



TRANSCRIPTIONAL PROFILES OF MITOCHONDRIAL DYNAMICS MARKERS IN HUMAN SPERMATOZOA ARE ASSOCIATED WITH DIFFERENT TYPES OF SPERMIOGRAMS



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INTRODUCTION:

Infertility has become one of the greatest health issues today, affecting millions of people worldwide, with significant contribution of male factor in many reported cases. Bearing in mind the increasing number of unexplained cases of infertile men in the peak of reproductive period and the lack of an accurate test for assessment of spermatozoa functionality, World Health Organization urges for the development of a new prognostic/diagnostic tool for detection of male infertility. Since mitochondria play important role in spermatozoa, regulating their homeostasis and functionality, it is reasonable to presume that they could be involved in these types of abnormalities and markers of their dynamics could be used as "mitochondrial-sperm-signature", to test the spermatozoa functionality. Regardless of that, little is known about mitochondrial dynamics markers in human spermatozoa. Therefore, the main objective of this research was to assess transcriptional profile of mitochondrial dynamics markers in the spermatozoa of men diagnosed with some of the most common types of sperm disorders.

RESULTS

Transcript levels of some of the main mitochondrial dynamics markers showed significant changes in spermatozoa of patients diagnosed with teratozoospermia.



(C) Main mitochondrial fission markers

(A) Main mitochondrial biogenesis markers

(B) Main mitochondrial fusion markers

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METHODS







(D) Main mitochondrial autophagy markers



Figure 1. RNA isolated from spermatozoa obtained from men diagnosed with normozoospermia, teratozoospermia, asthenoteratozoospermia and oligoasthenoteratozoospermia were used for analysis of the transcriptional profile of markers of mitochondrial biogenesis (**A**), mitochondrial fusion (**B**), mitochondrial fission (**C**) and mitochondrial autophagy (**D**). All obtained values were normalized to a normozoospermic group, used as a control and *GAPDH*, as a reference gene. Since the sizes of AT, AT+H and OAT groups were too small to apply statistical tests, they were excluded from further analysis. For comparison between N and T group t-test was used, in the case of normal data distribution, otherwise, Mann-Whitney test was applied. Statistical significance was set at the level p < 0,05 (*), p < 0,01 (**).

No significant difference in testosterone level in seminal plasma was noticed between groups.

Mitophagy

Mitofission

Testosterone level in seminal plasma

Figure 2. Testosterone level (ng/ml) in seminal plasma of men diagnosed with normozoospermia, teratozoospermia, asthenoteratozoospermia, asthenoteratozoospermia hypospermia and oligoasthenoteratozoospermia. Since the sizes of AT, AT+H and OAT groups were too small to apply statistical tests, they were excluded from further analysis. For comparison between N and T group Mann-Whitney test was used, since the data were not normally distributed.



Teratozoospermia

Based on the obtained results it is evident that the markers of mitochondrial dynamics in

human spermatozoa exerted different

patterns depending on the type of

spermiogram. However, testosterone level in

seminal plasma remaines unchanged.

PPARGC1A

MFN1

PPARGC1B

Mitogenesis

Mirorusion

It is important to point out that research was conducted on a small sample (1-10 individuals per group), so the results should be considered preliminary!

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Although trends of stimulation in transcription were observed for some markers in asthenoteratozoospermic and oligoasthenoteratozoospermic group, due to a small group sizes, statistical tests could not be applied, therefore, the most remarkable changes were observed for teratozoospermic group.

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