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Identification of the glycolytic pathway enzymes as potential biomarkers of male infertility

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Poor sperm motility remains predominantly a clinical sign of infertility, rather than a true diagnosis of the cause of infertility. Considering that sperm motility is one of the essential factors for normal fertility, research on proteins or protein functions related to sperm motility is sparse. However, our current understanding of spermatozoa, including their different physiological and pathological aspects, is still limited and not well defined. Therefore, to explore the biological display of the human genome, the physiological functions of each protein should be understood first. Proteomics involves the comprehensive study of proteins with their particular structural and functional aspects. As such, proteomics has the potential to transform our understanding of how mature sperm cells work. Hence, we proposed to identify all the protein molecules that differ in the normal and non-motile conditions of sperm using proteomics methods and validated by immunocytochemistry. The diagnosis of asthenozoospermia was made in the andrology lab of the department of reproductive biology when the sperm motility was observed to be less than 20% as per WHO recommendations. 50 samples each of non-motile and 50 normal samples of semen were used in this study. Proteomics analysis of asthenozoospermia and fertile individuals were done using standard protocol. After identification of proteins were validated by immunocytochemistry. Our results and reports from others suggest that mammalian spermatozoa need local ATP production for flagellar movement and control of the acrosomal reaction. Hence, we demonstrate that glycolysis is very important for human sperm motility. Glyceraldehyde-3-Phosphate dehydrogenase (GAPDH), Enolase and Pyruvate Kinase (PK) can serve as potential targets for the development of biomarkers and can be used as diagnostic indicators and their potential implications to assist fertility or to develop a male contraceptive strategy.

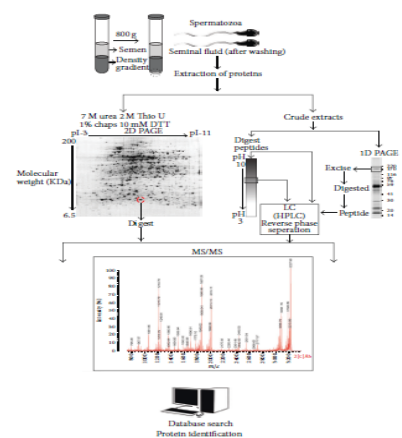


Figure-1: Schematic diagram showing the extraction and analysis of proteins from sperm cells. Proteome is done from an aliquot of the sperm cells by using two-dimensional polyacrylamide gel electrophoresis (2D-PAGE) followed by excision of protein spots from the 2D-PAGE gels and ionization-mass spectroscopy (ESI-MS/MS) or tandem MS (MS/MS) identification.

Recent Publications

1. Rashmi Tomar Rana, Gurseen Rakhra, Daisy Masih, Annu Vats, Saroj K. Verma, Vijay K. Singh, Vandana Kirar, Som Nath Singh. Effect of physical activity and age on plasma Copper, Zinc, Iron and Magnesium concentration in physically active healthy males. *Nutrition Journal* 43-44, P 75–82, 2017.
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5. Baker M A, Naumovski N, Hetherington L, Weinberg A, Velkov T, Aitken R J (2013) Head and flagella sub compartmental proteomic analysis of human spermatozoa. *Proteomics*; 13: 61-74.

Biography

Rashmi Tomar Rana working as a Scientist in Department of Research at Sir Ganga Ram Hospital (SGRH), New Delhi, India. And she worked as Research Associate III at Defense Institute of Physiology and Allied Sciences, DRDO, Delhi, India. Her research interest is in Biomarker Discovery, proteomics and Nano medicine.

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