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RESEARCH ARTICLE

GENETIC REGULATION OF EPIDIDYMAL MICROENVIRONMENT

*Debjani Nath

Department of Zoology, University of Kalyani, Kalyani, Nadia, West Bengal, India

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ABSTRACT

During their transit through the epididymis, spermatozoa undergo many biochemical modifications necessary to acquire flagellar motility and fertilizing ability. These modifications, collectively called sperm maturation, are well orchestrated along the epididymis. Sperm maturation requires the interaction of spermatozoa with proteins that are synthesized and secreted in a region-specific manner by principle cells of the epididymal epithelium and depend on highly regionalized gene expression patterns. But the regulatory processes that establish the discrete epididymal microenvironments remain yet largely unknown. Based on clinical observations, the role of the epididymis in human sperm maturation has been questioned but results obtained using animal models can be extrapolated to human with caution

INTRODUCTION

The epididymis consists of a single, highly coiled and convoluted tubule that Antoine De Graaf, the famous seventeenth century anatomist, compared to a thread thickening to a string. The mammalian epididymis is a segmented organ comprised of a single, highly coiled tubule conventionally divided into caput, corpus, and cauda regions in larger sections. As mammalian spermatozoa pass from the testis into the epididymis they possess a specialized and distinct morphology, but are infertile and are bathed as they progress from seminiferous tubule to the ductus deferens. Through a number of absorptive, secretory, and contractile processes, each region of the epididymis contributes to the concentration, maturation, transport, or storage of sperm (Robaire 1988; Cornwall 2002). The hallmarks of the maturational process are the acquisition of motility and the competence to undergo capacitation, leading to the ability to fertilize an egg (Turner 1995; Visconti *et al.*, 1995). Spermatozoa are transcriptionally and translationally inactive. Therefore, extratesticular maturation of spermatozoa is not under the control of the germinal genome; rather, it is mediated by factors within the epididymal fluid. The composition of the luminal environment of the epididymis changes continually due to both secretion and removal of specific ions, small organic molecules, and proteins from the luminal compartment of the organ. The microenvironment created along the length of the epididymal tubules are essential to the molecular modification of spermatozoa that results in fertile gametes. Each epididymal region is characterized by its own gene expression pattern encoding its specific secretome sequentially interacting with the maturing spermatozoa (Kirchhoff 1999). But the regulatory processes that establish the discrete epididymal microenvironments remain largely yet unknown.

Segment specific microenvironment

Most studies to date have used relatively large epididymal regions (caput, corpus, cauda) as boundaries for analysis of intraepididymal

gene expression patterns (Cornwall *et al.*, 1992, 1999). In describing the localization of epididymal gene expression, these regions have also been further divided (e.g., proximal, mid, and distal caput). The epididymal regions can also be definitively subdivided into discrete, intraregional segments or testes lobules of coiled tubule bounded by connective tissue septae (Vernet *et al.*, 1997; Eberspaecher *et al.*, 1995). Over the past decade it has become evident that many gene expression patterns within these regions are restricted to one or more segments (Eberspaecher *et al.*, 1999). This implies that these segments are distinct regulatory subunits of the epididymis (Eberspaecher *et al.*, 1999; Rankin *et al.*, 1992) and may play an important role in directing the tightly regulated composition of the epididymal tubule fluid. In addition to being region-specific, a number of epididymal genes are tissue-specific, expressed exclusively in the adult epididymis. Such genes include the initial segment (IS)-specific *ros1* proto-oncogene (*Ros1*) (Sonnenberg-Riethmacher *et al.*, 1996) and lipocalin 8 (*Lcn8*) 9 (Lareyre *et al.*, 2001) and the distal caput-specific lipocalin 5 (*Lcn5*) (Lareyre *et al.*, 1998). In addition, there are numerous other genes that are expressed predominantly in the epididymis and only at lower levels in other tissues. IS-specific cystatin 8 (*Cst8*) (Cornwall *et al.*, 1992, 1999), caput-specific glutathione peroxidase 5 (*Gpx5*) (Vernet *et al.*, 1997), and corpus- and cauda specific cysteine-rich secretory protein 1 (*Crisp1*) (Eberspaecher *et al.*, 1995) fall into this category. In addition to genes with sharply restricted expression in certain epididymal regions (Lareyre *et al.*, 2001), some exhibit more gradual changes of expression between the different regions, leading to characteristic checkerboard-type expression patterns for many epididymal genes (Eberspaecher *et al.*, 1999; Rankin *et al.*, 1992; Lareyre *et al.*, 1998). Furthermore, there are several epithelial cell types present in the ductus epididymis, and several epididymal genes exhibit cell specificity, most of them being expressed only in the principal cells (Blomqvist 2006). Most recently the application of gene profiling technology to the epididymis has yielded volumes of information of segment-specific gene expression that is available to the public. Because the gene chips used in these studies represented sequences derived from early-stage embryos, the microarray analysis was biased

