

**THE CONSEQUENCES ON THE RAT EPIDIDYMIS OF
INHIBITING 5-ALPHA-REDUCTASE**

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Dedication

This thesis is dedicated with much love and thanks to my family.

To my parents, Carl and Lillian, for their unconditional love, guidance and support throughout all my endeavours in life.

To my sister and brother, Tobi and Ryan, for their encouragement and lasting friendship.

To Scott, who shared this journey with me, I thank you for your love, immeasurable patience and unwavering belief in my capabilities.

ABSTRACT

The epididymis functions in the transport, maturation, storage and protection of spermatozoa. The structure and functions of the epididymis are dependent on androgens, primarily dihydrotestosterone (DHT). 5 α -Reductases (types 1 and 2) are thus key enzymes in this tissue because of their role in converting testosterone to DHT. The goal of this thesis was to examine the consequences on the rat epididymis and epididymal sperm of inhibiting DHT formation using novel dual 5 α -reductase inhibitors (i.e. inhibitors specific to both isoforms of 5 α -reductase). The first objective was to analyze the effects of 5 α -reductase inhibitor treatment on gene expression in the four epididymal segments (initial segment, caput, corpus and cauda epididymidis) using cDNA arrays. Treatment had highly segment specific effects on epididymal gene expression. Affected genes included those involved in fatty acid and lipid metabolism, regulation of ion and fluid transport, luminal acidification, oxidative defense and protein processing and degradation; these are essential processes contributing to the formation of an optimal luminal microenvironment required for proper sperm maturation. The next objective was to determine whether the observed changes in gene expression actually translated into effects on epididymal sperm functions. Fertility and several key facets of epididymal sperm maturation were analyzed. The percentages of motile and progressively motile sperm from the cauda epididymidis decreased and characteristic sperm motion parameters were altered. An elevated proportion of sperm from this region also retained their

cytoplasmic droplet. Matings with treated males resulted in fewer successful pregnancies and a higher rate of preimplantation loss. Lastly, cDNA arrays and quantitative real-time RT-PCR were used to elucidate potential signaling mechanisms via which DHT mediates and/or regulates its differential effects on epididymal gene expression and functions. Analysis of the expression of the 5 α -reductase isozymes, androgen receptor and members of the IGF, FGF, TGF and VEGF families revealed novel segment-specific expression profiles in the epididymis that were differentially affected by 5 α -reductase inhibition. Collectively, these studies established dual 5 α -reductase inhibition as a useful approach to study DHT action in the epididymis and revealed many novel aspects of epididymal physiology as well as avenues for future research.

RÉSUMÉ

L'épididyme est impliqué dans le transport, la maturation, le stockage et la protection des spermatozoïdes. La structure et les fonctions de l'épididyme dépendent des androgènes, principalement de la dihydrotestostérone (DHT). Les enzymes 5 α -réductases de types 1 et 2 jouent un rôle clé au niveau de l'épididyme en convertissant la testostérone en DHT. L'objectif de cette thèse a été de déterminer les effets de l'inhibition de la formation de DHT sur l'épididyme et les spermatozoïdes chez le rat en utilisant de nouveaux inhibiteurs doubles de 5 α -réductases (i.e. inhibiteurs spécifiques aux deux types d'isoformes). Le premier objectif a été d'analyser les effets de l'inhibition des enzymes 5 α -réductases sur l'expression des gènes au niveau des quatre segments épididymaires (le segment initial, le caput, le corpus et le cauda) à l'aide de microdéploiements (microarray) d'ADNc. Ce traitement a induit des effets hautement spécifiques sur l'expression des gènes en fonction du segment épididymaire. Les gènes affectés incluent ceux impliqués dans le métabolisme des acides gras et des lipides, la régulation du transport des ions et des fluides, l'acidification de la lumière, les défenses oxydatives et le traitement ainsi que la dégradation des protéines; des processus essentiels qui contribuent à la formation d'un microenvironnement optimal nécessaire à la maturation des spermatozoïdes. Le second objectif a été de déterminer si les changements observés au niveau de l'expression des gènes étaient répercutés sur les fonctions des spermatozoïdes épididymaires. La fertilité et différents aspects de la maturation des spermatozoïdes ont été analysés. Le pourcentage de

spermatozoïdes motiles et ceux ayant une mobilité progressive obtenus du cauda diminue et les paramètres caractéristiques du mouvement des spermatozoïdes sont altérés. Une proportion élevée de spermatozoïdes de ce segment épидидymaire ont retenu leur gouttelette cytoplasmique. L'accouplement de rats mâles traités a résulté en une diminution du nombre de grossesses et une augmentation du taux des pertes de pré-implantation. Finalement, des microdéploiements d'ADNc et l'analyse quantitative par qRT-PCR en temps réel ont été employés afin d'élucider les mécanismes potentiels de signalisation par lesquels la DHT transduit et/ou régule ses différents effets sur les fonctions et l'expression des gènes épидидymaires. L'analyse de l'expression des isozymes de la 5 α -réductase, du récepteur à androgènes, et des membres des familles des IGF, FGF, TGF, et VEGF ont révélé de nouveaux profils d'expression génique spécifiques à des segments de l'épididyme qui sont affectés de façons différentielles par l'inhibition des 5 α -réductases. L'ensemble de ces études établi que la double inhibition des 5 α -réductases est une approche utile à l'étude de l'action de la DHT au niveau de l'épididyme et a révélé plusieurs nouveaux aspects de la physiologie épидидymaire ainsi que de nouvelles possibilités pour de futures recherches.

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PREFACE

FORMAT OF THE THESIS

This is a manuscript-based thesis and conforms to section I.C. of the “Guidelines for Thesis Preparation” of the Faculty of Graduate Studies and Research of McGill University. This thesis is comprised of five chapters. Chapter one includes a general introduction to the male reproductive system and a comprehensive review of the literature regarding the structure, functions and regulation of the epididymis and the roles of 5 α -reductase in the male reproductive system. Chapter one concludes with the rationale for the studies presented in this thesis. Chapters two to four are data chapters presented as the duplicated text of published papers or papers submitted for publication. Chapter two was published in Journal of Endocrinology: Henderson NA, Cooke GM, Robaire B. Effects of PNU157706, a dual 5 α -reductase inhibitor, on gene expression in the rat epididymis. 2004 May;181:245-261. Chapter three was published in Biology of Reproduction: Henderson NA, Robaire B. Effects of PNU157706, a dual 5 α -reductase inhibitor, on rat epididymal sperm maturation and fertility. Biol Reprod. 2005 Feb;72:436-443. The copyright agreements of the respective publishers, Journal of Endocrinology by the Society for Endocrinology (<http://www.endocrinology-journals.org/>) and Biology of Reproduction by the Society for the Study of Reproduction (<http://www.biolreprod.org/>), permit the inclusion of these manuscripts in this thesis provided they are for non-commercial use. Chapter four has been submitted for publication. Connecting texts are included between these chapters

to ensure continuity of the thesis. Chapter five contains a summary and discussion of the results of this thesis and the List of Original Contributions. References are included at the end of each chapter. The appendix contains the ethics certificates for work on animal subjects and for the use of radioactive material, the proprietary rights notices for the Journal of Endocrinology and Biology of Reproduction and the co-author permission waiver for inclusion of manuscripts as part of this thesis.

CONTRIBUTIONS OF AUTHORS

All of the experiments and analyses were completed by the candidate with the sole exception of the *in vitro* 5 α -reductase activity assays included in chapters two and four. These assays were done by Dr. Gerry M. Cooke, who appears as a coauthor of these manuscripts; Dr. Cooke is affiliated with the Toxicology Research Division, Health Products and Foods Branch, Food Directorate, Health Canada, and the Reproductive Biology Unit, and Departments of Cellular and Molecular Medicine and Obstetrics and Gynecology of the University of Ottawa.

CHAPTER 1

INTRODUCTION

A. General Introduction: Male Reproductive System

The main focus of this thesis is the epididymis, however, in order to fully appreciate this unique tissue, it is necessary to understand the biological context in which it exists. Hence, a general overview of the structure, functions and regulation of the male reproductive system will be presented. Since androgens are crucial regulators of reproductive function, special focus is paid to the mechanisms of androgen action. The general background presented will also provide a means of comparing the regulation and functions of the epididymis to those of the other reproductive tissues. Consideration of the unique spermatozoa-related functions and regulatory mechanisms pertaining to the epididymis is imperative for the development of therapies that target the epididymis, for example, as a means of contraception. Later sections of the introduction will deal exclusively with the epididymis and the key role of 5 α -reduced androgens in this tissue.

In the simplest terms, the predominant role of the male reproductive system is to create and maintain functional spermatozoa and deliver them to the female reproductive tract. Achieving these tasks actually requires complex and coordinated interactions between the different cells, tissues and secretions of the male reproductive system.

1. The Testis

The testes are the primary organs of the male reproductive system. The testes occur in pairs and are located within the scrotum where a temperature 2-3

degrees lower than body temperature is maintained, a necessity for proper testicular function (1). The testis is protected by the tunica albuginea, a thick fibrous membrane composed of connective tissue and muscle fibers that encapsulates the testis and has contractile ability (2, 3). The testis is anatomically and functionally divided into two major compartments: the seminiferous epithelium and the interstitium. These compartments carry out the testicular functions of spermatogenesis and steroidogenesis, respectively. The complexity and significance of these processes warrant their own sections and are presented below.

The structural units of the seminiferous epithelium are the long, convoluted seminiferous tubules. Layers of peritubular myoid cells encase the seminiferous tubules; the tubules consist of both somatic cells (Sertoli cells) and developing germ cells. Sertoli cells were named after Enrico Sertoli who first described these very unique cells in the mid 1800s (4); since then, much has been learned about these tall, columnar cells that extend from the basement membrane to the lumen of the seminiferous tubule. Intercellular tight junctions between adjacent Sertoli cells form a major component of the blood-testis barrier, thus providing a protected and intimate environment for spermatogenesis to occur (5). Furthermore, the Sertoli cells are sustentacular or “nursing” cells with very unique shelf-like cytoplasmic processes that support and nourish the developing germ cells (6). As they differentiate, the germ cells progressively migrate across the seminiferous epithelium while maintaining essential contact with the Sertoli cells. This intimate physical association was first established by

Russell (6); since then the intricate communications between the Sertoli and germ cells have been extensively studied (reviewed in 7, 8). The cellular communication network is bi-directional and very elaborate involving paracrine factors, signaling molecules, proteases and antiproteases, transport/binding proteins, extracellular matrix components, energy metabolites and membrane components (7, 8).

The interstitium surrounds the seminiferous tubules and is comprised of blood vessels, lymphatics, nerves and several different cell types (9). Most notably, the steroid-producing Leydig cells are found in the interstitial space. Over 150 years ago, Franz von Leydig discovered these cells, noting their abundance and location in the testicular interstitium clustered around blood vessels and the seminiferous tubules (10). The significance of their anatomical location became apparent many years later upon the elucidation of the endocrine nature of these cells as the primary producer and supplier of testosterone to the blood stream and directly to the seminiferous epithelium (11). Leydig cell characteristics indicative of their steroidogenic role are the presence of abundant smooth endoplasmic reticulum, mitochondria with tubular cristae, and lipid droplets (12). Less common cell types in the interstitium include macrophages, monocytes, mast cells and fibroblasts (9, 13).

1.1. Spermatogenesis

In the early 1950s, landmark studies by Leblond and Clermont first defined the well-organized and highly regulated process of spermatogenesis (14). Each

spermatogenic cycle essentially consists of three phases. In the initial proliferative phase, diploid spermatogonial cells, from a self-renewing stem cell pool, undergo a period of mitotic divisions giving rise to spermatocytes, which then enter a meiotic phase (DNA synthesis and two meiotic divisions) that gives rise to haploid spermatids. In the last phase, termed spermiogenesis, the round spermatids mature morphologically into elongated spermatids. This is a critical process that not only involves the differentiation of sperm into the familiar head, midpiece and tail structures, but also the shedding of all but a small remnant of cytoplasm (cytoplasmic droplet), and nuclear events such as extensive chromatin remodelling (chromatin condensation) facilitated by the replacement of histones first by transition proteins and then by protamines (15, 16).

Spermatogenesis is a unique process that begins during fetal life, is arrested in infancy and restarts at puberty to continue throughout life in the male. The duration of the spermatogenic cycle differs among species (e.g., 64 days in humans, 49-52 days in rats (depending on the strain)), and new cycles are initiated prior to the completion of previous cycles such that older germ cells are continuously pushed toward the lumen (14, 17). These spermatogenic “waves” give rise to the distinctive stratification of the seminiferous epithelium, wherein groups of germ cells in different stages of development reside longitudinally within the same tubule. Upon reaching the luminal border, elongated spermatids disconnect from the Sertoli cells, cast off their excess cytoplasm (residual body) and are released as spermatozoa into the tubular lumen in a process called

spermiation (17). The residual bodies are engulfed and digested by the Sertoli cells (18).

1.2. Steroidogenesis

Testosterone is the primary male sex steroid. Greater than 95% of circulating testosterone is produced by the testicular Leydig cells (11). Within Leydig cells, cholesterol, the precursor of all steroids, is transferred from the outer to the inner mitochondrial membrane by steroidogenic acute regulatory protein (StAR), where the conversion of cholesterol to pregnenolone is catalyzed by the cholesterol sidechain cleavage cytochrome P-450 enzyme complex (P450ssc) (19). This is the rate-limiting step in the androgen biosynthetic pathway. The subsequent enzymatic steps occur in the smooth endoplasmic reticulum: 17 α -hydroxylase/C17-20-lyase converts pregnenolone to dehydroepiandrosterone, 17 β -hydroxysteroid dehydrogenase converts dehydroepiandrosterone to androstenediol, and finally 3 β -hydroxysteroid dehydrogenase converts androstenediol to testosterone (20).

While testosterone acts locally within the testis itself, the extent of its functions go well beyond the tissue where it is produced. Testosterone, bound to carrier proteins (i.e., SHBG and albumin), travels via the blood stream to carry out specific functions throughout the body. In addition to extratesticular components of the reproductive system, androgens also target many tissues including fat, muscle, bone, the central nervous system, the cardiovascular system and the immune system (21-25). Importantly, within specific target

tissues, testosterone can be reduced by 5 α -reductase to the more potent androgen dihydrotestosterone (DHT), or be converted to estradiol by the enzyme P450-aromatase (26, 27). These conversions allow testosterone to achieve an even greater range of complex physiological functions.

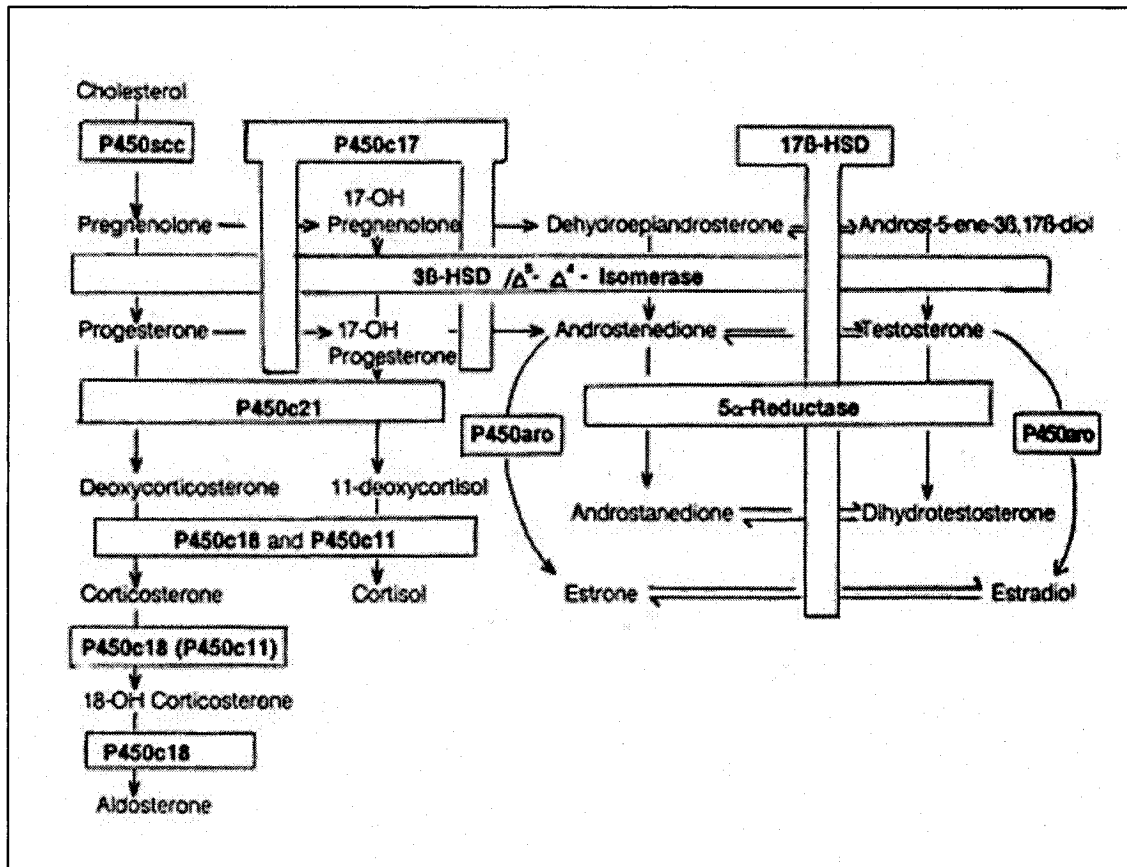


Figure 1. The steroidogenic pathway.

2. The Extratesticular Components

In addition to the testes, there are several other important components of the male reproductive system; these tissues include a series of sperm-conducting ducts, the sex accessory glands and the external genitalia (penis and scrotum).

2.1. The Excurrent Ducts

The sperm conducting tissues, referred to as the excurrent duct system, provide a pathway for sperm from the seminiferous epithelium in the testis to the site of ejaculation; sequentially, this pathway is comprised of the efferent ducts, epididymis, and vas deferens (28).

The rete testis, not technically part of the excurrent duct system as it is located within the testis, is a network of anastomosing channels lined by a cuboidal epithelium that collects sperm from the terminal ends of the seminiferous tubules. Connected to the rete testis are the efferent ducts (vasa efferentia) that carry sperm out of the testis proper. The efferent ducts are a series of straight or slightly convoluted tubules with a columnar epithelium that eventually anastomose to form one tubule that connects to the head of the epididymis. The efferent ducts are unique in that they are the only region in the excurrent duct system lined by cilia (29); initially thought to propel sperm towards the epididymis, it is now believed the cilia actually serve to mix the fluid contents of the lumen since these cilia do not beat in the same direction (30). Upon leaving the efferent ducts, sperm pass through the epididymis. The epididymis will be presented in depth in a subsequent part of this introductory chapter. The vas deferens (ductus deferens) is a straight muscular tube that transports sperm out of the epididymis upon ejaculation. Composed mainly of principal cells (columnar cells), the epithelium lining the proximal, distal and terminal regions of the vas deferens is morphologically distinct.

Several forces are involved in moving the sperm through the excurrent duct system, including hydrostatic pressure created by constant secretion of testicular fluid, contractions of the tunica albuginea of the testis, the peritubular myoid cells surrounding the seminiferous tubules, the smooth muscle surrounding the excurrent ducts and a vacuum force created by the ejaculation of stored sperm (28).

Originally viewed as a simple conduit system for sperm, it is now known that the excurrent duct system has more specialized roles. For example, it was postulated as early as 1920 that the epithelium of the efferent ducts had fluid reabsorption capabilities (31); this was confirmed in 1959 by tracer re-uptake studies (32). It is now known that, depending on the species, the efferent ducts are responsible for the reabsorption of up to 95% of the fluid produced by the testis (reviewed in 33). Furthermore, the reabsorption of fluid and the absorption and secretion of various molecules by the specialized epithelium lining the excurrent ducts actively modulates the composition of the luminal fluid bathing the sperm. Lastly, the efferent ducts and the vas deferens are also capable of spermiophagy (phagocytosis of spermatozoa) that usually occurs in response to abnormal conditions (e.g., tubule obstruction) but potentially under normal conditions as well (34-36).

2.2. The Sex Accessory Tissues

The sex accessory glands include the seminal vesicles and bulbourethral (Cowper's) glands, which occur in pairs, and the prostate (37). All species have

a prostate gland, while some species lack the seminal vesicles and/or bulbourethral glands. Located near the vas deferens-urethra junction, the predominant role of these glands is the secretion of seminal fluids that provide a vehicle for sperm at the time of ejaculation (37-39). The seminal vesicles contribute the largest amount of seminal fluid (~65%) and all together the sex accessory gland secretions make up greater than 95% of the ejaculate volume (37). The composition of the seminal fluid includes rich energy sources (sorbitol, fructose), protective factors such as buffering ions and proteins that shield the sperm from the foreign female reproductive tract environment, proteolytic enzymes that facilitate sperm penetration of the cervical mucous, prostaglandins believed to stimulate the female tract and some molecules of unknown function (e.g., spermine) (38, 40-42). Additionally, in rodent species, the seminal fluid coagulates to form a hard copulatory plug that ensures the retention and transport of sperm in the female reproductive tract (43).

B. Regulation of the Male Reproductive System

The regulation of the male reproductive system is extremely complex, involving numerous external and internal factors and the interplay between its different components. Many reviews have been published that extensively cover the numerous factors and mechanisms involved in the regulation of male reproductive function (28, 37, 44, 45). Therefore, the following section will only serve to present major regulatory mechanisms and some factors particularly

relevant to this thesis. Special attention is focussed on the roles of androgens and subsequently the mechanisms of androgen action.

1. The Hypothalamus-Pituitary-Testis Axis

Very early studies using the classic endocrinology technique of endocrine gland removal followed by replacement with glandular extracts first revealed the important neuroendocrine regulation of reproductive function mediated by the hypothalamus and pituitary (46, 47). The pulsatile release of gonadotropin-releasing hormone (GnRH) from the hypothalamus controls the synthesis and secretion of two circulating gonadotropins, luteinizing hormone (LH) and follicle stimulating hormone (FSH), from the anterior pituitary. Both LH and FSH target the testis; LH, secreted in a pulsatile fashion, stimulates Leydig cells to produce testosterone while FSH acts on the Sertoli cells and is required for the initiation of normal spermatogenesis. FSH also stimulates Sertoli cells to secrete androgen-binding protein (ABP), a carrier molecule for extracellular androgens.

The integrated hypothalamus-pituitary-testicular axis is controlled by complex negative feedback mechanisms. Testosterone feeds back to the hypothalamus and pituitary where it negatively controls the release of LH, and to a lesser extent FSH (48-50). The active metabolites of testosterone, estradiol and DHT, have different effects on the hypothalamic-pituitary-testicular axis; like testosterone, estradiol can also diminish LH release while DHT appears to have little or no effect on gonadotropin release (48, 50-53). In addition to steroidal feedback control, FSH secretion from the pituitary is also negatively regulated by

the Sertoli cell-produced peptide hormone inhibin, thus forming a separate testis-pituitary feedback loop (54, 55).

2. Steroid Hormones

Androgens are crucial regulators of sexual differentiation and development of the male phenotype and sexual maturation at puberty. Androgen insensitivity syndromes (AIS), caused by various androgen receptor gene mutations that impair androgen receptor function, unequivocally demonstrate the fundamental roles of androgens in male reproductive physiology (reviewed in 56). First described over 50 years ago, AIS range from the total abolishment of androgen receptor (AR) function causing complete feminization at birth, to partial disruptions of AR function resulting in different degrees of feminization or ambiguous genitalia, to subtle AR mutations that depress spermatogenesis while causing no overt sexual phenotype (56-58).

Testosterone and its active metabolite, DHT, both act via the single androgen receptor. DHT is more potent than testosterone due to a higher binding affinity for the AR leading to the formation of a more stable receptor-androgen complex (59-61). The relative potency of DHT is tissue dependent; in the prostate for example, DHT is approximately 4-5 times more potent than testosterone (62). Initially thought to simply amplify the action of testosterone, it is now also believed that DHT has biologically separate roles during development and sexual maturation, as well as in adulthood. Supporting this is the occurrence of mutations in the gene encoding 5 α -reductase, the enzyme responsible for

converting testosterone to DHT, that result in a unique form of male pseudohermaphroditism despite normal or elevated plasma testosterone levels (63). Though genetically male (46, XY) and possessing bilateral testes and normal internal Wolffian-duct structures (epididymides, vasa deferentia, seminal vesicles, ejaculatory ducts), individuals deficient in 5 α -reductase have highly underdeveloped prostates and ambiguous external genitalia at birth with subsequent virilization (including phallic growth) at the time of puberty (63, 64).

It is now commonly accepted that during embryogenesis, testosterone is responsible for the normal development of the Wolffian-duct structures and DHT is responsible for the development of the prostate, urethra, penis and scrotum that derive from the urogenital sinus and tubercle. Additionally, DHT appears to be responsible for sexual maturation at puberty characterized by altered facial and body hair growth patterns and maturation of the external genitalia while testosterone mediates the pubertal and post pubertal increase in muscle mass and the development of male sex drive (libido) (65, 66). Androgens are also fundamental for the control and maintenance of sexual function and behaviour during adulthood (65).

Testosterone, once secreted from the Leydig cell, binds to ABP and is maintained at very high concentrations within the testis where it is the primary hormonal regulator of spermatogenesis. Interestingly, the effect of testosterone on spermatogenesis is biphasic; depending on the dose, testosterone can both promote or inhibit the process *in vivo* (67-69). The testosterone-dependent regulation of spermatogenesis in different species has recently been reviewed

(70). In particular, several studies have demonstrated that testosterone is critical for later stages of spermatogenesis and spermiogenesis (68, 71-73) as well as spermiation (74).

O'Donnell et al. reported a peak in 5 α -reductase isoenzymes and 5 α -reduced metabolite production in the testis during puberty that coincided with the first wave of spermatogenesis in the rat, suggesting a role for 5 α -reduced metabolites in the initiation, but not the maintenance, of spermatogenesis (75). Earlier studies by this group showed that 5 α -reduced androgens are important for maintaining androgen action on rat spermatogenesis (particularly mid-spermiogenesis) only when testicular testosterone concentrations are experimentally reduced (76, 77). Under normal physiological conditions, the need to amplify testosterone signaling in the testis by conversion to DHT seems unlikely given that local testosterone concentrations are already extremely high. For example, within the human testis, testosterone concentrations are greater than 100-fold serum levels (78). Indeed, the very low levels of testicular 5 α -reductases present in the adult do not appear to play an important role in spermatogenesis.

While the testis is regarded as a primarily testosterone-dependent tissue, DHT is known to be the primary androgen acting in other reproductive tissues. The prostate is perhaps the most well characterized DHT-dependent tissue in the male reproductive system. This is largely due to the prevalence of two clinically important diseases (benign prostatic hyperplasia and prostate cancer) that has engendered numerous studies aimed at understanding the physiology of this

tissue. There are numerous reviews that describe the important role of DHT in the prostate (79, 80). The seminal vesicles are also highly dependent on androgens, and DHT is the primary androgen in this tissue (37, 81).

Furthermore, evidence indicates a role for DHT in seminal vesicle development, which brings into question the generally accepted role of testosterone in the development of this particular Wolffian-duct derived tissue (82). The roles for DHT in epididymal physiology will be discussed in later sections.

Clearly, androgens are the predominant hormonal regulators of reproductive function; however, roles for other hormones are quickly emerging. The ability of exogenous estrogen exposure to adversely affect spermatogenesis and male fertility was the first indication that estrogens may play a role in male reproduction (83, 84). A clear confirmation of the role of estrogen in the male is the perturbed reproductive phenotypes of recently generated transgenic mice lacking estrogen receptors or p450-aromatase (85-87). Interestingly, detailed histological studies of the estrogen receptor α knockout mice (ER α KO) carried out by Hess et al. have shown that the efferent ducts are primary targets for estrogen regulation (87, 88). The inability of the efferent ducts to carry out their primary function of fluid reabsorption is largely responsible for the impairment of spermatogenesis and fertility in the ER α KO mice. These observations highlight the important contributions of the extratesticular components of the male reproductive system to normal fertility.

3. Mechanisms of Androgen Action

The traditional mode of androgen action is via the androgen receptor, a classical nuclear receptor comprising an amino-terminal domain, a DNA-binding domain, a hinge region and a ligand-binding domain (89). Basically, within an androgen target cell, testosterone (or DHT depending on the target tissue) binds to the ligand-binding domain of the androgen receptor causing the dissociation of accessory proteins (e.g., heat shock proteins), receptor conformation changes that reveal the DNA-binding domain and subsequent translocation of the receptor into the nucleus where the DNA-binding domain interacts with specific DNA sequence elements (androgen response elements or AREs) on target genes to modulate transcriptional activity. The first link between steroid hormones and gene activation was established more than 40 years ago by Clever and Karlson (90) who injected the steroid ecdysone into insect larvae and observed changes in chromosome structure (so-called "puff reactions") within a certain time interval. Since then the genomic actions of steroid hormones have been firmly established and extensively reviewed (91-94). The discovery of coregulators has added a new layer of complexity to androgen receptor-dependent transcriptional regulation (reviewed in 95); essentially, coregulators (coactivators and corepressors) comprise a novel group of proteins that modulates the nuclear receptor transactivation function in a cell- and tissue-specific manner.

Interestingly, while the expression of many genes has been described as androgen-regulated, a biologically functional androgen response element (ARE) within the promoter and/or intronic regions of only a handful of genes has been

demonstrated thus far. The human prostate-specific genes PSA and hKLK2 and the rat prostate-specific genes probasin and the C subunit of prostatein are among these genes (96-99). Advances in genome sequencing should facilitate the identification of putative ARE sequences among known androgen-regulated genes as well as the discovery of candidate androgen-regulated genes.

In contrast to the well-characterized genomic events mediated by androgens, research accumulated over the past 20 years has revealed unequivocal non-genomic or “extranuclear” effects of these same hormones. These effects are rapid (seconds to minutes) and therefore incompatible with the classic genomic model of hormone action characterized by latent effects due to the time-course of transcriptional and translational events. Indeed, unlike the genomic effects, the non-genomic effects are insensitive to inhibitors of transcription and translation. These alternative steroid effects have been described for all classes of steroids and in a number of different tissues (reviewed in 100, 101).

In regards to the non-genomic effects of androgens in particular, testosterone has been shown to induce increases in Ca^{2+} levels by both influx of Ca^{2+} into target cells and Ca^{2+} release from intracellular stores, and to induce Ca^{2+} -mediated diacylglycerol and inositol 1,4,5-triphosphate formation (102-104). DHT has also been shown to rapidly and reversibly activate mitogen-activated protein kinases (MAPKs) in prostate cancer cell lines (105) and to interact with the Src/Raf-1/Erk-2 pathway (106, 107). As with other steroid hormones, the non-genomic actions of androgens are widely presumed to be mediated by cell-

surface membrane receptors as evidenced by studies using plasma-membrane impermeable testosterone-BSA conjugates (104). Treatment with antiandrogens either attenuates or does not affect the non-genomic actions of testosterone, indicating that the androgen receptor itself is likely only involved in some cases of non-genomic androgen action (100, 101). While the current knowledge of non-genomic steroid action is by no means complete, the diversity of the mechanisms of non-genomic actions is very evident and presents a fascinating and challenging new area of research.

4. Growth Factors

As with all tissues, growth factors have obvious roles in regulating the growth and development of the male reproductive system. Furthermore, growth factors are also known to figure prominently in reproductive tissue pathologies, for example, during tumour growth and benign prostatic enlargement (108-111). It is therefore not surprising that growth factors are thought to be involved in regulating the functions of normal adult reproductive tissues.

In the case of the testis, the expression, localization and production of components of several different growth factor systems (IGF, TGF, EGF, FGF, PDGF, NGF) have been characterized (reviewed in 112). IGF-1, for example, has well-documented effects on the gonad and data indicate that this particular growth factor is essential for reproductive maturation (reviewed in 113). Furthermore, IGF-1 is a potential regulator of adult neuro-endocrine functions via actions at the level of the hypothalamus where it is co-expressed with the IGF-1

receptor (113, 114). Other studies indicate that both IGF-1 and TGF- β 1 regulate Leydig cell function in an autocrine manner; IGF-1 is a positive regulator while TGF- β 1 inhibits Leydig cell function (115). In fact, the TGF- β family is one of the best characterized growth factor families acting in the testis; in addition to roles in testis development, various TGF- β isoforms are known to regulate spermatogenesis, steroidogenesis, extracellular matrix synthesis and Sertoli cell tight junction dynamics in this tissue (reviewed in 116).

In the case of the prostate, it is likely that the androgen sensitivity of this tissue is mediated by the production of peptide growth factors from stromal cells which act in a paracrine manner as direct intermediates of androgen action on epithelial cells (117). Different growth factors have stimulatory (e.g. FGFs, IGFs) and inhibitory (e.g. TGF- β 1) effects that maintain an equilibrium of prostate epithelial cell numbers (117). Interestingly, studies using prostate cell lines have provided evidence to support androgen receptor cross talk with growth factor signaling pathways, resulting in both enhanced androgen responses and receptor ligand-independent activation and modulation of androgen receptor transactivation (118-121).

Though the local expression and production of growth factors and growth factor receptors in healthy adult reproductive tissues certainly implies important functions for these molecules, for the most part, definitive local roles for most growth factor systems in these tissues remain unresolved. This is especially true for reproductive tissues other than the testis and prostate where data concerning growth factor expression, localization and production is even sparser.

C. The Epididymis

Early researchers in reproduction generally thought that sperm from the testis were already functionally mature, in other words, they were fully motile and possessed all the features required for fertilization of the egg. When it was observed as early as 1897 that fluid and sperm from the proximal and distal parts of the epididymis had different characteristics, a controversy on the role of the epididymis in sperm maturation was born (122, 123). Some researchers maintained that sperm were already fully mature before reaching the epididymis, others believed that sperm maturation was intrinsic to the germ cells themselves and was fulfilled by the time it took sperm to traverse the epididymis, while still others speculated that the epididymis, via its secretions, was actively involved in sperm maturation (124-127). This controversy lasted throughout much of the first half of the 20th century until renewed interest and advances in methodology allowed it to be resolved. An excellent historical perspective on the epididymis, from its earliest mention in the 4th century BC up to the present time, was documented by Orgebin-Crist and provides useful insight and accounts of the breakthroughs and advances in epididymal research over the years (128). In the late 1960s, pioneering studies by Orgebin-Crist (129) herself as well as Bedford (130) were the first to demonstrate that sperm maturation was not simply due to the passage of time, rather, the acquisition of motility and fertilizing ability required the exposure of sperm to the changing luminal environment of the epididymis. These findings finally revealed an important role for the epididymis in sperm maturation, sparking a renewed interest in this tissue. Since then,

research efforts devoted to increasing our understanding of epididymal physiology have dramatically increased. The following part of the introduction will focus on the structure, functions and regulation of the epididymis, highlighting the unique attributes of this tissue in comparison to other components of the male reproductive system.

1. Structure

Epididymides occur in pairs, one attached to the back of each testis. They are the major components of the excurrent duct system, receiving testicular inputs of sperm and fluid via the efferent ducts and emptying into the vas deferens (28, 131). The epididymis is a single, long and highly convoluted tubule comprised of two main compartments: the epididymal epithelium and the interior lumen. The lumen contains fluid with a complex and evolving composition and the maturing germ cells. The tubule is surrounded by connective tissue occupied by layers of smooth muscle, nerves, blood vessels and lymphatics (28, 131). Depending on the species, the tubule measures between 3 and 80 meters when unwound (132, 133) and it takes sperm approximately 8-11 days to travel from one end of the duct to the other (28, 134). The epididymis is structurally divided into four major segments: the initial segment closest to the testis, followed by the caput, corpus and cauda epididymides (28, 131, 135). These divisions are not only based on gross anatomical and morphological differences along the duct, but biochemical and functional differences as well. There is also evidence to suggest that the proximal part of the epididymis stems from a different

embryological origin (mesonephric tubules) than the rest of the duct (mesonephric or Wolffian duct) (136).

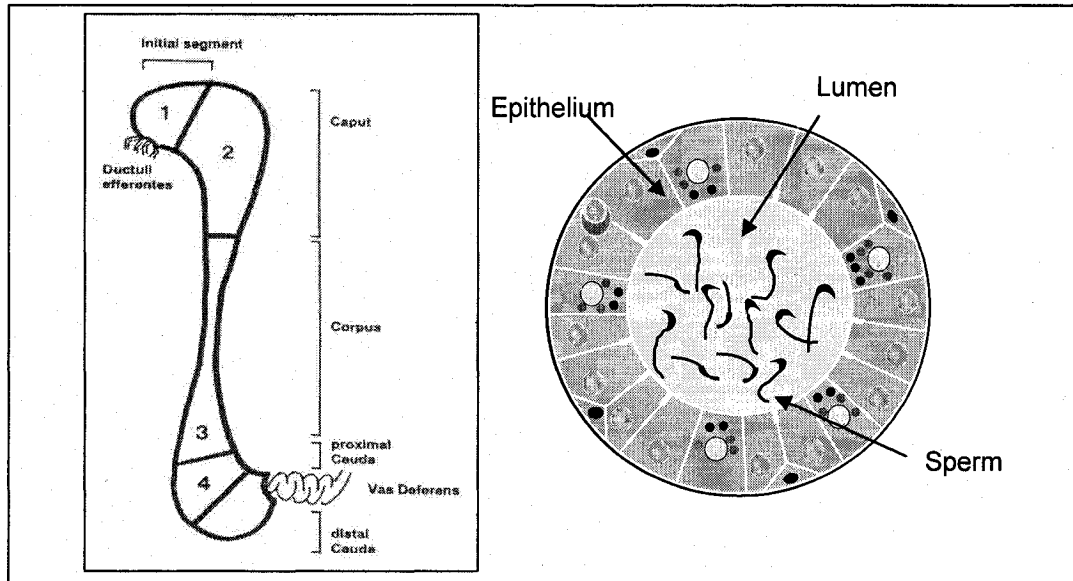


Figure 2. Epididymal segments and tubule compartments.

