9th Yazd International Congress and Student Award on Reproductive Medicine with 4th Congress of Reproductive Genetics

Oral Presentations

O-45
Exploring the dysregulated mRNAs–miRNAs–lncRNAs interactions associated to idiopathic non-obstructive azoospermia

Sabetian S[1], Zarei M[2], Namavar Jahromi B[1, 3], Morowvat MH[2], Tabei SMB[4], Cava C[5].

1. *Infertility Research Center, Shiraz University of Medical Sciences, Shiraz, Iran.*
2. *Pharmaceutical Sciences Research Center, Shiraz University of Medical Sciences, Shiraz, Iran.*
3. *Department of Obstetrics and Gynecology, School of Medicine, Shiraz University of Medical Sciences, Shiraz, Iran.*
4. *Department of Medical Genetics, Shiraz University of Medical Sciences, Shiraz, Iran.*
5. *Institute of Molecular Bioimaging and Physiology (IBFM), National Research Council (CNR), Milan, Italy.*

Email: soudabehsabet@gmail.com

Background: Non-obstructive azoospermia (NOA) is the most clinical problem in case of infertility. About 70% of NOA patients are idiopathic with uncharacterized molecular mechanisms.

Objective: This study aimed to analyze the possible pathogenic miRNA-target gene interaction and lncRNA-miRNA association involved in NOA.

Materials and Methods: In the current study, differentially expressed (DE) nRNAs, miRNAs and lncRNAs were determined using the microarray dataset and statistical software R. miRNAs–mRNA and miRNA-lncRNA interactions were identified and the base-pair binding between the seed region of miRNAs and complementary nucleotides in 30 UTR of mRNAs were analyzed. The influence of the validated single nucleotide polymorphisms was described by calculating the minimum free energy (MFE) of the interaction.

Results: A total of 74 mRNAs, 14 miRNAs, and 10 lncRNAs were identified to have significant differential expression in testicular tissue between patients and the fertile group. Four of the DE-mRNAs and all of the reported DE-miRNAs were upregulated. In addition, all of the represented DE-lncRNAs were showed to be downregulated. miR-509-5p and miR-27b-3p were found to interact with target gene polo-like kinase 1 (PLK1) and Cysteine-rich secretory protein2 (CRISP2), respectively. Rs550967205 (A > G) positioned at 30 UTR CRISP2 and rs544604911 (T > C) located at 30 UTR PLK1, with lowest MFE in miRNA-mRNA interaction, were assumed to have possible pathogenic roles linked to spermatogenesis arrest.

Conclusion: The results of the study provide new clues to understand the regulatory roles of miRNAs and lncRNAs in the pathogenesis and diagnosis of idiopathic azoospermia.

Key words: *Azoospermia, mRNA, miRNA, lncRNA, Gene expression.*

The original full text of this abstract has been published in Journal of Biomolecular Structure and Dynamics 2021: 16: 1-9. https://doi.org/10.1080/07391102.2021.1875879.

How to cite to this article: *Sabetian S, Zarei M, Namavar Jahromi B, Morowvat MH, Tabei SM, Cava C. Exploring the dysregulated mRNAs–miRNAs–lncRNAs interactions associated to idiopathic non-obstructive azoospermia. Journal of Biomolecular Structure and Dynamics 2021: 16: 1-9.*