*Corresponding author: Debjani Nath, Department of Zoology, University of Kalyani, Kalyani, Nadia, West Bengal, India.

Gene knockout in relation with different epididymal segmental microenvironment

Gene	Expression in epididymal region
Apolipoprotein E receptor 2 (apoer2)	Expressed in initial segment. Member of low density lipoprotein receptor gene family. Increased level of clusterin in epididymal luminal fluid of the knockout suggests apoer2 also function as a clusterin receptor (Andersen 2003).
Apolipoprotein B (apob)	Expressed in testis and epididymis.
Estrogen receptor- alpha (Es1)	Maintain lipid absorption and triglyceride homeostasis. (Huang 1996) Expressed in efferent duct and initial segment
Anion exchanger 2 (slc4a2)	Transcription factor Helps in fluid reabsorption (Hess1997; Zhou 2001)
HE6(Gpr64)	Expressed in initial segment caput and less expressed in cauda. Na dependent anion transporter (Medina <i>et al.</i> , 2003)
c-ros tyrosine kinase receptor (Ros 1)	Expressed in efferent ducts and initial segment. Member of G-protein coupled receptor (Davies <i>et al.</i> , 2004)
Nuclear oxysterol receptor LXR alpha and beta (lxr)	Expressed in initial segment Tyrosine kinase receptor (Sonnenberg-Riethmacher <i>et al.</i> , 1996; Yeung <i>et al.</i> , 2002; 2004 Frenoux <i>et al.</i> , 2004; Morales <i>et al.</i> , 2000)
Prosaposin (psap)	Highest in caput Transcription factor activated by oxysterol (Frenoux <i>et al.</i> , 2004)
Nuclear phospholipids hydroperoxide glutathione (Gpx4)	Expressed in epididymal lumen Lysosomal activator (Morales <i>et al.</i> , 2000)
Inositol polyphosphate 5-phosphatase (Inpp5b)	Expressed in epididymal germ cells Member of glutathione peroxidase family (Conrad <i>et al.</i> , 2005)
FSH receptor (Fshr)	Expressed in Sertoli cells, germ cells. Signaling protein in IP3 pathway. (Hellsten <i>et al.</i> , 2001)
Cathepsin A (Ctsa)	Follicle stimulating hormone receptor Expressed in sertoli cells, decreased in caput and corpus. (Grover <i>et al.</i> , 2005)
β -hexosaminidase A and B (Hexa b)	Expressed in caput and corpus Lysosomal carboxypeptidase (Korah 2003)
Mononuclear phagocytic growth factor stimulating colony factor (Csf1)	Expressed in initial segment Lysosomal enzyme (Adamali <i>et al.</i> , 1999)
Somatic and testis specific angiotensin converting enzyme (Ace)	Expressed in caput and cauda epididymis. (Pollard <i>et al.</i> , 1997) Regulator of the rennin-angiotensin system
Bone morphogenetic protein 8A (Bmp8A)	Help in sperm transport and zona binding (Hagaman 1998; Fuchs <i>et al.</i> , 2005; Zhao <i>et al.</i> , 1998) Maintain epididymal epithelium (Kondoh <i>et al.</i> , 2005)
γ - Glutamyl transpeptidase (Ggtp)	Mainain structure of epidymis (Lieberman <i>et al.</i> , 1996)
Hoxa 10 and Hoxa 11	Transcription factors Helps in epidymis morphogenesis during development. (Hsieh-Li <i>et al.</i> , 1995; Satokata 1995)