2. Histology

The epididymal epithelium is comprised of several different cell types; the presence and proportion of the different cell types is region-specific. A brief review of the different cell types will be presented. A more thorough description of the structural features of these cells can be found in comprehensive reviews (28, 137).

The principal cell is the predominant cell type within the epididymis. Present throughout the length of the duct, principal cells represent nearly 80% of the epithelial cell content in the initial segment and approximately 65% in the cauda epididymidis. The principal cells are columnar in shape and extend from the basement membrane to the lumen. They show regional differences in cell height; principal cells are very tall in the initial segment and become much

shorter in the cauda epididymidis. This is consistent with the increased luminal diameter of the more distal regions of the duct. Regional differences also exist in the appearance and organization of the secretory and endocytic organelles (28, 137). These differences likely reflect their different functions along the epididymis. Indeed, the coordinated secretory and endocytic activities of the principal cells and other epithelial cell types within the different epididymal segments directly modulate the composition of the luminal fluid (28, 137, 138-142). Exposure of the germ cells to the continuously changing luminal environment is crucial for proper sperm maturation, as will be discussed later on.

Basal cells are also found throughout the epididymis and constitute the second most abundant cell type in the epithelium (28, 137). Unlike principal cells, basal cells do not come in contact with the lumen; rather, they reside in between principal cells at the base of the epithelium in close contact with the basement membrane. Basal cells are flat, elongated cells with processes that extend along the basement membrane and sometimes up towards the lumen (143). Specific functions have yet to be ascribed to this cell type. A role in local immune defense has been proposed by some investigators who found that basal cells express macrophage antigens (144, 145); however, this feature appears to be species-specific (146, 147).

The clear cells are large cells that span the epithelium; they are most abundant in the cauda epididymidis but are also present in the caput and corpus epididymides. Clear cells have endocytic properties and are thought to actively remove material from the luminal compartment (28, 137). Part of this material

appears to be the contents of the cytoplasmic droplet that is shed from sperm as they transit through the epididymis (148).

The halo, narrow and apical cells are the least abundant cell types in the epididymis (28, 137). Halo cells are small cells located throughout the epididymis. Data exists to suggest that the halo cells are the primary immune cells in the epididymis; this cell type consists of helper T lymphocytes, cytotoxic T lymphocytes and monocytes (147). Narrow and apical cells are confined to the initial segment of the epididymis. Aside from endocytic capability, little is known regarding the function of either of these cell types.

2.1. The Blood-Epididymis Barrier

The blood-epididymis barrier prevents the transfer of materials from the general circulation into the epididymal lumen. Structurally, apical tight junctions between adjacent principal cells are responsible for the formation of the blood-epididymis barrier. Functionally, these cellular contacts are crucial for creating a protective and selective microenvironment for sperm maturation to occur (reviewed in 149).

The existence of a blood-epididymis barrier was first established in the early 1970s (150). In 1995, Cyr et al. observed that there were regional differences in the ultrastructural features of tight junctional complexes between epididymal principal cells (151). Ongoing work from Cyr's lab has focused on the characterization of the integral membrane proteins involved in epididymal tight-junction formation (e.g., cadherin, occludin, claudin-1); these studies, as well as

others, have contributed to our knowledge of the development, localization and regulation of tight-junctional complexes in the epididymis (149, 152-154).

3. Functions

In addition to sharing sperm transport functions with the other components of the excurrent duct system, the epididymis carries out other crucial sperm-related functions including sperm maturation, storage and protection.

3.1. Sperm Maturation

Sperm released from the testis are not yet functionally mature; in other words, they cannot swim or fertilize eggs. The acquisition of forward motility and fertilizing ability is referred to as maturation; sperm mature as they pass through the epididymis (129). While sperm passage through the epididymis is an absolute requirement for maturation, the exact region in the epididymis where sperm first acquire fertilizing potential varies among species. Generally, sperm become fertile by the time they reach the distal corpus/proximal cauda epididymidis (155-158). Similarly, sperm gain the potential for progressive motility by the time they reach the cauda epididymidis (155, 159). The gradual acquisition of potential for forward motility is reflected by the characteristic motion patterns of sperm isolated from the caput and cauda epididymides; caput epididymal sperm display a curved or circular swimming pattern, while cauda epididymal sperm are more vigorous and swim in a straight path (159).

3.1.1. Sperm Modifications During Epididymal Transit

In addition to the obvious changes in motility and fertilizing potential, several morphological and biochemical changes in spermatozoa also occur during epididymal transit (160). Morphologically, the most apparent change is the migration of the cytoplasmic droplet along the midpiece of the sperm and its eventual shedding in the distal regions of the epididymis (160, 161). Intracellular sperm organelles are also modified during maturation. For example, structural changes in several organelles, including the nucleus and mitochondria, arise due to the formation of stabilizing disulfide bonds (162, 163). The extensive remodelling of the lipid, protein and glycoprotein composition of the sperm plasma membrane is another feature of sperm maturation (164-167). The ratios of cholesterol:phospholipid and saturated:unsaturated fatty acids are altered in the maturing sperm membrane leading to changes in membrane fluidity (164, 168). The acquisition of new proteins and/or the modification of existing sperm membrane proteins is important for the capacitation of sperm in the female reproductive tract and sperm interaction with the female gametes (164, 165).

Since spermatozoa are generally considered to be biosynthetically inert once they leave the testis, maturational changes are necessarily mediated by proteins that were already present in sperm within the testis that become modified and activated in the epididymis (e.g., by proteolysis), or by the permanent or transient interaction of sperm directly with enzymes, binding molecules and other components present in the epididymal luminal fluid (165). Either way, sperm maturation ultimately relies on the proper functioning of the

epididymal epithelium, which controls the regional composition of the luminal fluid (169).

3.1.2. Creation of the Epididymal Luminal Environment

Micropuncture studies have been instrumental in determining the composition of the luminal fluid in the different epididymal regions (170). It is now known that the fluid microenvironment is very dynamic and dependent on the selective absorption and secretion of components by the epididymal epithelium (28, 137, 171). Major constituents include small organic molecules, ions, amino acids, peptides, proteins and lipids (172-177).

Many individual processes are involved in the formation of the luminal environment; these processes include fluid and ion transport, luminal acidification as well as protein and lipid secretion, processing and degradation.

3.1.2.1. Fluid and Ions

The major role of fluid transport across the epididymal epithelium is to concentrate sperm as they travel through the tubule (177); by the time spermatozoa reach the cauda epididymidis, they have been concentrated twenty-fold (171). In addition, this process regulates the concentration of constituents in the luminal fluid to which sperm are exposed.

Much of the fluid reabsorption occurs in the efferent ducts and the proximal portion of the epididymis (171). The expression of aquaporins (water channels), a local renin-angiotensin system and active ion transport are factors

involved in fluid transport (177, 178). In fact, the ionic composition of epididymal luminal fluid is markedly different in the different epididymal regions (177). Ions involved in mediating the absorption of water include chloride (caput) and sodium (cauda) (179, 180).

The ionic composition of the luminal fluid also determines its pH. In the rat, intraluminal pH decreases between the initial segment (pH 7.2) and the cauda epididymidis (pH 6.8) (181, 182). The distribution of luminal bicarbonate ions along the epididymis mirrors the pattern of pH decline (181, 183). In 1980, Au and Wong showed that the epithelial reabsorption of both bicarbonate and sodium ions were responsible for the decline in pH (184). Anion exchangers, ion channels, specific ATPases and carbonic anhydrase are implicated in the acidification process (176, 185, 186). Still, a specific role for luminal acidification in sperm maturation remains unclear. Several lines of evidence do however suggest a role for luminal acidification in sperm storage (176).

3.1.2.2. Proteins and Lipids

In earlier studies, SDS polyacrylamide gel electrophoresis was used to characterize the protein content of the luminal fluid from the different regions of the epididymis and compare it to that of blood or rete testis fluid (187, 188). These studies revealed very few similarities between the protein content of epididymal luminal fluid and blood or rete testis fluid; in addition, the protein profiles from the different epididymal regions differed markedly. The conclusion was that the epididymis must be able to synthesize and secrete new proteins into

the lumen. This was confirmed in 1980 by Brooks and Higgins who showed that epididymal tissues *in vitro* incorporated the radioactive amino acid precursor ³⁵S-methionine into new proteins and secreted them into the incubation medium (189). Since then, the characterization and identification of proteins secreted by the epididymal epithelium have been the focus of intense investigation (138, 190-192). Advances in proteomic analysis techniques have greatly aided in these tasks, allowing the elucidation of various secreted proteins including different types of binding proteins, glycosidases, antioxidant enzymes, clusterin, proteases and protease inhibitors (193, 194).

The sequential exposure of sperm to the various types of proteins synthesized and secreted by the epididymal epithelium is imperative for proper sperm maturation (139, 193, 194). Moreover, while fluid regulation assures the right quantity of proteins present in the epididymal lumen, the qualitative evolution of proteins along the tubule involves post-secretory events such as protein processing and degradation and reabsorption of proteins by the epithelium. Indeed, the ability of the epididymal epithelium to endocytose specific proteins has been demonstrated; for example, the endocytosis of androgen binding protein, clusterin, alpha-2 macroglobulin and transferrin has been characterized in the rat (140, 142, 195, 196).

The epididymal lumen contains many lipids and lipid substrates (176). The lipid-rich luminal environment is thought to be important for the maturation of the sperm plasma membrane as well as the maintenance of the apical membrane of epididymal epithelial cells. However, lipid-dependent mechanisms

that may mediate these events remain unresolved (164). Nevertheless, it is well established that the modification and exchange of sperm membrane lipids is an important feature of sperm maturation (166-168).

It has been known for many decades that some of the most highly concentrated constituents in the lumen are the phospholipid glycerylphosphorylcholine (GPC) and the organic compound carnitine (197, 198). Epididymal principal cells synthesize GPC and the concentration of GPC in the lumen increases towards the cauda epididymidis (197, 199). In addition to a presumed role in sperm membrane maturation, GPC and other phospholipids may act as oxygen radical scavengers in the lumen. Still, future studies are required to confirm the exact roles for lipids in epididymal function.

Carnitine is involved in the β -oxidation of fatty acids in tissues such as skeletal and cardiac muscle (200), however the reason for high carnitine concentrations in epididymal luminal fluid remains unresolved. The absorption of carnitine in the proximal epididymis may have a role in sperm motility (201, 202). Also, the infertility observed in male mice with a primary carnitine deficiency implicates a necessary role for carnitine in epididymal function (203).

3.2. Sperm Transport and Storage

It was initially thought that the only role of the epididymis was the transport of sperm from the testis to the site of ejaculation. As with other components of the excurrent duct system, the transport of sperm through the epididymis is mediated by hydrostatic pressure and contractions of smooth muscle

surrounding the tubule (28). Innervation of the epididymis is functionally important for epididymal contractility (204). The cauda epididymidis in particular has prominent innervation coinciding with the prevalence of smooth muscle in this region (205, 206). Neuronal input controls sperm movement through the tubule and expulsion of sperm into the vas deferens during ejaculation (204, 207).

The cauda epididymidis is the primary site for sperm storage. In mammals, between 50 to 80% of spermatozoa within the excurrent ducts are located in this region (208). Sperm have acquired full forward motility by the time they reach the cauda epididymidis, however they are kept in an immotile state until ejaculation (159, 209, 210). In the rat, immobilin, a large mucus-like protein secreted by the proximal epididymal segments, closely associates with sperm in the cauda epididymis rendering them immotile (141, 211). This interaction is thought to protect sperm from mechanical shearing forces during ejaculation. Clear cells in the distal cauda epididymidis selectively endocytose immobilin to maintain steady concentrations within the lumen (141). The acid pH of cauda luminal fluid may also play a role in the immobilization of sperm during storage, but this has yet to be confirmed *in vivo* (209, 212, 213).

3.3. Sperm Protection

The blood-epididymis barrier can protect sperm from most external factors by preventing their access to the luminal environment (149); however, sperm remain susceptible to damage from factors that arise internally. Spermatozoa

generate reactive oxygen species required for capacitation and chromatin condensation, however, spermatozoa are also highly susceptible to the damaging effects of reactive oxygen species (214). Antioxidant defense mechanisms are thus of great importance in the epididymis to protect maturing spermatozoa as well as the epididymal epithelium from oxidative damage.

The epididymis has many antioxidant defense mechanisms. Epididymal plasma contains vitamin E, zinc and taurine which can act as antioxidants (172, 215, 216). Important antioxidant and glutathione-cycle enzymes are also present. For example, indoleamine dioxygenase, superoxide dismutase and several glutathione peroxidases have been characterized in the epididymis (215-221). Moreover, high glutathione-S-transferase (GST) activity and the expression of different GSTs have been established in the epididymis (143, 222-224). Lastly, multiple gamma-glutamyl-transpeptidases (GGTs II-IV), enzymes responsible for glutathione degradation, are differentially expressed along the epididymis (225).

4. Gene Expression in the Epididymis

Underlying the many integrated functions of the epididymal epithelium is the controlled expression of a multitude of genes. A large amount of research has focused on examining gene expression in the epididymis (reviewed in 226-229). From these numerous studies, one major feature of epididymal gene expression has emerged, namely, epididymal gene expression profiles are highly segment specific. This is not surprising since segment-specific morphology,

biochemistry and function are hallmark characteristics of the tissue. Moreover, epididymal gene expression responds in a segment-specific manner to the experimental circumstances of androgen withdrawal, stress and aging (230-232).

Much like the diverse nature of proteins secreted by the epididymal epithelium, genes expressed in the epididymis encode a vast array of gene products (226-229). While the expression patterns of several epididymis-specific and/or epididymis-relevant genes have been analyzed along the epididymis, understanding the structure and function of this complex tissue requires more than analyzing the properties of isolated genes. Recently, gene array technology has provided a powerful method for large-scale, parallel gene expression analysis thereby generating greater insight into the link between epididymal gene expression and epididymal function (233). In conjunction with advances in genomic technology, proteomic studies are now possible due to the technique of matrix-assisted laser desorption/ionization (MALDI) imaging mass spectrometry (IMS). Using this technique to analyze mouse epididymal tissue sections and laser-captured microdissected epididymal cells, Chaurand et al. have monitored over 400 different protein profiles in the epididymis (234). The identity of only a few of these proteins is known, however, it was noted that more than 50 of these proteins show a regionalized epididymal expression or secretion pattern which is consistent with what is observed at the level of gene expression. Further elucidation of these proteins should contribute greatly to our understanding of epididymal physiology and allow specific links to be made between epididymal gene transcription, translation and function.

D. Regulation of the Epididymis

Many factors are involved in the regulation of epididymal functions, including estrogens, retinoids, growth factors and unidentified testicular factors (235-238). Androgens, however, are recognized as the primary hormonal regulators of epididymal structure and functions (239-241). As early as 1926, Benoit demonstrated that orchidectomy (removal of the testes) had consequences on the epididymis (242). It was determined a few years later that the testicular substance that maintained the epididymis was testosterone (243). When deprived of androgens, the epididymis atrophies and sperm do not survive (239, 242, 244). The structural, morphological, cellular and ultrastructural changes in the epididymis that occur in response to androgen withdrawal have been well documented (239, 245, 246). The following section focuses primarily on the androgen regulation of epididymal functions, though other modes of regulation are also addressed.

1. Steroid Hormones

The epididymis is a highly androgen-dependent tissue. Androgen sources include androgens directly input by the adjacent testis via the efferent ducts and circulating androgens supplied by the vasculature. Androgen levels in the testicular fluid entering the epididymis are approximately ten-fold higher than circulating androgen levels (247). Androgen action is mediated by binding of androgens to the androgen receptor; androgen receptor levels are relatively constant throughout the epididymis (248, 249). Additionally, androgens are also

expected to exert non-genomic effects in the epididymis, as they have been shown to do in other tissues (100, 101).

Several in vivo and in vitro studies have confirmed that it is not testosterone, but rather dihydrotestosterone (DHT), that is the main androgen acting in the epididymis (247, 250-254). Despite these important findings, little effort has focused on distinguishing between the effects of total androgens and DHT in the epididymis. Indeed, the main methodologies used to study the androgen-dependence of epididymal functions are based on the removal of total androgens by orchidectomy (often accompanied by testosterone replacement studies), suppression of androgen synthesis (GnRH antagonists, hypophysectomy) or blocking androgen action (AR receptor antagonists). Nevertheless, using these various methods, most of the previously described epididymal functions have been shown to be regulated by androgens (reviewed in 246). The role of 5 α -reduced androgens in the epididymis will be further discussed in a later section. The drastic effect of androgen withdrawal on epididymal sperm clearly reflects the crucial role for androgens in regulating all facets of epididymal function. Some of the epididymal epithelial processes that have been shown to be dependent on androgens include the transport of specific ions and small organic molecules across the epididymal epithelium and regulation of intraluminal pH. For example, androgens influence fluid balance in the epididymis by regulating sodium and anion transport across the epithelium (179, 255, 256). Additionally, the transport of carnitine and inositol across the epithelium is regulated by androgens (257, 258). The anti-androgen flutamide

has been shown to elevate epididymal luminal pH in rats, thus indicating that acidification is under the control of androgens (259).

Studies where androgens have been shown to regulate proteins and enzymes involved in the numerous epididymal functions at the mRNA, protein and/or activity levels are plentiful (246); the following cases constitute only a few representative examples. The regulation of protein processing enzymes such as cathepsin B (260, 261) and lipid metabolizing enzymes such as phospholipase A (262) is androgen-dependent. In regard to fluid transport, androgens modulate the epididymal expression of aquaporins (263) as well as specific components of the renin-angiotensin system, namely angiotensinogen and angiotensin II receptor type 1 (256, 264). The mRNA for the acidification enzyme carbonic anhydrase IV, predominantly expressed in the corpus epididymidis, decreases following androgen withdrawal by castration (186). The expression of another enzyme implicated in acidification, $H^+K^+ATPase$, depends on testosterone in all regions of the epididymis except the initial segment (265). Relating to the protective functions of the epididymis, orchidectomy and androgen replacement studies demonstrate that the epididymal glutathione S-transferases are under separate control and are differentially regulated by androgens (143, 266). Similarly, multiple gamma-glutamyl transpeptidases are differentially regulated by androgens in different segments of the epididymis (225). Lastly, androgens are known to regulate components of tight junctions in the epididymis that are critical for the formation of the protective blood-epididymis barrier (154, 267).

Less well characterized are the roles for other hormones in the regulation of epididymal functions. An important role for estrogens in regulating the uptake of fluid in the efferent ducts has already been clearly established. Whether this finding is indicative of a similar regulatory role for estrogens in the epididymis remains unclear, though the abnormal epididymal phenotype in ER α KO mice suggests that it is (88).

As early as 1975, Danzo speculated that estrogen could bind to receptors in the epididymis (268). Autoradiographical techniques confirmed this binding nearly ten years later (269). Unfortunately, attempts to differentiate between the estrogen receptor subtypes (ER α and ER β) in the epididymis using multiple immunocytochemical techniques have yielded conflicting results, particularly for ER α , necessitating further studies to clarify their localization within the epididymis (reviewed in 235). Notably, estrogen (estradiol) is an active metabolite of testosterone. There exists no evidence to date that estradiol can be synthesized by the epididymal epithelium. This is unlike the case for the other active metabolite of testosterone, DHT, which is well known to be made by the epididymis. Alternatively, germ cells can synthesize estrogen (270) and p450-aromatase has been localized to the cytoplasmic droplet attached to epididymal sperm (271). This suggests that the germ cells act as “endocrine” cells providing estrogen to the epididymis where it may be involved in regulating epididymal functions.

2. Testicular factors

It has been well established that the epididymis, in particular the initial segment, is dependent on the testicular input of factors other than androgens directly to the epididymal lumen (245, 272-275); depriving the epididymis of these testicular factors has well-documented effects on morphology and gene expression in the initial segment (28, 229, 238, 276). This type of regulation has been called "lumicrine" by some and refers specifically to "the regulation of cells via factors secreted or produced by another group of cells through a luminal or ductal system" (238, 274). Such regulation has been demonstrated by two different methods: efferent duct ligation (EDL) and orchidectomy followed by androgen replacement. EDL results in the blockage of direct testicular input to the epididymis but leaves androgen production (though not spermatogenesis) by the testes intact and thus capable of synthesizing and supplying androgens to the epididymis via the bloodstream; consequently, EDL allows a method of differentiating between the testicular delivery of androgens and nonandrogenic factors to the epididymis. Effects of EDL on the histology of the initial segment of the epididymis were reported over 25 years ago (272, 273). Orchidectomy generally induces a loss of function that can often be recovered by the reintroduction of exogenous androgens; a lack of recovery following androgen replacement indicates regulation by a non-androgenic testicular factor.

Many examples of lumicrine regulation of the epididymis exist. For instance, the accumulation of carnitine in the cauda epididymidis decreases with orchidectomy and carnitine uptake is only partially restored by subsequent

androgen replacement (277). Accordingly, carnitine accumulation in the cauda epididymidis also decreases after EDL (277). More often, lumicrine regulation is observed within the proximal regions of the epididymis, particularly the initial segment. For example, the expression of 5 α -reductase, gamma-glutamyl transpeptidase IV, claudin-1, proenkephalin and cystatin-related epididymal specific (CRES) in the initial segment is dependent on luminal factors from the testis (154, 225, 278-280).

3. Growth Factors

Investigation of growth factor systems in the epididymis has been fairly limited; however, several clues suggest they may play a key role in this tissue. Vascular endothelial growth factor (VEGF) protein has been shown to be localized in the rat epididymal epithelium in a region- and cell-specific pattern (281). Interestingly, the overexpression of VEGF in the testis and epididymis of transgenic mice causes infertility (282). This finding suggests a role for VEGF in the male reproductive system that is likely different from its classical role in regulating endothelial (blood vessel) growth and permeability. Future studies are needed to determine whether the infertility in these mice stems from a testicular or epididymal effect, or a combination of both. In a different animal model, the GH-deficient dwarf (dw/dw) rat, the administration of insulin-like growth factor 1 increases motility and improves morphology of immature spermatozoa (283). Again, whether an epididymal mechanism contributes to this effect is not yet clear.

Several different fibroblast growth factor (FGF) receptors are expressed in the initial segment of the rat epididymis (284). This is interesting since FGF is a candidate testicular factor that regulates the epididymis in a lumicrine fashion (237). It has also been suggested that certain growth factors secreted by the proximal epididymis may act as paracrine regulators of the more distal epididymal segments. Candidates for this paracrine mechanism of regulation include platelet-derived growth factor, transforming growth factor β and nerve growth factor (285-288). It thus seems plausible that several different growth factor systems are involved in epididymal regulation. Further investigation is needed to elucidate mechanisms of growth factor regulation in the epididymis and to determine their reliance on androgens.

E. 5α -Reductase

5α -Reductase (EC 1.3.1.22) is the enzyme that catalyzes the conversion of testosterone into DHT. In species including humans, monkeys, dogs, rats and mice, two isoforms of 5α -reductase have been identified and are termed type 1 and type 2 (289, 290). The presence of two isozymes that carry out the same reaction likely underscores the need for 5α -reduced androgens in male physiology. Research efforts focused on the characterization of both isozymes of 5α -reductase have revealed differences in sequence and chromosomal location as well as differences in tissue, cellular and subcellular distributions, enzyme kinetics, and regulation.

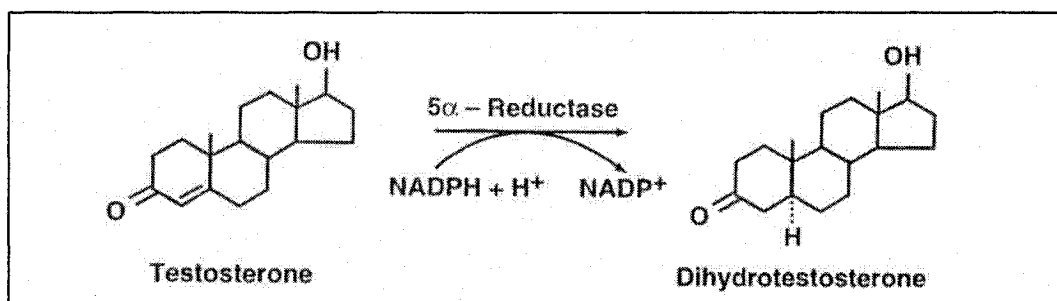


Figure 3. Reaction catalyzed by 5 α -reductase.

In humans, the 5 α -reductase isozymes share similar gene structures and are approximately 46% homologous in sequence; type 1 is located on chromosome 5 and type 2 is located on chromosome 2 (291-293). Mutations in the 5 α -reductase type 2 gene are responsible for 5 α -reductase deficiency in humans that results in male pseudohermaphroditism; more than 20 different mutations of this gene have been reported (63, 64, 291). Rat 5 α -reductase type 1 and type 2 are approximately 60% and 77% identical in sequence to their respective human homologs, and approximately 44% homologous to each other (289, 290). The 5 α -reductase genes encode a highly hydrophobic membrane-bound protein; because of these properties, attempts to purify this protein have been unsuccessful to date.

Type 2 5 α -reductase is the predominant isoform in male reproductive tissues such as the prostate (290). The type 1 isoform predominates in peripheral tissues such as the liver and skin, however, it is also present in male reproductive tissues (290). Liver 5 α -reductase, along with 3 α -hydroxysteroid dehydrogenase, is presumably involved in the catabolism or breakdown of steroid hormones in preparation for their elimination (294). In other tissues,

rather than inactivating steroid hormones, 5 α -reductase potentiates hormone action via the formation of DHT (26). While tissue localization may predict catabolic or anabolic roles for 5 α -reductase, it remains unknown whether there are independent physiological roles for each isozyme.

1. 5 α -Reductase in the Male Reproductive System

A comparison of 5 α -reductase within two different androgen-dependent reproductive tissues, the testis and the prostate, serves to illustrate the differences in cellular and subcellular distribution and regulation of this enzyme.

1.1. Testis

Within the testis, 5 α -reductase activity has been predominantly localized to cells in the interstitial compartment, especially during development (295-297). Supporting this is the demonstration that purified immature Leydig cells have substantial 5 α -reductase activity (295). Indeed, it was already mentioned that peaks in 5 α -reductase isoenzyme expression and 5 α -reductase activity in the testis occur at puberty, reflecting a likely role for 5 α -reduced androgens in the initiation of spermatogenesis at this time (75). It would seem that androgens do not have a prominent role in the regulation of testicular 5 α -reductase activity. This is evidenced by studies in hypophysectomized rats where LH administration increases 5 α -reductase activity independent of testosterone production (298, 299). More recently, however, it has been shown that the two isozymes of 5 α -reductase in the testis are differentially regulated by testosterone at the mRNA

level: testosterone regulates 5 α -reductase type 1 mRNA and activity in a negative manner but does not affect 5 α -reductase type 2. Conversely, FSH regulates 5 α -reductase type 1 mRNA in a positive manner and also appears to regulate type 2 (300). The activity of both 5 α -reductase isozymes decreases dramatically after puberty, consistent with a limited role for DHT in the adult testis (301). Testicular 5 α -reductase activity has been primarily localized to the microsomal subcellular fraction (302). The role of each 5 α -reductase isozyme in the testis remains unclear; however, it appears that 5 α -reductase type 1 is predominant in this tissue (75).

1.2. Prostate

5 α -reductase has been extensively studied in the prostate because of the well-established role for DHT in the development of prostate diseases. Within the prostate, 5 α -reductase activity increases post-pubertally and reaches a stable plateau in adulthood (303). This is in marked contrast to testicular 5 α -reductase activity. In the prostate, 5 α -reductase activity has been localized to both microsomal and nuclear subcellular fractions (304, 305). The prostate is composed of stroma and epithelium and studies have localized 5 α -reductase activity to both compartments (306). 5 α -reductase activity in the prostate has been shown to be regulated by androgens. For example, testosterone administration rescues the loss of 5 α -reductase activity that occurs following orchidectomy (307). Additionally, androgens control the expression of both 5 α -reductase isozymes in the prostate (308). Unlike the testis, LH does not appear

to regulate 5 α -reductase in the prostate (309). While some studies suggest that type 2 5 α -reductase predominates in the prostate, both isozymes have been localized in the tissue (305, 310). Furthermore, specific 5 α -reductase type 1 enzyme activity has been demonstrated in the prostate, supporting a significant role for both isozymes in this tissue (311).

2. 5 α -Reductase in the Epididymis

A number of key studies have unequivocally demonstrated that DHT is the main androgen acting in the epididymis. Several different groups have demonstrated the ability of epididymal cells to synthesize 5 α -reduced metabolites from testosterone *in vitro* (250-252). In 1972, Tindall et al. showed that the active androgen present in epididymal cell nuclei after injection of radiolabelled testosterone is DHT (253). Subsequently, in 1974, Orgebin-Crist demonstrated that 5 α -reduced androgens are more potent than testosterone in maintaining epididymal functions *in vivo* (254). Finally, micropuncture experiments confirmed that, beyond the efferent ducts, the predominant androgens in epididymal luminal fluid are the 5 α -reduced metabolites of testosterone (247). More recently, epididymal 5 α -reductases have been characterized at the activity, mRNA and protein levels.

2.1. Enzyme Activity

In the epididymis, 5 α -reductase activity is present in both the microsomal and nuclear fractions (312). Microsomal 5 α -reductase activity is expressed at

low levels throughout the epididymis (313). In contrast, nuclear 5 α -reductase activity exists in a striking positional gradient along the epididymis; it is highest in the initial segment and drops significantly towards the end of the tubule (314). Following bilateral orchidectomy, nuclear 5 α -reductase activity declines dramatically, especially in the proximal regions, and is only partially rescued by testosterone replacement, even at supraphysiological levels (314). Thus it is apparent that nuclear 5 α -reductase activity is regulated in a lumicrine manner by a factor coming from the testis. The decreased activity observed following efferent duct ligation and unilateral castration is also consistent with this mode of regulation (314, 315).

Attempts have been made to identify the lumicrine factor regulating 5 α -reductase activity. Experimentally removing sperm, by administering testosterone at a dose that suppresses spermatogenesis, has no effect on nuclear 5 α -reductase activity, thereby eliminating the possibility that sperm (or a sperm-associated substance) is the testicular factor in question (316). Alternatively, hypophysectomy (removal of the pituitary) followed by administration of testosterone at a dose that maintains spermatogenesis and Sertoli-cell secretion, also maintains nuclear 5 α -reductase activity (317). A Sertoli-cell product secreted under the control of androgens was thus proposed as the testicular factor regulating nuclear 5 α -reductase activity. Androgen-binding protein (ABP) is a likely candidate given that its synthesis by Sertoli cells is androgen dependent (318). Moreover, ABP is actively endocytosed by the

epithelium in the initial segment of the epididymis, the region where nuclear 5 α -reductase activity is highest (319, 320).

2.2. mRNA Levels

Analysis of the localization and regulation of the mRNAs for 5 α -reductase type 1 and type 2 in the rat epididymis was done by Viger in the early 1990s (278, 321). The expression of 5 α -reductase type 1 mRNA is highest in the initial segment and decreases longitudinally. As with nuclear 5 α -reductase activity, the expression of 5 α -reductase type 1 mRNA decreases significantly following orchidectomy and efferent duct ligation. Following orchidectomy, exogenous testosterone can recover the expression of type 1 mRNA in all regions of the epididymis except the initial segment (321). These findings indicate that a lumicrine factor originating in the testis is required for the regulation of 5 α -reductase type 1 expression uniquely in the initial segment while the expression in the rest of the tissue is regulated by circulating androgens.

5 α -Reductase type 2 mRNA is expressed at higher levels than 5 α -reductase type 1 in all segments of the epididymis. Longitudinally, type 2 expression is high in the initial segment, peaks in the caput epididymidis and then decreases in the corpus and cauda epididymides, though to a lesser extent than type 1 expression (278). Surprisingly, levels of 5 α -reductase type 2 mRNA increase nearly 2-fold in the initial segment in response to efferent duct ligation, while expression in the rest of the tissue is unaffected (278). This was in marked contrast to the effects of efferent duct ligation on 5 α -reductase type 1 mRNA

expression, and was the first instance where the differential regulation of both isozymes of 5 α -reductase in the same tissue was observed. Interestingly, the developmental expression profiles for type 1 and type 2 5 α -reductase are also different in the epididymis; the segment-specific expression of 5 α -reductase type 1 mRNA varies dramatically at different postnatal ages while 5 α -reductase type 2 expression is not altered post-natally (278, 321).

2.3. Protein Levels

The development of antibodies specific to each 5 α -reductase isozyme has proved challenging. Consequently, there has yet to be a clear differentiation of the localization of type 1 and type 2 5 α -reductase proteins along the epididymis. Nevertheless, immunohistochemical studies using an antibody raised against the rat type 1 isoform have shown that the pattern of protein expression in the epididymis is similar to the expression profiles for 5 α -reductase type 1 mRNA and nuclear 5 α -reductase activity; the localization was most intense in a discrete lobule of the initial segment and decreased longitudinally (322). Efferent duct ligation abolished 5 α -reductase type 1 protein staining in the initial segment exclusively (249).

3. 5 α -Reductase Inhibitors

Several characteristics of the 5 α -reductase deficiency phenotype, including underdeveloped prostates, altered facial and body hair growth patterns, decreased incidences of temporal hairline regression and decreased incidences

of acne, were the first indicators that the inhibition of 5 α -reductase may be of therapeutic potential in normal, non-deficient males. Biomedical research and drug discovery efforts have since led to the development of 5 α -reductase inhibitors, primarily for the treatment of benign prostatic hyperplasia (BPH), which is extremely prevalent in older males (>60% of men over 55 years old) (323). More recently, 5 α -reductase inhibitors have also been marketed for the treatment of male pattern baldness (324), and basic and clinical research indicates potential roles for 5 α -reductase inhibitors in the treatment of acne (325) and the early treatment or prevention of prostate cancer (326, 327).

It has been shown that inhibitors have different selectivity for the two isoforms of 5 α -reductase. Finasteride, a type 2 selective 5 α -reductase inhibitor, was first marketed for the treatment of benign prostatic hyperplasia in 1992 (328). Consequently, the long-term efficacy and safety of finasteride have been extensively studied for this indication (reviewed in 79, 80). Finasteride treatment decreases serum and prostate DHT levels by approximately 65-70% and 85-90% respectively (80). The lack of specificity of finasteride for the type 1 isoform has been proposed as the reason why this drug is only moderately effective in the treatment of benign prostatic hyperplasia (79, 80). Efforts to discover more therapeutically effective compounds, i.e., that decrease DHT levels to a greater extent, have led to the development of a novel class of dual 5 α -reductase inhibitors (329-332). For example, dutasteride (GI198745) is a dual 5 α -reductase inhibitor that was selected for clinical development due to its remarkable potency. It is perhaps the most potent 5 α -reductase inhibitor

reported thus far, reducing serum DHT levels to >95% (331). In early 2003, dutasteride (GI198745) became the first dual 5 α -reductase inhibitor available for the treatment of BPH (333). In comparison to finasteride, dutasteride and other dual compounds achieve almost total suppression of DHT levels (329, 330, 333).

Compared to the multitude of studies investigating the effects of 5 α -reductase inhibition in the prostate, there are a limited number of studies that examine the effects of finasteride on other reproductive tissues or fertility (334-337) and fewer still that examine the extraprostatic effects of the novel class of dual inhibitors (329, 333).

As early as 1981, Cohen *et al.* presented data that a 5 α -reductase inhibitor could affect fertility (338). However, interpretation of these early studies needs to be made with caution since many of the earlier inhibitory compounds employed in these studies also have known effects on other steroid metabolizing enzymes (e.g., 3 α -hydroxysteroid dehydrogenase) or on the androgen receptor (339-342). Therefore any effect cannot solely or conclusively be attributed to the inhibition of 5 α -reductase.

Later inhibitor studies employed the type 2 selective inhibitor finasteride. In 1991, Cukierski *et al.* (334) reported a partial decrease in fertility following chronic finasteride treatment (80 mg/kg/day for 24 weeks) of adult male rats. Wise *et al.* reported a similar effect in a related study (335). In these earlier studies, testis weight and histology were unaffected by treatment and the subfertility was attributed solely to a deficit in the formation of copulatory plugs due to the effects of treatment on seminal vesicle and prostate weights.

However, any data pertaining to the epididymis were lacking, therefore it is possible that the compromised fertility could have been due to an effect on this tissue as well.

Interestingly, with respect to other 5 α -reductase inhibitor studies, no adverse effects of 5 α -reductase inhibitor treatment on testis weight, histology and/or sperm counts, and hence spermatogenesis, have been reported following treatment with either finasteride or a novel dual inhibitor (79, 337, 343, 344). To date, however, still little or no information exists pertaining to the effects of 5 α -reductase inhibition in the epididymis and no studies have focused on the epididymal consequences of inhibiting both isozymes of 5 α -reductase with a dual inhibitor.

F. Formulation of the Project

Scientific research into the physiology of male reproduction has obvious clinical implications for the development of novel treatments for reproductive tissue cancers and age-related pathologies such as BPH, for discerning the treatable causes of male infertility or subfertility, as well as for the design of effective male contraceptives. For these reasons, both the prostate and the testis have historically been the focus of major research efforts; however, over the past few decades it has become increasingly apparent that epididymal research is also of great importance. Of particular relevance are the multiple sperm-related functions of the epididymis that have made this tissue an appealing post-testicular target for the development of safe, rapid and reversible

male contraceptives. Additionally, the epididymis is clearly a potential site of origin of male infertility and therefore, elucidating epididymal causes of male infertility has therapeutic potential for the management of this prevalent pathology. Despite these therapeutic incentives, much remains to be learned about the specific factors and mechanisms involved in mediating and regulating epididymal functions. Therefore, novel approaches are required to further our understanding of epididymal physiology.

