

**Function** 

**SPERMATOGENESIS** 

(GO:0007283)

**TRANSCRIPTION** 

(GO:0006351)

**CELL DEATH** 

(GO:0008219)

CELL

**PROLIFERATION** 

(GO:0008283)

**Function** 

**SPERMATOGENESIS** 

(GO:0007283)

**TRANSCRIPTION** 

(GO:0006351)

**CELL DEATH** 

(GO:0008219)

Symbol

GGT1

CAB39L

TRY1

ADAM29

**CABYR** 

HMGB2

RPS3

NKX3-1

RPS3

RPS3A

RPS15A

NKX3-1

**Symbol** 

**CREM** 

DDX4

PRM2

LMNA

MEA1

SPATA4

CREM

**SAP130** 

SPZ1

LMNA

SPATA4

# TRANSCRIPTOMIC ANALYSIS OF MALE INFERTILITY



#### INTRODUCTION

- Infertility: Disease defined as failure to achieve a clinical pregnancy after 12 months or more of unprotected sex (World Health Organization).
- ✓ Affects approximately 10-15% of couples of reproductive age. About **50**% of these cases can be associated with male factors.
- ✓ Causes: Epigenetic, genetic, physiological and endocrine failure, testis pathologies...
- ✓ A normal seminal evaluation does not necessarily indicate a fertile potential. Transcriptomics represents a promising approach for the discovery of new biomarkers able to improve the management of male factor infertility.
- ✓ **Transcriptome**: Collection of all molecules of RNA derived from genes whose biological information is required by the cell, at a specific time and under certain conditions.

#### OBJECTIVE

Get a list of candidate genes, with alterations in the transcriptome, as potential markers for the diagnosis of different forms of male infertility: idiopathic [1], azoospermia [2], asthenozoospermia [3], oligozoospermia [4] and teratozoospermia [5].

#### **Review of transcriptomic** studies in infertility

#### **Inclusion criteria**

METHODOLOGY

- Infertility classification

- N° patients (>10)
- Microarray analysis
- RT-PCR validation



**Functional annotation and** 

classification by gene ontology (GO)



## **IDIOPATHIC**





2678

81617

5644

51686

11086

26256

3148

6188

4824

6188

6189

6210

4824

1390

5620

202051

79595

84654

4000

202051

- √ TRY1, 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.

Infertility markers may not be related to sperm production in terms of sperm count, but are probably related to sperm function. [1]

Trypsin 1

Name

Gamma-glutamyltranspeptidase 1

Ornithine decarboxylase antizyme 3

ADAM metallopeptidase domain 29

phosphorylation-regulated protein

Name

DEAD (Asp-Glu-Ala-Asp) box

Spermatogenesis-associated protein 24

Spermatogenesis-associated protein 24

cAMP-responsive element modulator

Sin3A-associated protein, 130kDa

Spermatogenic leucine zipper 1

cAMP-responsive element modulator

Calcium-binding tyrosine

High mobility group box 2

40S ribosomal protein S3

NK3 homeobox 1

NK3 homeobox 1

polypeptide 4

Protamine-2

Lamin A/C

Lamin A/C

Ribosomal protein S3

Ribosomal protein S3A

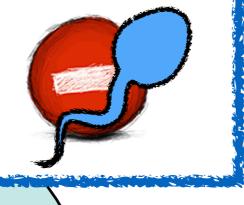
Ribosomal protein S15A

Male-enhanced antigen 1

Calcium binding protein 39-like







- ✓ Yq microdeletions study is useful for azoospermia diagnosis (AZF deletions).
- ✓ YBX2 network: **ODF1**, **TNP1** and **PRM2**.
- ✓ ARNT2 network: CRISP, TSSK2, MDM4 and EGR4.

The **DAZ1** gene is the leading candidate that causes the failure of the spermatogenesis process [2].



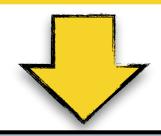
Function	Symbol	Name	ID
SPERMATOGENESIS (GO:0007283)	DAZ1	Deleted in azoospermia protein 1	1617
	TSSK2	Testis-specific serine/threonine-protein kinase 2	23617
	CRISP2	Cysteine-rich secretory protein 2	7180
	YBX2	Y-box-binding protein 2	51087
	TNP1	Nuclear transition protein 1	7141
	PRM2	Protamine-2	5620
	ODF1	Outer dense fiber of sperm tails 1	4956
CELL PROLIFERATION (GO:0008283)	AIF1	Allograft inflammatory factor 1	199
	ARNT2	Aryl-hydrocarbon receptor nuclear translocator 2	9915
	EGR4	Early growth response 4	1961
	MDM4	MDM4, p53 regulator	4194
	SOD2	Superoxide dismutase 2, mitochondrial	6648
CELL DEATH (G0:0008219)	ARNT2	Aryl-hydrocarbon receptor nuclear translocator 2	9915
	MDM4	MDM4, p53 regulator	4194
	HMGB1	High mobility group box 1	3146
FERTILIZATION (GO:0009566)	CLGN	Calmegin	1047
	DAZ1	Deleted in azoospermia protein 1	1617
	TNP1	Nuclear transition protein 1	7141

### **ASTHENOZOOSPERMIA** > 40% of sperm with reduced motility



- ✓ ANXA2, 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.

