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A proteomic analysis on human sperm tail: comparison between normozoospermia and asthenozoospermia

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Introduction: Asthenozoospermia is a common cause of human male infertility characterized by reduced sperm motility. The molecular mechanism that impairs sperm motility is not fully understood. This study purposed to identify novel biomarkers by focusing on sperm tail proteomic analysis of asthenozoospermic patients.

Materials & Method: Sperm were isolated from normozoospermic and asthenozoospermic semen samples. Tail fractions were obtained by sonication followed by Percoll gradient. The proteins were extracted by solubilization and subjected to two-dimensional gel electrophoresis (2-DE); then, the spots were analyzed using ImageMaster 2D Platinum software. The significantly increased/ decreased amounts of proteins in the two groups were exploited by matrix-assisted laser desorption-ionization time-of-flight/time-of-flight (MALDI-TOF-TOF) mass spectrometry.

Results: Three hundred and ninety protein spots were detected in both groups. Twenty-one protein spots that had significantly altered amounts (p<0.05) were excised and exploited using MALDI-TOF-TOF mass spectrometry. They led to the identification of the following 14 unique proteins: Tubulin beta 2B; glutathione S-transferase Mu 3; keratin, type II cytoskeletal 1; outer dense fiber protein 2; voltage-dependent anion-selective channel protein 2; A-kinase anchor protein 4; cytochrome c oxidase subunit 6B; sperm protein associated with the nucleus on the X chromosome B; phospholipid hydroperoxide glutathione peroxidase-mitochondrial; isoaspartyl peptidase/L-asparaginase; heat shock-related 70 kDa protein 2; stress-70 protein, mitochondrial; glyceraldehyde-3-phosphate dehydrogenase, testis-specific and clusterin.

Conclusion: Fourteen proteins present in different amounts in asthenozoospermic sperm tail samples were identified, 4 of which are reported here for the first time. These proteins might be used as markers of male infertility, targets for male contraceptive development and to predict embryo quality.

Biography

Susan Sabbagh is an educated physiotherapy at Shiraz University of Medical Science and she has post graduated from anatomical science in Ahwaz University of Medical Science. Since then she started teaching at Dezful University of Medical Science as a faculty member. Her main research was on neurology field and done some researches on multiple sclerosis, neural tube defects and hearing loss and published 8 papers in reputed journals. From 2014, she was attracted to proteomics and learned about it. Her project on sperm tail proteomics was published in journal of assisted reproduction and genetics on 2015.

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