The maintenance of epididymal structure and functions is known to be highly dependent on the presence of androgens. Furthermore, several *in vivo* and *in vitro* studies have confirmed that it is not testosterone, but rather dihydrotestosterone (DHT), that is the main androgen acting in this tissue. Despite the central role for DHT in epididymal physiology, very few studies have examined the specific consequences on the epididymis of inhibiting 5 α -reductase, the enzyme that catalyzes DHT formation. The availability of suitable inhibitors may have precluded these studies; however, with the advent of specific dual inhibitors that concurrently inhibit both isozymes of 5 α -reductase, this is no longer the case. Indeed, studying the consequences of inhibiting DHT formation is likely to provide important information regarding the androgen-regulation of epididymal functions. Additionally, given that all current evidence precludes an effect of 5 α -reductase inhibition on the testis, the inhibition of DHT production is an interesting experimental approach for studying the regulation of sperm maturation in the epididymis while presumably having little or no effect on sperm production in the testis. The goal of the present thesis is to use novel 5 α -

reductase inhibitors in combination with advanced gene expression and sperm analysis techniques in order to increase our current understanding of the roles of DHT in epididymal physiology.

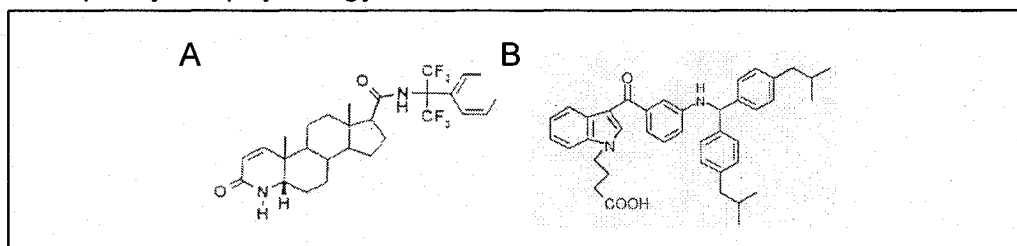


Figure 4. Structures of dual 5 α -reductase inhibitors. A) PNU157706, Pharmacia & Upjohn. B) FK143, Fujisawa Pharmaceutical Co.

Specifically, the studies comprised in chapter 2 of the present thesis employ the novel dual 5 α -reductase inhibitor PNU157706 to examine the effects of inhibiting DHT formation on epididymal gene expression. This is accomplished on a large-scale with cDNA array technology. Subsequently, the studies in chapter 3 examine the effects of PNU157706 treatment on epididymal sperm maturation, enabling a correlation between changes in epididymal gene expression and epididymal function. For the first time, techniques are used to assess sperm morphology, motility and fertilizing ability following treatment with a dual 5 α -reductase inhibitor. Lastly, in chapter 4, previous effects of inhibiting DHT formation on epididymal gene expression are confirmed by using another dual 5 α -reductase inhibitor, FK143. Additionally, gene expression analysis following treatment with both inhibitor compounds is expanded using real-time quantitative RT-PCR techniques to include genes involved in mediating androgen action and in multiple growth factor signaling pathways. Conclusively, these studies give insight into the role of DHT in regulating epididymal gene expression

and functions, establish 5 α -reductase inhibition as a new approach to study epididymal physiology and identify novel directions and targets for continued epididymal research.

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CHAPTER 2

Effects of PNU157706, a Dual 5 α -Reductase Inhibitor, on Gene Expression in the Rat Epididymis

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¹ G.M. Cooke did the *in vitro* 5 α -reductase enzyme assays described in this chapter.

Abstract

The epididymis is the site of sperm maturation and storage. 5 α -Reductases (types 1 and 2) are key enzymes in this tissue because they convert testosterone to dihydrotestosterone (DHT), the main androgen regulating epididymal functions. Examining the consequences of inhibiting DHT formation is likely to provide important information regarding the regulation of epididymal functions, yet few inhibitor studies have focused on this tissue. To understand better DHT-mediated regulation of epididymal gene expression, we employed a dual 5 α -reductase inhibitor and cDNA microarrays to examine the effects of 5 α -reductase inhibition on gene expression in the initial segment, caput, corpus, and cauda epididymidis. Inhibition of epididymal 5 α -reductase activity by PNU157706 was confirmed by *in vitro* enzyme assays. Rats were treated with 0, 0.1, 1.0 or 10 mg/kg/day of PNU157706 for 28 days. The weights of DHT-dependent tissues, including the epididymis, were decreased following treatment. The effect of treatment on gene expression was dose-dependent and highly segment-specific. The initial segment responded uniquely in that a similar number of genes increased and decreased in expression compared with the other segments where the majority of affected genes decreased in expression. Some of the more dramatically affected genes were involved in signal transduction as well as fatty acid and lipid metabolism, regulation of ion and fluid transport, luminal acidification, oxidative defense and protein processing and degradation. These are essential processes contributing to the formation of an optimal luminal microenvironment required for proper sperm maturation. These

results provide novel insight into the DHT-dependent mechanisms that control epididymal functions.

Introduction

The epididymis is a single, highly convoluted tubule that receives the input of sperm and fluid from the testis and that empties into the vas deferens (Robaire & Hinton 2002). It is structurally divided into four main segments (initial segment, caput, corpus and cauda epididymidis) and functions in the transport, protection, maturation and storage of spermatozoa (Robaire & Hinton 2002, Orgebin-Crist 1967). The multifaceted sperm-related functions of the epididymis have made this tissue an appealing target for the control of male contraception and fertility. Achieving these therapeutic goals, however, necessitates a greater understanding of the mechanisms regulating epididymal structure and functions.

Not surprisingly, given the complexity of this tissue, many factors are involved in the regulation of epididymal functions, including estrogens, retinoids, growth factors and unidentified testicular factors (Hess *et al.* 2002, Orgebin-Crist *et al.* 2002, Lan *et al.* 1998, Hinton *et al.* 1998). Androgens, however, are recognized as the primary hormonal regulators of epididymal structure and functions (Orgebin-Crist & Tichenor 1973, Blaquier *et al.* 1972). Furthermore, several *in vivo* and *in vitro* studies have confirmed that it is not testosterone, but rather dihydrotestosterone (DHT), that is the main androgen acting in this tissue (Orgebin-Crist *et al.* 1976, Tindall *et al.* 1972, Turner *et al.* 1984, Gloyna & Wilson 1969). 5 α -Reductase (EC 1.3.1.22) is thus a key enzyme in the

epididymis because of its role in locally converting testosterone to DHT. Two isoforms of 5 α -reductase have been identified and are termed type 1 and type 2 (Andersson & Russell 1990, Normington & Russell 1992). Both isoforms are present in the epididymis and are differentially expressed along the tubule (Viger & Robaire 1996).

Examining the consequences of inhibiting DHT formation is likely to provide important information regarding the regulation of epididymal functions, yet very few inhibitor studies have focused on this tissue (de Larminat & Blaquier 1979, Cohen *et al.* 1981, Cooke & Robaire 1986, Zoppi *et al.* 1992). In order to elucidate specific functions of 5 α -reductase in the epididymis using inhibitors, compounds that are specific only to 5 α -reductase and that inhibit both isoforms of the enzyme (i.e. dual inhibitors) are required. The latter is necessary as it has not yet been determined if one or both of the isoforms are important for mediating the androgen regulation of epididymal structure and functions. Specificity and toxicity were problems with early compounds such as diethyl-4-methyl-3-oxo-4-aza-5 α -androstane-17 β -carboxamide (4-MA) (Cooke & Robaire 1986, DiSalle *et al.* 1994). Modification of 4-MA yielded finasteride, the first clinically available 5 α -reductase inhibitor (Sudduth *et al.* 1993, Li *et al.* 1995, Steers 2001). With the discovery of two isoforms of 5 α -reductase, it was shown that finasteride is selective for the type 2 isoform. The lack of specificity of finasteride for the type 1 isoform has been proposed as the reason why this drug is only moderately effective in the treatment of benign prostatic hyperplasia (Steers 2001, Bartsch *et al.* 2002). Drug development efforts to create more

therapeutically effective compounds for the treatment of androgen-dependent disorders such as benign prostatic hyperplasia have provided compounds that fulfill the requirements of specificity and dual action. PNU157706 is a novel dual 5α -reductase inhibitor for the potential treatment of benign prostatic hyperplasia (di Salle *et al.* 1998). It is more potent than finasteride in decreasing DHT levels. This compound is of express interest as it has been reported to have an effect on epididymal weight (di Salle *et al.* 1998).

Hormones often effect changes in their target tissues by altering the expression of specific sets of genes. The expression patterns of several epididymis-specific and/or epididymis-relevant genes have been analyzed along the epididymis (for review see Cornwall *et al.* 2002); however, understanding the structure and function of this complex tissue requires more than analyzing the properties of isolated genes. The biological function of sperm maturation arises from the interactions of many components. cDNA array technology provides a powerful method for large-scale, parallel gene expression analysis that can provide insight into these interactions, and how they are regulated. Our objective in this study is to use cDNA array technology in combination with a novel 5α -reductase inhibitor to help elucidate the DHT-dependent regulatory networks that govern segment-specific gene expression in the epididymis. We demonstrate that the inhibition of DHT formation in the epididymis alters the expression of many genes potentially involved in sperm-related functions. Furthermore, the present studies indicate that DHT-dependent regulation of gene expression is highly segment-specific and involves components of different signaling pathways.

Materials and Methods

Animals

Adult male Sprague-Dawley rats (325-350g) were obtained from Charles River Canada (St. Constant, PQ, Canada), maintained under controlled light (14L:10D) and temperature (22°C), and freely provided with food and water. Caput-corpus epididymides from 90-day old animals that were previously stored at -80°C were used for *in vitro* enzyme assays. For the *in vivo* study, rats were randomly divided into 4 groups of 5 animals each and gavaged with 0.5 ml/kg of 0 (control), 0.1 (low), 1.0 (medium) or 10 mg/kg (high) of PNU157706 (generously provided as a gift by Pharmacia & Upjohn, Italy) suspended in 0.5% methylcellulose solution (BDH, Montreal, QC) containing 0.4% Tween 80 (A&C American Chemicals Ltd, Montreal, QC) for 28 consecutive days. Doses were selected based on reported effects on rat ventral prostate; the dosing regimen with 10 mg/kg/day PNU157706 has been shown to decrease prostatic dihydrotestosterone levels by >90% (di Salle *et al.* 1998). At killing, animals were anesthetized and seminal vesicles, testes, ventral prostates and epididymides from the left side were collected. Epididymides were sectioned into initial segment, caput, corpus and cauda, and immediately frozen in liquid nitrogen. Tissues were stored at -80°C until used for RNA extraction. All animal studies were conducted in accordance with the principles and procedure outlined in the Guide to the Care and Use of Experimental Animals prepared by the Canadian Council on Animal Care.

Statistical Analysis

One-way ANOVA followed by Tukey's test was used to detect significant effects of PNU157706 treatment on tissue weights. The level of significance was taken as $p < 0.05$.

In vitro 5 α -reductase assays

Unlabeled steroids were purchased from Steraloids Inc. (Newport, RI). (1,2,6,7-³H) testosterone (74.0 Ci/mmol) was from Dupont/NEN (Boston, MA). Organic solvents were from BDH, (Montreal, QC). Dimethylglutaric acid (DMG), NADPH and dimethyl sulfoxide (DMSO) were from Sigma Chemical Co. (St Louis, MO). Plastic coated WhatmanTM PE SIL G silica gel chromatography plates were purchased from Chromatographic Specialties (Montreal, QC). PNU157706 solutions were prepared in DMSO.

Frozen caput-corpus epididymides (only normal, untreated tissues were used) were thawed, homogenized (Polytron) in DMG buffer (50 mM 2,3-dimyristoylglycerol (DMG), 5% glycerol, NaOH, 0.5mM NADPH) pH 6.5, and the nuclear and microsomal fractions were assayed for 5 α -reductase activity as previously described (Cooke & Robaire 1987); protein was estimated using the method of Lowry (Lowry *et al.* 1951). Initial studies were done to determine the linearity of nuclear and microsomal activity with time and protein concentration (data not shown). Purification and quantification of steroids was by thin-layer chromatography and scintillation counting (Cooke & Robaire 1987). Reaction

rates were obtained by linear regression analysis ($r > 0.97$). At pH 4.5, no 5 α -reductase activity was measurable at any concentration of testosterone.

Kinetic studies of 5 α -reductase activity were done at pH 6.5 with testosterone (nine concentrations ranging from 5 to 375 nM). To determine the effects of PNU157706 on 5 α -reductase activity, PNU157706 was included at concentrations of 0, 1, 3 and 10 nM. A single incubation time of 1h and an incubation volume of 1 ml were used in kinetic studies. To obtain the apparent Michaelis constant ($K_{m(app)}$) and apparent maximum velocity ($V_{max(app)}$), the Wilkinson method (non-linear least squares analysis of a rectangular hyperbola (Wilkinson 1961)) was used. Slope and intercept replots were obtained from, respectively, $K_{m(app)} / V_{max(app)}$ versus $[I]$ and $1/V_{max(app)}$ versus $[I]$. Linear regression analysis of the replots was employed to determine the $K_{i(app)}$ values.

RNA extraction

Total RNA was extracted from each sample using guanidine thiocyanate as described previously (Jervis & Robaire 2001). Following isolation, RNA samples were DNase-treated (Atlas Pure Isolation Kit user manual, section IV, Clontech, Palo Alto, CA) to remove contaminating genomic DNA and RNA concentration was assessed by optical density determination at 260 nm (Beckman DU7 spectrophotometer, Montreal, PQ, Canada). In addition to spectrophotometric readings, RNA quality was verified by gel electrophoresis. Each sample consisted of a single epididymal segment obtained from individual rats; no tissues were pooled.

Complementary DNA arrays and hybridization

RNA samples were used to probe cDNA arrays (Atlas Rat 1.2K; Clontech) according to the manufacturer's instructions. Five arrays per epididymal segment per treatment group (control, low, medium and high PNU157706) were probed and referred to as replicates ($n=5/\text{treatment}/\text{segment}$), with the following exceptions: 4 replicates per group were used ($n=4/\text{group}$) for the initial segment in the high PNU157706 group, the initial segment and cauda in the medium PNU157706 group and the initial segment and caput in the low PNU157706 group; 3 arrays were used ($n=3/\text{group}$) for the corpus in the medium PNU157706 group. A total of 75 arrays were screened for this experiment. Arrays were exposed to phosphorimager plates (Molecular Dynamics; Sunnyvale, CA) 24 h before scanning with a phosphorimager (Storm, Molecular Dynamics). Analysis of array images with Atlas Image (Version 2.0; Clontech) was performed to quantify the intensity of each cDNA spot, which reflects the relative abundance of RNA in the sample. The raw data for each gene (intensity minus the background) were imported into Genespring 4.0.7 (Silicon Genetics, Redwood, CA) for further analysis. For each replicate array in a given treatment group, a gene was considered detected if its intensity was above threshold, with threshold defined as two times the average background of that individual array. A gene was considered expressed if it was detected in at least three replicates in that group.

To minimize experimental variation and allow for comparison of different treatment groups, data were normalized with the standard experiment-to-experiment normalization (Genespring). Specifically, the median level of

expression on each array was defined as 1 and expression of each gene was normalized relative to 1; this value was averaged for all replicates in a group to generate what is referred to as the relative intensity for a given gene. All individual gene profiles are shown using the standard experiment-to-experiment normalization. Gene expression changes of 2-fold or greater (i.e. 50% decrease or 100% increase) are focused on throughout the text except for genes belonging to specific gene families. The importance of replication for validation of gene expression studies has been documented (Lee *et al.* 2000, Herwig *et al.* 2001). Conventional statistical analysis was not applicable to our large normalized data sets. We include errors of the mean (SEM) of individual genes to show variability among replicates in a given group.

As a means to validate our gene array expression data, we examined the control expression profiles of three genes with well-established epididymal expression profiles (Fig. 1). As expected, the expression of 5 α -reductase type 2 was highest in the initial segment and caput epididymidis, angiotensin converting enzyme expression peaked dramatically in the caput epididymidis in comparison to the other segments, and androgen receptor gene expression remained constant throughout the epididymis (Viger & Robaire 1996, Strittmatter & Snyder 1984, Robaire & Viger 1993).

Results

Tissue Weights

There were no significant changes in body weights among any of the groups of animals (data not shown). As expected, the weights of the seminal vesicle and ventral prostate, both DHT-dependent tissues, were significantly decreased with all doses of PNU157706 while there was no effect of treatment on testis weights (Fig. 2A-C). A 10% decrease in epididymal weight was observed with the low and medium PNU157706 treatment groups with a further decrease to 82% of control in the high PNU157706 group (Fig. 2D).

5 α -Reductase Activity

The addition of PNU157706 to incubations at concentrations of 0, 1, 3 and 10 nM inhibited epididymal 5 α -reductase as shown in Fig. 3A (nuclear) and B (microsomal) fractions. Kinetic analyses demonstrated that PNU157706 caused the $K_{m(app)}$ values to increase (about three to four fold) without affecting the $V_{max(app)}$ values. Confirmation of these findings was achieved with slope ($K_{m(app)}/V_{max(app)}$ vs. $[I]$) and intercept ($1/V_{max(app)}$ vs. $[I]$) replots, shown in Fig. 3C (nuclear) and D (microsomal); the slopes of the replots were positive and the slopes of the intercept replots were almost horizontal or exhibited a negative slope. The values for the inhibition constant ($K_{i(app)}$) for PNU157706 from the slope replots were lower than those obtained from the intercept replots (Table 1) indicating that this drug is a competitive inhibitor of 5 α -reductase. Furthermore,

since the K_i is lower than the $K_{m(app)}$, the affinity of 5 α -reductase for PNU157706 is greater than the affinity for testosterone.

Number of genes expressed

The expression of 1176 genes was examined simultaneously using cDNA arrays. In each epididymal segment, similar numbers of transcripts were detected in the control and high PNU157706 treatment groups. In the initial segment, transcripts for 34% (397) and 31% (368) of genes were detected in tissues from control and treated rats, respectively. Similarly, in the caput epididymidis, transcripts for 35% (411) of genes were detected in tissue from control animals and 31% (360) in those from treated rats. A lower number of transcripts was detected in the corpus epididymidis compared to the other segments: 25% (295) of genes in control, 21% (247) in treated. Slightly more transcripts were detected in the cauda epididymidis; 36% (420) of genes in control, 37% (438) in treated.

Overall changes in gene expression with PNU157706 treatment

The range of gene expression changes in the initial segment following high PNU157706 treatment extended from a greater than 80% decrease (c-met proto-oncogene) to a 6.6-fold increase (set β + set α isoform). In the caput epididymidis, the range was from a 73% decrease in expression (cathepsin B) to a 9.7-fold increase in expression (P2X purinoceptor 1). In addition to having the

lowest number of genes with detected expression, the corpus epididymidis also demonstrated the smallest range of gene expression changes following treatment; expression changes ranged from a 78% decrease (carbonic anhydrase 4 (CA4)) to a 4.8-fold increase (muscarinic acetylcholine receptor M4). The largest range of gene expression changes was observed in the cauda epididymidis which was from a greater than 90% decrease (elastase 2) to a 7.3-fold increase (serine proteinase rPC7).

As expected, using the criterion of 2-fold changes in gene expression, i.e., a 100% increase or 50% decrease, the expression of a large proportion of genes was unaffected by PNU157706 treatment in each epididymal segment. Analysis of the number of genes undergoing a minimum 2-fold change in expression between control and high PNU157706 treatment groups revealed a unique response to treatment in the initial segment (Fig. 4). In this segment, a similar number of genes increased and decreased in expression by 2-fold or greater. In contrast, in more distal epididymal segments, there were more genes decreasing than increasing in expression by 2-fold or more following treatment (Fig. 4).

Segment-specific changes in gene expression

A total of 81 genes changed in expression by 2-fold or greater in the epididymis following treatment with high PNU157706. The expression of the majority of these genes was affected uniquely in one segment. The few transcripts that changed in expression by at least 2-fold in more than one segment are indicated in Table 2. Transcripts of particular interest that changed

in a segment specific manner were examined in the control, low, medium and high PNU157706 treatment groups in order to visualize dose-response profiles.

Initial Segment. A total of 25 transcripts changed by a minimum of 2-fold in the initial segment. Differential expression was observed for 4 genes that are mediators or modulators of signal transduction (Fig. 5A). Two oncogenic proteins (NF-2, retinoblastoma protein pp105) and ras-GTPase activating protein (p120GAP) decreased in expression. The maximum decrease was achieved only with the high dose of PNU157706. The fourth gene, Crk-associated substrate (CAS), a kinase substrate, showed increased expression with medium and high PNU157706 treatment. Another important group of transcripts affected in the initial segment were those involved in fatty acid/lipid metabolism: fatty acid amide hydrolase, corticosteroid 11- β dehydrogenase 1, very long chain acyl-CoA dehydrogenase (VLCAD) and 5-lipoxygenase (5-LO) (Fig. 5B). Transcripts for these 4 genes increased following PNU157706 treatment. For the two dehydrogenases and fatty acid amide hydrolase, the maximum increase was observed with the low dose while for 5-lipoxygenase, an increase in expression was only achieved with the high dose. Interestingly, two genes with roles in regulating ion and water balance in body fluids were also affected by PNU157706 treatment; atrial natriuretic peptide clearance (ANP-C) receptor expression decreased while chloride channel CLC-7 expression increased (Fig. 5C).

Caput. Only 14 genes changed in expression by a minimum of 2-fold in the caput epididymidis. Specifically, the expression of three signaling genes was differentially affected by PNU157706 treatment (Fig. 6A). One transcript, cAMP-dependent protein kinase type II-beta regulatory chain (cAMP dep PK Type 11 β), showed a decrease only with the high dose of PNU157706. In contrast, Ehk 3, a tyrosine kinase, and neural thrombospondin 1-like protein (NELL-1), a protein kinase C-binding protein, both increased and the maximum effect was achieved with the low dose of PNU157706. Cathepsins, a family of cysteine proteases that function in protein degradation and processing, have been shown previously to change in expression in the epididymis under certain conditions (McGrath 1999, Jervis & Robaire 2002). In the caput epididymidis, cathepsin B expression decreased following treatment only with the high dose of PNU157706 (Fig. 6B). Also of note in the caput epididymidis was the increase in expression of short chain acyl-CoA dehydrogenase (SCAD), another gene involved in fatty acid/lipid metabolism (Fig. 6C). As seen with other genes, the maximum increase in expression was obtained with the low dose of PNU157706. Other transcripts specifically affected by treatment in the caput epididymidis included two transforming growth factor β family members; TGF β receptor 1 and TGF β masking large subunit decreased maximally in expression with the low dose of PNU157706.

Corpus. In the corpus epididymidis, 15 genes showed expression changes of 2-fold or greater. Of particular interest in this segment was the dose-dependent

decrease in expression of carbonic anhydrase 4 (CA-4), a gene implicated in the acidification of the epididymal lumen (Fig. 7A). Three signaling-related genes also decreased in expression in a dose-dependent manner (Fig. 7B). These were ras related protein rab13, a G-protein involved in trafficking and targeting, ephrin B1, a receptor tyrosine kinase ligand, and Jak1 tyrosine-protein kinase.

Cauda. A total of 38 genes changed a minimum of 2-fold in expression in the cauda epididymidis. Once again, transcripts involved in mediating or modulating signal transduction were differentially affected by inhibitor treatment (Fig. 8A). Rab-related GTP-binding protein and muscle/brain cAMP-dependent protein kinase inhibitor (PKI-alpha) showed the same dose-response profile where the maximum decrease in expression was achieved with the low dose of PNU157706. Transcripts for phosphatidylinositol 4-kinase (PI4-K) and the putative protein kinase C regulatory protein, 14-3-3 protein gamma subtype, also similarly decreased in a dose-dependent manner with the maximum decrease achieved with the medium dose. The ras-related GTPase rab4B followed a different profile decreasing in a dose-dependent manner. In addition to these signalling genes, phospholipase expression was also affected. Phospholipases hydrolyze ester bonds in phospholipids to generate second messengers such as diacyl glycerol and inositol triphosphate. Specifically in the cauda epididymidis, three phospholipase C (PLC) family members decreased in expression following PNU157706 treatment (Fig. 8B). PLC gamma-2, PLC delta-1 and PLC gamma-1 expression decreased in a dose-dependent manner, but the expression of the

latter two genes was not affected by the low dose of PNU157706. Three different ion transporters decreased specifically in the cauda epididymidis (Fig. 8C). Hydrogen-potassium transporting ATPase alpha 2a subunit, implicated in the acidification of bodily fluids, decreased in expression maximally with the low dose of PNU157706. In contrast, the sodium/potassium transporting ATPase beta 2 subunit decreased in expression maximally only with the high dose of PNU157706. The anion exchanger, band 3, which contributes to the regulation of cell pH and of cell volume, decreased in expression in a dose-dependent manner. Other genes that changed in expression specifically in the cauda epididymidis after inhibitor treatment included genes with metabolic functions (e.g. aldolase C and ceruloplasmin decreased), proteases (elastase 2 decreased, cathepsin S increased) and growth-factor related genes (e.g. platelet derived growth factor receptor α and vascular endothelial growth factor D decreased).

Expression by gene family

An advantage of cDNA array technology is the capability of examining the effects of 5 α -reductase inhibitor treatment on the overall expression of gene families that are known to be of importance in the epididymis. The expression patterns of two functionally relevant gene families, oxidative stress-related genes and proteasomal genes, were examined along the epididymis.

Oxidative stress-related genes. The expression of four glutathione S-transferases (GSTs), one glutathione peroxidase (GPX) and glutathione synthetase (GSH synthetase) was examined along the epididymis following PNU157706 treatment (Fig. 9). GST mu expression decreased by 30% in the initial segment but remained unchanged in the other segments. GST Yrs-Yrs expression also decreased in the initial segment as well as in the cauda epididymidis by approximately 33%, and 48%, respectively. In contrast, expression of this particular GST increased in the corpus by 2.5-fold. Interestingly, GST subunit 5 theta expression was also differentially affected by treatment in a segment-specific manner; expression decreased in the initial segment by 52% and increased in the cauda by 3-fold. GST subunit 13 expression was decreased by 38% in the initial segment and by 67% in the corpus. Also changing in the initial segment was the expression of GPX3 which decreased 57%. Lastly, the expression of GSH synthetase was increased specifically in the caput by approximately 1.6-fold. Clearly, the expression of oxidative-stress related genes was most affected in the proximal epididymis, particularly in the initial segment. Furthermore, with few exceptions, the predominant effect of treatment was decreased expression.

Proteasomal genes. We examined the expression of eight proteasomal proteins along the epididymis following treatment with PNU157706 (Fig. 10). The predominant effect of treatment was a decrease in expression of the proteasomal genes, particularly in the distal epididymis (corpus and cauda epididymidis).

Differential expression of the proteasomal genes was not observed in the initial segment. In this region, the greatest fold-change in expression was a 1.4-fold increase for proteasome component C3. Proteasomal gene transcript levels in the caput were also relatively unaffected by treatment with the exception of proteasome activator rPA28 subunit alpha that decreased 33% in expression and proteasome subunit RC10-II that decreased approximately 52% in expression. In the corpus epididymidis, transcript levels for proteasome subunit R-delta, component C8, subunit R-iota and beta subunit decreased by approximately 33%, 33%, 63% and 30% respectively. The greatest effect of treatment was seen in the cauda epididymidis. In this region, the greatest decrease in expression was observed for proteasome subunit rPA28 (69%). Additionally, proteasome components C2 and C3 both decreased in expression by 33% and proteasome component C8 and beta subunit decreased in expression by nearly 50%.

Discussion

In the present study, we have confirmed that PNU157706 is a competitive inhibitor of microsomal and nuclear epididymal 5 α -reductase activity and has effects, *in vivo*, on the weights of DHT-dependent tissues, including the epididymis. Furthermore, we demonstrate that dual inhibition of 5 α -reductase has a highly segment-specific effect on the expression of a wide range of genes in the epididymis, thus indicating that DHT is a global mediator of many epididymal functions.

Perhaps the most important function of the epididymis is the creation of a continuously changing luminal environment that allows for proper sperm concentration, maturation, and storage in different segments of the epididymis (Robaire & Hinton 2002, Turner 1991). A large number of studies have demonstrated that many of the individual processes that contribute to the creation of an optimal luminal microenvironment are regulated by androgens (Ezer & Robaire 2002). These processes include fluid and ion transport, luminal acidification as well as protein and lipid secretion, processing and degradation. Our analysis of 2-fold changes in gene expression following inhibitor treatment revealed the segment-specific increase and decrease in expression of many genes potentially involved in these processes.

The major role of fluid transport across the epididymal epithelium is to concentrate sperm as they travel through the tubule. In addition, this process regulates the concentration of constituents in the luminal fluid to which sperm are exposed. Androgens influence fluid balance in the epididymis by regulating sodium and anion transport across the epithelium (Wong & Yeung 1977, Au *et al.* 1978, Leung *et al.* 2002) and modulate the epididymal expression of specific aquaporins, water channels that mediate water transport in many tissues (Pastor-Soler *et al.* 2002). In this study, we have shown an effect of 5 α -reductase inhibition on the expression of several genes involved in fluid and ion transport. In the initial segment, expression of the clearance receptor for atrial natriuretic peptide decreased with treatment. This is of particular interest in light of the fact that atrial natriuretic peptide interacts physiologically with the renin-angiotensin

system to control the fluid balance important for hemodynamic and renal function (Suzuki *et al.* 2001, Melo *et al.* 2000, Oliveira-Souza *et al.* 2002). Furthermore, in the epididymis, androgens regulate the expression of specific components of the renin-angiotensin system, namely angiotensinogen and angiotensin II receptor type 1 (Leung *et al.* 2002, Leung *et al.* 2000). Thus, we propose that DHT-dependent expression of specific components regulates this system mediating fluid transport in the epididymis.

Acidification of the luminal fluid is believed to be necessary for proper sperm maturation as well as storage, particularly in the distal epididymis (Turner & Reich 1985). The anti-androgen flutamide has been shown to elevate epididymal luminal pH in rats, thus indicating that acidification is under the control of androgens (Cafilisch 1993). Anion exchangers, ion channels, specific ATPases and carbonic anhydrase are implicated in the acidification process (Turner 2002, Jensen *et al.* 1999, Kaunisto *et al.* 1999). The mRNA for carbonic anhydrase IV, predominantly expressed in the corpus epididymidis, decreases following androgen withdrawal by castration (Kaunisto *et al.* 1999). In the present study, carbonic anhydrase IV is also shown to be expressed predominantly in the corpus epididymidis. Furthermore, carbonic anhydrase IV showed the highest fold decrease in expression with inhibitor treatment, specifically in this segment, suggesting that the androgen regulating the expression of this gene is DHT. In the cauda epididymidis, we describe a further effect of inhibitor treatment on the expression of two other genes involved in pH

regulation; the expression of the alpha 2a subunit of the H⁺/K⁺ transporting ATPase decreased as did that of band 3 anion exchanger.

Sequential exposure of sperm to epididymal luminal contents, including proteins, is necessary for proper maturation (Turner 1991). While fluid regulation assures the right quantity of proteins present in the epididymal lumen, the qualitative evolution of proteins along the tubule involves protein processing and degradation events. Furthermore, protein processing is required for direct modification of sperm surface proteins, a major feature of epididymal sperm maturation (Phelps *et al.* 1990, Jones 1998). Some of the genes showing the highest fold segment-specific changes in expression following inhibitor treatment are those involved in protein processing/degradation (cathepsin B, elastase 2, serine proteinase rPC7), suggesting that DHT is an important regulator of this function. Of these three genes, only cathepsin B has been characterized previously in the epididymis at the protein and enzyme activity levels (Igdoura *et al.* 1995, Tomomasa *et al.* 1994). Notably, elastase 2 has angiotensin II forming ability (Santos *et al.* 2002) and might therefore represent another DHT-regulated component of the renin-angiotensin system in the epididymis.

A striking effect of inhibitor treatment was the increased expression of five genes involved in fatty acid/lipid metabolism in the proximal epididymis. These results are not altogether surprising since the epididymal lumen is a lipid-rich environment and the modification and exchange of sperm membrane lipids is another major feature of sperm maturation occurring in the proximal epididymis (Jones 1998). Interestingly, modification of the phospholipid environment

regulates 5 α -reductase activity (Cooke & Robaire 1985). Lipid metabolizing enzymes have been shown previously to be androgen regulated in the prostate (Swinnen *et al.* 1997) and the epididymis (Beck 1980). Our results suggest that DHT regulates lipid metabolism by endogenously repressing the expression of specific enzymes.

An important advantage of gene expression profiling is the ability to analyze, in an integrated way, the expression of genes that carry out important functions as well as genes that regulate these functions. Inhibitor treatment clearly has a segment-specific effect on the expression of genes involved in signal transduction, indicating possible mechanisms through which DHT signals to promote sperm-related functions. For example, the protein kinase C (PKC) binding protein, NELL2, increased in expression in the caput epididymidis, while expression of 14-3-3 protein gamma subtype, a PKC regulator, decreased in the cauda epididymidis. The PKC family is interesting as various important PKC isoforms have been shown to be androgen-regulated in the rat ventral prostate (Montalvo *et al.* 2002). Inhibitor treatment also altered the expression of several *ras/rab* related genes in a segment-specific way. These are members or regulators of the small G protein superfamily that mediates cellular processes such as cytoskeletal reorganization, vesicular and nuclear transport, and notably, gene expression (Paduch *et al.* 2001). An example of one such gene is *rab13*, which decreased in expression in the corpus epididymidis following inhibitor treatment. DHT-dependent regulation of this gene is of note because *rab13* has been shown to regulate the assembly of functional tight junctions in epithelial

cells (Marzesco *et al.* 2002) and androgens are known to regulate components of tight junctions in epithelial cells of the epididymis (Cyr *et al.* 1996, Gregory *et al.* 2001). Tight junctions are important components of occluding barriers, including the blood-epididymis barrier, which enables the creation of the optimal luminal microenvironment.

In addition to their functional relevance in the epididymis, lipids also play key roles in signaling (Cantley 2002). Inhibitor treatment decreased the expression of three phospholipase C (PLC) enzymes specifically in the cauda epididymidis. Phosphoinositides are classical signaling lipids and the importance of phospholipases in regulating phosphoinositide metabolism has been well characterized. More recently, a role for lipids in nuclear signal transduction has emerged that requires the activation of phospholipase C (Dygas & Baranska 2001). This nuclear location has implications for direct control of gene expression (Dygas & Baranska 2001, Martelli *et al.* 2002). DHT-dependent regulation of PLC expression might therefore indirectly control the expression of other important genes.

Spermatozoa generate reactive oxygen species required for capacitation and chromatin condensation, however, spermatozoa are also highly susceptible to the damaging effects of reactive oxygen species (Aitken 2002). Antioxidant defense mechanisms are thus of great importance in the epididymis to protect maturing spermatozoa as well as the epididymal epithelium from oxidative damage. Orchidectomy and androgen replacement studies demonstrate that the epididymal glutathione S-transferases are under separate control and are

differentially regulated by androgens (Robaire & Hales 1982). Our results further support the importance of DHT in regulating enzymes of the glutathione cycle, predominantly in the proximal epididymis where the glutathione antioxidant enzymes are concentrated.

The key function of the proteasome, a large, multicatalytic protease, is protein degradation (DeMartino & Slaughter 1999, Coux *et al.* 1996). In the epididymis, controlled protein degradation via the proteasome pathway not only regulates the luminal protein repertoire and contributes to sperm membrane remodeling during maturation, it also provides an important secondary defense against oxidative stress by preventing the accumulation of oxidized and damaged proteins (Mehlhase & Grune 2002, Grune 2000). Furthermore, the regulated degradation of proteins is involved in the control of various signal transduction pathways (Callis & Vierstra 2000). The overwhelming effect of inhibitor treatment was a decrease in proteasomal gene expression predominantly in the corpus and cauda epididymidis, implying that proteasomal gene expression is DHT-dependent in these two segments. Of particular relevance is a recent study in prostate cancer cells indicating an important role of the proteasome system in the regulation of androgen receptor transcriptional activity (Lin *et al.* 2002). Evidence suggests that the proteasome exerts its regulatory role by affecting androgen receptor transactivation, nuclear translocation, degradation and interaction with coregulators. This finding is supported by plant studies where the proteasome has been implicated in hormone signaling (Callis & Vierstra 2000, Gray & Estelle 2000). Thus, it is also plausible that regulation of proteasomal gene expression

by DHT affects the downstream expression of other androgen dependent genes in the epididymis.

In summary, our study of the effects of 5 α -reductase inhibition on gene expression in the epididymis has shown DHT to be a major regulator of the segment-specific expression of a wide array of genes and gene families. The nature of the genes affected enhances our understanding of the androgen-regulated processes contributing to optimal sperm maturation in this tissue. Several novel genes were identified and further investigation is required to determine their functional relevance and potential as therapeutic targets in the control of male fertility and contraception.

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Figures and Legends

Figure 1. Expression of 5 α -reductase type 2 (dotted line), angiotensin-converting enzyme (solid line) and androgen receptor (dashed line) in the initial segment (IS), caput (CA), corpus (CO) and cauda (CD) epididymides of vehicle treated (control) rats. Gene expression is presented as relative intensity (mean \pm SEM, 3-5 replicates/group).

Figure 1

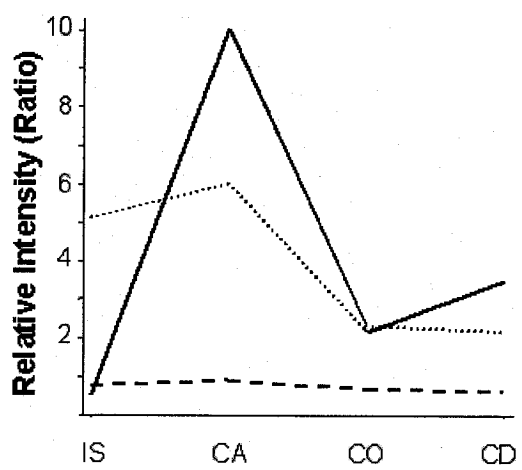


Figure 2. Effect of PNU157706 treatment on weights of seminal vesicles (A), left ventral prostates (B), testes (C) and epididymides (D). Data are represented as the mean \pm SEM for each treatment group on the x-axis: Control/0 mg/kg (0), Low dose/0.1mg/kg (0.1), Medium dose/1.0 mg/kg (1), High dose/10 mg/kg (10). * indicates $p < 0.05$.