toward identifying new subsets of genes expressed in the adult epididymis. Johnston *et al.* examined the varying expression profiles of genes from all segments of the mouse epididymis using Affymetrix mouse gene chips. This information is available in a searchable website at the Mammalian Reproductive Genetics database (<http://mrg.genetics.washington.edu>). Because each study used different sources of sequences, a broad representation of sequences is presented. During epididymal transit, sperm-associated proteins including ADAM2 (fertilin), ADAM3 (cyritestin), ADAM24 (testase), CE9, and others are proteolytically processed to their mature and presumably functionally active forms (Lum *et al.*, 1997; Kim *et al.*, 2004 Zhu *et al.*, 2001; Petruszak *et al.*, 1991). Although the identity of the proteases involved in the activation of these proteins is not known, furin-like proteases have been implicated for several of these processing events (Lum *et al.*, 1997). Recent studies showed that several members of the prohormone convertase family of proprotein processing enzymes including furin, PC7, PC4, and PACE4 are expressed in the epididymis in a regionalized manner and several are present in epididymal fluid suggesting a possible role for these proteases in sperm maturational events. Indeed, PC4 knockout male mice are infertile despite normal spermatogenesis and motility, suggesting that critical fertilization molecules may not be processed correctly (Mbikay *et al.*, 1997). Other proteases expressed in a segment-specific manner in the epididymis include several of the matrix metalloproteases, MMP2, MMP3, MMP9 (Metayer *et al.*, 2002), ADAM28 (Oh *et al.*, 2005), and procathepsin L (Okamura *et al.*, 1995). Several protease inhibitors that show segment-specific expression have also been identified. Several members of the cystatin-related epididymal spermatogenic (CRES) subgroup of family 2 cystatins of cysteine protease inhibitors including CRES,

CRES2, CRES3, and cystatin E2 are highly restricted to the initial segment region of the mouse epididymis (Cornwall 1002; 2003; Hsia *et al.*, 2003; Li *et al.*, 2003). Although the function of these secretory proteins in vivo is not known, in vitro CRES is an inhibitor of several members of the prohormone convertases (Cornwall *et al.*, 2003), suggesting CRES may regulate proprotein processing events in the epididymis. Other protease inhibitors expressed in the epididymis include Eppin, a member of the whey acidic protein type four-disulfide core gene family. In the human, Eppin associates with semenogelin on the surface of ejaculated spermatozoa and may provide antimicrobial activity for spermatozoa (Wang *et al.*, 2005). Studies in which primates were immunized with Eppin resulted in a contraceptive effect in 78% of the monkeys that was reversible in 71%, suggesting an important function for this protein in fertility and a possible role as a male contraceptive (O'Rand *et al.*, 2004). Other gene and gene products expressed in a region-dependent manner in the epididymis include those encoding antioxidant enzymes such γ -glutamyl transpeptidase, glutathione peroxidases, and superoxide dismutase (Palladino *et al.*, 1994; Ghyselincx *et al.*, 1990; Schwaab *et al.*, 1998; Perry *et al.*, 1993). Because the epididymal lumen is oxygen-rich, unsaturated fatty acids in sperm membranes may be susceptible to oxidative damage. The expression of these enzymes may protect spermatozoa from oxidative damage. Lysosomal enzymes such as β -hexosaminidase, α -mannosidase, and α -galactosidase are secreted into the epididymal lumen, where they may affect sperm function either directly or indirectly by modifying carbohydrate moieties (Cornwall *et al.*, 2002; Hermo *et al.*, 1997). A variety of signaling molecules are also expressed in a region dependent manner in the epididymal epithelium. It is likely that these proteins respond to various external stimuli in the luminal environment, ultimately affecting epithelial cell function. For

