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Epididymal proteome, transcriptome, what else?

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In order to understand the mammalian species specificities of the epididymal functionality, proteomic analysis of epididymal proteins from different mammalian species as well as transcripomic of epididymal tissues have been done.
The luminal protein content (luminal proteome) and secretory activity obtained by metabolic 35S-methionine labeling (secretome) were analyzed from human to monotreme epididymis by one and two dimensional electrophoresis. These studies have shown that the protein composition changed continuously throughout the duct and that several hundred epididymal proteins are present under numerous isoforms. There is a wide range of dynamics in the abundance of these proteins (~10 orders of magnitude) and about 15–20 proteins represent more than 60–80% of the total protein concentration. Proteomic approaches have allowed the identification of the common proteins between species: lactoferrin, procathepsin D, NCP2 (HE1, CTP), GPX5 (glutathione peroxidase 5), beta-Nacetyl- hexosaminidase, mannosidase, galactosidase, PGDS (prostaglandin D2 synthase), clusterin, CRISP (cystein-rich secretory protein) and E-RAPB (LCN5). It is probable that these major epididymal proteins, which surround the gametes, are mainly involved in sperm preservation and or epididymis function than in inducing specific and localized modifications on the sperm surface. In top of the soluble proteins, recent data have shown that epididymal fluid contained also particulate components. For example small membraneous vesicles of different sizes and specific compositions (exosome-types « epididymosomes ») have been found within the fluid along the duct.
Other types of protein associations, may be of micellar types, have also been described and contain proteins clustered mainly by their hydrophobic properties. Changes in sperm membrane proteins during maturation have also been clearly demonstrated, resulting from proteolysis and changes in the glycosylation state of preexisting components as well as acquisition of secreted proteins from the fluid. Meanwhile only few mechanisms have been studied in details.
One of the future major goals will be to achieve a complete proteomic study of the membrane changes during maturation and understanding which types of modifications the surface components undergo. This will give some clues to analyze the underlying mechanisms as well the methods of transfer, that can be the vesicular or micellar systems, the intrinsic hydrophobocity of the secreted proteins, the presence in the fluid or on the sperm membrane of proteases (such as sheddases) and proteases inhibitors or the modifications induced by the different glycosydases. At least the increase in transcriptomic studies of the testis and the epididymis on different species have described new genes or genes not yet reported and new control mechanisms both at the level of the tissue but also within the fluid. Nowadays studies have been done mainly in rodents and human, and recently we have done it in the boar. These studies have increased our knowledge on the high level of epididymal regionalization, but a large work at analyzing the different pathways and gene ontology they provide still remains to be done. These studies may also use to determine a certain numbers of specific epididymal region « markers » that could be use to search for their specific promoters and regulation.
This should help to understand the genesis and maintenance of the epididymal regionalization. These studies will provides the basis to address the final question of what biochemical processes at cellular level are responsible for the development of a fertile spermatozoa during the epididymal maturation .