Figure 2

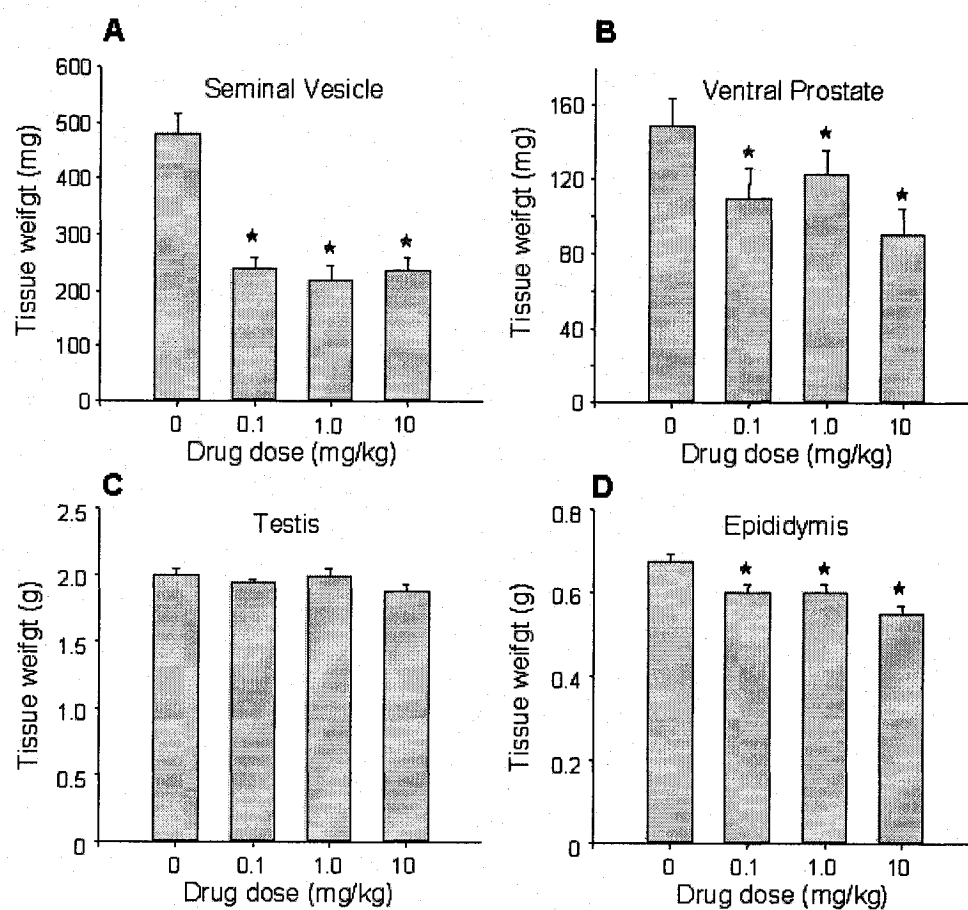


Figure 3. Inhibition of rat nuclear (A) and microsomal (B) 5 α -reductase activity *in vitro* by different concentrations of PNU157706 (PNU). For nuclear (C) and microsomal (D) 5 α -reductase, slope replots (squares) were obtained from $K_{m(app)}/V_{max(app)}$ vs. (PNU) and intercept replots (triangles) were obtained from $1/V_{max(app)}$ vs. (PNU).

Figure 3

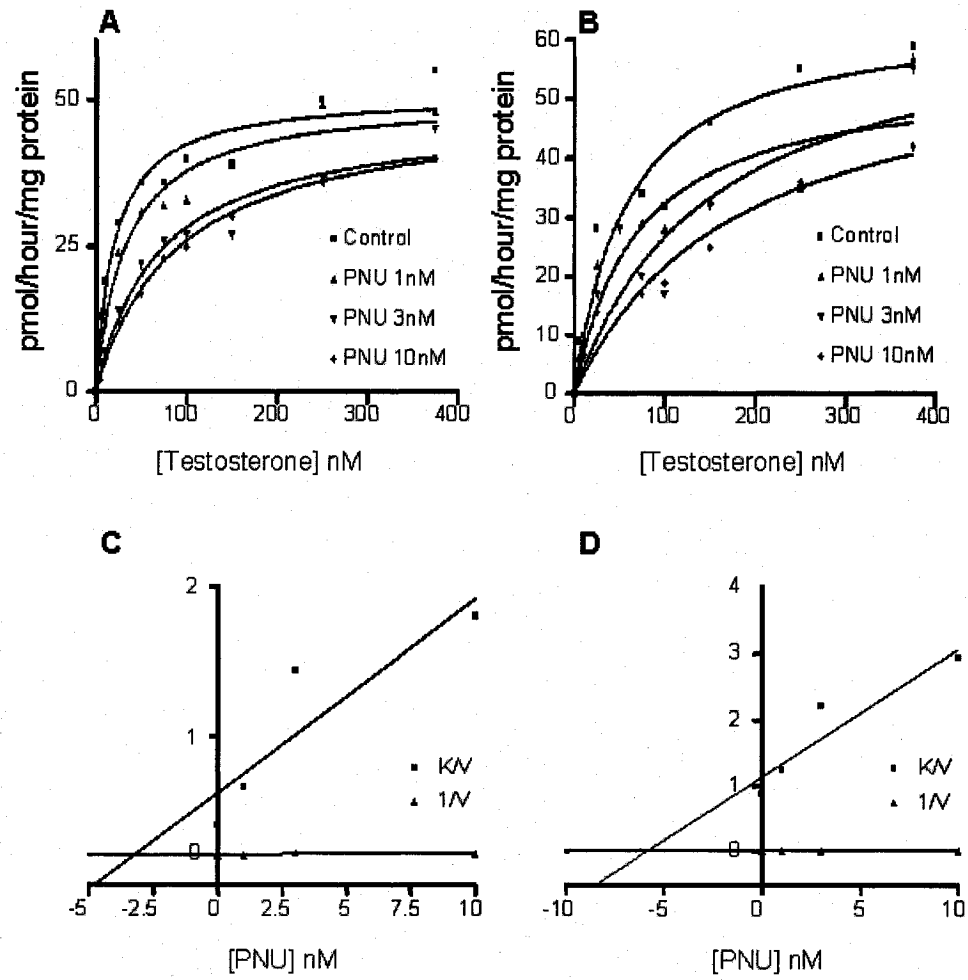


Figure 4. Number of genes in each epididymal segment showing changes in gene expression following 10 mg/kg/day PNU157706 treatment. The vertical scale represents the total number of genes that showed at least a 2-fold change in expression in either direction (100% increase or 50% decrease). The dark grey bars indicate the number of genes increasing in expression (above x-axis); the light grey bars indicate the number of genes decreasing in expression (below x-axis). Initial segment (IS), Caput (CA), Corpus (CO), Cauda (CD).

Figure 4

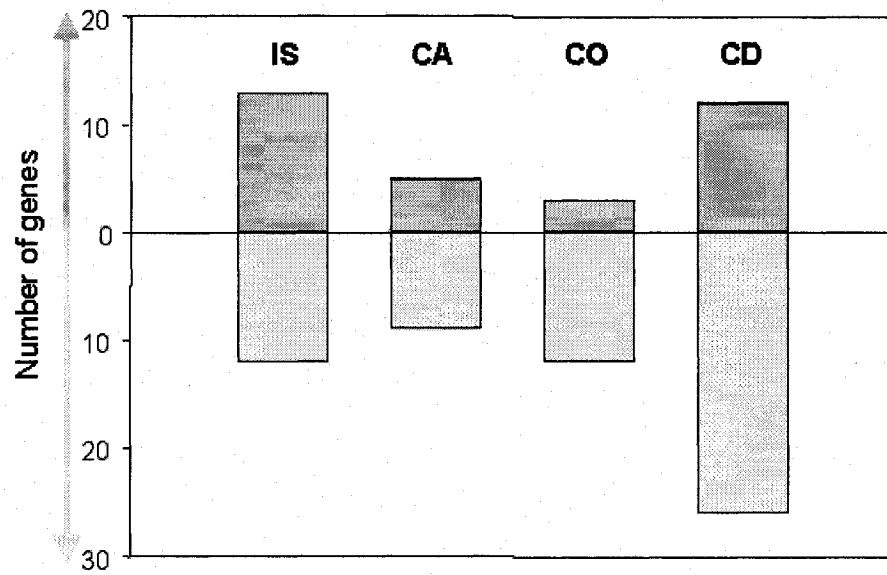


Figure 5. Genes with altered expression in the initial segment following PNU157706 treatment for 28 days. Each line represents one gene. (A) Signalling-related genes: NF-2, retinoblastoma protein pp105 (RBpp105), ras-GTPase activating protein (p120GAP), Crk-associated substrate (CAS). (B) Fatty acid/lipid metabolism genes: Fatty acid amide hydrolase (f.a. amide hydrolase), corticosteroid 11 β -hydroxysteroid dehydrogenase (corticosteroid 11 β -HSD), very long chain acyl-CoA dehydrogenase (VLCAD), 5-lipoxygenase (5-LO). (C) Fluid/ion balance related genes: atrial natriuretic peptide clearance receptor (ANP-C), chloride channel CLC-7 (CLC-7). Gene expression is presented as relative intensity (mean \pm SEM, 3-5 replicates/group) on the y-axis for each treatment group on the x-axis: Control/0 mg/kg (0), Low dose/0.1mg/kg (0.1), Medium dose/1.0 mg/kg (1), High dose/10 mg/kg (10).

Figure 5

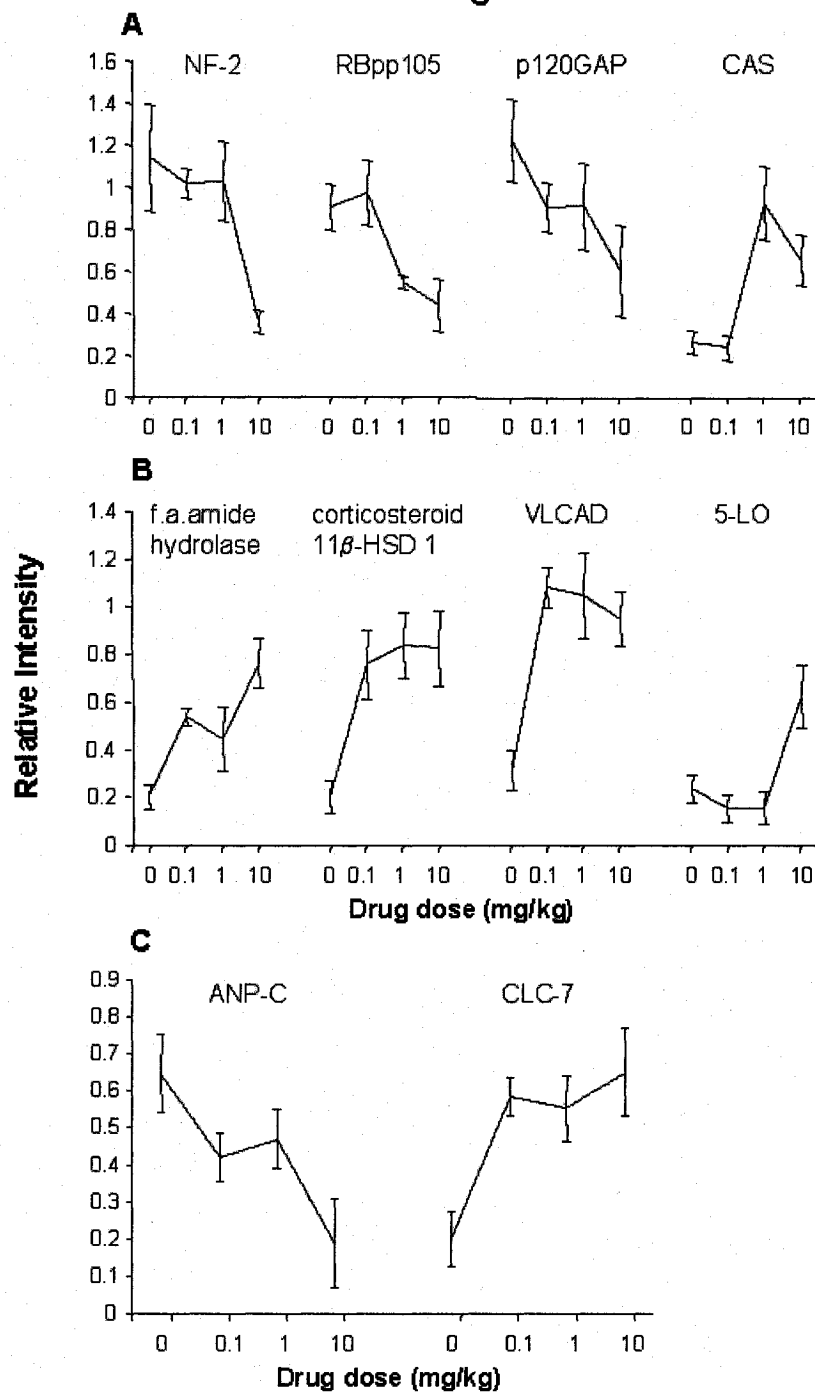


Figure 6. Genes with altered expression in the caput epididymidis following PNU157706 treatment for 28 days. Each line represents one gene. (A) Signalling-related genes: cAMP-dependent protein kinase type II-beta regulatory chain (camp dep. PK type II β), Ehk3, neural thrombospondin1-like protein (NELL-1). (B) Cathepsin B. (C) Short chain acyl-CoA dehydrogenase (SCAD). Gene expression is presented as relative intensity (mean \pm SEM, 3-5 replicates/group) on the y-axis for each treatment group on the x-axis: Control/0 mg/kg (0), Low dose/0.1mg/kg (0.1), Medium dose/1.0 mg/kg (1), High dose/10 mg/kg (10).

Figure 6

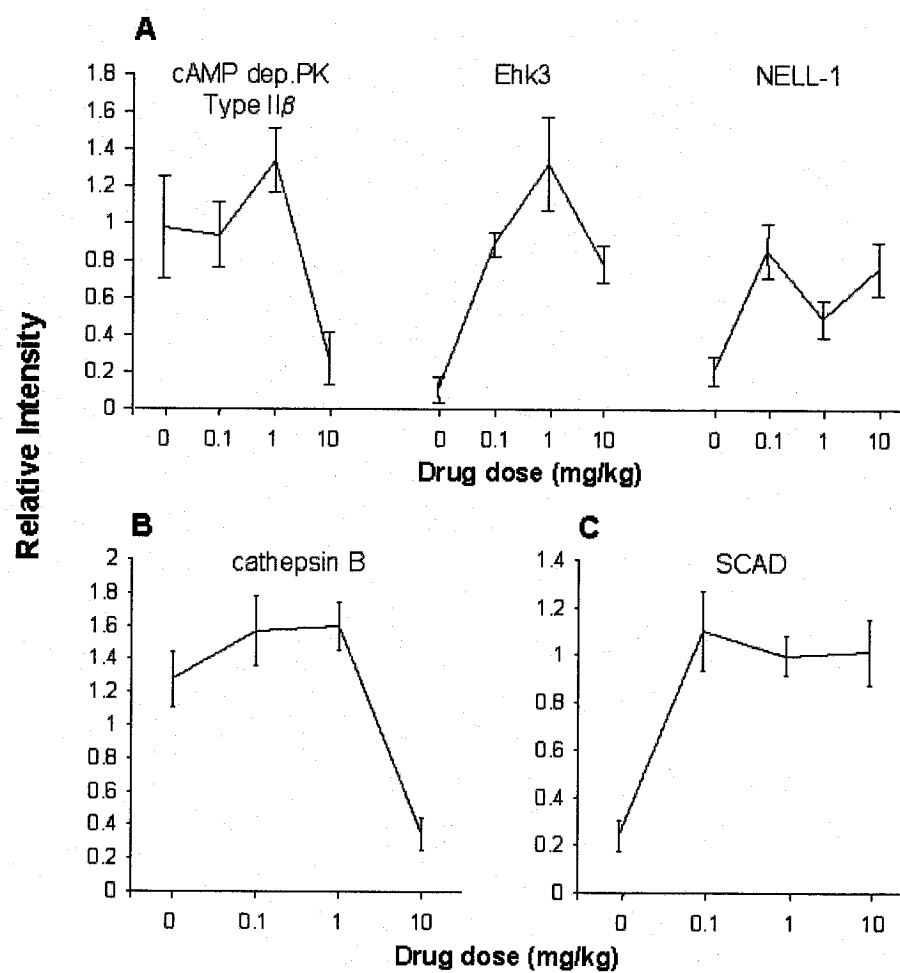


Figure 7. Genes with altered expression in the corpus epididymidis following PNU157706 treatment for 28 days. Each line represents one gene. (A) Carbonic anhydrase 4 (CA4). (B) Signalling-related genes: ras related protein RAB13 (rab13), ephrinB1, Jak1 tyrosine-protein kinase (Jak1). Gene expression is presented as relative intensity (mean \pm SEM, 3-5 replicates/group) on the y-axis for each treatment group on the x-axis: Control/0 mg/kg (0), Low dose/0.1mg/kg (0.1), Medium dose/1.0 mg/kg (1), High dose/10 mg/kg (10).

Figure 7

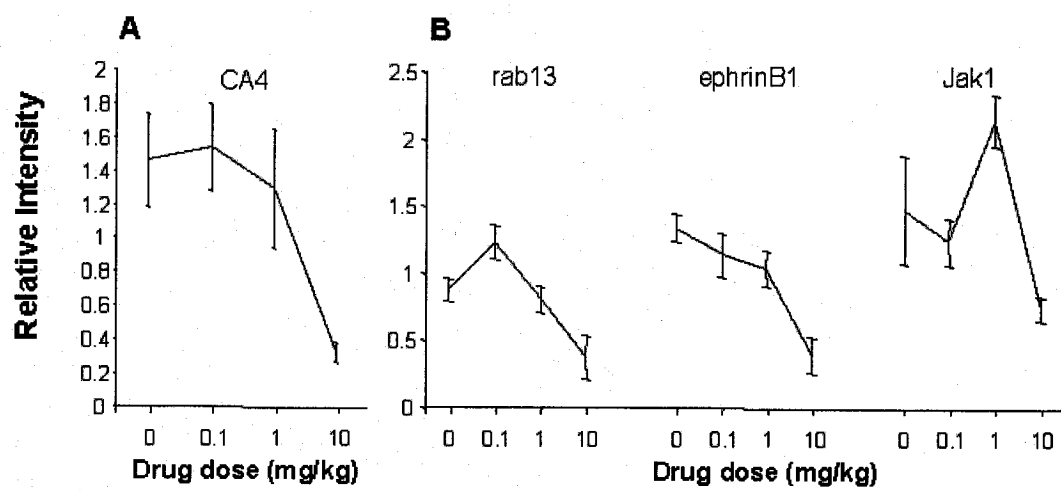


Figure 8. Genes with altered expression in the cauda epididymis following PNU157706 treatment (10mg/kg) for 28 days. Each line represents one gene.

(A) Signalling-related genes: Rab-related GTP-binding protein (Rab-related GBP), muscle/brain cAMP-dependent protein kinase inhibitor (PKI-alpha), phosphatidylinositol 4-kinase (PI4-K), 14-3-3 protein gamma subtype, ras-related GTPase rab4B (rab4B). (B) Phospholipase genes: Phospholipase C gamma 2 (PLC gamma 2), phospholipase C delta 1 (PLC delta 1), phospholipase C gamma 1 (PLC gamma 1). (C) Ion transporter genes: Hydrogen-potassium transporting ATPase alpha 2a subunit (H⁺/K⁺ ATPase alpha 2a sub.), sodium/potassium transporting ATPase beta 2 subunit (Na⁺/K⁺ ATPase beta 2 sub.), band 3 anion exchanger (Band 3). Gene expression is presented as relative intensity (mean \pm SEM, 3-5 replicates/group) on the y-axis for each treatment group on the x-axis: Control/0 mg/kg (0), Low dose/0.1mg/kg (0.1), Medium dose/1.0 mg/kg (1), High dose/10 mg/kg (10).

Figure 8

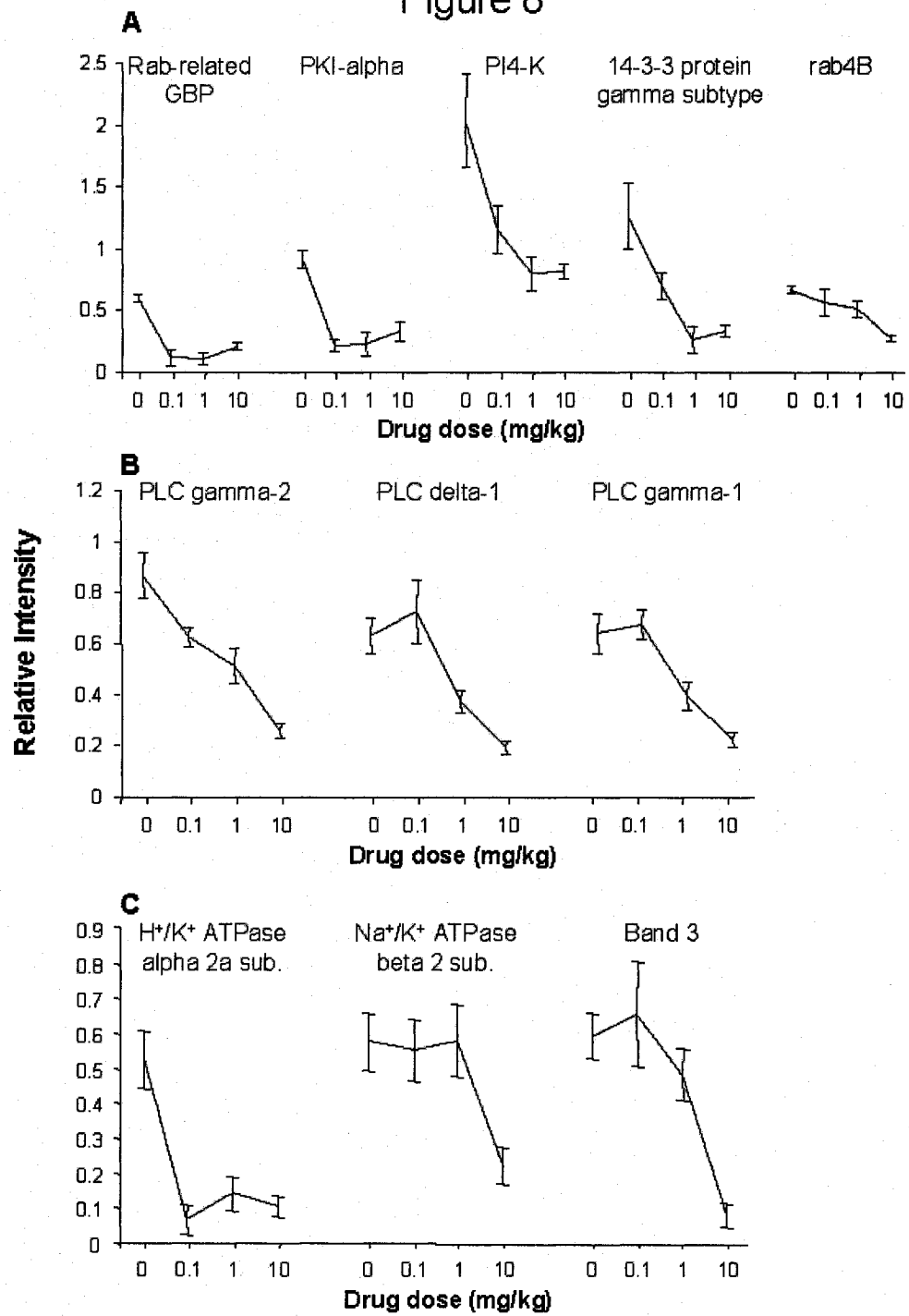


Figure 9. Expression of oxidative stress related genes in the control (light grey bars) and high PNU157706 treatment (dark grey bars, 10mg/kg/day) groups in the initial segment (IS), caput (CA), corpus (CO) and cauda (CD) epididymidis. Gene expression is presented as relative intensity (mean \pm SEM, 3-5 replicates/group) on the y-axis for each specific gene on the x-axis: GST mu (μ), GST Yrs-Yrs (Yrs-Yrs), GST subunit 5-theta (5-theta), GST subunit 13 (13), GPX3, and glutathione synthetase (GSH synth).

Figure 9

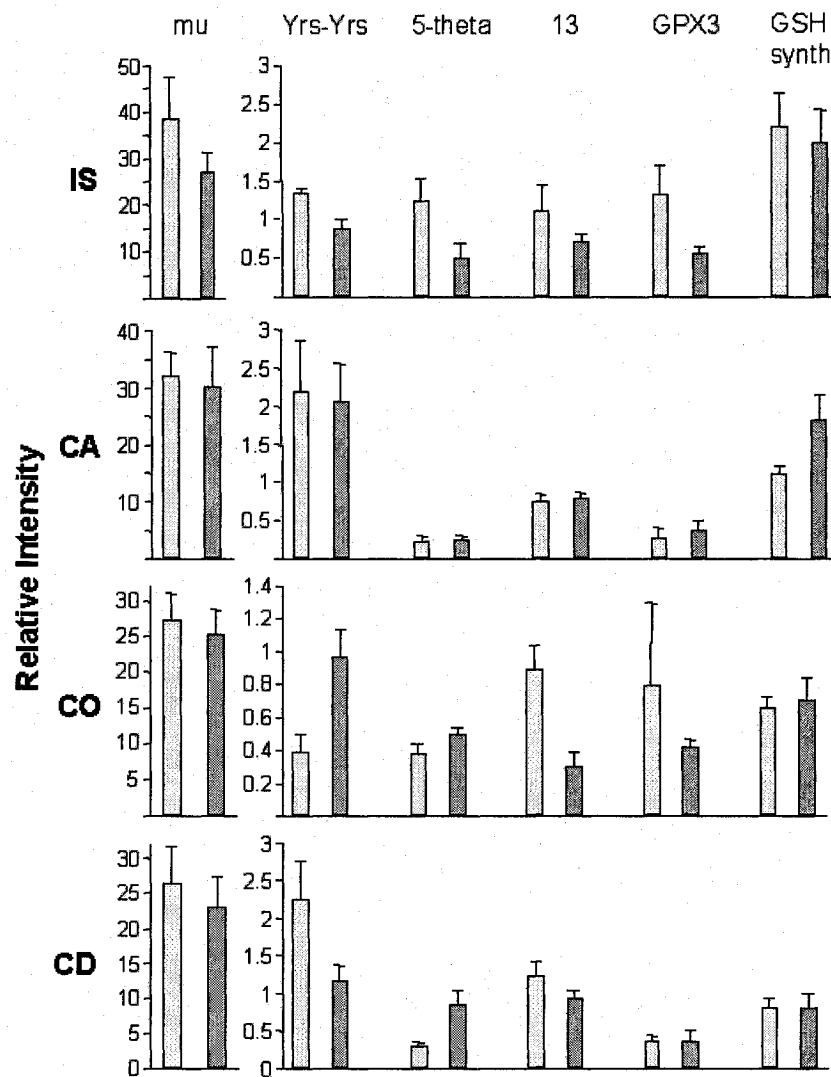
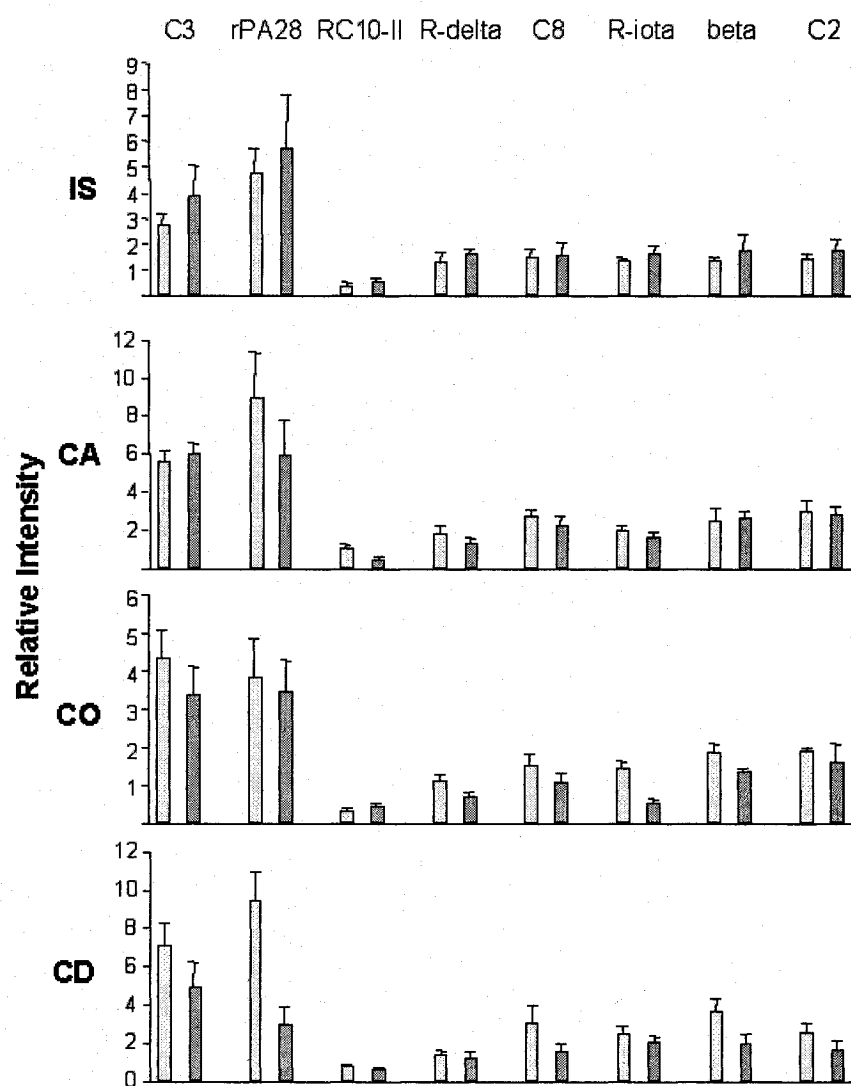


Figure 10. Expression of proteasomal genes in the control (light gray bars) and high PNU157706 treatment (dark grey bars, 10mg/kg/day) groups in the initial segment (IS), caput (CA), corpus (CO) and cauda (CD) epididymidis. Gene expression is presented as relative intensity (mean \pm SEM, 3-5 replicates/group) on the y-axis for each specific gene on the x-axis: proteasome component C3 (C3), proteasome activator rPA28 subunit alpha (rpA28), proteasome subunit RC10-II (RC10-II), proteasome subunit R-delta (R-delta), proteasome component C8 (C8), proteasome subunit R-iota (R-iota), proteasome subunit beta (beta), and proteasome component C2 (C2).

Figure 10



Tables and Legends

Table 1. Summary of the in vitro effect of PNU157706 on epididymal nuclear and microsomal 5 α -reductase enzyme kinetics. Non-linear least squares analysis was used to obtain the $K_{m(app)}$ and $V_{max(app)}$ values. Linear regression analysis of the slope and intercept replots was used to obtain the $K_{i(app)}$ values.

	Experiment 1					Experiment 2				
	$K_{m(app)}$	$V_{max(app)}$	r	$K_{i(app)}$	r	$K_{m(app)}$	$V_{max(app)}$	r	$K_{i(app)}$	r
Nuclear 5α-reductase										
0 nM PNU	20.5	51.1	0.95	-	-	20.7	45.7	0.86	-	-
1 nM PNU	33.1	50.4	0.97	-	-	40.9	48.5	0.93	-	-
3 nM PNU	68.7	47.8	0.96	-	-	64.4	53.5	0.90	-	-
10 nM PNU	88.2	49.1	0.99	-	-	96.7	48.6	0.96	-	-
Slope replot ($K_{m(app)}/V_{max(app)}$ vs [PNU])	-	-	-	3.13	0.90	-	-	-	4.02	0.98
Intercept replot ($1/V_{max(app)}$ vs [PNU])	-	-	-	74.5	0.51	-	-	-	-ve	0.23
Microsomal 5α-reductase										
0 nM PNU	57.1	64.4	0.94	-	-	32.4	63.9	0.95	-	-
1 nM PNU	67.7	54.4	0.88	-	-	62.2	64.5	0.83	-	-
3 nM PNU	145.3	65.7	0.91	-	-	60.8	49.7	0.91	-	-
10 nM PNU	174.6	59.7	0.95	-	-	172.7	66.8	0.94	-	-
Slope replot ($K_{m(app)}/V_{max(app)}$ vs [PNU])	-	-	-	4.76	0.94	-	-	-	3.1	0.99
Intercept replot ($1/V_{max(app)}$ vs [PNU])	-	-	-	-ve	0.01	-	-	-	-ve	0.13

Table 2. Genes with minimum 2-fold changed expression in more than 1 epididymal segment following 10 mg/kg PNU157706 treatment. The arrows represent the direction of change in expression. The dash (-) indicates no change in expression by 2-fold or greater. Accession numbers are for the GenBank database. Functional classifications are according to Clontech™.

Accession Number	Name	Change in gene expression				Functional classification
		Initial Segment	Caput	Corpus	Cauda	
U65007	c-met proto-oncogene	↓81%	↑564%	-	-	Growth factor/chemokine/protein kinase receptor
M95735	Syntaxin B	↓73%	-	-	↓77%	Trafficking & targeting protein
L11651	Eukaryotic translation initiation factor 5	↓72%	-	↓71%	↑458%	Translation factor
M76767	Fatty acid synthase	↓68%	-	-	↑469%	Fatty acid metabolism
M31602	Carboxypeptidase E	↓64%	↓66%	-	-	Metalloproteinase
X67654	Glutathione-S-transerase sub. 5 theta	↓58%	-	-	↑196%	Oxidative metabolism
X14977	Aldehyde dehydrogenase 2	↑140%	-	-	↑100%	Other metabolism
X80477	P2X purinoceptor 1	-	↑873%	↑156%	↑220%	ATP-gated ion channel

Connecting Text

In the previous chapter, cDNA array studies revealed changes in the expression of numerous genes following 5 α -reductase inhibitor treatment, indicating that DHT is an important regulator of epididymal gene expression. The nature of the affected genes suggested their involvement in processes that are essential for the formation of the dynamic luminal microenvironment that is required for proper sperm maturation in the epididymis. Therefore, the next objective was to determine if the observed changes in epididymal gene expression following 5 α -reductase inhibitor treatment actually translated to effects on epididymal sperm functions.

CHAPTER 3

Effects of PNU157706, a Dual 5 α -Reductase Inhibitor, on Rat Epididymal Sperm Maturation and Fertility

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Abstract

Sperm entering the epididymis gain progressive motility and fertilizing ability in a process termed maturation. The functional dependence of the epididymis on dihydrotestosterone (DHT) is well established, yet few studies have examined the consequences on the epididymis of inhibiting DHT formation. We have shown that inhibition of both isoforms of 5 α -reductase (types 1 and 2), the enzyme that converts testosterone to DHT, has pronounced effects on epididymal gene expression. In the present study, we investigate whether inhibiting 5 α -reductase has consequences on epididymal sperm maturation. Rats were treated with vehicle or 10 mg/kg/day PNU157706, a dual-type inhibitor, for 28 days. Fertility and several key facets of sperm maturation were analyzed. Changes in sperm motility were assessed by computer-assisted sperm analysis (CASA). Changes in sperm morphology were assessed by CASA and electron microscopy. The motility of spermatozoa from the cauda epididymidis of treated animals showed a significant decrease in both the percentage of motile and progressively motile sperm as well as altered motion parameters. The morphology of cauda epididymal spermatozoa was also adversely affected by the treatment; the most prominent effect was a markedly elevated proportion of sperm that retained their cytoplasmic droplet. Matings with treated males resulted in fewer successful pregnancies and a higher rate of pre-implantation loss. Progeny outcome was unaffected. The compromised sperm motility and morphology likely contribute to the subfertility of inhibitor-treated rats. Our results indicate a role for dual 5 α -reductase inhibitors in further

studies of epididymal physiology and as a potential component of a male contraceptive.

Introduction

Within the testis, several complex sequential stages of germ cell differentiation give rise to spermatozoa [1, 2]. Sperm are then introduced to the epididymis, a single highly convoluted tubule structurally divided into four main segments (initial segment, caput, corpus and cauda). This tissue is the site of sperm maturation and additionally functions in sperm transport, protection and storage [3, 4]. Sperm maturation in the epididymis involves various morphological and biochemical changes, the initiation of progressive motility and the acquisition of fertilizing ability [3, 5-7]. In comparison with spermatogenesis in the testis, an elaborate process requiring approximately 2 mo in the adult male primate [8], sperm maturation in the epididymis does not involve cell division and is accomplished in a significantly shorter period of time [9]. These features of sperm maturation have generated significant interest in the epididymis as an advantageous posttesticular target for the development of safe, rapid and reversible male contraceptives. Achieving this therapeutic goal as well as elucidating epididymal causes of male infertility require an increased understanding of epididymal physiology.

The maintenance of epididymal structure and functions is known to be highly dependent on the presence of androgens [10, 11]. Furthermore, several in vivo and in vitro studies have confirmed that it is not testosterone, but rather

dihydrotestosterone (DHT), that is the main androgen acting in this tissue [12-15]. In contrast, testicular spermatogenesis is a testosterone-dependent process [16, 17, reviewed in 18]. Therefore, the inhibition of DHT production is an interesting experimental approach for studying the regulation of sperm maturation in the epididymis while presumably having little or no effect on sperm production in the testis.

