OBJECTIVE: The global proteomic analysis of different fractions of spermatozoa from fertile and infertile men is performed to identify specific proteomic signatures that may shed light on defective sperm function in infertile men.

MATERIALS AND METHODS: This study by the Institutional Review Board. Semen samples were collected from 17 fertile and 12 proven fertile men. All enrolled patients provided written consent to participate in the study. Following liquefaction, manual semen analysis was performed according to WHO 2010 guidelines to determine sperm concentration and motility. Sperm samples were stained with a DPX oil kit for assessment of sperm morphology. Sample was tested for Leukocytospermia, i.e., >1 X 10⁶ WBC/ml, where the round cell concentration was >1 X 10⁶ and confirmed by the peroxidase or the Endtz test.

RESULTS: Pathway analysis revealed that proteins involved in mitochondrial function, fatty acid metabolism and maintenance of euchromatin were overexpressed in fertile group, while proteins involved in spermatogenesis, sperm maturation and sperm function were overexpressed in infertile group. The Reactome pathway revealed a gradual decrease in the proteins involved in protein synthesis, gene expression and cell cycle along the process of maturation in fertile group (Figure 3A) while those involved in cytokinesis and cytoskeletal protein expression leading to sperm dysfunction.

CONCLUSIONS: Global proteomic analysis sheds light on defective sperm function in infertile men. Future work is in progress to validate the expression leading to sperm dysfunction.