SPERMATOGENESIS
✓
✓
✓

TRANSCRIPTOMIC ANALYSIS OF MALE INFERTILITY

PROTAME mRNAs appear to have a role in the formation of fully functional mature spermatozoa including sperm motility [3].

Function | Symbol | Name | ID
---|---|---|---
DAZ1 | Deleted in azoospermia protein 1 | [617]
TSSK2 | Calcium-specific sarko/calcimodulin protein kinase 2 | [23617]
CRISPS2 | Cysteine-rich secretory protein 2 | [7180]
YBX2 | Y-box-binding protein 2 | [51087]
PRM2 | Protamine-2 | [5620]
ODF1 | Outer dense fiber of sperm tail 1 | [4956]
AIF1 | Apoptosis-inducing factor 1 | [199]
ARNT2 | Aryl-hydrocarbon receptor nuclear translocator 2 | [9015]
EGFR | Early growth response 4 | [1961]
MDM4 | MDM4, p53 regulator | [4194]
SOD2 | Superoxide dismutase 2 | [6648]
ARNT2 | Aryl-hydrocarbon receptor nuclear translocator 2 | [9015]
MDM4 | MDM4, p53 regulator | [4194]
HMG1B | High mobility group box 1 | [3146]

OLIGOZOOSPERMIA

Function | Symbol | Name | ID
---|---|---|---
SPERMATOGENESIS | (GO:0007230) | | 
Sperm maturation | BRD2 | Bromodomain-containing protein 2 | [5620]
PRM2 | Protamine-2 | [5620]
PRM1 | Protamine-1 | [5619]
PRM2 | Protamine-2 | [5620]
TNP1 | Nuclear transition protein 1 | [7141]
TNP2 | Nuclear transition protein 2 | [7142]

AZOOSPERMIA

FUNCTIONS OF PROTEIN Ratios:

AXAN2, BRD2, OAZ3 and IL6ST: significant positive correlation between the sperm progressive motility and the relative mRNA levels.

PRM1, PRM2, TNP1 and TNP2 reduction increased DNA strand breaks, which may induce the inactivation of mitochondria.

Proteasomal mRNAs appear to have a role in the formation of fully functional mature spermatozoa including sperm motility [3].

Trynl, CAB39L, GGT1 and ribosomal proteins (+ other 133) were found to be differentially expressed at least two times.

If the over- or under-expressed genes are grouped by function, between 80 and 100% of them are involved in spermatozoa differentiation.

Sperm count, but are probably related to sperm function [1].

CONCLUSIONS

Omic technologies have provided a powerful tool for transcriptomic profiling of male factor infertility and the identification of the potential diagnosis biomarkers [6].

Despite the evidences to support these applications, there are several deep uncertainties to be established.

From basic functional significance of the mRNAs in mature sperm, to the molecular mechanisms and the determination the mRNAs of male factor infertility.

What is the reason for this difference in gene expression?

As transcriptional disorder is common within infertile men, the possibility of a genetic cause decreases, thereby increasing the interest of the hypothesis that the environment, through epigenetic marks, could play a key role in this problem.

REFERENCES

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