cycle regulation sustaining cell proliferation. Aromatase overexpression seems to be concomitant with an enhanced IGF-I signaling in R2C cells as well as in our *in vivo* model, supporting the hypothesis of a cooperation between estrogen and IGF-I in Leydig cell tumorigenesis, which is also observed in other tumor tissues. The observation that antiestrogens and aromatase inhibitors as well as IGF-I signaling blockers are able to reduce R2C proliferation is indicative of possible applications of these drugs as new adjuvant therapeutic tools for the treatment of testicular cancer.

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