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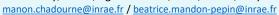
Topaz1 suppression disrupts the expression of testicular long non-coding RNAs during murine spermatogenesis.





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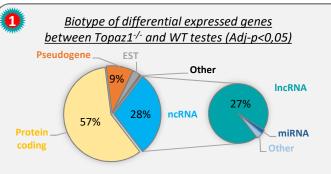


<u>Background of Topaz1</u>: Topaz1, for <u>Testis and Ovary specific PAZ</u> domain gene <u>1</u>, has been characterized in our lab as a new germ cell specific gene highly conserved in vertebrates with a role during gametogenesis of mammals¹. To study the role of this gene, a line of Topaz1-depleted mice has been generated. Thus, whereas female mice are fertile, homozygous male mutants are infertile². Abnormal meiosis occurs in testes Topaz1^{-/-} mice causing cell death and an absence of spermatozoa. Previous transcriptional study of Topaz1^{-/-} mice by microarray comparative analysis highlighted the significant proportion of deregulated long non-coding RNA (IncRNA) in mutant testis.

The aim of this work is to study (1) the whole transcriptome of Topaz1-/- mouse testes and (2) the involvement of IncRNA in murine spermatogenesis.

Methodologies:

- RNA sequencing (RNA Seq) to identify all deregulated genes in Topaz1-/- testis whose IncRNA.
- Localization by In Situ hybridization (ISH) of some deregulated lncRNA.
- Generation of a new line of knockout mice (CrispR/Cas9 technology) without one of these IncRNA → Studies of the phenotype.



<u>Fig.1.</u> Overview of 2748 deregulated transcripts in P18.5 testes lacking Topaz1. 91% (2491) are down-regulated; 9% (257) are upregulated. A large proportion (27%) of deregulated genes are lncRNAs.

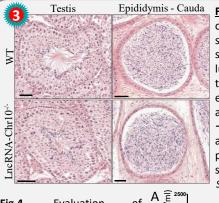
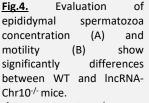


Fig. 3. Histological analysis of 2 month-old testis showed the presence of spermatozoids in the lumen of the seminiferous tube and in the cauda of epididymis in both WT and lncRNA-Chr10^{-/-} mice.

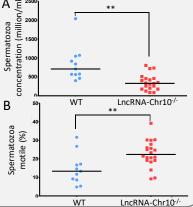
→ LncRNA-Chr10^{-/-} mice are fertile with a normal progression of spermatogenesis.

Scale bar = 50 μm



→ LncRNA-Chr10^{-/-} mice have a 57% decrease of spermatozoa concentration and motility was significantly higher.

**: pvalue<0,01



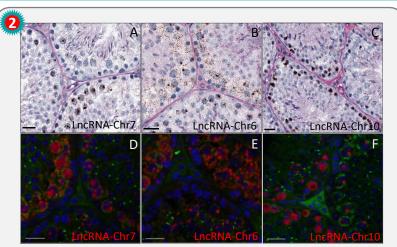
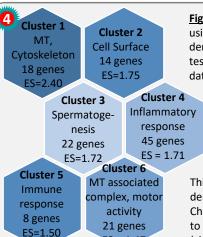


Fig.2. A-C: ISH (RNAscope® Brown) of different deregulated IncRNAs: LncRNA-Chr7(A), LncRNA-Chr6 (B) and LncRNA-Chr10 (C) in 2 months-old WT testis section. **D-F**: Merge images showing ISH with IncRNA (red) probes, immunodetection of VASA (DDX4) (green) and DAPI staining (blue).

→ LncRNAs are expressed in different spermatocytes depending on the stage of the seminiferous epithelium: IncRNA-Chr10 seems nuclear whereas IncRNA-Ch6 cytoplasmic. LncRNA-Chr7 looks as if located in both cytoplasm and nuclei.

Scale bar = 20µm



ES = 1.47

Fig.5. Functional annotation clustering using DAVID analysis with 206/258 deregulated genes in lncRNA-Chr10^{-/-} testes compared to WT (from RNAseq data of P18.5 testes; data not show).

→ Despite the absence of noticeable phenotype in IncRNA^{-/-} mouse line, transcriptomic analysis of P18.5 testes indicated that 6 gene clusters are significantly deregulated (ES >1,3).

This higlighted the biological process deregulated in absence of the lncRNA-Chr10 with the most interesting referred to microtubule (MT) base process (cluster 1 and 6) and spermatogenesis (cluster 3).

Conclusion:

Number of LncRNA expressed in the testes is significant. In Topaz1 null mice, with male meiotic arrest, a large number of testicular lncRNA are significantly deregulated (Fig1). Three of them were observed by ISH showing different localisations into spermatocyte cells, suggesting distinct roles during spermatogenesis (Fig2). To determine a potential spermatogenetic role, a new mouse line deleted of one of them (LncRNA-Chr10, expressed in nuclear germ cells) has been created. These mice are fertile in both sexes (Table 1) and spermatogenesis of mutant takes place normally (Fig3). However, they have a decrease of epididymal spermatozoa concentration and an increase of spermatozoa motility (Fig5). Moreover, transcriptomic analysis of P18.5 lncRNA-Chr10-/- testes (by RNAseq) shows more than 250 deregulated genes involved particularly in cytoskeleton and spermatogenesis (Fig5).

ES = Enrichment Score

→ Thus, although LncRNA-Chr10, expressed exclusively in the testes with an expression linked with Topaz1 expression, its depletion does not appear crucial for fertility in mice. The IncRNA-Chr10 seems to play role in spermatozoa motility and concentration. This IncRNA may regulate protein coding gene expression especially genes in relation to the cytoskeleton.

References: (1) Baillet A, et al. PLoS One. 2011;6(11):e26950; (2) Luangpraseuth-Prosper A, et al. Dev Biol 2015;406:158-171.