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



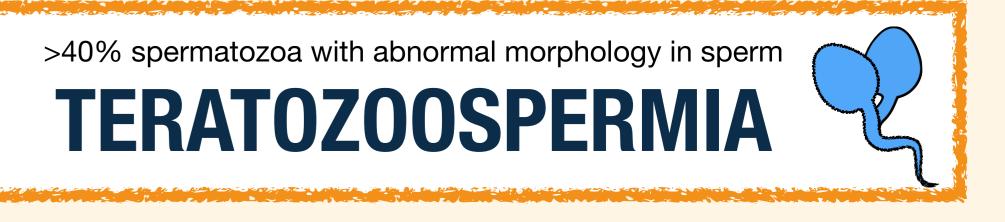
Function	Symbol	Name	ID
SPERM MOTILITY (GO:0030317) & CELL MOTILITY (GO:0048870)	IL6ST	Interleukin 6 signal transducer	3572
	OAZ3	Ornithine decarboxylase antizyme 3	51686
	TNP1	Nuclear transition protein 1	7141
	TNP2	Nuclear transition protein 2	7142
	ANXA2	Annexin A2	302
	PRM1	Protamine-1	5619
	PRM2	Protamine-2	5620
	CRISP2	Cysteine-rich secretory protein 2	7180
	LDHC	Lactate dehydrogenase C	3948
	HILS1	Spermatid-specific linker histone H1-like protein	54388
	NOS3	Nitric oxide synthase 3	4846
SPERMATOGENESIS (G0:0007283)	BRD2	Bromodomain-containing protein 2	6046
	PRM1	Protamine-1	5619
	PRM2	Protamine-2	5620
	TNP1	Nuclear transition protein 1	7141
	TNP2	Nuclear transition protein 2	7142

Function	Symbol	Name	ID
SPERMATOGENESIS (G0:0007283)	HSPA2	Heat shock 70kDa protein 2	3306
	ODF1	Outer dense fiber of sperm tails 1	4956
	ODF2	Outer dense fiber of sperm tails 2	4957
	ODF3	Outer dense fiber of sperm tails 3	113746
	ODF4	Outer dense fiber of sperm tails 4	146852
FERTILIZATION (GO:0009566)	PLCZ1	Phospholipase C, zeta 1	89869
	SPAM1	Sperm adhesion molecule 1 (PH-20 hyaluronidase, zona pellucida binding)	6677
CELL PROLIFERATION (G0:0008283)	CDKN3	Cyclin-dependent kinase inhibitor 3	1033

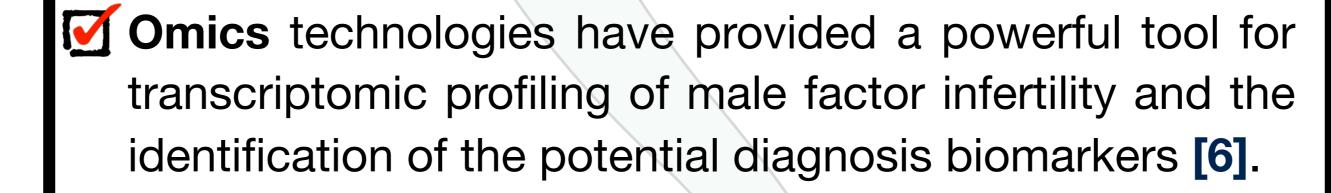


#### The lack of certain transcripts is indicative of a failure in the late phase of spermatogenesis [5].

- √ Ubiquitin proteasomal pathway (UPP) completely suppressed. Involved in morphological progression of spermiogenesis.
- Reduction in HSPA2 mRNA was resonant with depletion of ODF 1-4 mRNAs and acrosomal proteins ACRV1 and SPAM1.



#### 4000 17256 CONCLUSIONS



- 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.

#### functional mature spermatozoa including sperm motility [4]. ✓ Aberrant PRM1/PRM2 protein ratio is responsible for an unstable chromatin condensation.

DDX4 gene expression significantly decreased in the sperm of oligozoospermic men.

Protamine mRNAs appear to have a role in the formation of fully

<10 million spermatozoa per one ml of ejaculate

# **OLIGOZOOSPERMIA**

# REFERENCES

- 1. Garrido, N. et al. Microarray analysis in sperm from fertile and infertile men without basic sperm analysis abnormalities reveals a significantly different transcriptome. Fertil. Steril. 91, 1307–1310 (2009).
- 2. Gatta, V. et al. Testis transcriptome analysis in male infertility: new insight on the pathogenesis of oligo-azoospermia in cases with and without AZFc microdeletion. BMC Genomics 11, 401 (2010).
- 3. Jodar, M. et al. Differential RNAs in the sperm cells of asthenozoospermic patients. Human Reproduction 27, 1431–1438 (2012). Montjean, D. et al. Sperm transcriptome profiling in oligozoospermia. J. Assist. Reprod. Genet. 29, 3-10 (2012).
- 5. Platts, A. E. et al. Success and failure in human spermatogenesis as revealed by teratozoospermic RNAs. Hum. Mol. Genet. 16, 763–773 (2007).
- 6. Lee, L. K. & Foo, K. Y. Recent insights on the significance of transcriptomic and metabolomic analysis of male factor infertility. Clin. Biochem. 47, 973–982 (2014).