5 α -Reductase (EC 1.3.1.22) is the enzyme that catalyzes the conversion of testosterone into DHT. Two isoforms of 5 α -reductase have been identified and are termed type 1 and type 2 [19, 20]; the contributions of each isozyme to male reproductive biology have not been fully elucidated. It is known that both 5 α -reductase isozymes are present in the epididymis, where they are differentially distributed and regulated [21]. Though the importance of each isozyme in the epididymis remains unclear, a synergistic or additive contribution of both isozymes to epididymal functions is a plausible likelihood. Supporting this concept is the observation of a more pronounced virilization defect in dual 5 α -reductase knockout mice when compared to the single 5 α -reductase type 2 knockout animals [22] as well as greater decreases in serum and prostate DHT levels when both isozymes are inhibited simultaneously [23-25].

The utility of 5 α -reductase type 2 inhibitors (e.g. finasteride) for treatment of androgen-dependent disorders such as benign prostatic hyperplasia and alopecia has been demonstrated [reviewed in 24-26]. Recently, drug development efforts to create even more therapeutically effective compounds have led to the production and testing of a novel class of 5 α -reductase inhibitors,

termed dual inhibitors, that concurrently inhibit both 5 α reductase type 1 and type 2. PNU157706 is one such inhibitor developed for the potential treatment of benign prostatic hyperplasia. PNU157706, *in vitro*, has been shown to be a specific competitive inhibitor of epididymal 5 α -reductase activity and it decreases DHT-dependent tissue weights (i.e., seminal vesicle and ventral prostate) *in vivo* [23, 27]. Furthermore, PNU157706 was shown to be more potent than finasteride in decreasing DHT levels [23]. In a previous study, we have shown that treatment of adult male rats with PNU157706 has a highly segment-specific effect on epididymal gene expression [27]. Importantly, some of the more dramatically affected genes are potentially involved in essential processes contributing to the formation of an optimal luminal microenvironment required for proper sperm maturation. For example, genes involved in fatty acid and lipid metabolism, regulation of ion and fluid transport, luminal acidification, oxidative defense, and protein processing and degradation were affected [27].

Studying the consequences of inhibiting DHT formation is likely to provide important information regarding the androgen-regulation of epididymal functions; however, very few recent studies have examined the effects of 5 α -reductase inhibition, specifically in the epididymis. The present study was designed to evaluate the effects of an altered androgen environment on epididymal sperm maturation by taking advantage of a novel drug and sperm analysis technology to determine the effects of 5 α -reductase inhibition on sperm morphology, motility and fertilizing ability.

Materials and Methods

Animals and Treatment Protocol

Adult Sprague-Dawley rats were obtained from Charles River Canada (St. Constant, PQ, Canada), maintained under controlled light (14L:10D) and temperature (22°C), and provided with food and water ad libitum. Male rats (325-350g) were randomly divided into 2 groups and gavaged with 0.5 ml/kg of 0 (control) or 10 mg/kg (treated) of PNU157706 (Pharmacia & Upjohn, Italy) suspended in 0.5% methylcellulose solution (BDH, Montreal, QC) containing 0.4% Tween 80 (A&C American Chemicals Ltd, Montreal, Quebec) for 28 consecutive days. The dose was selected based on reported effects on rat ventral prostate; the dosing regimen with 10 mg/kg/day PNU157706 has been shown to decrease prostatic dihydrotestosterone levels by >90% [23]. Virgin female rats (200-250g) were used for the mating study. All animal studies were conducted in accordance with the principles and procedure outlined in the Guide to the Care and Use of Experimental Animals prepared by the Canadian Council on Animal Care.

Sperm Motility

All chemicals were purchased from Sigma Chemical Co. (St. Louis, MO) unless otherwise noted. At the time of killing, animals were anesthetized and seminal vesicles, testes, ventral prostates and one epididymis, sectioned into initial segment, caput, corpus and cauda segments; were collected and

immediately frozen in liquid nitrogen. Tissues were stored at -80°C for future use. Sperm samples were collected from the distal caput and distal cauda of the remaining epididymis and used for computer-assisted sperm analysis (CASA) as previously described [28, 29], with the exception that the medium used for motility analysis was as follows: Hanks balanced salts solution (Gibco Invitrogen Co., Grand Island, NY), buffered with 4.2 g/L Hepes and 0.35 g/L NaHCO_3 and containing 2.0 g/L BSA, 0.9 g/L D-glucose, 0.1 g/L sodium pyruvate and 0.025 g/L soybean trypsin inhibitor, pH 7.4, at 37°C [30]. Briefly, the epididymis was trimmed free of fat and clamped at the caput-corpus and corpus-cauda junctions, then severed on the corpus side of the clamp and blotted. While still clamped, the caput and cauda epididymides were rinsed in separate 35-mm Petri dishes containing 2 ml of motility media and then transferred to separate Petri dishes containing 3 ml of fresh media. A #11 scalpel blade was used to pierce several tubules of the distal caput and distal cauda regions allowing sperm to diffuse into the medium. The tissue was removed and sperm were allowed to disperse for approximately 5 min. Sperm concentrations were optimized prior to aliquoting into an 80- μm -deep glass cannula for CASA on the HTM-IVOS, (Hamilton-Thorne Research, Beverly, MA) using version 12 of the Toxicology software. Approximately 3500 caput epididymal sperm and 6000 cauda epididymal sperm were analyzed for each treatment group ($n=5-7$). The percentages of motile and progressively motile sperm and the following kinematic parameters were determined by CASA: average-path velocity (VAP), curvilinear velocity (VCL), straight-line velocity (VSL), amplitude of lateral head displacement (ALH), beat

cross frequency (BCF), linearity ($\text{LIN} = \text{VSL}/\text{VCL} \times 100$) and straightness ($\text{STR} = \text{VSL}/\text{VAP} \times 100$).

Sperm Morphology

The morphology of spermatozoa from the cauda epididymidis was evaluated by phase-contrast microscopy using the HTM-IVOS. Sperm from the original dilution for motility analysis were fixed with 10% neutral buffered formalin (1:3, Sigma-Aldrich, Oakville, Ontario). Samples were aliquoted onto regular slides and sperm were analyzed using the 10x phase contrast objective. This system allowed clear visualization of cytoplasmic droplets [28]. Approximately 300 to 500 sperm per sample were analyzed and the percentage of sperm retaining their cytoplasmic droplet was calculated. Similarly, broken sperm (head only, tail only, other breakages) and angulated sperm (bent at midpiece) were also clearly detectable using this system and the frequency of these abnormalities was calculated.

In addition to the HTM-IVOS analysis of sperm morphology, spermatozoa from the cauda epididymidis of four control and four treated rats were also processed for electron microscopic analysis. A #11 scalpel blade was used to pierce the cauda several times and sperm were collected by shaking in Hanks minimum essential medium (Invitrogen Canada Inc., Burlington, Ontario). Spermatozoa were washed in Hanks media, fixed in the same media containing 1% glutaraldehyde (Mecalab Ltd., Montréal, Québec), and embedded for electron microscope analysis. Briefly the samples were washed three times in sodium

cacodylate buffer (0.1M) containing 3% sucrose, pH 7.4, postfixed in 1% osmium tetroxide and 1.5% potassium ferrocyanide and embedded in epoxy resin.

Sperm ultrastructure was then analyzed on the electron microscope (Philips 410 electron microscope, Eindhoven, The Netherlands). For analysis of cytoplasmic droplet retention, a minimum of 100 midpiece sperm tail (flagellum) cross sections per animal were photographed, and the number of sperm tails with cytoplasmic droplets recorded.

Mating Study

A mating study was designed to determine the effects of PNU157706 treatment on male fertility. Vaginal smears from female rats were analyzed daily for a minimum of 2 weeks to confirm normal estrous cycles. On the last day of treatment, each male rat was paired overnight with 2 female rats in proestrus. Female rats were examined the next morning for the presence of sperm in vaginal smears; this was defined as day 0 of gestation for sperm-positive animals. The male reproductive indices that were calculated are: copulation index (number of sperm positive females / number of pairings), pregnancy index (number of pregnancies / number of sperm positive females), and fertility index (number of pregnancies / number of pairings).

Pregnancy Outcome

To examine the effect of inhibitor treatment on pregnancy outcome, female rats underwent a cesarean section on Day 20 of gestation. The ovaries

were removed and the number of corpora lutea was counted; uteri were opened, and the numbers of implantation sites were counted. The status of each implantation site was classified as resorption, dead or live fetus. For each treatment group, the overall implantation rate (number of implantations / number of corpora lutea), preimplantation loss per female [(number of corpora lutea - number of implantation sites) / number of corpora lutea], overall resorption rate (number of resorptions / number of total implantations) and postimplantation loss per female [(number of implantations – number of live fetuses)/ number of implantations] were calculated. Fetuses were sexed, weighed and examined for external malformations.

Statistical analysis

Statistical analysis of frequency data (reproductive indices, fetal sex ratio) was done by the Fisher Exact test. The implantation and resorption rates were analyzed by the test of proportions (Z-test). The remaining data assessing male fertility and pregnancy outcome, sperm motility and sperm morphology were analyzed for differences between the control and treated groups by Student's *t* test or the Mann-Whitney U test (in cases of failed normality or equal variance tests). Data are presented as mean \pm SEM. For all analyses, the level of significance was set at $p < 0.05$.

Results

Effects of PNU157706 Treatment on Sperm Motility

In the control group, a pattern of spermatozoal motility from circular, in the caput epididymidis, to progressively forward, in the cauda epididymidis, was observed. This progression was reflected in the sperm motion parameters measured by CASA where sperm from the cauda epididymides had higher straight line velocity (VSL) and straightness (STR) (Table 1), as well as an increase in the percent that was progressively motile (Fig. 1). For sperm taken from the caput epididymidis, there was no effect of PNU157706 treatment on any of the motion parameters (Table 1), or on the percentage of motile and progressively motile sperm (Fig. 1). In contrast, treatment with the 5 α -reductase inhibitor caused a significant decrease in the VSL, STR and linearity (LIN) of sperm from the cauda epididymidis (Table 1). There was also a significant decrease in the percentage of motile and progressively motile sperm from the cauda epididymides of PNU157706-treated rats when compared to control rats (Fig. 1).

Effects of PNU157706 Treatment on Sperm Morphology

A major morphological feature of epididymal sperm maturation is the displacement of the cytoplasmic droplet along the midpiece of sperm travelling from the caput to the cauda epididymal regions [7, 31]. Analysis of sperm from the cauda epididymidis under phase-contrast microscopy using the CASA

system allowed clear visualization of the cytoplasmic droplet (Fig. 2A). As expected, a low percentage (approximately 12%) of sperm from this segment of the tissue of control males retained their cytoplasmic droplet. However, sperm samples from the cauda epididymides of males treated with PNU157706 had a significantly higher percentage of retained cytoplasmic droplets compared to controls, doubling to nearly 25% (Fig. 2B).

Some sperm abnormalities such as bent (angulated) sperm and sperm breakages (i.e., headless, tailless) were also easily visualized using the CASA system; examples of these defects are shown in Figure 3. Sperm samples from the cauda epididymides of control and treated males had similar percentages of bent sperm (Table 2). In contrast, there was a higher incidence of sperm breakage in sperm from the cauda epididymides of males treated with the inhibitor; the percentages of headless, tailless and other breaks all increased significantly with treatment, as did the percentage of overall abnormalities observed using CASA (Table 2).

Analysis of the ultrastructure of sperm from the cauda epididymidis revealed an apparent increase in the proportion of mid-piece spermatozoa having cytoplasmic droplets; examples of sperm cross-sections with and without the droplet are shown in Figure 4. The droplet appears as a membrane-bound structure surrounding the sperm tail. There was a significant effect of treatment on the percentage of mid-piece sperm cross-sections surrounded by cytoplasmic droplets (Fig. 4C). This is consistent with our CASA analysis of cytoplasmic droplet retention in sperm from the cauda epididymidis. Very few ultrastructural

abnormalities were observed in sperm samples from either control or treated rats.

Effects of PNU157706 Treatment on Male Fertility

In this study, each male (n=8 / treatment group) was paired with 2 virgin females in proestrus for a total of 16 pairings for each treatment group. The effects of 5 α -reductase inhibitor treatment on indices of male reproduction are shown in Table 3. All of the control males successfully mated with at least one female, with the majority mating with both females. All of these successful matings resulted in pregnancies. In contrast, there was a decrease in the number of sperm-positive (successfully mated) females exposed to PNU157706-treated males. In some cases, approximately 50 or more sperm were present and easily detected in the vaginal smears of females exposed to treated males (comparable to controls), while in other cases as few as 2 sperm were detected. Furthermore, not all of the sperm-positive females exposed to treated males became pregnant. Overall, the number of females with successful pregnancies that resulted from pairings with treated males was significantly reduced.

Effects of PNU157706 Treatment on Pregnancy Outcome

As expected, females exposed to either control or PNU157706-treated males had similar numbers of corpora lutea (17.1 ± 0.7 and 17.2 ± 1.8 , respectively). In contrast, the implantation rate, reflecting the number of released

ova that were successfully fertilized and implanted in the uterus, was significantly decreased in females exposed to treated males (80.6%) compared to those exposed to control males (95%). Approximately half of the pregnant females that were mated with control males had some degree of preimplantation loss (7/13) compared to 83% of the pregnant females exposed to treated males (5/6). The mean preimplantation loss per litter increased from 5.3% in females exposed to control males to nearly 19% in females exposed to treated males (Fig. 5). Upon examination of the data for individual pregnant females, it is apparent that there is a heterogeneous effect of treatment on pre-implantation loss. Of the females mated with PNU157706-treated males, three had low rates of preimplantation loss (<15%) that were comparable to females mated with control males. Of the three remaining females, one had a higher rate of preimplantation loss (>18%) while two females had exceedingly high preimplantation loss at approximately 37 and 41%. In addition, three females exposed to treated males showed evidence of successful copulation (sperm-positive vaginal smears) that failed to result in pregnancy. This occurrence can be considered as 100% preimplantation loss due to failure of sperm to fertilize the released ova. Analysis of preimplantation loss based on the number of sperm positive females showed a significant increase in females exposed to males treated with PNU157706 (nearly 46%) when compared to control-mated females.

There was no significant effect of inhibitor treatment on postimplantation loss (Fig. 5). There were no late fetal deaths (non-live fetuses) observed in this study, therefore the postimplantation loss observed was due solely to

resorptions. Approximately half of the pregnant females exposed to either control or treated males had resorptions (control 6/13; treated 3/6) and the resorption rate was not significantly higher for those exposed to treated males.

The fetuses sired by control and treated males showed no gross external malformations. There was no difference in ano-genital distance between fetuses sired by PNU157706 treated males (male 3.69 ± 0.12 mm; female 1.97 ± 0.02 mm) and control males (male 3.92 ± 0.04 mm; female 1.95 ± 0.02 mm). The sex ratio (male/female) was also unaffected by treatment (control 96/107; treated 39/40). Fetuses sired by males treated with PNU157706 did not differ in weight (males 3.95 ± 0.36 g; females 3.81 ± 0.41 g) when compared to those sired by control males (males 4.23 ± 0.23 g; females 3.98 ± 0.23 g).

Discussion

Finasteride, a type 2 selective 5α -reductase inhibitor, was first marketed for the treatment of benign prostatic hyperplasia in 1992 [32]. Consequently, the long-term efficacy and safety of finasteride have been extensively studied for this indication [reviewed in 24, 25]. Finasteride treatment decreases serum and prostate DHT levels by approximately 65-70% and 85-90% respectively [25]. Efforts to discover more therapeutically effective compounds, i.e., that decrease DHT levels to a greater extent, have led to the development of a novel class of dual 5α -reductase inhibitors. In early 2003, dutasteride (GI198745) became the first dual 5α -reductase inhibitor available for the treatment of BPH [33]. In

comparison to finasteride, dutasteride and other dual compounds achieve almost total suppression of DHT levels [23, 33, 34].

There are a limited number of studies that examine the effects of finasteride on other reproductive tissues and/or fertility [35-38] and fewer still that examine the extraprostatic effects of the novel class of dual inhibitors [33, 34]. In 1991, Cukierski *et al.* [35] reported a partial decrease in fertility following chronic finasteride treatment (80 mg/kg/day for 24 weeks) of adult male rats. Wise *et al.* [36] reported a similar effect in a related study. In these earlier studies, testis weight and histology were unaffected by treatment and the subfertility was attributed solely to a deficit in the formation of copulatory plugs due to the effects of treatment on seminal vesicle and prostate weights. However, any data pertaining to the epididymis were lacking; therefore it is possible that the compromised fertility could have been due to an effect on this tissue as well.

In recent years, Mahendroo *et al.* [22] have developed and studied type-specific and dual 5 α -reductase null mutation mice. The dual knockout mice were fertile (pregnancy rates of 60% compared to 96% for wild-type animals). Unexpectedly, type 2 or dual knockout male mice showed only a mild virilization defect such that their internal and external genitalia were fully formed, but their prostates and seminal vesicles were smaller. These findings were markedly different from the phenotype of type 2 5 α -reductase deficiency in humans that results in a form of male pseudohermaphroditism [for review, see 39]. The authors concluded that, in mice, testosterone alone is required for differentiation of the male urogenital tract and that the synthesis of DHT serves largely as a

signal amplification mechanism. In contrast, both testosterone and DHT are required for proper development of the reproductive system in men, and studies in male rats with pharmacological inhibitors also support a two-androgen model of sexual differentiation [41-42]. Thus, the rat appears to be a more suitable animal model for understanding the roles of DHT within the human male reproductive system and comparisons with the mouse should be made with caution.

With the recent novel use of finasteride for the treatment of androgenic alopecia in young men of reproductive age [26] and the emergence of dual inhibitors that decrease DHT levels to a greater extent [33, 34], a renewed focus on the effects of 5α -reductase inhibition on the testis and fertility has emerged. To date, no adverse effects of 5α -reductase inhibitor treatment on testis weight, histology and/or sperm counts, and hence spermatogenesis, have been reported [24, 38, 43, 44], nor do 5α -reductase knockout mice show any testicular phenotype [22]; however, epididymal studies still remain scarce. Given the important role of the epididymis in sperm maturation, and the dependence of this tissue on DHT, a closer examination of the effects of 5α -reductase inhibition on epididymal sperm was considered necessary.

In the current study, we show that PNU157706 treatment of adult male rats for 28 days resulted in decreased fertility. It is unlikely that the effects of PNU157706 treatment on male fertility were due to an effect on sexual behaviour since 100% of the treated males showed evidence of successful copulation and 75% sired at least one litter. Current evidence does not suggest a role for DHT

in regulating sexual behavior. While the physiological functions of brain 5 α -reductase activity have not been fully elucidated, evidence points to roles predominantly during brain ontogenesis and the sexual differentiation of specific brain regions, as well as possible anesthetic/anxiolytic actions evoked when progesterone and/or corticoid levels are high, i.e. during stress, and neuroprotective roles mediated via the catabolism of potentially neurotoxic levels of steroids [reviewed in 45]. Additionally, the very low incidence of sexual side effects in men treated with finasteride or the dual inhibitor dutasteride provides support for a minimal or nonexistent role for DHT in regulating sexual behavior [32-34].

Examination of pregnancy outcome demonstrated an effect of treatment on implantation rate and preimplantation loss per pregnant female. Preimplantation loss represents either failure of sperm to fertilize the released ova or the death of the fertilized embryo before implantation. The latter suggests involvement of genetic damage (chromosomal aberrations) leading to early death and is proposed as the reason for increased preimplantation loss and decreased fetal weight seen with increased paternal age and long-term paternal exposure to the alkylating agent cyclophosphamide [46, 47]. It is unlikely that the genetic integrity of spermatozoa in this study is compromised since the testis, the site of continuous sperm cell division, has not been shown to be affected by 5 α -reductase inhibitor treatment [24, 38, 43, 44]. Furthermore, treatment had no effect on any of the fetal parameters measured, including fetal weight, which might be indicative of genetic impairment, nor were there any abnormal or dead

fetuses sired by treated males. It is more plausible that the sperm were unable to reach and fertilize the released ova due to compromised sperm motility and/or morphology. Supporting this is the observation of fewer sperm in the vaginal smears of some females mated with treated males and a lower pregnancy index.

We showed a decrease in both overall motility and progressive motility of sperm from the cauda epididymidis, accompanied by decreases in some motion parameters. The sperm tail encompasses the structural components directly involved in sperm motility [for review, see 48]; consequently, compromised tail ultrastructure could lead to impaired motility. In the present study, however, electron microscopic analysis of mid-piece flagellar ultrastructure revealed no effects of treatment that could account for the reduced sperm motility. Again, these findings are consistent with a lack of effect of 5 α -reductase inhibitor treatment on the testis, where sperm ultrastructure is established. The acquisition of sperm motility is a key element of epididymal sperm maturation [3]. By the time sperm reach the distal regions of the epididymis, maximum progressive motility is achieved that enables sperm to reach and penetrate the egg [3, 49]. This transition to progressive motility requires interactions between sperm and the surrounding epididymal luminal environment [3, 4, 50]. In fact, in reproductive toxicology studies, altered sperm motility is a valuable indicator of toxicity arising from an exclusive effect on the epididymis or sperm within the epididymis [51]. In the current study, it is likely that the reduced sperm motility observed is due to exposure of sperm to a compromised epididymal luminal environment. Notably, in a previous study we have shown that PNU157706

treatment affects the segment-specific expression of many genes in the epididymis potentially involved in the creation of the luminal environment that is critical for proper sperm maturation [27].

While the characteristic head, midpiece and tail structures of spermatozoa are already present before sperm leave the testis, other morphological changes occur during sperm transit through the epididymis. One prominent change is the migration of the cytoplasmic droplet along the midpiece of the sperm and its eventual shedding in the distal regions of the epididymis [7, 31]. The percentage of sperm retaining their cytoplasmic droplet was increased in rats treated with PNU157706. Interestingly, while the reason for shedding of the droplet remains unclear, some evidence suggests that cytoplasmic droplet retention can be correlated with altered epididymal function and decreased fertility [52-55]. Shedding of the droplet is thought to be related to the well-characterized changes in sperm plasma membrane lipid composition and fluidity that occur during epididymal transit [5, 56]. It is tempting to speculate that the increased cytoplasmic droplet retention, and possibly the increased sperm breakages observed in the current study are due to altered sperm membrane composition and dynamics arising from exposure to a suboptimal epididymal milieu. In fact, we have shown that PNU157706 treatment alters the epididymal expression of genes involved in oxidative defense that protect the highly susceptible sperm membrane lipids from oxidative damage [27]. Indeed, proper redox chemistry is essential within the epididymis as it regulates pathways involved in important sperm functions such as motility and sperm-egg interaction [52]; thus any

perturbation of the redox system likely has manifold consequences on epididymal sperm. Additionally, PNU157706 treatment also alters the expression of genes involved in fatty acid and lipid metabolism within the epididymis [27]. Of relevance to the current study is the reported reproductive impairment observed in mouse models of sphingolipid storage disorders (Niemann-Pick, Tay-Sachs, and Sandhoff diseases) that exhibit gross lipid accumulation within cells and tissues, including those of the male reproductive tract [58-60]. Interestingly, there do not appear to be any changes in testis weight, morphology or sperm counts in these animals; hence, the reproductive pathologies are believed to result from lipid accumulation in lysosomes of the epididymis that give rise to a dysfunctional sperm maturation environment. These models not only highlight the importance of lipid regulation within the epididymis, but also clearly support an important role for the epididymis in sperm-related functions that are unique and separate from the testis.

In conclusion, while an effect on sperm fertilizing ability was reported in earlier 5 α -reductase inhibitor studies, to our knowledge, this is the first study that clearly demonstrates an effect of inhibitor treatment on sperm maturation in the epididymis. It is highly likely that the compromised sperm motility and morphology observed in the current study contribute to the subfertility observed in 5 α -reductase inhibitor-treated rats. Furthermore, our results support a role for both 5 α -reductase isozymes within the epididymis and indicate the potential of dual 5 α -reductase inhibition as an experimental model for more in-depth study of

epididymal sperm-related functions separate from testicular sperm-related functions.

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Figures and Legends

Figure 1. Effect of PNU157706 treatment on sperm motility. The percentages of motile sperm (top) and progressively motile sperm (bottom) from the caput (left) and cauda (right) are indicated for the control (0 mg/kg/day, light grey bars) and treated (10 mg/kg/day, dark grey bars) groups. * $P < 0.05$ versus the control group, $n = 5-7$.

Figure 1

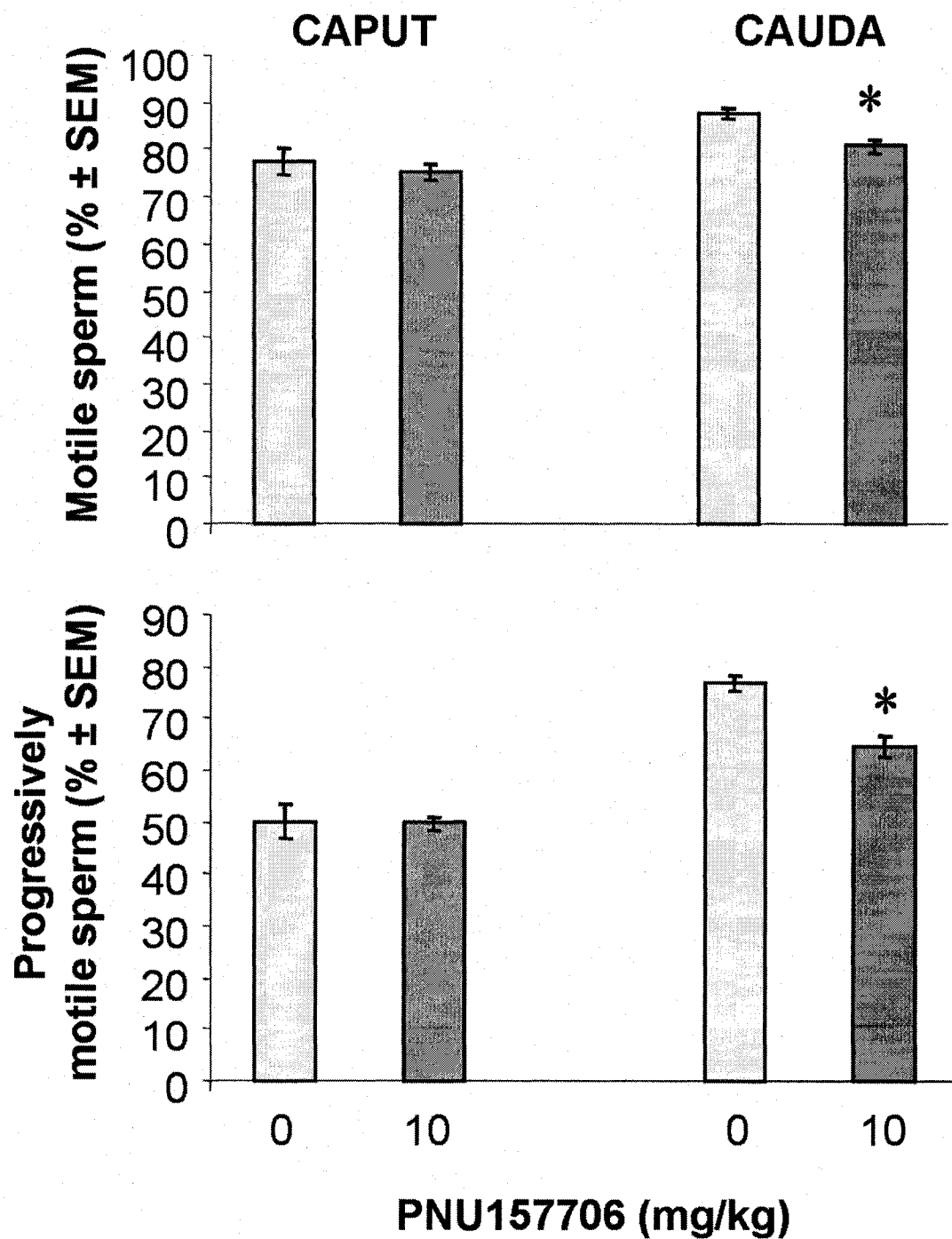


Figure 2. HTM-IVOS (phase-contrast microscopy) analysis of the effect of PNU157706 treatment on cytoplasmic droplet retention in cauda sperm. **A)** Example of a phase-contrast image from the HTM-IVOS system showing the absence or presence (white arrows) of the cytoplasmic droplet on cauda sperm. Bar = 16 μm . **B)** Calculation from phase-contrast images of the percentage of cauda sperm retaining the cytoplasmic droplet in the control (0 mg/kg/day, light grey bars) and treated (10 mg/kg/day, dark grey bars) groups. 300-500 sperm per sample (n=5) were analyzed. * $P < 0.05$ versus the control group.

Figure 2

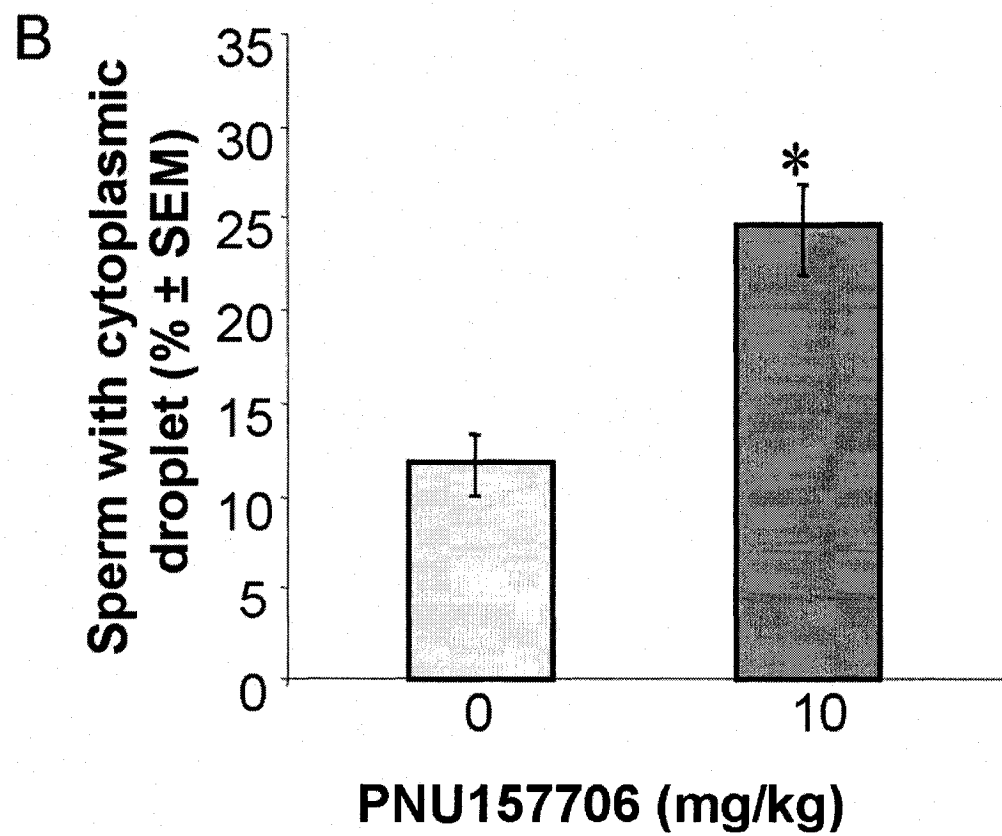
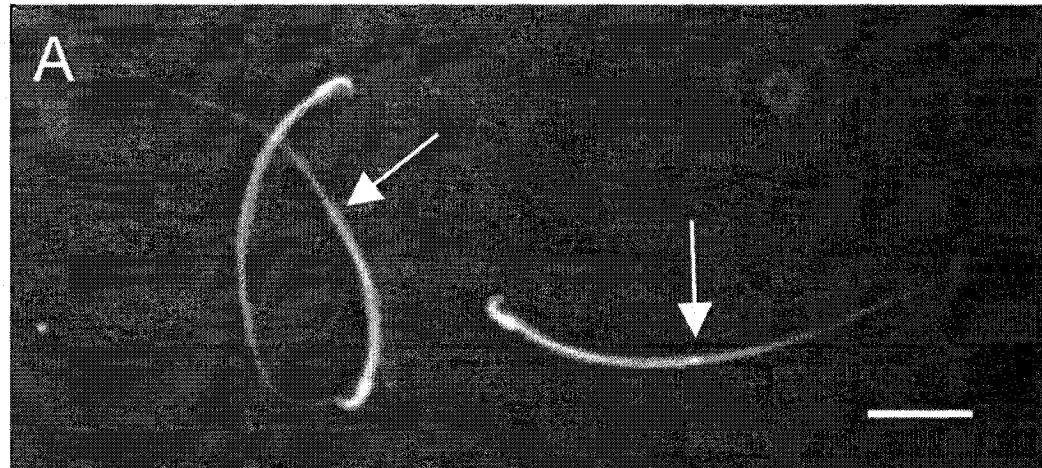


Figure 3. Examples of phase-contrast images of abnormal sperm morphologies detected using the HTM-IVOS system. **A)** Tail only. **B)** Bent. **C)** Broken. **D)** Head only. Bar = 16 μm .

Figure 3

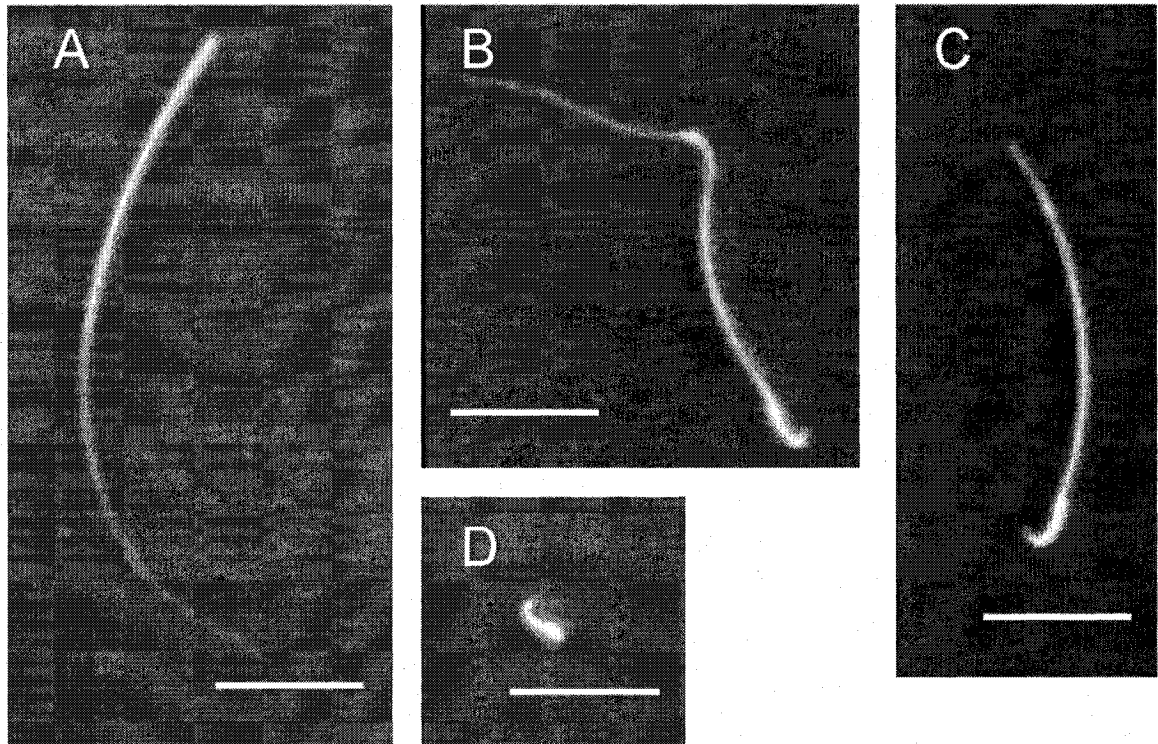


Figure 4. Electron microscopic analysis of the effect of PNU157706 treatment on cytoplasmic droplet retention in cauda sperm. **A)** Example of an electron micrograph showing several tail mid-piece cross-sections of cauda sperm. Cytoplasmic droplets surrounding the sperm midpiece are indicated by black arrows. Bar = 0.5 μm . **B)** Higher magnification of the cytoplasmic droplet. Bar = 2 μm . **C)** Calculation from electron micrographs of the percentage of cauda sperm retaining the cytoplasmic droplet in the control (0 mg/kg/day, light grey bars) and treated (10 mg/kg/day, dark grey bars) groups. A minimum of 100 midpiece sperm tail (flagellum) cross-sections per animal (n=4) were analyzed. * $P < 0.05$ versus the control group.