example, in the caput, several members of the retinoid signaling pathway are expressed such as epididymis-specific extracellular retinoic acid-binding protein and the related MEP17, mMUP4-L, and mEP19, cellular retinoic acid binding protein and retinoic acid receptor (Okamura *et al.*, 1995). It is likely that these proteins participate in the delivery and trafficking of retinoids to and within the epididymal cells. The bone morphogenetic proteins belong to the transforming growth factor-superfamily of growth factors and function as signaling molecules. Bone morphogenetic protein (BMP) 7 and BMP8a are both expressed in the epididymis and the loss of Bmp8a gene function leads to epididymal degeneration that ultimately results in infertility (Orgebin-Crist *et al.*, 2003). Interestingly, although both BMPs are expressed in the initial segment, the degenerative effects observed in the Bmp8a knockout are observed in more distal epididymal regions, suggesting a possible paracrine role for BMP8a in the epididymis. Several peptides such as proopiomelanocortin, endorphin, proenkephalin, and neuropeptide Y are expressed in the epididymis and may also function in paracrine signaling pathways (Perry *et al.*, 1993). The region-dependent expression of genes implies that there are region-dependent transcription factors. Perhaps the most well studied are the members of the Etv4 subfamily including Etv4, Etv5, and Etv1. All family members are expressed in the initial segment, and their messenger RNAs (mRNAs) are profoundly reduced following the loss of signaling from the testis, suggesting these transcription factors may regulate a subset of genes dependent on testicular luminal fluid factors (Zhao *et al.*, 1998). Other transcription factors expressed in the initial segment include the androgen receptor (Yang *et al.*, 2006), estrogen receptor (Viger *et al.*, 1995), B-myc (Cornwall *et al.*, 2001), C/EBP(Hsia *et al.*, 2001), and Pem (Pitman *et al.*, 1998). Estrogen receptor expression is important for normal fluid resorption by the epithelium and specifically is necessary for expression of a critical transporter NA/H exchanger 3 as evidenced by examination of the knockout mouse (Huang *et al.*, 1996; Hess *et al.*, 1997). C/EBP function is necessary for transactivation of the CRES gene (Hsia *et al.*, 2001). Although the epididymal gene targets for B-myc are not known, cell culture studies suggest that it is involved in the regulation of cell growth (Gregory *et al.*, 2000). Although the regional or segment-specific expression of genes has been well-documented in the epididymis, the biological roles their gene products carry out is for the most part unknown. However, recent generation of knockout mouse models have revealed the critical roles some of these epididymal expressed genes play. The loss of several genes that are involved in fluid transport or signaling in the initial segment region including that for apolipoprotein E receptor 2 (Blomqvist *et al.*, 2006), estrogen receptor (Esr1) (Huang *et al.*, 1996; Hess *et al.*, 1997), HE6 (Gpr64) (Medina *et al.*, 2003), or the complete loss of the initial segment region resulting from the loss of the c-ros tyrosine kinase receptor (Ros1) (Sonnenberg-Riethmacher *et al.*, 1996) leads to an inability of sperm to regulate their cell volume, resulting in a characteristic hairpin loop of the sperm flagella. Other epididymal expressed genes, including those for lysosomal proteins, such as β -hexosaminidase and cathepsin A (ctsa) or follicle-stimulating hormone receptor (Fshr), exhibit an altered epithelium and/or changes in lysosomal size (refs. Korah 2003; Grover *et al.*, 2005; Adamali *et al.*, 1999).

Testis/lumacrine regulation of the initial segment

Studies have clearly established that the epididymis is an androgen dependent organ. Indeed, following castration, epididymal weight decreases to 25% of intact after 2 wk. Restoration of circulating testosterone reverses the cellular changes in the caput, corpus, and cauda epididymis but not in the initial segment (Ezer *et al.*, 2002). Supra-physiological levels of androgens also do not reverse these changes in the initial segment. Interestingly, ligation of the efferent ducts, which connect the testis to the epididymis and are the passageway for sperm and luminal components to enter the initial segment from the testis, results in a profound regression of the initial segment region (Ezer *et al.*, 2002). Because ligation of the efferent

