IDENTIFICATION OF FERTILITY ASSOCIATED PROTEOMICS BIOMARKERS IN NORMOZOOSPERMIC INFERTILE MEN

Ashok Agarwal¹, Manesh Kumar Panner Selvam¹, Peter N. Pushparaj²

¹Cleveland Clinic, American Center for Reproductive Medicine - Department of Urology, Cleveland, Ohio, USA
²Center of Excellence in Genomic Medicine, King Abdulaziz University, Jeddah, Saudi Arabia

INTRODUCTION

• Up to 30% of men with normal semen parameters are diagnosed as infertile and the reason for their infertility is unknown.
• Change in the expression of sperm proteins may be a major cause of fertility issues seen in these men.
• The main aim of the current study was to examine the proteomic changes in the spermatozoa that could affect the fertility as a potential cause of infertility in normozoospermic men.

STUDY DESIGN AND PARTICIPANTS

• Participants: - Normozoospermic fertile men (n=5).
  - Normozoospermic infertile men (n=5).
• Global proteomic analysis was performed using liquid chromatography tandem-mass spectrometry (LC-MS/MS).
• The normalized spectral abundance factor (NSAF) ratio was calculated to categorize the expression profile of differentially expressed proteins (DEPs).
• Functional pathway analysis of the DEPs was done using the Ingenuity Pathway Analysis (IPA) software.
• Selected DEPs were validated by Western Blot.

RESULTS

Figure 1: DEPs in normozoospermic fertile men and normozoospermic infertile men

- Normozoospermic fertile men (n=5)
- Normozoospermic infertile men (n=5)

DEPs (n=162)

Normozoospermic fertile men
Normozoospermic infertile men

10
138
14

UE - underexpressed
OE - overexpressed
UE=63 and OE=74

Figure 2: Molecular and cellular functions enriched in normozoospermic infertile men.

-log (B-H p-value)

Cell Death and Survival
Protein Degradation
Protein Synthesis
Post-Translational Modification
Free Radical Scavenging
Cell-To-Cell Signaling and Interaction
Cellular Function and Maintenance
Cellular Movement
Small Molecule Biochemistry
Energy Production
Molecular Transport
Nucleic Acid Metabolism
Amino Acid Metabolism
Cell Cycle

Figure 3: Protein expression levels of a) ANXA2, b) PRDX2, c)SPA17, d) SERPINA5 by Western blot

Western blot analysis
• ANXA2 (0.49-fold change)
• PRDX2 (0.57-fold change)
• SPA17 (3.25-fold change)
• SERPINA5 (2.39-fold change)

CONCLUSION

• Sperm functions such as hyperactivation, capacitation and acrosome reaction are compromised in normozoospermic infertile men.
• SPA17, ANXA2 and SERPINA5 can serve as potential non-invasive protein biomarkers in cases of unexplained male infertility.