Figure 4

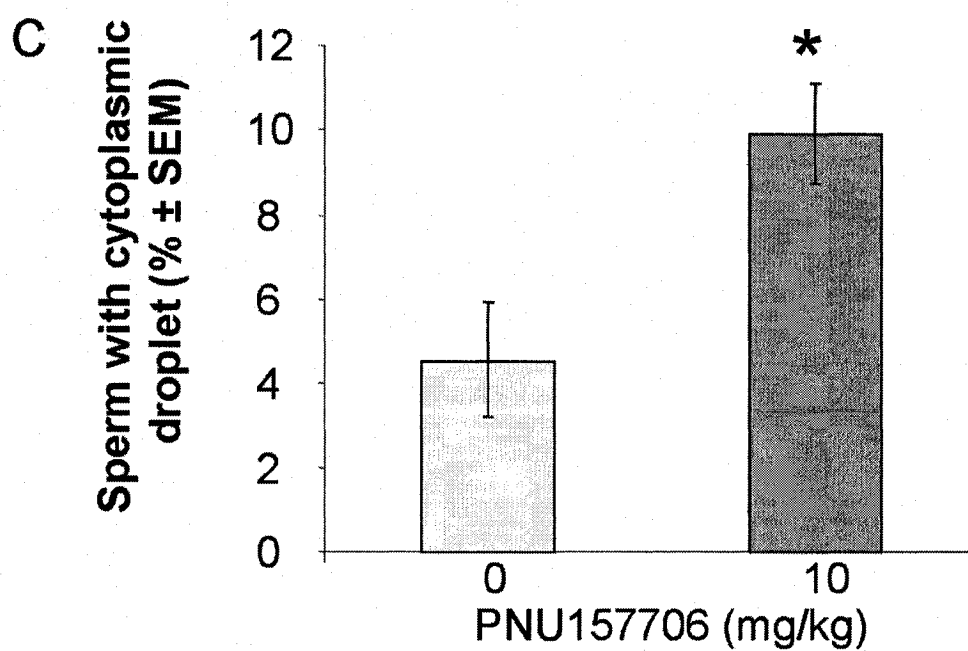
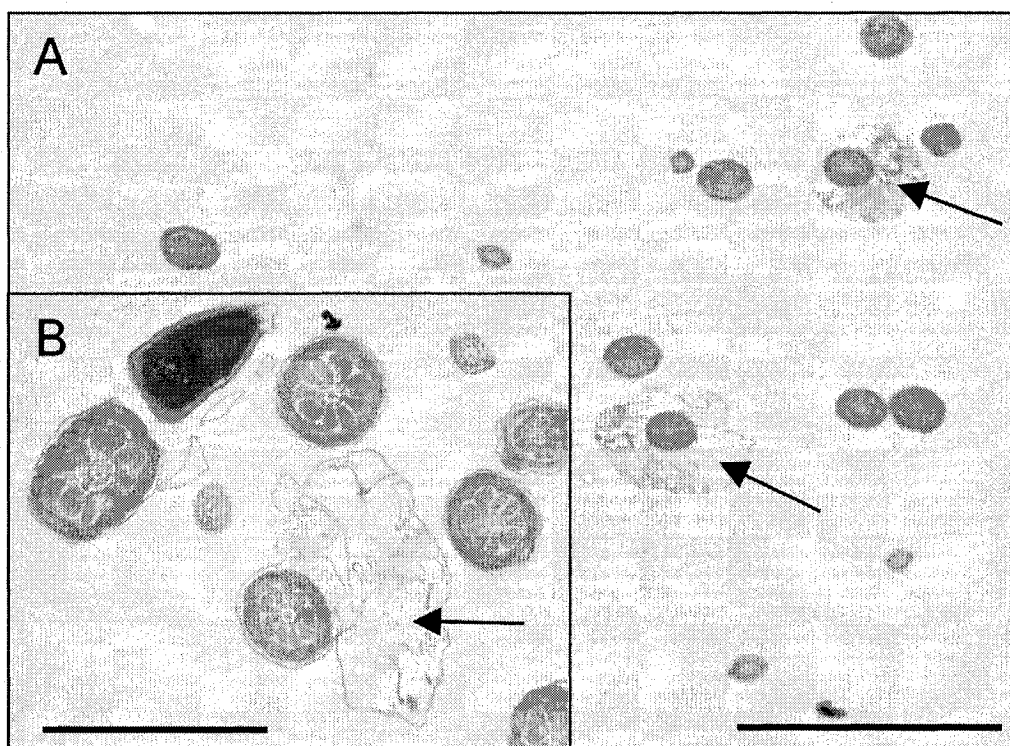
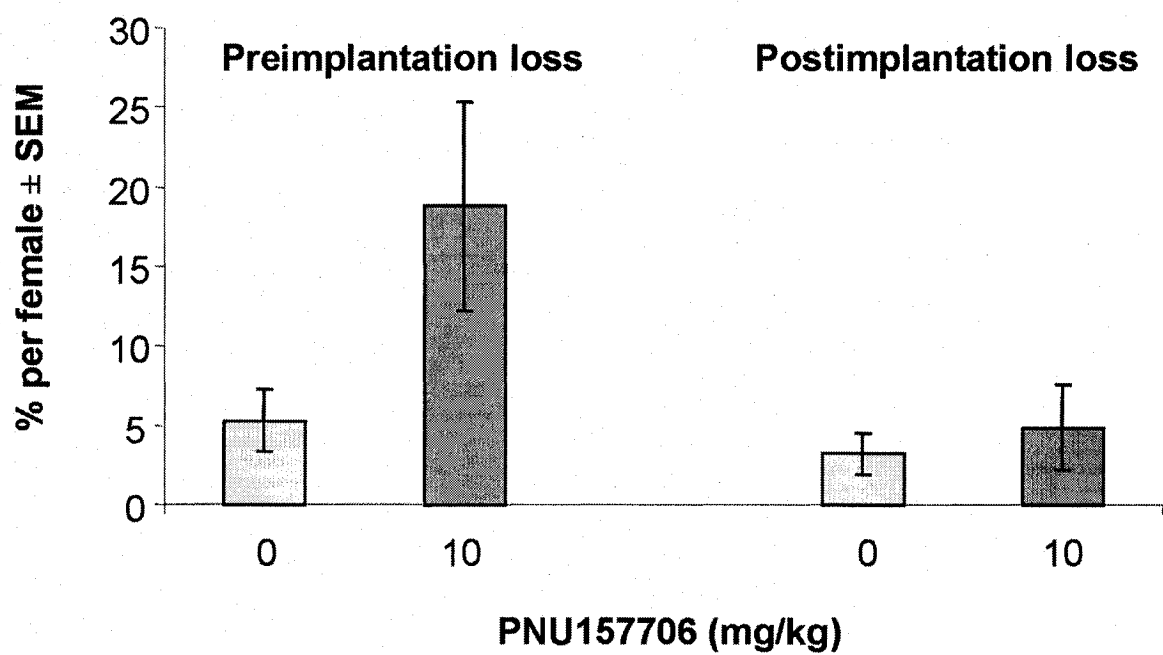


Figure 5. Effect of PNU157706 treatment on pregnancy outcome on Day 20 of gestation. The rates of preimplantation and postimplantation loss are shown as percentage per female on the y-axis for the control (0 mg/kg/day, light grey bars) and treated (10 mg/kg/day, dark grey bars) groups on the x-axis.

Figure 5



Tables and Legends

Table 1. Effect of PNU157706 treatment on motion parameters of caput and cauda epididymal sperm.^a

^a Values represent mean \pm SEM (n = 5-7). Average-path velocity (VAP), straight-line velocity (VSL), curvilinear velocity (VCL), amplitude of lateral head displacement (ALH), beat cross frequency (BCF), straightness (STR), linearity (LIN).

^b $P < 0.05$ versus control group.

PNU157706 (mg/kg)	Caput		Cauda	
	0	10	0	10
Velocity parameters				
VAP ($\mu\text{m}/\text{sec}$)	143.8 ± 5.3	143.7 ± 7.3	157.7 ± 3.1	155.5 ± 4.9
VSL ($\mu\text{m}/\text{sec}$)	81.5 ± 3.2	82.1 ± 3.5	103.3 ± 2.6	92.4 ± 3.7^b
VCL ($\mu\text{m}/\text{sec}$)	309.6 ± 9.2	307.8 ± 12.4	348.1 ± 4.8	335.6 ± 8.1
Head motion parameters				
ALH (μm)	19.9 ± 0.6	20.1 ± 0.7	22.1 ± 1.0	23.4 ± 0.7
BCF (Hz)	27 ± 0.3	25.8 ± 0.7	22.7 ± 1.1	21.5 ± 0.6
Derived parameters				
STR (%)	59.2 ± 0.8	59.5 ± 1.3	66.8 ± 2.2	60.7 ± 1.5^b
LIN (%)	28.5 ± 0.2	28.4 ± 0.4	30.4 ± 0.7	28.0 ± 0.6^b

Table 2. Effect of PNU157706 treatment on cauda epididymal sperm morphology.^a

^a Values represent mean \pm SEM (n = 5-7).

^b $P < 0.05$ versus control group.

PNU157706 (mg/kg)	Abnormalities observed with HTM-IVOS				
	Head only (%)	Tail only (%)	Bent (%)	Other (%)	Total (%)
0	0.43 ± 0.3	0.38 ± 0.1	2.4 ± 0.4	0.18 ± 0.1	3.4 ± 0.7
10	2.03 ± 0.5 ^b	1.17 ± 0.3 ^b	4.21 ± 0.8	0.74 ± 0.2 ^b	8.2 ± 0.8 ^b

Table 3. Effect of PNU157706 treatment on male reproductive indices.

^a Copulation index = number of sperm positive females / number of pairings (% value in parentheses)

^b Pregnancy index = number of pregnancies / number of sperm positive females (% value in parentheses)

^c Fertility index = number of pregnancies / number of pairings (% value in parentheses)

^d $p < 0.05$ versus control group.

	<i>Treatment group</i>	
	Control	PNU157706
Copulation index ^a	13/16 (81.3%)	9/16 (56.2%)
Pregnancy index ^b	13/13 (100 %)	6/9 (66.7%)
Fertility index ^c	13/16 (81.3%)	6/16 (37.5%) ^d

Connecting Text

Thus far, the studies presented clearly demonstrated that DHT has an important role in regulating gene expression and sperm maturation in the epididymis and it does so in a highly segment-specific manner. What remained unclear was the identity of segment-specific signaling/regulatory molecules and pathways acting upstream and/or downstream of DHT to mediate its actions in the epididymis. Therefore, the elucidation of potential DHT signaling mechanisms in the epididymis formed the basis of the final objective. Two main groups of genes were chosen for gene expression analysis: 1) The isozymes of 5 α -reductase and the androgen receptor, which are directly involved in mediating androgen action in the epididymis and 2) Different growth factor families, which were chosen based on increasing evidence for the involvement of growth factor signaling in other reproductive tissues such as the prostate.

CHAPTER 4

Segment-Specific Expression of Signaling Pathway Genes in the Rat Epididymis and the Effects of Dual 5 α -Reductase Inhibition

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¹ G.M. Cooke did the in vitro 5 α -reductase enzyme assays described in this chapter.

Abstract

Dihydrotestosterone (DHT) is the primary androgen acting in the epididymis, the site of sperm maturation. Previously, we showed that treatment of male rats with PNU157706, an inhibitor that acts on both isoforms of 5 α -reductase to prevent DHT formation, has effects on the expression of genes implicated in processes that create the optimal luminal microenvironment required for sperm maturation, and on sperm maturation itself. However, signaling pathways involved in regulating or mediating DHT actions in the epididymis remain largely unknown. The goals of this study were to determine the expression profiles of different signaling genes in the epididymis and assess their DHT-dependence by using two different dual 5 α -reductase inhibitors. Rats were untreated or gavaged with vehicle, 10 mg/kg/day of PNU157706 or 32 mg/kg/day of FK143 for 28 days and epididymal gene expression was analyzed. Gene array analysis revealed analogous effects of FK143 on overall epididymal gene expression when compared to previous PNU157706 studies. Quantitative RT-PCR analysis of the expression of the 5 α -reductase isozymes, androgen receptor and members of the IGF, FGF, TGF and VEGF families revealed novel segment-specific expression profiles in the epididymis that were differentially affected by 5 α -reductase inhibition; the two inhibitors had parallel effects. Specifically, in proximal regions, 5 α -reductase 1, androgen receptor and TGF- β 1 expression increased after treatment while in distal segments expression of IGF-1, IGFBP-5, IGFBP-6, and FGF-10 decreased. These results provide novel insight into epididymal signaling mechanisms and indicate potential candidates

acting either upstream or downstream of DHT to regulate and/or mediate its actions in the epididymis.

Introduction

The epididymis is a highly specialized tissue within the male excurrent duct system that functions in the transport, maturation, protection and storage of spermatozoa (1, 2). There are four distinct regions of the epididymis that carry out the sperm-related functions: the initial segment, caput, corpus and cauda epididymidis. Importantly, the acquisition of progressive motility and fertilizing ability (i.e. sperm maturation) requires the successive exposure of spermatozoa to the particular luminal environment created by the different epididymal segments (1, 2). The functional segmentation of the epididymis is reflected at the molecular level by complex segment-specific gene expression profiles (3, 4). The unique patterns of gene expression along the duct contribute to the evolving repertoire of components that make up the highly specialized luminal fluid.

The structure and functions of the epididymis are highly dependent on androgens (5, 6). More specifically, several studies have clearly shown that the primary androgen acting in this tissue is dihydrotestosterone (DHT) (7-10). 5 α -Reductase (EC 1.3.1.22) is the enzyme that catalyzes the conversion of testosterone to DHT. Both isoforms of 5 α -reductase (type 1 and type 2) are present in the epididymis and are differentially expressed along the tubule (11).

Previously, using gene expression profiling, we have shown that treatment of adult male rats with the dual 5 α -reductase inhibitor, PNU157706, has a highly

segment-specific effect on epididymal gene expression (12). The affected genes are involved in fatty acid and lipid metabolism, regulation of ion and fluid transport, luminal acidification, oxidative defense, and protein processing and degradation; these are essential processes that contribute to the formation of the optimal luminal microenvironment (12).

Importantly, distinctive segment-specific epididymal gene expression changes also occur during aging and in response to other experimental manipulations such as orchidectomy, caloric restriction and vitamin E treatments (13-16). These unique responses clearly demonstrate the differential regulation of this tissue, however, surprisingly little is known about how this regulation is achieved. While DHT clearly has a prominent role in the epididymis, the involvement of unique signaling molecules and pathways acting upstream and/or downstream of DHT remains to be deciphered. Therefore, the main objective of the present study was to examine the effects of 5 α -reductase inhibition on the expression of specific signaling genes in the epididymis in order to elucidate possible mechanisms of DHT action in this tissue.

In the present study, gene arrays were used to analyze the effects of a second 5 α -reductase inhibitor, FK143, on gene expression; FK143 is a non-steroidal, non-competitive inhibitor of both isozymes of 5 α -reductase (17, 18). The cumulative array data from this study and our previous PNU157706 study (12), as well as the current literature, were used as a guide in the selection of genes potentially involved in epididymal regulatory mechanisms for further characterization in the epididymis. The genes chosen include both isozymes of

5 α -reductase and the androgen receptor, which are directly involved in mediating androgen action in the epididymis, as well as those involved in different growth factor signaling systems. Interestingly, there is recent evidence supporting a role for various growth factors in epididymal function; for example, the overexpression of VEGF in the testis and epididymis of transgenic mice results in infertility (19). In a different animal model, the GH-deficient dwarf (dw/dw) rat, the administration of insulin-like growth factor 1 increases the motility and improves the morphology of immature spermatozoa (20). Whether an epididymal mechanism contributes fully or in part to the effects of these growth factors in such animal models has not yet been determined, but it is certainly possible that these and other growth factor systems are involved in epididymal regulation.

The steady-state epididymal expression profiles of the selected genes were analyzed using the sensitive technique of quantitative real-time RT-PCR. We then assessed the effects of both 5 α -reductase inhibitors (PNU157706 and FK143) on the epididymal expression of these signaling genes to determine whether they are dependent on DHT, and thus potentially acting as upstream (i.e. the 5 α -reductase isozymes) or downstream regulators of DHT-dependent gene expression and function.

Materials and Methods

Animals

Adult male Sprague-Dawley rats (325-350g) were obtained from Charles River Canada (St. Constant, PQ, Canada), maintained under controlled light

(14L:10D) and temperature (22°C), and provided with food and water ad libitum. Caput-corpus epididymides from 90-day old animals that were previously stored at -80°C were used for *in vitro* enzyme assays. For *in vivo* studies, adult male rats were left untreated (for determination of steady-state mRNA profiles, n=5) or they were randomly divided into 3 treatment groups (n=5) and gavaged with 0.5 ml/kg of either the vehicle alone (control group) or 10 mg/kg PNU157706 or 32 mg/kg FK143 (inhibitor treatment groups) suspended in vehicle (0.5% methylcellulose solution (BDH, Montréal, QC) containing 0.4% Tween 80 (A&C American Chemicals Ltd, Montreal, QC)) for 28 consecutive days. Doses were selected based on reported effects on rat ventral prostate; the dosing regimen with 10 mg/kg/day PNU157706 or 32 mg/kg/day of FK143 has been shown to decrease prostatic dihydrotestosterone levels by >90% (18, 21). Epididymides from untreated and treated rats were sectioned into initial segment, caput, corpus and cauda epididymides and immediately frozen in liquid nitrogen. Tissues were stored at -80°C until used for RNA extraction. The changes in reproductive tissue weights with treatment were consistent what has previously been reported for both compounds (12, 18, 21). All animal studies were conducted in accordance with the principles and procedures outlined in the Guide to the Care and Use of Experimental Animals prepared by the Canadian Council on Animal Care (McGill Animal care Committee protocol #206).

In vitro 5 α -Reductase Assays

Unlabelled steroids were purchased from Steraloids Inc. (Newport, RI). (1,2,6,7-³H) testosterone (74.0 Ci/mmol) was from Dupont/NEN (Boston, MA). Organic solvents were from BDH (Montréal, QC). Dimethylglutaric acid (DMG), NADPH and dimethyl sulfoxide (DMSO) were from Sigma Chemical Co. (St Louis, MO). Plastic coated WhatmanTM PE SIL G silica gel chromatography plates were purchased from Chromatographic Specialties (Montréal, QC). FK143 solutions were prepared in DMSO.

Frozen caput-corpus epididymides (only control, untreated tissues were used) were thawed, homogenized (Polytron) in DMG buffer (50 mM DMG, 5% glycerol, NaOH, 0.5mM NADPH) pH 6.5, and the nuclear and microsomal fractions were assayed for 5 α -reductase activity as previously described for PNU157706 (12). Briefly, kinetic studies of 5 α -reductase activity were done at pH 6.5 with testosterone (9 concentrations ranging from 5-375 nM). To determine the effects of FK143 on 5 α -reductase activity, FK143 was included at concentrations of 0, 3, 15 and 45 nM. A single incubation time of 1h and an incubation volume of 1 ml were used in kinetic studies. To obtain the apparent Michaelis constant ($K_{m(app)}$) and apparent maximum velocity ($V_{max(app)}$), the Wilkinson method (non-linear least squares analysis of a rectangular hyperbola) was used (22). Slope and intercept replots were obtained from, respectively, $K_{m(app)} / V_{max(app)}$ versus [I] and $1/V_{max(app)}$ versus [I]. Linear regression analysis of the replots was employed to determine the $K_{i(app)}$ values.

RNA Extraction

From each sample, total RNA was extracted using the RNeasy extraction kit with DNase1 treatment (Qiagen Inc., Mississauga, ON, Canada) according to the manufacturer's protocol with the exception that the on-column DNase digestion was extended to 1 hour. RNA concentration was assessed by optical density determination at 260nm (Beckman DU7 spectrophotometer, Montréal, PQ, Canada). In addition to spectrophotometric reading, RNA quality was verified by conventional gel electrophoresis. Each sample consisted of a single epididymal segment obtained from individual rats, i.e., no tissues were pooled.

Complementary DNA Arrays and Hybridization

The effects of FK143 treatment on epididymal gene expression were analyzed with cDNA arrays as described previously (12). Briefly, RNA samples were used to probe cDNA arrays (BD Biosciences Atlas Rat 1.2K array) according to the manufacturer's instructions. Four arrays per epididymal segment per treatment group (control, FK143) were probed and referred to as replicates (n=4/treatment/segment). Arrays were exposed to phosphorimager plates (Molecular Dynamics, Sunnyvale, CA) 24 hours before scanning with a phosphorimager (Storm, Molecular Dynamics). Analysis of array images with Atlas Image (Version 2.0, BD Biosciences) was done to quantify the intensity of each cDNA spot, which reflects the relative abundance of RNA in the sample. The raw data for each gene (intensity minus the background) were imported into GeneSpring 4.0.7 (Silicon Genetics, Redwood, CA) for further analysis. For each

replicate array in a given treatment group, a gene was considered detected if its intensity was above threshold, with threshold defined as two times the average background of that individual array. A gene was considered expressed if it was detected in at least three replicates in that group.

To minimize experimental variation and allow for comparison of different treatment groups, data were normalized with the standard experiment-to-experiment normalization (GeneSpringTM). Specifically, the median level of expression on each array was defined as 1 and expression of each gene was normalized relative to 1; this value was averaged for all replicates in a group to generate what is referred to as the relative intensity for a given gene. A transcript was considered differentially expressed if the change in relative intensity between the control and treatment group was 2-fold or greater (i.e. 50% decrease or 100% increase). The importance of replication for validation of gene expression studies has been documented (23, 24).

Quantitative Real-Time RT-PCR

The expression of selected genes (Table 1) was analyzed by quantitative real-time RT-PCR. Analysis of the steady-state expression profiles for the selected genes along the epididymis was done using RNA samples extracted from the epididymides of untreated adult rats (n=4-5). Analysis of the effects of 5 α -reductase inhibition on the epididymal expression profiles of selected genes was done using RNA samples extracted from the epididymides of vehicle, PNU157706 and FK143 treated rats (n=4-5). As expected, the steady-state

(untreated) and vehicle-treated expression profiles for all the genes examined were indistinguishable. For simplicity, only the vehicle-treated profiles are shown which are representative of the steady-state expression profiles discussed in the results section. The steady-state real-time RT-PCR expression profiles generated from untreated epididymides are available as a supplemental figure (suppl Fig. 1).

First strand complementary DNA (cDNA) was synthesized from 1 µg of total RNA using SuperScript-II reverse transcriptase (Invitrogen-Life Technologies, Carlsbad, CA) and oligo dT₍₁₂₋₁₈₎ primers (Invitrogen-Life Technologies) according to manufacturer's instructions, with the exception that only half the concentration of DTT was used (25). The reverse transcription (RT) reactions were then diluted 1:3 and 1 µl aliquots of the diluted RT samples were used for subsequent quantitative real-time PCR analysis.

Quantitative real-time PCR was carried out on the LightCycler system (Roche, Indianapolis, IN) using the Quantitect SYBR green PCR kit (Qiagen) according to the manufacturer's protocol. The gene-specific primer sequences (Table 1) were obtained from the literature or designed using Primer3 software (<http://frodo.wi.mit.edu/cgi-bin/primer3/primer3.cgi/>). Briefly, each PCR reaction contained 1 µl of cDNA (RT sample), 0.5 µM of gene-specific primers and 10 µl of the SYBR green master mix. The PCR cycling conditions were as follows: initial denaturation/enzyme activation for 15 minutes at 95°C followed by 40-60 cycles of denaturation at 95°C for 10 sec, annealing at 57–60°C for 5 sec and elongation

at 72°C for 10 sec. The production of a single PCR product was confirmed by melting curve analysis and conventional gel electrophoresis.

The relative quantification of mRNA was done according to the standard curve method (refer to Applied Biosystems User Bulletin # 2, reviewed in 26). The same RT sample was used to assay each target gene and the reference gene cyclophilin in separate (LightCycler) PCR runs. Cyclophilin was chosen as the endogenous control because of its invariant expression throughout the epididymis and its lack of response to androgen status (27). A stock of standard curve cDNA was made as follows: total RNA was extracted from the 4 epididymal segments (initial segment, caput, corpus and cauda epididymides) of an untreated adult rat and then equal amounts of RNA from each segment were mixed together to create a standard 1µg/µl RNA solution. Subsequently, several 1 µl aliquots of RNA standard were reverse-transcribed into cDNA as described previously and then pooled together to create one standard cDNA stock that was used in all PCR experiments. For each analysis, 6 serial dilutions of the standard cDNA were run as a calibration curve in parallel to the samples. The levels of mRNA for each gene (target and reference genes) were determined by comparing each sample to the appropriate standard curve. All standards and samples were assayed in duplicate. Average values for the target gene RNA concentrations determined from each RT sample preparation were normalized to the average value for cyclophilin RNA concentration determined from the same RT sample preparation.

Statistical Analysis

For the steady-state real-time PCR gene expression profiles, differences between epididymal segments were analyzed by ANOVA followed by Tukey's test. To analyze the differences in gene expression between the vehicle (control) and inhibitor treatment groups, ANOVA followed by Dunnett's test was done. The level of significance was set at $p \leq 0.05$ for all analyses.

Results

Effect of FK143 on Epididymal 5 α -Reductase Activity

The inhibitory effect of FK143 on 5 α -reductase was assessed *in vitro* by examining the effects of FK143 on the 5 α -reductase activity of nuclear and microsomal epididymal fractions. The addition of FK143 to incubations at concentrations of 0, 3, 15 and 45 nM inhibited epididymal 5 α -reductase as shown in Fig. 1A (nuclear fraction) and B (microsomal fraction). Kinetic analyses demonstrated that FK143 caused the $V_{\max(\text{app})}$ values to decrease (by about 75%) with no consistent effect on the $K_{\text{m}(\text{app})}$ values. Confirmation of these findings was achieved with slope ($K_{\text{m}(\text{app})}/V_{\max(\text{app})}$ vs. $[I]$) and intercept ($1/V_{\max(\text{app})}$ vs. $[I]$) replots, shown in Fig. 1C (nuclear) and D (microsomal); the slopes of the slope replots were negative or almost horizontal whereas the slopes of the intercept replots were positive. The values for the inhibition constant ($K_{\text{i}(\text{app})}$) for FK143 determined from the slope and intercept replots respectively were 56.6 and 26.5 for the nuclear 5 α -reductase fraction and 44.5 and 53.4 for the microsomal 5 α -

reductase fraction. Since the $K_{i(\text{app})}$ values from both slope and intercept replots were almost identical, it was clear that the $K_{m(\text{app})}$ did not influence the $K_{i(\text{app})}$ values determined; these findings were consistent with FK143 being a non-competitive inhibitor of 5 α -reductase, as has been reported for other tissues (17).

Effects of FK143 on Epididymal Gene Expression

Comparison of the gene array data from the present FK143 study to our previous study using PNU157706 (12) revealed analogous effects of the different inhibitors on epididymal gene expression; both the nature of the affected genes and the direction of expression changes (i.e. increased or decreased expression) were very similar (refer to Suppl Table 1). In the current study, the expression of a greater number of genes met our detection analysis criteria (i.e. were detectable above the set background expression threshold) therefore, a greater number of genes were analyzed. Novel changes in gene expression (2-fold minimum) that were revealed in the current gene array study are reported in a supplemental table (Suppl Table 2).

The comparison of the effects of two different inhibitors added greater power to our analyses such that we could identify genes with expression changes that were less than 2-fold but were consistently affected by treatment with both inhibitors. Among these genes was 5 α -reductase type 2, which is of particular relevance to the present study as it is one of the isozymes that catalyzes the formation of DHT; the averaged response of this gene to 5 α -reductase inhibitor treatment (determined from the array studies) was 1.4-, 1.6- and 1.8-fold

decreased expression in the initial segment, caput and corpus epididymides, respectively. Also among these genes were several insulin-like growth factor (IGF) family members. For example, following inhibitor treatment, the expression of IGF binding protein-5 (IGFBP-5) decreased by an average of 1.1-, 1.4- and 1.5-fold in the caput, corpus and cauda epididymides, respectively, and IGFBP-6 expression increased by an average of 1.1-fold in the initial segment and decreased by an average of 1.4-fold in the corpus epididymidis. Lastly, the expression of IGF-1 and IGF-1 receptor (IGF-1R) decreased by an average of 1.4- and 1.6-fold, respectively, in the cauda epididymidis following 5 α -reductase inhibitor treatment.

In accordance with the main objective of this study to identify potential signaling systems involved in epididymal regulation, we undertook to characterize the expression of the above-mentioned genes as well as other mediators of androgen action (5 α -reductase type 1, androgen receptor) and other growth factor family members (chosen based on the current literature) using the more sensitive technique of quantitative real-time RT-PCR.

Expression of 5 α -Reductases and the Androgen Receptor in the Epididymis

We examined the steady-state expression levels of 5 α -reductase types 1 and 2 and of the androgen receptor in the epididymis using real-time RT-PCR (Fig. 2, black bars). These three genes have been previously characterized in the epididymidis by Northern blot analysis (11, 28). The gene expression results obtained using these two techniques were analogous for all three genes. 5 α -

Reductase type 1 was expressed in the initial segment at levels approximately 4-fold higher than the other regions of the epididymis. 5 α -Reductase type 2 was also highly expressed in the initial segment, peaked slightly in the caput epididymidis and then decreased in the corpus and cauda epididymides. Androgen receptor gene expression was relatively constant throughout the epididymis.

Dual 5 α -reductase inhibitor treatment had differential effects on the expression of 5 α -reductase type 1 and 2 and the androgen receptor in the epididymis (Fig. 2). Both compounds had similar effects on the different gene expression profiles. 5 α -Reductase type 1 expression was uniquely affected in the initial segment where it increased maximally with FK143 treatment by approximately 2.5-fold. Androgen receptor gene expression also increased following treatment uniquely in the caput epididymidis. In contrast, the expression of 5 α -reductase type 2 remained essentially unaffected by treatment except for an approximate 66% decrease in the corpus epididymidis. The corpus epididymidis was also the segment where the greatest decrease in 5 α -reductase type 2 expression was detected using gene array technology.

Expression of IGF Family Members in the Epididymis

We examined the steady-state expression of four IGF family members along the epididymis (Fig. 3, black bars). The expression of IGF-1 was significantly lower in the caput epididymidis compared to the other segments where it was expressed at similar levels. The expression of IGF-1R escalated

longitudinally, increasing nearly 3-fold between the initial segment and the cauda epididymidis. The expression of IGFBP-5 was also highest in the cauda epididymidis, being on average 3-fold higher than in the other segments. The high relative expression values for IGFBP-5 suggest that it is more highly expressed in the epididymis compared to the other IGF family members. However, direct comparisons between the different genes cannot be made conclusively since different target gene primer pairs may not exhibit the same amplification efficiency in PCR experiments. Lastly, the expression profile of IGFBP-6 in the epididymis was very similar to that of IGF-1 such that it was significantly lower in the caput epididymidis compared to the remaining segments.

The effects of dual 5 α -reductase inhibition on the expression profiles of the four IGF family members are shown in Figure 3. Again, treatment with the two different dual inhibitors had similar effects on the expression profiles of all the IGF family members examined, with FK143 having a more pronounced effect. Interestingly, the effects of 5 α -reductase inhibitor treatment were gene- and segment-specific. The expression of all four genes remained unaffected by treatment in the initial segment. In the more distal segments of the epididymis, treatment with either inhibitor caused a general decrease in the expression of most IGF family members examined. More specifically, the expression of IGF-1 and IGFBP-5 was the most affected by treatment, maximally decreasing by 60% and 84% in the cauda epididymidis, respectively. Decreased expression was also observed for IGFBP-6, reaching significance in the corpus epididymidis.

These changes in gene expression reflect what has been found using gene array technology.

Expression of FGF Family Members in the Epididymis

The steady-state expression profiles for the ligand, fibroblast growth factor-10 (FGF-10), and the receptor, fibroblast growth factor receptor-2 (FGFR-2), were examined in the epididymis (Fig. 4, black bars). The steady-state expression of FGF-10 was significantly lower in the caput epididymidis compared to all other segment. The steady-state expression of FGFR-2 was significantly higher in the cauda epididymidis compared to the more proximal regions. The high relative expression values for FGFR-2 suggest that it is quite highly expressed in the epididymis compared to the other genes analyzed.

The effects of PNU157706 and FK143 treatment on the epididymal expression of FGF-10 and FGFR-2 expression were analyzed (Fig. 4). FGF-10 gene expression was significantly affected by both inhibitor treatments; it decreased maximally with FK143 treatment in the corpus and cauda epididymides by approximately 45% and 31%, respectively. Inhibitor treatments did not result in a significant decrease in FGFR-2 expression.

Expression of TGF Family Members in the Epididymis

The steady-state expression profiles for the ligand, transforming growth factor- β 1 (TGF- β 1), and the receptor, transforming growth factor- β 1 receptor

(TGF- β 1R), were examined in the epididymis (Fig. 5, black bars). The expression of TGF- β 1 was relatively constant in the initial segment, caput and corpus epididymides and peaked in the cauda epididymidis to nearly double the levels in the proximal regions. In contrast, TGF- β 1R was expressed in the in the initial segment and corpus epididymidis at approximately twice the levels in the caput and cauda epididymides. The relative expression values for TGF- β 1R were the highest of all the genes examined, suggesting that it is very highly expressed in the epididymis.

The effects of dual 5 α -reductase inhibitor treatment on epididymal TGF- β 1 and TGF- β 1R expression were analyzed (Fig. 5). The only significant effects of 5 α -reductase inhibitor treatment were on the expression of TGF- β 1 in the caput epididymidis, which nearly doubled following treatment, and TGF- β 1R in the cauda epididymidis, which decreased following treatment.

Expression of VEGF Family Members in the Epididymis

The steady-state expression profiles for the ligand, vascular endothelial growth factor (VEGF), and the receptor, vascular endothelial growth factor receptor-2 (VEGFR-2), were examined in the epididymis (Fig. 6, black bars). Both genes were most highly expressed in the initial segment. VEGF expression was lowest in the caput epididymidis and increased slightly towards the cauda epididymidis. VEGFR-2 was expressed in the caput, corpus and cauda epididymides at approximately 63-74% of the initial segment expression level.

The effects of dual 5 α -reductase inhibitor treatment on epididymal VEGF and VEGFR-2 expression were analyzed (Fig. 6). In contrast to all the other growth factors analyzed, there were no significant effects of treatment with either inhibitor in any segment of the epididymis.

Discussion

Previously we demonstrated that the dual 5 α -reductase inhibitor PNU157706 inhibited epididymal 5 α -reductase activity *in vitro* and had extensive effects on epididymal gene expression *in vivo* (12). In the present study, we confirmed that a second compound, FK143, is a noncompetitive inhibitor of nuclear and microsomal epididymal 5 α -reductase activity *in vitro*. Furthermore, it was found that treatment with FK143 elicited changes in epididymal gene expression that were analogous to those observed with PNU157706, as evidenced by gene array studies. These corroborating findings clearly indicate that the observed changes in gene expression are due to the common effect of both compounds on the inhibition of DHT formation, as opposed to a mechanism different than 5 α -reductase inhibition.

Recently, we showed that treatment of male rats with PNU157706 affects epididymal sperm maturation as evidenced by changes in epididymal sperm morphology, motility and fertilizing ability (29). It is highly likely that the effects of dual 5 α -reductase inhibition on epididymal sperm maturation are linked to the effects of inhibitor treatment on the expression of genes that can be functionally categorized according to important epididymal epithelial processes (i.e.,

processes that contribute to the formation of the epididymal luminal environment). What remains unclear is the identity of segment-specific signaling/regulatory molecules and pathways involved in mediating the upstream and/or downstream effects of DHT on epididymal gene expression and function.

In the present study we focused specifically on signaling mechanisms in the epididymis and therefore chose to analyze the expression of both 5 α -reductase isozymes and the androgen receptor, as well as several components of different growth factor systems. Moreover, we determined whether the expression of these genes was dependent on DHT by assessing the effects of dual 5 α -reductase inhibition. For the most part, these genes have not been extensively characterized in the epididymis, with the exception of the 5 α -reductase isozymes and the androgen receptor. Thus, this is the first study demonstrating the differential distribution and regulation of many of these genes.

Expression of 5 α -Reductases and the Androgen Receptor in the Epididymis

The expression of both 5 α -reductase isozymes has been previously characterized in the epididymis (11, 30, 31). Moreover, the segment-specific epididymal expression profiles of these genes show different patterns during development and aging and respond differently to efferent duct ligation and bilateral orchidectomy (11, 28, 30-32). However, this is the first study to employ 5 α -reductase inhibitors to specifically examine the DHT regulation of the expression of these genes in the epididymis. Our results are consistent with the differential regulation of the 5 α -reductase isozymes in this tissue. Type 1 5 α -

reductase expression was specifically increased in the initial segment following inhibitor treatment, suggesting a negative feedback mechanism of regulation by DHT in this segment. In contrast, the expression of 5 α -reductase type 2 was affected only in a limited manner by treatment in the corpus epididymidis. Interestingly, androgen status has been shown to regulate the expression of both 5 α -reductase isozymes differently in different tissues. For example, in the rat brain, type 1 5 α -reductase expression increases following castration, and androgen replacement with DHT reverses this increase to a larger extent than testosterone replacement (33). In contrast, 5 α -reductase type 2 expression falls in the rat prefrontal cortex after castration and increases dramatically with testosterone replacement compared to DHT replacement (33). In fact, the exogenous administration of testosterone, and to a lesser extent DHT, increased type 2 5 α -reductase expression even in intact animals (33). Testosterone has also been shown to control the expression of 5 α -reductase type 2 in the rat prostate while both testosterone and DHT positively regulate 5 α -reductase type 1 expression in the rat liver (34, 35). The differential regulation of both 5 α -reductase isozymes suggests that they play physiologically distinct roles in different tissues. Further studies are needed to fully characterize these distinct roles.

As expected, the present real-time PCR expression results were analogous to what has been previously described for the androgen receptor in the epididymis; androgen receptor gene expression is relatively constant throughout the tissue with levels slightly higher in the caput epididymidis

compared to those in the cauda epididymidis (28, 36, 37). Studies have also shown that circulating androgens regulate the expression of the androgen receptor in the epididymis (36, 37); however, as with most of the genes previously examined in the epididymis, no differentiation was made between total androgens (i.e., testosterone plus DHT) and DHT alone. Our results suggest that androgen receptor expression is regulated by DHT specifically in the caput epididymidis.

Growth Factor Signaling Pathways in the Epididymis

Studies using prostate cell lines have provided evidence to support androgen receptor cross talk with growth factor signaling pathways, resulting in both enhanced androgen responses and receptor ligand-independent activation and modulation of androgen receptor transactivation (38-41). Thus, it seems plausible that similar interactions occur in other reproductive tissues, including the epididymis; however, this remains to be examined. The characterization of recently established epididymal cell-lines should facilitate further investigation into the interactions between androgen and growth factor signaling pathways in the epididymis (42, 43).