ducts does not affect circulating androgen levels, these studies suggest that the maintenance of initial segment morphology requires components in the luminal fluid from the testis (i.e., lumacrine regulation) (Hinton *et al.*, 1998). Furthermore, gene expression studies revealed a subset of initial segment expressed genes that are down regulated following efferent duct ligation, including CRES subgroup and members, and others, suggesting that luminal factors are not only needed for the maintenance of initial segment morphology but for function as well (Cornwall 1002; 2003; Hsia *et al.*, 2003; Hinton *et al.*, 1998). Although it is not known if one or many testis factors are required to maintain initial segment function, studies by Lan *et al.* (1998) suggest that basic fibroblast growth factor may be one such factor. Administration of fibroblast growth factor-2 but not epidermal growth factor to efferent duct-ligated rats restored GGT mRNA, protein, and activity in the initial segment to control levels. Furthermore, these investigators proposed that fibroblast growth factor may elicit its effects on Ggt_pr4 gene expression via activation of the ras-raf-mitogen-activated protein kinase pathway and downstream activation of the ETV4 transcription factor (Hinton *et al.*, 1998, 2003; Lan *et al.*, 1998). Most recently, studies by these investigators suggest that, not surprisingly, not all testis-regulated genes respond the same to changes in ETV4 transcriptional activity. The administration of an ETV5-dominant negative plasmid by in vivo electroporation to the rat initial segment resulted in the down regulation of Etv5, Etv4, and Etv1 mRNAs in the initial segment as well as putative target genes γ -glutamyl transpeptidase (Ggt_pr4), steroid 5 α reductase (Srd5a1), and glutathione peroxidase (Gpx5). However, although the testis-regulated genes CRES (cst8) and MEP17 (len8) contain ETS-binding sites within their promoters, they did not respond to the dominant negative, suggesting that there either may be several testis factors, each differentially regulating specific subsets of genes, or that one or a few testis factors may mediate different downstream effects via the activation of multiple signaling pathways and subsequent effector molecules (Robaire *et al.*, 2007).

Androgenic regulation of epididymal microenvironment

The epididymis is critically dependent on the presence of testis. A variety of epididymal functions are regulated directly or indirectly by androgens. For example, epididymal histology, intermediary metabolism, ion transport, synthesis and secretion of a number of epididymal proteins, and activity of certain enzymes have been shown to be under the control of androgens. Furthermore, transport, acquisition of fertilizing capacity, and storage of spermatozoa are dependent on androgens (Orgebin-Crist *et al.*, 1996; Robaire *et al.*, 1998). Androgenic control is mainly mediated by 5 α -dihydrotestosterone (DHT) and less clearly by testosterone [T] (Robaire *et al.*, 1998; 2000), which is avidly converted to DHT by steroid 5 α -reductase isoenzymes, type 1 and 2, in the epididymis. The expression patterns of the two steroid 5 α -reductases (Srd5a) in the epididymis exhibit a gradient. While the IS expresses high levels of both isoforms, their expression decreases in the more distal segments (Viger *et al.*, 1991; 1996). DHT acts via binding to the androgen receptor (AR), which is expressed in all epididymal regions and in most of the epididymal cell types (Zhou *et al.*, 2002). Although the expression of many epididymal genes is regulated by androgens, only a few of them have been shown to contain androgen response elements (AREs) in their promoter region. However, the 5'-flanking region of murine Crisp1 contains several putative AREs (Roberts *et al.*, 2001); also, the murine Gpx5 (Ghyselinck *et al.*, 1993; Lareyre *et al.*, 1997), Lcn5 (Lareyre *et al.*, 2000), and reproductive homeobox 5 (Rhox5) (Barbulescu *et al.*, 2001) promoter regions contain functional AREs. Interestingly, certain epididymal genes with a wider tissue distributions, such as gamma-glutamyltransferase 1 (Ggt1), are androgen regulated only in the epididymis; furthermore, Ggt1 transcripts are regulated differentially by androgen in the different epididymal regions (Palladino *et al.*, 1994), which suggests the possibility that they play a role as AR co-regulators in the regulation of Ggt1 expression. Examples of tissue-specific co-regulators of AR are known from other tissues (Puigserver *et al.*, 1998; Muller

et al., 2000), and the findings on Ggt1 expression after gonadectomy suggest that a tissue-, segment-, and cell-specific combination of transcription factors and co-regulators mediates the androgen regulation of epididymal genes. In addition to androgens, mostly unknown testicular factors present in efferent duct fluid have been shown to regulate the maintenance of the epithelial structure and gene expression in the IS (Nicander *et al.*, 1983; Abe *et al.*, 1984). These genes include Cst8 (Cornwall *et al.*, 1992), v-raf murine sarcoma 3611 viral oncogene homolog (Araf) (Winer *et al.*, 1995), Gpx5 (Vernet *et al.*, 1997; Rigaudiere *et al.*, 1992), a disintegrin and metallopeptidase domain 7 (Adam7) (Cornwall *et al.*, 1997), and Lcn8 (Lareyre *et al.*, 2001). Similar to androgens, these testicular factors can also act as inhibitors of transcription (Brooks *et al.*, 1983), and in addition, they have been shown to stabilize the mRNA of Ggt1 (Rudolph *et al.*, 1997). Several testicular factors have been suggested, such as the androgen binding protein, which regulates the expression of Srd5a1 (Robaire *et al.*, 1995), the basic fibroblast growth factor that regulates the expression of Ggt1 (Lan *et al.*, 1998), and the germ cells themselves, or germ cell associated factors, that regulate the expression of preproenkephalin 1 (Penk1) (Garrett *et al.*, 1980).

Conclusion

While there are numerous forms of contraception available worldwide, it is clear that there is no single method that fulfills the requirements, preferences and intentions of all individuals during their reproductive lifetime (Harrison *et al.*, 1996). Men, in particular, have few contraceptive choices, though it has been estimated that male methods of contraception account for 37% of all contraceptive use (Darroch 2000). The primary targets for male-based contraceptives are the testis and the epididymis. Intervention in the testis has potential endocrine sequelae, may have problems posed by the blood–testis barrier, and must avoid teratogenic effects arising from sperm that may have completed spermatogenesis but with damaged DNA. An alternative strategy is to direct attention to the processes of sperm maturation, which occurs in the epididymis. Inhibition of these post-testicular maturation events in the sperm by modulating normal epididymal microenvironment represents an attractive option for contraceptive intervention. The challenge is to identify novel targets which, if inhibited, would prevent sperm maturation and successful fertilization but are also devoid of the side effects commonly encountered with current contraceptive products or strategies (T.T. Turner *et al.*, 2006). This implies that any potential target would optimally have a tissue-distribution pattern limited to the epididymis, though this is not required. The development of a drug addressing such a target would be novel and would move the field away from therapeutics that affect multiple genes towards therapeutics that act on a single gene product. Comparison of the gene expression data from this study to a Wyeth internal microarray database allowed for the identification of genes that exhibit a higher level of expression in the epididymis than in 22 other tissues. At the microarray level of sensitivity these genes were categorized as either epididymis selective (307 genes) or epididymis-specific (75 genes). A number of genes had distinctive patterns of expression in the epididymis but were neither selective nor specific, e.g. ATP binding cassette, subfamily B, member 9 (*Abc9*), while others had distinctive, segmental patterns of expression and were epididymal specific, e.g. *Gpx-5*. A number of other genes previously studied in the epididymis, e.g. *cres2* (cystatin-11), *lcn5* (lipocalin5, ERABP) and *Gpx-5* were epididymal-specific at this level of sensitivity. Mining of human genome databases has revealed that of these epididymal-specific mouse genes, 41 have homologues in the human epididymis. To speak of absolute specificity of the homologues in human tissues is complicated for technical reasons, but many of these genes have their highest expression in human epididymal tissue. Selected members of this gene set can be characterized with regard to protein synthesis and localization as discussed in this review. Proteins judged suitable for further study can be carried further in the pathway for contraceptive development or /and can be used to assess different pathological conditions.

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