A physiological role for IGF-1 in the regulation of epididymal functions was hypothesized over ten years ago due to the varied immunohistochemical localization of IGF-1 protein in the rat epididymis (44). IGF-1R protein and mRNA have also been localized to the epididymis (45, 46). Adult mice with a homozygous null mutation of the IGF-1 gene are infertile dwarfs with reduced

testosterone production, and consequently reduced spermatogenesis and reproductive organ size (45). Interestingly, the epididymal phenotype of IGF-1 null mice is more severe in the distal regions of the epididymis with greater reductions in weight and decreased coiling. In the present study, the expression of IGF-1 and IGF-1R was found to be highest in the distal epididymal segments. These results are consistent with a role for IGF signaling in the distal regions of the epididymis (corpus and cauda epididymides). Further corroborating this conclusion are results from the current study demonstrating the unique effects of 5 α -reductase inhibitor treatment on the expression of IGF-1 and possibly IGF-1R, predominantly in the corpus and cauda epididymides.

The IGF network also includes numerous IGF binding proteins that modulate the bioavailability and cellular functions of IGFs (47). We analyzed the epididymal expression of two high-affinity binding proteins, IGFBP-5 and IGFBP-6. Again, these genes were more highly expressed in the distal regions of the epididymis and were mainly affected by 5 α -reductase inhibitor treatment in these regions. IGFBP-5 expression was particularly affected by treatment, decreasing dramatically in the cauda epididymidis.

Various FGF receptors have been characterized exclusively in principal cells of the initial segment of the rat epididymis (48). Our results also indicate a role for FGF signaling in the distal part of the epididymis since the highest expression levels for FGF-10 and its receptor FGFR-2 were in the corpus and cauda epididymides. Furthermore, the effects of 5 α -reductase inhibitor treatment were most pronounced in these regions.

Differential expression profiles for TGF- β isoforms (TGF- β 1, TGF- β 2, TGF- β 3) have previously been characterized in the rat epididymis by Northern blot (49, 50). In these studies, substantial TGF- β 1 expression was observed compared to the other isoforms; TGF- β 1 expression was upregulated in the caput, corpus and cauda epididymides following total androgen ablation by orchidectomy. In the present study, we also observed the upregulation of TGF- β 1 expression most predominantly in the caput epididymidis with no changes in the distal regions. Taken together, these data suggest that TGF- β 1 is uniquely regulated by different androgens in the epididymis; our results indicate that there is a DHT-dependent repression of TGF- β 1 in the proximal epididymis while castration induced increases in TGF- β 1 expression in the corpus and cauda epididymides, indicating a specific role for total androgens or testosterone in these regions. Roles for the TGF- β family have also been implicated in other DHT-dependent reproductive tissues such as the seminal vesicle and ventral prostate (51, 52). TGF- β 1 in particular was also shown to be repressed by androgens in the regressing rat ventral prostate (53), similar to what was observed in the epididymis, further supporting a role for androgens in regulating the expression of this gene.

TGF- β is postulated to be involved in the regulation of programmed cell death in tissues that regress following androgen ablation. Interestingly, in the present study TGF- β 1 is induced despite the absence of tissue regression, thus indicating a novel role for TGF- β 1 in the epididymis that is separate from its role in apoptosis. To the best of our knowledge, this is the first study demonstrating the differential distribution of any TGF- β receptor mRNA in the epididymis. The

presence of both ligand and receptor strongly supports a role for the TGF- β system in the epididymis; however, DHT only appears to regulate this system at the level of the ligand.

Vascular endothelial growth factor (VEGF) protein was shown to be localized in the rat epididymal epithelium in a region- and cell-specific pattern (54); for example clear cells in the caput, corpus, and cauda epididymides were immunoreactive for VEGF. In humans, VEGF protein has been localized to peritubular and basal cells of the epididymal duct and VEGFR-2 protein has been localized to vascular endothelial cells of the epididymis (55). Interestingly, the overexpression of VEGF in the testis and epididymis of transgenic mice causes infertility (19). These findings suggest a role for VEGF in the epididymis, likely as a paracrine regulator of the epididymal vasculature as opposed to the epididymal epithelium. In the present study, we confirmed the differential distribution of both the VEGF and VEGFR-2 mRNAs in the rat epididymis. Interestingly, unlike the other growth factor families examined, 5 α -reductase inhibitor treatment had no significant effect on the expression of VEGF or VEGFR-2, reflecting a lack of DHT regulation of this growth factor system in the epididymis. This may be due to the predominantly vascular as opposed to epithelial localization of this system in the epididymis, which is unique from other growth factor signaling systems.

It is of interest to note that the testis has been shown to produce and secrete many different growth factors, including components of the IGF, TGF, EGF, FGF, PDGF, and NGF systems (reviewed in 56). It has been well established that the epididymis, in particular the initial segment, is dependent on

the testicular input of factors, other than androgens, directly to the epididymal lumen (57, 58); depriving the epididymis of these testicular factors (i.e. via efferent duct ligation) has well-documented effects on gene expression in the initial segment (reviewed in 59). This type of paracrine regulatory mechanism has been coined “lumocrine” regulation since it occurs via a ductal system (59). Thus, it is plausible that growth factors originating in the testis can act as “lumocrine” regulators of the epididymis by acting on their corresponding receptors present in the epididymal epithelium. Similarly, it is also likely that growth factors secreted in one segment of the epididymis can act on the receptors located in the same or more distal regions of the epididymis representing autocrine or paracrine regulatory mechanisms.

In summary, the collective findings of the present study suggest that sex steroid and growth factor signaling become dysregulated following 5 α -reductase inhibition, leading to altered epididymal gene expression and function. Furthermore, the results of this study support the involvement of differential signaling mechanisms in regulating and/or mediating the actions of androgens (predominantly DHT) in the different segments of the epididymis. This regulatory diversity is likely to be important in controlling segment-specific sperm-related functions.

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Figures and Legends

Figure 1. Inhibition of rat nuclear (A) and microsomal (B) 5 α -reductase activity *in vitro* by different concentrations of FK143 (FK). For nuclear (C) and microsomal (D) 5 α -reductase, slope replots (squares) were obtained from $K_{m(app)}/V_{max(app)}$ vs [FK] and intercept replots (triangles) were obtained from $1/V_{max(app)}$ vs [FK].

Figure 1

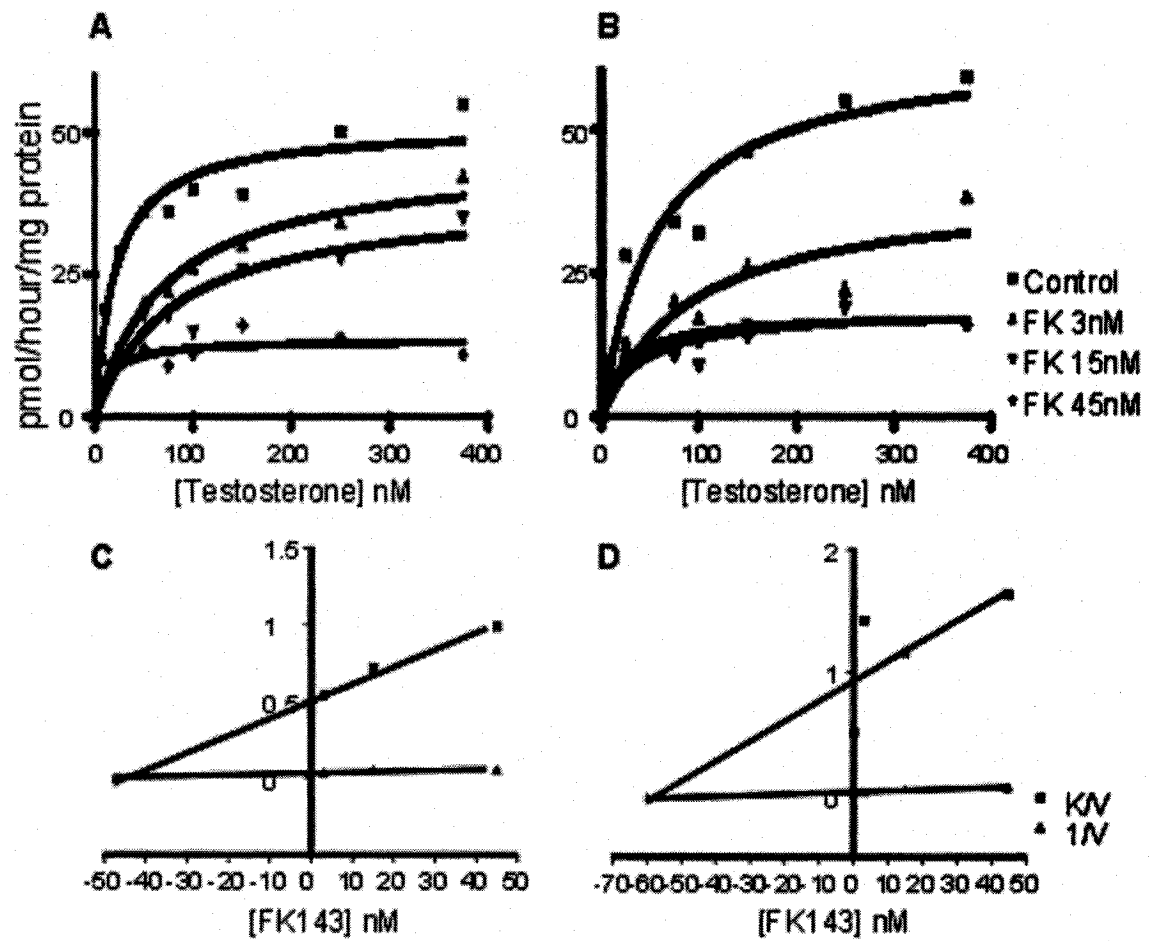


Figure 2. Quantitative real-time RT-PCR analysis of 5 α -reductase type 1 (5 α R-1), 5 α -reductase type 2 (5 α R-2) and androgen receptor (AR) mRNAs in the initial segment (IS), caput (CA), corpus (CO) and cauda (CD) epididymides. All gene expression values are expressed relative to the levels of cyclophilin mRNA and are represented as means \pm SEM. RNA extracted from epididymides of vehicle (black bars), PNU15776 (striped bars) and FK143 (white bars) treated rats (n=5/group) was used to analyze the effect of 5 α -reductase inhibitor treatment on mRNA expression profiles. Asterisks (*) indicate significant differences between the vehicle-treated and inhibitor-treated groups ($p < 0.05$).

Figure 2

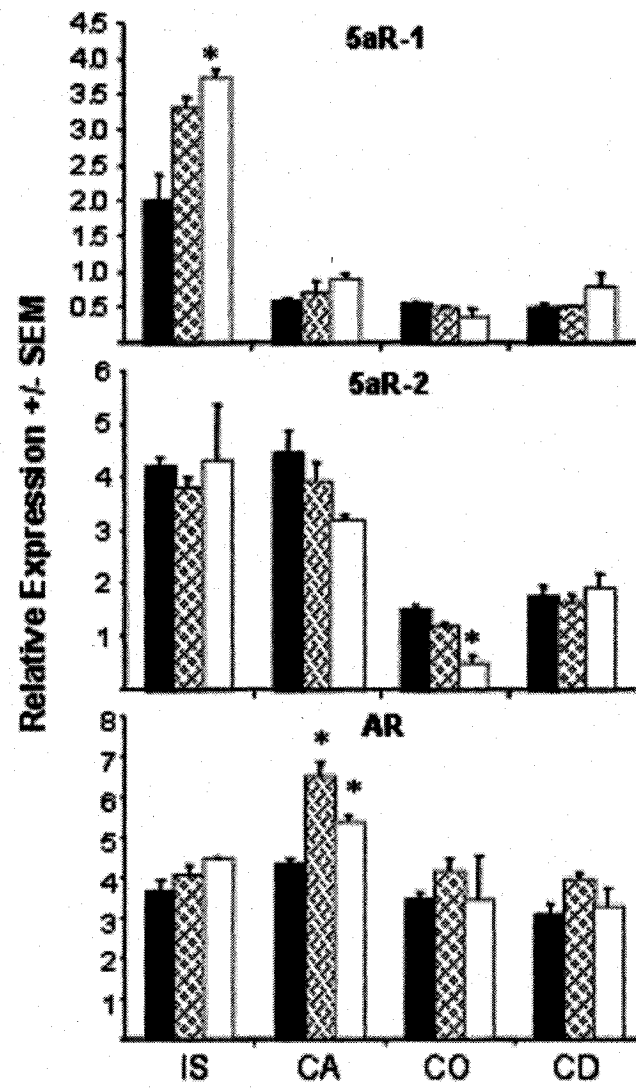


Figure 3. Quantitative real-time RT-PCR analysis of insulin-like growth factor-I (IGF-1), insulin-like growth factor-I receptor (IGF-1R), insulin-like growth factor-binding protein-5 (IGFBP-5) and insulin-like growth factor-binding protein-6 (IGFBP-6) mRNAs in the initial segment (IS), caput (CA), corpus (CO) and cauda (CD) epididymides. All gene expression values are expressed relative to the levels of cyclophilin mRNA and are represented as means \pm SEM. RNA extracted from epididymides of vehicle (black bars), PNU15776 (striped bars) and FK143 (white bars) treated rats (n=5/group) was used to analyze the effect of 5 α -reductase inhibitor treatment on mRNA expression profiles. Asterisks (*) indicate significant differences between the vehicle-treated and inhibitor-treated groups ($p < 0.05$).

Figure 3

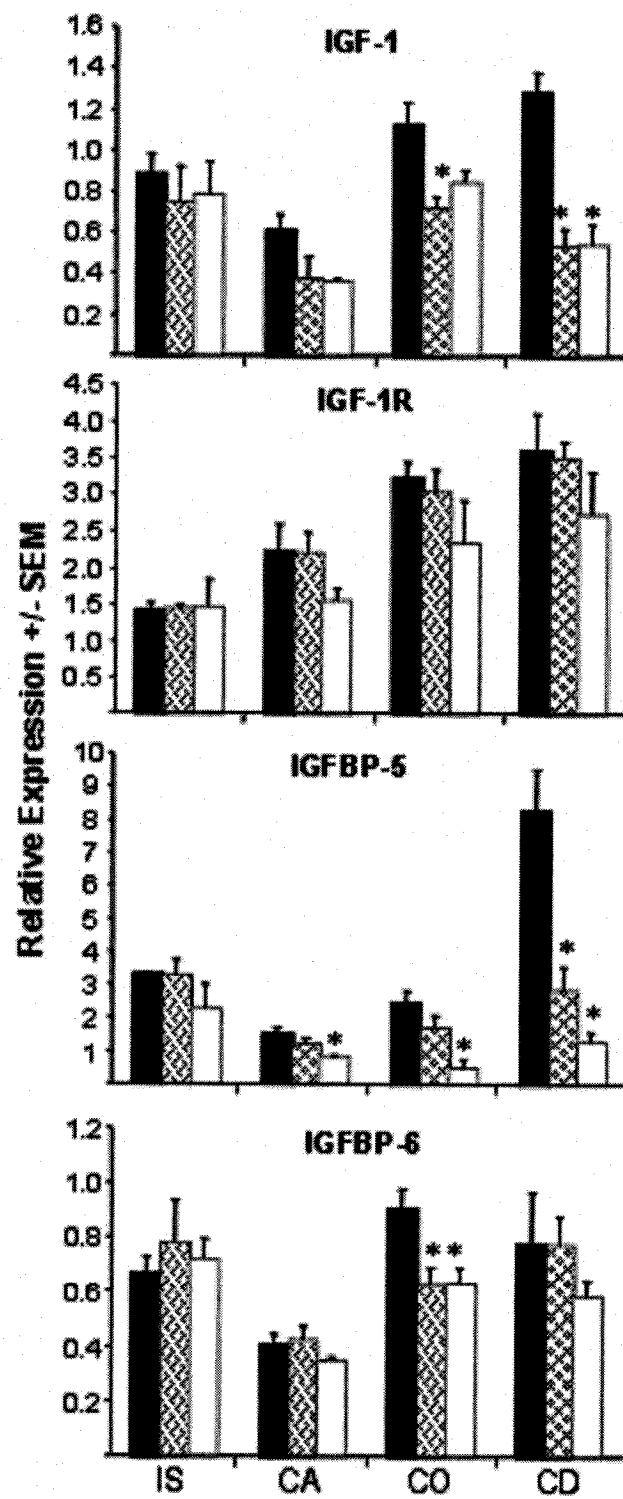


Figure 4. Quantitative real-time RT-PCR analysis of fibroblast growth factor-10 (FGF-10) and fibroblast growth factor receptor-2 (FGFR-2) mRNAs in the initial segment (IS), caput (CA), corpus (CO) and cauda (CD) epididymides. All gene expression values are expressed relative to the levels of cyclophilin mRNA and are represented as means \pm SEM. RNA extracted from epididymides of vehicle (black bars), PNU15776 (striped bars) and FK143 (white bars) treated rats (n=5/group) was used to analyze the effect of 5 α -reductase inhibitor treatment on mRNA expression profiles. Asterisks (*) indicate significant differences between the vehicle-treated and inhibitor-treated groups ($p < 0.05$).

Figure 4

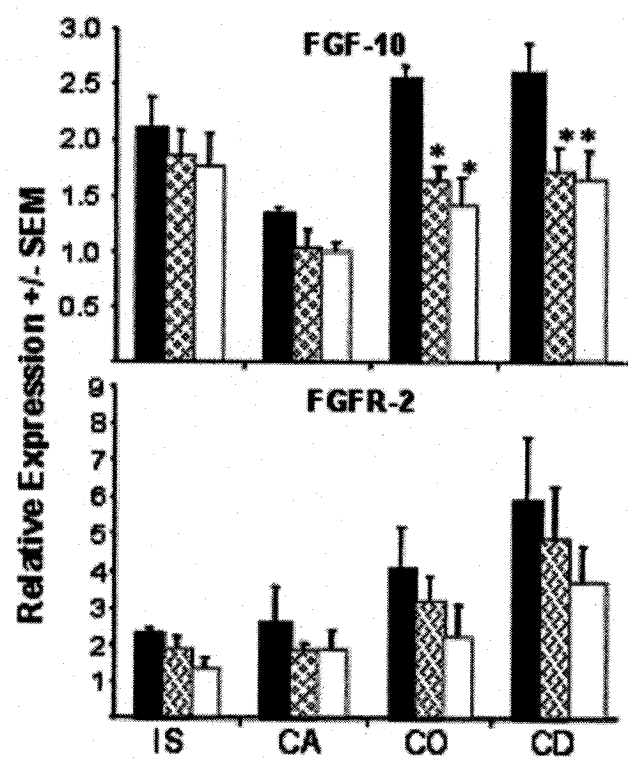


Figure 5. Quantitative real-time RT-PCR analysis of transforming growth factor- β 1 (TGF- β 1) and transforming growth factor- β 1 receptor (TGF- β 1R) mRNAs in the initial segment (IS), caput (CA), corpus (CO) and cauda (CD) epididymides. All gene expression values are expressed relative to the levels of cyclophilin mRNA and are represented as means \pm SEM. RNA extracted from epididymides of vehicle (black bars), PNU15776 (striped bars) and FK143 (white bars) treated rats (n=5/group) was used to analyze the effect of 5 α -reductase inhibitor treatment on mRNA expression profiles. Asterisks (*) indicate significant differences between the vehicle-treated and inhibitor-treated groups (p<0.05).

Figure 5

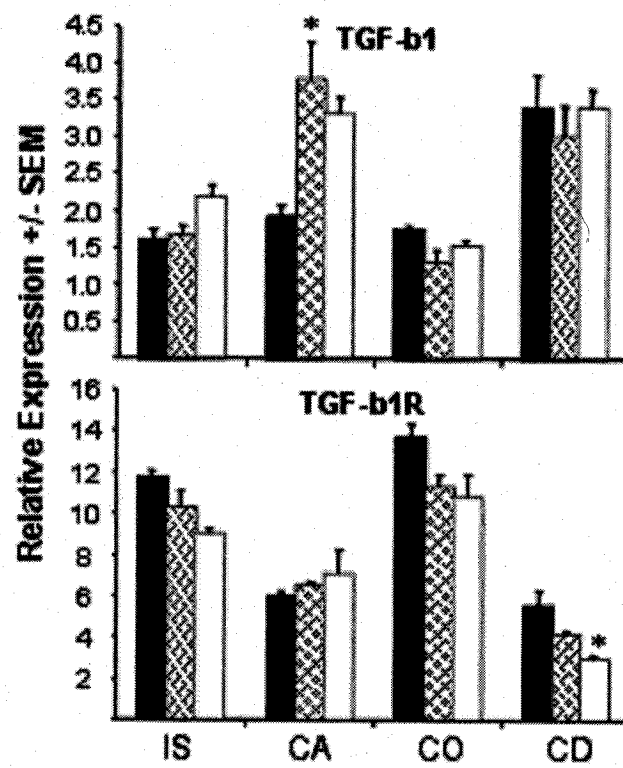
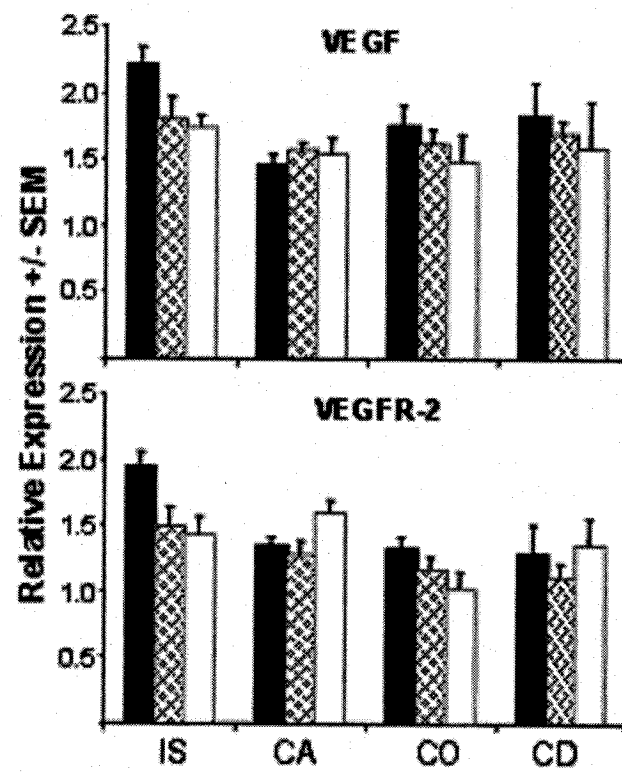


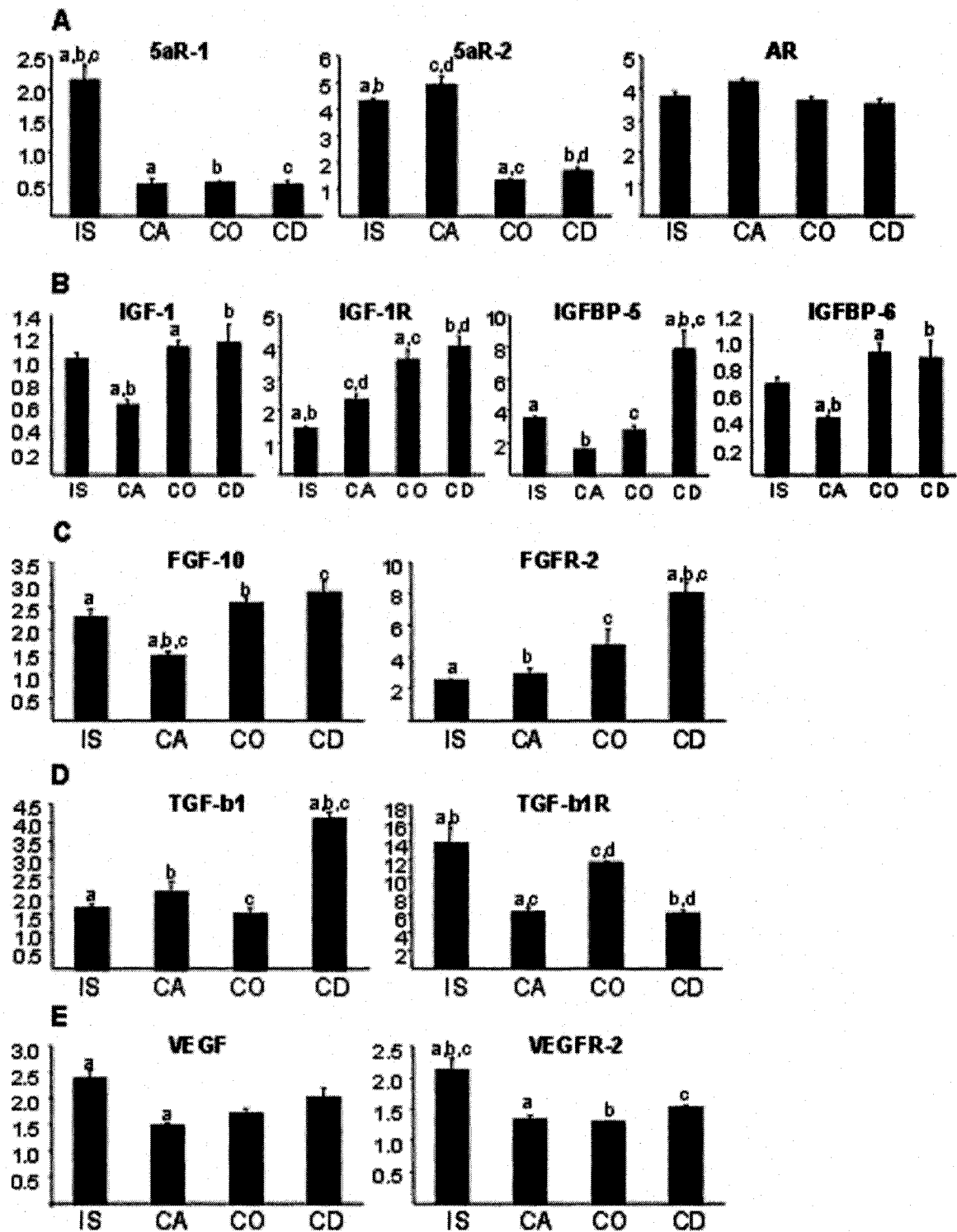
Figure 6. Quantitative real-time RT-PCR analysis of vascular endothelial growth factor (VEGF) and vascular endothelial growth factor receptor-2 (VEGFR-2) mRNAs in the initial segment (IS), caput (CA), corpus (CO) and cauda (CD) epididymides. All gene expression values are expressed relative to the levels of cyclophilin mRNA and are represented as means \pm SEM. RNA extracted from epididymides of vehicle (black bars), PNU15776 (striped bars) and FK143 (white bars) treated rats (n=5/group) was used to analyze the effect of 5 α -reductase inhibitor treatment on mRNA expression profiles. Asterisks (*) indicate significant differences between the vehicle-treated and inhibitor-treated groups ($p < 0.05$).

Figure 6



Supplemental Figure 1. Quantitative real-time RT-PCR analysis of steady-state gene expression in the initial segment (IS), caput (CA), corpus (CO) and cauda (CD) epididymides. A. 5 α -Reductase type 1 (5 α R-1), 5 α -reductase type 2 (5 α R-2) and androgen receptor (AR) expression profiles. B. Insulin-like growth factor-I (IGF-1), insulin-like growth factor-I receptor (IGF-1R), insulin-like growth factor-binding protein-5 (IGFBP-5) and insulin-like growth factor-binding protein-6 (IGFBP-6) expression profiles. C. Fibroblast growth factor-10 (FGF-10) and fibroblast growth factor receptor-2 (FGFR-2) expression profiles. D. Transforming growth factor- β 1 (TGF- β 1) and transforming growth factor- β 1 receptor (TGF- β 1R) expression profiles. E. Vascular endothelial growth factor (VEGF) and vascular endothelial growth factor receptor-2 (VEGFR-2) expression profiles. Paired superscripts (a, b, c, d) indicate significantly different values ($p < 0.05$).

Supplemental Figure 1



Tables and Legends

Table 1. Details of primers used in quantitative real-time RT-PCR experiments.

NA: Not Applicable.

Accession numbers are from the Genbank database.

Gene	Accession No.	Forward primer	Reverse primer	Reference
5aR- 1	NM_017070	CGTCCTGCTGGCTATGTTTC	GAAGGCCAAGACAAAGGTGA	NA
5aR- 2	NM_022711	GGACCCTGATCCTGTGCTTA	ACACCACAAAGGAAGGCAAC	NA
AR	NM_012502	CTAGCGCGTGCCTTCCTTTACA	CCCACCTGCGGGAAGCT	60
IGF-1	NM_178866	CACAGGCTATGGCTCCAGCAT	TCTCCAGCCTCCTCAGATCACA	60
IGF-1R	NM_052807	CGCTGTGTGGACCGGGATTT	GCATGCACTCGCCATCGTG	60
IGFBP-5	NM_012817	GTGACCGCAAAGGATTCTACAAGA	GGCAGCTTCATCCCATACTTGTC	60
IGFBP-6	NM_013104	ACCTCGGCTGCCCCTATAAGG	TCAGTCTGGAGCTGCTGCAGTAC	60
FGF-10	NM_012951	GCTGCTGTTGCTGCTTCTTGTTG	GCTGCTGTTGCTGCTTCTTGTTG	60
FGFR-2	XM_341940	TTCCCCAGATTACCTGGAGATAGC	TCGTGGTCTTCATTTCGGCAA	60
TGF- β 1	NM_021578	GTTCTTCAATACGTCAGACATTG	CATTATCTTTGCTGTCACAAGAGC	61
TGF- β 1R	NM_012775	AATGTTACGCCATGAAAATATCCT	TACAACAGGTTCCATTTTTCTTCA	61
VEGF	NM_031836	CAGCTATTGCCGTCCAATTGA	CCAGGGCTTCATCATTGCA	62
VEGFR-2	NM_013062	TCAGAGACACTGAGCATGGAA	GTTTTGAGCTCTTCTGAGGCAA	62
Cyclophilin	NM_008907	ACACGCCATAATGGCACTGG	ATTTGCCATGGACAAGATGCC	63

Supplemental Table 1. Previously reported genes that showed a minimum 2-fold change in expression uniquely in one epididymal segment following PNU157706 treatment (reported in 12).

¹ The fold-changes expression values following PNU157706 treatment (PNU) were obtained from a previous study (12) and are included for comparison purposes.

² The fold-change expression values following FK143 (FK) treatment were obtained in the present study.

Accession numbers (Acc. Numbers) are for the Genbank database.

	Fold-change in expression		Acc. Number
	PNU ¹	FK ²	
Initial Segment			
neurofibromatosis 2 (NF-2)	↓3.1	↓3.2	U61772
retinoblastoma protein (RBp105)	↓2.1	↓3.2	D25233
ras-GTPase-activating protein (p120GAP)	↓2.0	↓3.6	L13151
Crk-associated substrate (Cas)	↑2.5	-	D29766
fatty acid amide hydrolase	↑3.8	↑2.5	U72497
corticosteroid 11β-dehydrogenase 1	↑4.0	↑4.9	J05107
very long chain acyl-CoA dehydrogenase	↑3.0	↑4.0	D30647
5-lipoxygenase	↑2.7	-	J03960
atrial natriuretic peptide clearance receptor	↓3.4	↓3.5	L27339
chloride channel protein 7	↑3.2	↑4.1	Z67744
Caput epididymidis			
cAMP-dependent protein kinase type II-beta regulatory chain	↓3.6	↓4.8	M12492
Ehk 3	↑7.5	-	U21954
neural thrombospondin 1-like protein (NELL1)	↑3.7	↑5.0	U48246
cathepsin B	↓3.7	↓5.4	X82396
short chain acyl-CoA dehydrogenase	↑4.2	↑3.5	J05030
Corpus epididymidis			
carbonic anhydrase 4	↓4.5	↓5.3	S68245
ras-related protein RAB13	↓2.3	↓5.7	M83678
ephrin B1	↓3.4	↓4.3	U07560
Janus tyrosine-protein kinase 1 (JAK1)	↓2.0	↓1.0	AJ000556
Cauda epididymidis			
RAB-related GTP-binding protein	↓2.8	↓1.1	M94043

muscle/brain cAMP-dependent protein kinase inhibitor	↓2.8	↑1.2	L02615
phosphatidylinositol 4-kinase	↓2.5	↓3.4	D83538
14-3-3 protein gamma subtype	↓3.8	↓3.5	S55305
ras-related protein RAB4B	↓2.4	-	X78605
phospholipase C gamma 2	↓3.3	↓4.1	J05155
phospholipase C delta 1	↓3.2	↓4.3	M20637
phospholipase C gamma 1	↓2.9	↓4.3	J03806
ATPase, hydrogen-potassium, alpha 2a subunit	↓5.0	↓3.9	M90398
sodium/potassium-transporting ATPase alpha 2 subunit	↓2.6	↓1.1	M14512
Band 3	↓7.3	↓5.0	J05167

Supplemental Table 2. Genes that showed a minimum 2-fold change in expression uniquely in one epididymal segment following FK143 treatment.

¹The fold-change expression values following FK143 (FK) treatment were obtained in the present study.

²The fold-changes expression values following PNU157706 treatment (PNU) were obtained from a previous study (12) and are included for comparison purposes.

Accession numbers (Acc. Numbers) are for the Genbank database. Functional classifications are according to BD Bioscience (Clontech).

	Fold-change in expression		Acc.	Functional
	FK ¹	PNU ²	Number	Classification
Initial Segment				
Decreased expression				
glucose-regulated 78-kDa protein	2.7	1.4	M14050	Chaperones & Heat Shock Proteins
Increased expression				
Prohibitin	2.9	1.5	M61219	Intracellular Adaptors & Receptor-Associated Proteins
neural visinin-like Ca ²⁺ -binding protein NVP-3	2.8	1.1	D13126	Calcium-Binding Proteins
adenylyl cyclase type VIII			L26986	Adenylate/Guanylate Cyclases & Diesterases
Cytoplasmic β-actin	2.3	1.1	V01217	Cytoskeleton & Motility Proteins
Vasopressin V2 receptor	2.3	1.2	Z11932	Hormone/G Protein-Coupled Receptors
dual-specificity MAPKK2	2.2	1.1	D14592	Intracellular Kinase Network Members
Casein kinase II	2.2	1.1	L15619	Intracellular Kinase Network Members
Elongation factor 2	2.2	1.0	K03502	Translation Factors
Aminopeptidase B	2.1	1.1	U61696	Metalloproteinases
Macrophage migration inhibitory factor	2.1	1.5	U62326	Growth Factors, Cytokines & Chemokines
Cathepsin L	2.0	1.5	Y00697	Cysteine Proteases
Cofilin	2.0	1.3	X62908	Other Cytoskeleton & Motility Proteins
Caput epididymidis				
Decreased expression				
Gastric inhibitory polypeptide precursor	4.5	1.8	L08831	Other Extracellular Communication Proteins
Sodium channel SCN2B	5.4	1.9	U37026	Voltage-Gated Ion Channels
Potassium channel Kir6.2	4.2	1.8	X97041	Voltage-Gated Ion Channels
C-type natriuretic peptide precursor	4.0	1.9	D90219	Hormones
insulin receptor-related receptor-α	3.0	1.3	M90661	Intracellular Kinase Network Members
rab12, ras related GTPase	2.9	1.5	M83676	G Proteins; Other Trafficking & Targeting Proteins

Gax, growth-arrest-specific protein	2.8	1.1	Z17223	Other Transcription Proteins; Telomere-Associated Proteins
cytochrome c oxidase, subunit IV	2.6	1.3	X14209	Energy Metabolism
CD2, membrane glycoprotein	2.5	1.2	X05111	Cell-Cell Adhesion Receptors; Cell Surface Antigens
vacuolar ATP synth. 16-kDa proteolipid subunit	2.3	1.4	D10874	ATPase Transporters
erbB4, proto-oncogene	2.3	1.6	U52531	Growth Factor/Chemokine/Protein Kinase Receptors
creatine kinase	2.1	1.2	X59737	Energy/Nucleotide Metabolism
apurinic/apyrimidinic endonuclease	2.1	1.3	D44495	DNA Damage Repair Proteins & Ligases

Corpus epididymidis				
<i>Decreased Expression</i>				
Ca ⁺⁺ -dependent phospholipase A2 precursor	3.1	1.6	U03763	Phospholipases & Phosphoinositol Kinases
DNA-binding protein inhibitor ID3	2.4	1.9	D10864	Transcription Activators & Repressors
Monocarboxylate transporter MCT1	2.2	1.8	D63834	Symporters & Antiporters
Pancreatic secretory trypsin inhibitor I precursor (PSTI-I)	2.1	1.8	M27882	Protease Inhibitors
G1/S-specific cyclin D2	2.0	1.8	D16308	Cyclins; Oncogenes & Tumor Suppressors
Increased expression				
Ral A; GTP-binding protein	3.5	1.3	L19698	G Proteins
angiotensin converting enzyme	3.1	1.1	U03734	Metalloproteinases
tissue inhibitor of metalloproteinase- 2	2.9	1.3	L31884	Protease Inhibitors
syntaxin 3	2.6	1.2	L20820	Trafficking & Targeting Proteins
14-3-3 protein theta	2.4	1.1	D17614	Kinase Activators & Inhibitors
GTP-binding protein; G-alpha-i2	2.4	1.0	M17528	G Proteins

Cauda epididymidis				
<i>Decreased expression</i>				
ATPase, transitional endoplasmic reticulum	2.6	1.4	U11760	Immune System Proteins
proteasome component C8	2.3	1.9	M58593	Proteasomal Proteins
SYNAPTOTAGMIN XI	2.2	1.4	AF000423	Exocytosis/Calcium-Binding

				Proteins
heterogeneous nuclear ribonucleoprotein K	2.1	1.5	D17711	RNA Processing, Turnover & Transport Proteins
Increased expression				
Plectin	2.6	1.3	X59601	Cytoskeleton & Motility Proteins
tissue carboxypeptidase inhibitor	2.1	1.1	U40260	Protease Inhibitors

CHAPTER 5

DISCUSSION

The androgen dependence of the male reproductive system has been established for decades; experimental manipulation or alteration of androgen status has been an important methodological approach for studying this complex system. In the present thesis, we have employed such an approach to exclusively study epididymal physiology. Importantly, however, we updated the methodology to better reflect our current understanding of the androgen-dependence of the epididymis, namely that DHT is the predominant androgen acting in this tissue (1-6) and furthermore, that both isozymes of 5 α -reductase, the enzyme catalyzing the local conversion of testosterone to DHT, are present in the epididymis (7). Thus, the androgen manipulation approach used throughout this thesis was inhibition of DHT formation, which was facilitated by the timely development of dual 5 α -reductase inhibitors (PNU157706, FK143) (8, 9). This chapter will discuss the advantages of our novel experimental approach and the significance of some of the key findings presented in this thesis. Special emphasis will be placed on future research directions that will not only serve to expand our current findings, but also to increase knowledge of epididymal physiology in general that will lay the basis for new therapeutic approaches targeted at the epididymis.

5 α -Reductase Inhibition as an Approach to Study Epididymal Physiology

The importance of DHT in the epididymis was deduced decades ago from a combination of *in vitro* studies of 5 α -reductase enzyme activity and direct *in vivo* measurements of steroid levels in this organ (1-6). Since then, however,

very few studies have attempted to show direct biochemical and functional consequences of decreased DHT in the epididymis. Rather, much of our current knowledge regarding androgen regulation of epididymal structure and functions was derived from total androgen ablation or withdrawal experiments with or without subsequent androgen replacement (reviewed in 10). Androgen ablation was achieved predominantly by bilateral orchidectomy (removal of the testes) and to a lesser extent by hypophysectomy (removal of the pituitary) which is a much more severe form of hormone withdrawal.

Structurally, orchidectomy causes a time dependent decrease in rat epididymis weight that reaches approximately 70% by 4 weeks post-orchidectomy; the decreased weight is associated with the loss of sperm and fluid input from the testis as well as with cell shrinkage and apoptotic cell death (11-13). Regressive changes occur predominantly in principal cells indicating that this cell type is particularly sensitive to androgens, while other epithelial cell types appear unaffected by orchidectomy (14).

Functionally, orchidectomy and hypophysectomy have demonstrated that the acquisition of sperm motility and fertilizing ability are dependent on androgens (15-17). Furthermore, using these kinds of techniques, important epithelial processes such as the transport and/or secretion of ions and small organic molecules, metabolic functions and protein and lipid secretion, processing and degradation have been shown to be dependent on androgens (reviewed in 10). At the molecular level, androgen ablation techniques have revealed the influence of androgens on the expression of specific genes within the different regions of

the epididymis including the 5 α -reductase isozymes, gamma-glutamyl transpeptidases, carbonic anhydrase isoforms and various metallothioneins to name a few (7, 18-20). Recently, gene array technology has enabled a larger scale analysis of the effects of orchidectomy on epididymal gene expression; this study identified novel orchidectomy-responsive genes and it permitted the visualization of global trends in gene expression in the epididymis post-orchidectomy, including transient upregulation of gene expression which had not previously been described (21).

While total androgen ablation techniques have been vital for determining the roles of androgens in the epididymis and other reproductive organs, it has become clear that even more insight into androgen action stands to be gained by differentiating between the roles of the two major androgens, testosterone and DHT. Even though both androgens act via the same receptor, several lines of evidence indicate that they have unique roles. Their differential roles during development are perhaps the best characterized; testosterone is responsible for the normal development of the Wolffian-duct structures, the pubertal and post pubertal increase in muscle mass and the development of male sex drive (libido) while DHT ensures the development of the prostate, urethra, penis and scrotum and sexual maturation at puberty (22, 23).

Additionally, there is growing evidence that testosterone and DHT carry out unique roles in adult tissues. For example, the unique roles of androgens in the prostate have been particularly well studied because of their prominent role in two hugely prevalent pathologies affecting this tissue, namely benign prostatic

hyperplasia and prostate cancer. In fact, the effects of orchidectomy and 5 α -reductase inhibitor treatment on prostate physiology have been extensively characterized (reviewed in 24-28).

Particularly relevant to this thesis are examples where T and DHT have been shown to elicit different gene expression responses in this tissue. Nearly 15 years ago, Rittmaster et al. first demonstrated the differential effects of castration and 5 α -reductase inhibitor treatment on androgen-regulated gene expression in the rat prostate (29). More recently, using similar experimental protocols (castration and 5 α -reductase inhibition) in combination with differential display PCR, Avila et al. identified several unique gene expression responses in the rat prostate that clearly suggested that some genes are regulated in different ways by testosterone and DHT in a manner that cannot simply be attributed to the differential affinity of these two hormones for the androgen receptor (30). Lastly, it is well known that the prostate regresses in orchidectomized rats and subsequent administration of exogenous testosterone stimulates prostatic regrowth (24-26). Dadras et al. showed that treatment with finasteride during the testosterone-stimulated prostatic regrowth in castrated rats, which prevents the conversion of testosterone to DHT by 5 α -reductase type 2, alters the expression patterns of certain androgen-response genes (31).

These studies indicate the important role of androgen status in the regulation of gene expression in the prostate. Indeed, the prostate is the only tissue where concrete efforts have been made towards discerning the roles of testosterone and DHT. This thesis represents the first comprehensive attempt to

assess the specific roles of DHT in the epididymis, at both a molecular level (gene expression) as well as a functional level, through the inhibition of 5 α -reductase. Additionally, this is the first set of studies specifically targeting the epididymis that employ dual 5 α -reductase inhibitors. The use of dual inhibitors is an important feature of our experimental approach due to the fact that both 5 α -reductase isozymes are now known to exist in the epididymis (7).

Our findings support the continued use of dual 5 α -reductase inhibition as an experimental approach to study epididymal physiology. In fact, there are several significant advantages to this approach in comparison to other androgen-manipulation techniques. Firstly, when examining a specific tissue, it is obviously desirable to use a technique that targets this tissue, in our case the epididymis, while having limited effects on other tissues and systems. Clearly, the more pervasive the effects of any treatment, the more difficult it is to distinguish between the direct and indirect effects of that treatment. Due to the prevalence of the androgen receptor throughout the body and the well-established roles for testosterone in multiple organ systems, removal of the primary site of testosterone biosynthesis (the testes) by orchidectomy will consequently have a broad spectrum of physiological effects that are not limited to the reproductive system, much less the epididymis. In rats, for example, the circulating androgen concentration decreases to less than 10% of intact control levels by 2 hours following orchidectomy (32), such that all androgen target tissues, whether dependent on testosterone, DHT or both, are rapidly affected. Hypophysectomy, being a more severe form of hormone withdrawal, has even more extensive

effects than orchidectomy (33). Comparatively, inhibiting the formation of DHT by inhibiting 5 α -reductase has less wide-ranging effects since testosterone (and other hormones) levels are essentially maintained at normal levels, forming the basis for a more specific approach with less confounding effects on other tissues.

Importantly, the testis itself does not appear to be affected by 5 α -reductase inhibitor treatment (27, 34-36). This is a second key advantage of this experimental approach. Spermatogenesis in the testis and sperm maturation in the epididymis are intimately linked androgen dependent phenomena, consequently it is very difficult to distinguish between true effects/responses that originate in the epididymis and those that manifest from abnormal testicular functions. Deciphering the unique roles of the testis and epididymis in sperm function has implicit consequences for understanding the origins of male infertility. In this regard, dual 5 α -reductase inhibition provides an intriguing method to study epididymal sperm-related functions separate from testicular sperm-related functions. Furthermore, with the emphasis in male contraceptive research on elucidating post-testicular targets for contraceptives, the need to uncover mechanisms of epididymal sperm maturation is even more apparent.

Finally, one last advantage of 5 α -reductase inhibition in comparison to orchidectomy is that the testis obviously remains intact such that the input of new sperm into the lumen of the epididymis, as well as blood flow to the tissue, also remain intact. The continuous introduction of sperm enables detailed analyses of sperm maturation dynamics in the epididymis, while maintenance of blood supply to the tissue is integral to its structure and functions.

The establishment of dual 5 α -reductase inhibition as a useful and advantageous approach to study the DHT dependence of the epididymis and the initial *in vitro* and *in vivo* characterization of two different inhibitor compounds was an important contribution of the present thesis; this has opened the door to many possible avenues of investigation.

It would have been desirable to measure the exact levels of testosterone and DHT present in each epididymal segment following 5 α -reductase inhibitor treatment; however, this type of analysis was not truly feasible at the time because of the limited amount of inhibitor compound made available to us for our studies, the amount of animal tissues (especially the smaller epididymal segments) required for accurate hormone measurements and the lack of validated protocols for the measurement of DHT in rat epididymides. Furthermore, based on previous studies, it is generally accepted that 5 α -reductase inhibitor treatment decreases DHT levels very significantly in serum and target tissues with limited effects on testosterone levels (27, 28, 34, 36). Therefore, the measurement of androgen levels was not considered a priority. Rather, in the present thesis, we used the approach of dual 5 α -reductase inhibition and sought to answer three main questions: 1) What are the consequences of DHT depletion on epididymal gene expression? 2) What are the consequences of DHT depletion on epididymal sperm functions and can they be correlated to changes in gene expression? 3) How does DHT mediate/regulate differential epididymal gene expression and functions? The next sections serve to highlight some of our significant findings and place them in the context of

current epididymal research. Furthermore, suggestions for future research initiatives will be presented.

DHT and Epididymal Gene Expression

The development and advancement of gene array technology has presented tremendous opportunities for large-scale gene expression analyses in all areas of research. The availability of this technology was a decisive factor in determining our first objective to elucidate the effects of dual 5 α -reductase inhibition on epididymal gene expression. To substantiate and strengthen the reliability of our gene array experiments, our studies incorporated many factors that were unprecedented in gene array experiments at the time this thesis was initiated, including the use of numerous replicates, stringent analysis criteria, dose-response expression profiling to analyze the effects of drug treatment (chapter 2) and additional analyses using a second drug of the same class (introduced in chapter 4).

While gene arrays have previously been used to examine gene expression in the epididymis (21, 37-39), to my knowledge, the study described in chapter 2 was the first report of the effects of treatment with a dual 5 α -reductase inhibitor on global gene expression in this tissue and as such contributes greatly to our understanding of DHT-dependent gene expression in the epididymis. The corroborative gene array findings presented in chapter 4 complement this initial study. Following 5 α -reductase inhibitor treatment, the expression of numerous genes increased and/or decreased in the epididymis, usually in a highly segment-

specific manner, reflecting the importance of DHT and the complexity of coordinated gene expression throughout the tissue that is likely fundamental to its multiple functions.

Among the many genes showing changes in expression following inhibitor treatment, one grouping I found particularly interesting were those involved in protein and lipid processing. Protein and lipid processing events are required for the direct modification of sperm surface components, a major feature of epididymal sperm maturation (40-43). Interestingly, the development of contraceptive vaccines that uniquely target sperm-specific antigens represents a widely researched approach for the regulation of male fertility (reviewed in 44). The viability of this approach was exemplified in a recent study by O'Rand et al. who found that a high percentage (78%) of male nonhuman primates immunized with Eppin, a testis/epididymis-specific protein, became infertile and the majority recovered fertility when immunization was stopped (45). In light of this study as well as others, it is certainly plausible that the DHT-directed processing of epididymal sperm-specific membrane components could provide unique epididymal targets for immunocontraception. Indeed, given that 5 α -reductase inhibition affected the expression of several protein and lipid processing enzymes in a highly segment-specific manner in the epididymis, it is tempting to speculate that DHT regulates the availability of these enzymes to ensure their activity only when and where it is needed during the course of epididymal sperm maturation. As such, it would be interesting to find out whether the protein and lipid processing enzymes identified in chapter 2 act on sperm surface molecules and if

so, to then determine whether their reactions yield antigens that are unique to sperm cells since the therapeutic value of an antigen as an immunocontraceptive target is contingent upon specificity to germ cells.

The large-scale nature of the analyses that are achievable with gene array technology generated a vast amount of information that conceivably points toward the most novel avenues for future research. While I singled out one group of genes that I found particularly intriguing as candidates for further investigation, following up on any of the genes or gene families identified in chapter 2 would further our understanding of epididymal physiology. A next logical step would be to investigate whether changes in gene expression following dual 5 α -reductase inhibitor treatment are paralleled by changes at the protein level using immunohistochemistry, provided that reliable antibodies are available for the proteins of interest. Immunohistochemistry would be preferable to Western blotting because the precise cellular localization of the proteins can be determined. Since unique functions of the various epididymal cell types have been and continue to be elucidated (46), identifying the cell type or types from which a specific protein originates can give additional insight into its potential role in the tissue.

The results presented in chapter 3 certainly suggest that the effects of 5 α -reductase inhibition on epididymal gene expression result in deficits in sperm function, however, direct links between any of the affected genes identified by gene arrays and specific functional consequences remain to be determined. As such, the true value of gene and protein analyses would be borne out to the

fullest extent by determining whether the actual functions of specific proteins are affected by 5 α -reductase inhibitor treatment as well. For example, given that a number of the genes identified in chapter 2 are enzymes involved in protein and lipid processing and metabolism, functional follow-up studies would naturally entail direct assays of enzymatic activity. Similarly, the expression of several oxidative stress-related genes were affected by 5 α -reductase inhibitor treatment therefore, assessing the capacity of the epididymal epithelium to respond to oxidative stress following inhibitor treatment is another possible follow-up experiment. A student in our lab is using treatment with buthionine sulfoximine, a chemical that induces oxidative stress by inhibiting the rate limiting enzyme in glutathione synthesis, to assess the capacity of the epididymis to handle oxidative stress in the context of aging (47). It would be feasible to employ this same methodology to assess the capacity of the epididymis to handle oxidative stress following 5 α -reductase inhibitor treatment as well.

Lastly, in regards to follow-up studies, epididymal intraluminal ion concentrations and pH represent other functional endpoints that could be measured following 5 α -reductase inhibitor treatment, given that the expression of genes involved in fluid and ion transport and luminal acidification were among those identified in chapter 2. In this case, learning and perfecting delicate micropuncture techniques (48, 49) would be required to collect uncontaminated samples of intraluminal fluid from the different epididymal segments following 5 α -reductase inhibitor treatment. Once accomplished, micropuncture techniques could also be used for the microanalysis of other luminal components, such as

proteins known to be secreted by the epididymal epithelium, to determine if they are affected by 5 α -reductase inhibitor treatment and hence under the control of DHT.

DHT and Epididymal Sperm Function

The nature of the gene transcripts that were altered following 5 α -reductase inhibitor treatment suggested their potential involvement in key epididymal epithelial processes that contribute to the formation of an optimal luminal microenvironment required for sperm maturation. These results prompted us to next determine whether sperm maturation was indeed compromised following 5 α -reductase inhibitor treatment. Therefore, we focused specifically on analyzing different facets of sperm maturation in the epididymis and found that 5 α -reductase inhibitor treatment had effects on sperm morphology, motility and fertilizing ability (chapter 3). It is reasonable to conclude that the cumulative effects of 5 α -reductase inhibitor treatment on gene expression resulted in the compromised sperm functions described in chapter 3, which reaffirms the value of following-up on the different functionally relevant gene families identified by gene array in order to elucidate the missing links between epididymal gene expression and sperm functions.

In chapter 3, a standard mating study demonstrated that 5 α -reductase inhibitor treatment resulted in subfertility; however, using this traditional method, the exact origin or cause of the subfertility could not be pinpointed. Due to the general lack of effect of 5 α -reductase inhibitor treatment on the testis (27, 34-36)

it is highly unlikely that the subfertility arises from effects on this tissue. In contrast, there are well-documented effects of 5 α -reductase inhibitor treatment on the seminal vesicles (50, 51), thus it is reasonable to postulate that deficiencies in seminal plug formation, one of the main functions of seminal vesicle secretions (52), may be contributing to the subfertility. I would venture to speculate however, that if the effects of 5 α -reductase inhibitor treatment on the seminal vesicles were to subsequently affect fertility, it would be an "all or nothing" effect rather than the variable effects we observed in the current study, mainly because of the dramatic and highly consistent treatment effects on this tissue that are apparent in our studies and numerous others. It is also tempting to speculate that the variability in the fertility observed in the current study is due to the sheer number of epididymal sperm that must be consistently affected in order to achieve complete infertility. In rats for example, a greater than 90% decrease in the number of epididymal sperm is required to achieve complete infertility (53).

Clearly, more in depth studies are required to pinpoint the exact nature of the subfertility described in chapter 3. Essentially, to achieve fertilization, sperm must be able to reach, recognize, contact and penetrate the egg, while withstanding exposure to the unfamiliar environment of the female reproductive tract. It is plausible to think that decreased progressive sperm motility, as is observed in the study described in chapter 3, may compromise the ability of sperm to travel through the female reproductive tract and reach the egg. This could be assessed by flushing out, fixing and examining the contents of the uterus and oviducts after mating to reveal the nature and number of sperm that

reached these sites within the female tract. In fact, this approach was used to determine the cause of infertility in *c-ros* tyrosine kinase receptor knockout male mice (54). These mice have a unique epididymal phenotype in that they completely lack the initial segment. Despite normal testicular sperm output, epididymal sperm from these animals have slightly lower velocity and head movement parameters (approximately 20% lower than wildtype mice) and display various forms of flagellar angulation predominantly in the distal regions of the epididymis (55). Examination of the uterine and oviductal contents of female mice mated with *c-ros* knockouts showed that sperm were unable to reach the oviduct as a result of their bent tails forming an entangled sperm mass and their compromised flagellar vigor (54).

In addition to facilitating sperm migration to the site of fertilization, sperm motility is also believed to be required for penetration of the surface coats that surround the egg. In particular, hyperactivated motility, described as a type of vigorous non-linear motion that mammalian sperm exhibit as they progress through the female oviduct, has been implicated in this process (56). Studies have suggested that hyperactivated sperm motility provides increased vigor and thrust that facilitates sperm penetration of the surrounding cumulus cells and the zona pellucida, a glycoprotein matrix that envelopes the plasma membrane of the egg (57-60).

Computer-assisted sperm analysis (CASA) has proven to be a valuable tool for studying epididymal sperm motility patterns, and this type of analysis has progressed to become a regular component of sperm functional studies due in

large part to the work of Perreault et al, who tested and defined the CASA criteria for optimal and objective measurements of epididymal sperm motility (61, 62). Standard CASA measures are made 10-30 minutes after sperm are collected in a medium that is not conducive to capacitation thereby making measures of hyperactivation impossible. Recently however, Perreault's group addressed this problem and established novel criteria for detecting and monitoring hyperactivation of rat sperm motility using CASA that was facilitated by advances in CASA computer and optical systems (63). Now that measurements of rat sperm hyperactivation are possible, it would be interesting to determine whether 5 α -reductase inhibitor treatment has an effect on this functional end-point as it does on other motility parameters.

Lastly, the ability of sperm to undergo the acrosome reaction, also a requirement for egg recognition and penetration (56), can be assessed following 5 α -reductase inhibitor treatment using staining methods (i.e. chlortetracycline fluorescence staining) (64). The acrosome reaction is highly dependent on complex sperm membrane dynamics therefore it would be a particularly interesting functional endpoint to measure given that 5 α -reductase inhibitor treatment affects the expression of numerous genes that potentially interact with and modify the sperm plasma membrane (chapters 2 and 4).

DHT Signaling Mechanisms in the Epididymis

The epididymis is not a homogeneous tissue; rather, it displays highly regionalized tissue organization, function and gene expression. Due to its

complexity, deciphering the regulatory mechanisms governing the epididymis is a challenging objective to tackle. Our experiments clearly demonstrated that DHT has an important role in regulating this tissue, and it does so in a highly segment-specific manner. What remained unclear was the identity of segment-specific signaling/regulatory molecules and pathways involved in mediating the effects of DHT on epididymal gene expression and function, which formed the basis of our third and final objective. We touched upon this matter using gene array technology (chapters 2 and 4) and identified transcription factors and other signaling molecules with altered gene expression following 5 α -reductase inhibitor treatment. For the most part however, the genes identified in this way were isolated signaling molecules (i.e. not from the same pathway) such that specific conclusions regarding the involvement of signaling pathways in epididymal regulation were difficult to make. We therefore wanted to approach our third objective in a more comprehensive manner by focusing our analyses on specific signaling systems using the novel and sensitive technique of quantitative real-time RT-PCR.

As we found out, DHT mediated regulation of the epididymis extends to the level of the enzymes that control its production (5 α -reductases) as well as the receptor that mediates its action (androgen receptor). The differential effect of 5 α -reductase inhibitor treatment on the expression of the two 5 α -reductase isozymes in the epididymis was particularly interesting. This finding was consistent with what has previously been reported regarding the regulation of 5 α -reductase expression in other tissues (65-67) and strongly suggests that the two

isozymes carry out unique roles despite the common reaction they catalyze. Whether or not this is the case has not yet been proven; the development of reliable type-specific inhibitors provides one approach that would help resolve this issue.

Alternatively, a more in depth examination of the phenotypes of the type specific 5 α -reductase knockout mice developed by Mahendroo et al. might also give insight into the unique roles of each isozyme (68). While it has been reported that there is no effect on reproduction in type 1 5 α -reductase knockout male mice and the type 2 5 α -reductase knockout males exhibit a mild virilization defect, thorough examinations and/or descriptions of many specific tissue phenotypes, including the epididymis, have not yet been reported. Unfortunately, despite the existence of 5 α -reductase knockout animals, they have not been made generally available such that these types of analyses can be undertaken. It should be noted that Mahendroo et al. concluded from their studies that testosterone alone is required for differentiation of the male mouse urogenital tract and that the synthesis of DHT serves largely as a signal amplification mechanism in this animal model (68). This is in contrast to the requirements for both testosterone and DHT in the proper development of the reproductive system in men. Furthermore, studies in male rats using pharmacological inhibitors also support a two-androgen model of sexual differentiation (34, 69, 70), indicating that the rat may be a more suitable animal model for understanding the roles of DHT within the male reproductive system.

We showed that the expression of the androgen receptor is affected in a segment-specific manner by 5 α -reductase inhibitor treatment *in vivo*. It would also be interesting to assess the effects of treatment on androgen receptor function *in vitro*, for example by examining androgen receptor transactivation of reporter gene constructs containing functional androgen response elements (AREs) in established cell culture systems such as the LnCAP prostate cancer cell line (71). Additionally, using similar *in vitro* reporter gene assays, it would be possible to test whether ligand-bound androgen receptor binds directly to the promoter regions of genes identified in chapters 2 and 4 that changed (increased or decreased) in expression following 5 α -reductase inhibitor treatment. These studies would have the potential of elucidating those genes that are direct targets of androgen action, reveal novel AREs, distinguish between AREs that lead to the induction or repression of gene expression as well as differentiate between the effects of testosterone and DHT-bound androgen receptor complexes on gene expression.

Determining the roles of growth factors and growth factor signaling in the development, regulation and pathogenesis of the reproductive system, particularly of the prostate, has become an intriguing and widespread area of research in the field of reproduction. Using quantitative real-time RT-PCR, we were able to analyze the longitudinal expression patterns of several growth factor family members in the epididymis and determine whether these patterns were regulated by DHT. While the results presented in chapter 4 suggest that DHT regulates diverse epididymal processes by activating different growth factor

signaling pathways, substantiating the activation of these pathways presents a challenging task for several reasons, not the least being the inherent difficulty in measuring the transient changes in gene expression and phosphorylation status that occur when a signaling cascade is activated.

Generally, in vitro cell-culture systems are better suited for signaling analyses. For example, studies using prostate cell lines have provided evidence to support androgen receptor cross talk with growth factor signaling pathways resulting in both enhanced androgen responses and receptor ligand-independent activation and modulation of androgen receptor transactivation (72-75). Given these findings and our current gene expression results, analogous studies of epididymal androgen and growth factor signaling interactions are certainly warranted. Until recently, however, studies of this type were not truly feasible due to the lack of viable epididymal cell culture systems. Fortunately, with the recent emergence of several different epididymal cell lines (reviewed in 76), new tools now exist that could enable more in depth studies of androgen and growth factor signaling in the epididymis. A study by Sipila et al. is a promising example of the viability of these cell lines for the analysis of signaling systems in the epididymis (77); in this particular study, inhibitors of specific signal transduction pathways were used to elucidate the epididymal regulation of PEA3, a member of the family of Ets transcription factors that is highly expressed in the adult epididymis (78).

In addition to evaluating signaling mechanisms, epididymal cell lines have numerous potential applications for studying epididymal genes and proteins and

their regulation by various endogenous and/or exogenous factors. It would certainly be interesting to determine the cellular consequences of different androgen treatments. In collaboration with another student, I have initiated ongoing studies in our lab to characterize the androgen-dependence of gene expression in available cell lines; using the same gene array technology employed throughout this thesis, we are assessing the effects of androgen status on gene expression in the mouse proximal caput cell line (79). Importantly, we have the benefit of our large-scale epididymal gene expression data with which to make comparisons in order to determine how representative the cell line is of the actual *in vivo* situation. Furthermore, these initial studies were designed to differentiate between the effects of testosterone and DHT to ultimately assess the suitability of this *in vitro* system for studying androgen action in the epididymis.

Finally, despite the numerous potential applications of the newly emerging epididymal cell lines and the insight into epididymal physiology that stands to be gained, it needs to be recognized that cell lines are only representative of one isolated epididymal segment. As such, cell lines could never truly represent the complex regionalized diversity of the epididymis as a whole, a hallmark feature that has made the epididymis such an interesting and unique tissue to study in the first place.

Final Conclusions

A novel androgen manipulation approach, dual 5 α -reductase inhibitor treatment, was designed and implemented in this thesis to specifically study the

roles of DHT in the epididymis. This approach revealed novel roles for DHT in the segment-specific expression of numerous genes implicated in important epididymal epithelial cell processes, in maintaining key features and function of epididymal sperm and in androgen and growth factor signaling mechanisms in the epididymis. Collectively, the studies presented in this thesis contribute greatly to our understanding of androgen action in the epididymis and lay the groundwork for many novel investigations of epididymal physiology. From a clinical standpoint, a greater understanding of epididymal sperm maturation would enable more informed diagnoses of the underlying epididymal causes of male infertility and indicate potential treatments for this pathology. Furthermore, the epididymis represents an extremely promising target for male contraceptive approaches that are highly specific with few to no side effects, especially when compared to testis-based or hormonal contraceptive approaches that are disadvantaged by delayed onset of effectiveness and reversibility, accompanying androgen-dependent side effects and documented ethnic variations in efficiency (80, 81).

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LIST OF ORIGINAL CONTRIBUTIONS

1. Treatment using novel dual 5 α -reductase inhibitors was shown, for the first time, to be a viable and useful approach to study DHT action in the rat epididymis. Prior to these studies, there were very few reported analyses of the effects of 5 α -reductase inhibitor treatment on the epididymis and none that used a dual inhibitor to maximally decrease DHT levels.
2. The effects of dual 5 α -reductase inhibitor treatment on gene expression in the rat epididymis were determined using cDNA arrays containing 1178 cDNAs. It was demonstrated that treatment affected epididymal gene expression in a dose-dependent and highly segment-specific manner.
3. Gene expression in the initial segment responded uniquely to dual 5 α -reductase inhibitor treatment in that a similar number of genes increased and decreased in expression, whereas in the other epididymal segments the predominant effect of treatment was decreased gene expression.
4. Insight was provided into the DHT regulation of genes potentially involved in important processes that contribute to the formation of the epididymal luminal microenvironment that is critical for proper sperm maturation; these processes included fatty acid and lipid metabolism, regulation of ion and fluid transport, luminal acidification, oxidative defense and protein processing and degradation.

5. Treatment with a dual 5 α -reductase inhibitor had segment-specific effects on sperm motility. There was no effect of treatment on the motility of sperm from the caput epididymidis. Treatment decreased the percentages of motile and progressively sperm and altered the characteristic sperm motion parameters of sperm from the cauda region.
6. Phase-contrast and electron microscopy showed that dual 5 α -reductase inhibitor treatment affected sperm morphological changes associated with epididymal sperm maturation, but did not affect sperm ultrastructural features that are established in the testis. Namely, treatment resulted in a higher proportion of sperm from the cauda epididymidis that retained their cytoplasmic droplet.
7. The effects of dual 5 α -reductase inhibition on male fertility were determined. Females naturally mated with treated males had fewer successful pregnancies and a higher rate of preimplantation loss. The rate of postimplantation loss and progeny outcome were unaffected.
8. The epididymal expression profiles of both 5 α -reductase isozymes and the androgen receptor were determined using the novel technique of quantitative real-time RT-PCR. These profiles were analogous to cDNA array and Northern blot analyses of gene expression.

9. Novel segment-specific expression profiles for IGF, FGF, TGF and VEGF family members were established in the epididymis using quantitative real-time RT-PCR.
10. Two different dual 5 α -reductase inhibitors were shown to have analogous effects on epididymal gene expression.
11. Dual 5 α -reductase inhibitor treatment had gene and segment-specific effects on the expression of genes involved in mediating androgen signaling in the epididymis. The expression of 5 α -reductase type 1 and androgen receptor increased in the proximal epididymis following treatment.
12. Dual 5 α -reductase inhibitor treatment had gene and segment-specific effects on the expression of growth factor signaling genes in the epididymis. The expression of IGF-1, IGFBP-5, IGFBP-6, and FGF-10 decreased in the distal epididymis following treatment.

APPENDIX

McGill University

Animal Use Protocol – Research

For office use only

Protocol #: 206

Investigator #: 365

Approval End Date: Jan 31, 2004

Facility Committee: MCD

Title: Regulation of epididymal functions
(must match the title of the funding source application)

New Application:

Renewal of Protocol: # 206

Pilot:

Category (see section 11): D

1. Investigator Data:

Principal Investigator: Bernard Robaire

Phone #: 398-3630

Department: Pharmacology and Therapeutics

Fax#: 398-7120

Address: 3655 Promenade Sir-William-Osler

Email: brobaire@pharma.mcgill.ca**2. Emergency Contacts:** Two people must be designated to handle emergencies.

Name: Bernard Robaire

Work #: 398-3630

Emergency #: 935-3828

Name: Trang Luu

Work #: 398-6241

Emergency #: 731-6517

3. Funding Source:

External: X

Internal:

Source (s): CIHR

Source (s):

Peer Reviewed: YES X NO**

Peer Reviewed: YES NO**

Status: Awarded Pending

Status: Awarded Pending

Funding period: ongoing 4/1/02 - 3/31/07

Funding period:

For Office Use Only:

ACTION	✓	DATE
CCS	✓	Feb 21/03
DELTA	✓	March 10/03
APPROVED		

** All projects that have not been peer reviewed for scientific merit by the funding source require 2 Peer Review Forms to be completed e.g. Projects funded from industrial sources. Peer Review Forms are available at www.mcgill.ca/rgo/animal

Proposed Start Date of Animal Use (d/m/y):

or ongoing: X

Expected Date of Completion of Animal Use (d/m/y):

or ongoing: X

Investigator's Statement: The information in this application is exact and complete. I assure that all care and use of animals in this proposal will be in accordance with the guidelines and policies of the Canadian Council on Animal Care and those of McGill University. I shall request the Animal Care Committee's approval prior to any deviations from this protocol as approved. I understand that this approval is valid for one year and must be approved on an annual basis.

Principal Investigator's signature:

Date: Feb 12, 2003

Approved by:

Chair, Facility Animal Care Committee:

Date: 12/2/2003

University Veterinarian:

Date: 2/20/03

Chair, Ethics Subcommittee (as per UACC policy):

Date: 2/20/03

Approved Animal Use

Beginning: Feb 1, 2003

Ending: Jan 31, 2004

This protocol has been approved with the modifications noted in Section 13.



McGill University Internal Radioisotope Permit

20050242

Permit Holder & Position BERNARD DR. ROBAIRE, PROFESSOR	Building (Office) MCINTYRE BUILDING	Building (Lab) MCINTYRE BUILDING	Laboratory Classification BASIC	PLEASE POST	Date Issued 2004/09/01
Department PHARMACOLOGY AND THERAPEUTICS	Room Number(s) 104	Telephone 398-3630	Room Number(s) 115,116	Telephone 398-6241	Expiry Date 2005/08/31

PERSON(S) APPROVED TO WORK WITH RADIOISOTOPES

Name	Train.	Cond(s)	Class(es)	Radioisotope(s)
BERNARD ROBAIRE, PROFESSOR	Y	2, 4, 3	1	P-32, H-3, C-14, I-125
NATALI HENDERSON, PH.D. STUDENT	Y	2, 4	1	P-32, H-3, C-14, I-125
KATIA ZUBKOVA, MSC STUDENT	Y	2, 4	1	P-32, H-3, C-14, I-125
SHAYESTA SEENUNDUN, MSC STUDENT	Y	2, 4	1	P-32, H-3, C-14, I-125
TRANG LUU, TECHNICIAN	Y	2, 4	1	P-32, H-3, C-14, I-125
MAHSA HAMZEH, QUALIFYING STUDENT	Y	2, 4	1	H-3, P-32
FARIDA VAISHEVA, RESEARCH ASSISTANT	Y	2, 4	1	H-3, P-32
LUDOVIC MORCOW, PH.D STUDENT	Y	2, 4	1	H-3, P-32
SOPHIE ANNE LAMOUR, GRADUATE STUDENT	Y	2, 4	1	P-32, H-3, C-14, I-125

GENERAL LICENCE CONDITIONS (OPEN AND/OR SEALED SOURCES)

- The permit must be posted with the CNSC safety poster in the permit holder's premises.
- Radioisotope handling shall be in accordance with the McGill Radiation Safety Policy Manual.
- The permit holder must ensure that all persons mandated to work with radioisotopes be properly trained in radiation safety prior to start of work.
- Radioactive work areas must be clearly identified with radiation warning signs.
- Smoking, eating, drinking, storage of foods or drink and the application of cosmetics and contact lenses are prohibited in areas where radioisotopes are used.
- All procedures involving radioactive materials should be carried out on spill trays or on benches lined with disposable absorbent material.
- Procedures that might produce airborne radioactive contamination should be carried out in a functioning fume hood.
- When hand or clothing contamination is possible, protective gloves and clothing must be worn.
- After handling radioactive material and especially before leaving the laboratory, personnel must ensure that all parts of their cloths are not contaminated.
- Purchase and disposal of radioisotopes must be kept electronically or documented in a log book.
- For disposal of radioactive waste, consult the McGill Radiation Safety Policy Manual and/or McGill WMP.
- Wipe tests must be performed and records be kept in a log book.
- The permit must reflect the exact conditions under which radioactive material is used. If changes must be made, contact the RSO at 398-1538.
- The device(s) containing the sealed source(s) must have a radiation symbol and an identification label bearing the name and telephone number of the permit holder.
- Leak tests must be performed on sealed sources equal to or greater than 50 MBq (1.35mCi).
- Extremity dosimeter (i.e. ring or wrist badges) must be worn if 50 MBq or more of P-32, Sr-89, Sr-90 & Y-90 are used.
- Workers using I-125 or I-131 on open bench (5 MBq), in a fume hood (50 MBq) or a vented glove box

Approved Unsealed Radioisotope(s) and Location(s)

Isotope	Possession Limit	Stored	Handled
H-3	< 400 MBq (11 mCi)	116	114, 115
C-14	< 40 MBq (1.1 mCi)	116	114, 115
P-32	< 1 GBq (27 mCi)	117, 116	114, 116
Sr-35	< 400 MBq (11 mCi)	116	114, 115
I-125	< 400 MBq (11 mCi)	116/1329	114, 116/1329

Approved Sealed Radioisotope(s) and Location(s)

Permanently Housed Source(s)				Accessible Source(s)			
Isotope	Activity	Stored	Handled	Isotope	Activity	Stored	Handled
Ra-226	10 uCi (remov	114	114	H-3	194,600 dpm	114	114
H-3	196000 dpm	114	114	C-14	71,700 dpm	114	114
C-14	105900 dpm	114	114				
RA-226	10uCi	114	114				

Personnel Conditions

- Must attend thyroid bioassays within 5 days of use if 50 MBq (1.35 mCi) of I-125 are manipulated in a fume hood.
- Must wear a whole-body film badge, if gamma, x-ray or high energy beta emitters are used.
- Must wear an extremity TLD dosimeter, if more than 50 MBq (1.35 mCi) of P-32, Sr-89, Sr-90 or Y-90 are used.
- Classified as Radiation User.
- Classified as Nuclear Energy Worker (NEW).
- Does not work with any radioisotopes but may be indirectly exposed.

Workload Classes

- Work load < 10MBq (270 uCi) of unsealed radioisotopes in open areas.
- Work load < 10MBq (270 uCi) of unsealed radioisotopes in a fume hood.
- Work load > 10MBq (270 uCi) of unsealed radioisotopes in open areas.
- Work load > 10 MBq (270 uCi) of unsealed radioisotopes in a fume hood.
- Work with sealed sources.
- Individual does not work with radioactive sources but normal working conditions involve presence in a room where radioactive material is used or stored.

Joseph Vincelli
RSO & Occupational Hygienist
McGill Environmental Health & Safety

For: Dr. Ian Butler, Chairperson
McGill University Laboratory Safety Committee
Associate Vice-Principal (Research)

Date 27/04/05



Health
Canada

Santé
Canada

Health Products
and Food Branch

Direction générale des produits
de santé et des aliments

20 May 2005

Natali Anne Henderson
Pharmacology & Therapeutics
McIntyre Medical Sciences Building, Room 115
McGill University
3655 Promenade Sir William Osler
H3G 1Y6

Dear Miss Henderson,

As per your request, I hereby grant you permission to reprint, as part of your thesis, the two following manuscripts that I have co-authored:

- 1) Henderson NA, Cooke GM, Robaire B. Effects of PNU157706, a dual 5-alpha-reductase inhibitor, on gene expression in the rat epididymis. J Endocrinol 2004 May; 181(2):245-261
- 2) Henderson NA, Cooke GM, Robaire B. Segment-specific expression of signaling pathway genes in the rat epididymis and the effects of dual 5-alpha-reductase inhibitor treatment. Submitted for publication.

Yours sincerely,



Gerard M. Cooke, Ph.D.

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