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

Award Winners

A-2
Whole-exome sequencing in patients with primary ovarian insufficiency

Akbari A[1], Padidar K[1, 2], Salehi N[1, 3], Mashayekhi M[4], Almadani N[1], Sadighi Gilani MA[5], Bashambou A[6], McElreavey K[6], Totonchi M[1, 7].

1. *Department of Genetics, Reproductive Biomedicine Research Center, Royan Institute for Reproductive Biomedicine, ACECR, Tehran, Iran.*
2. *Department of Molecular Genetics, Faculty of Basic Sciences and Advanced Technologies in Biology, University of Science and Culture, Tehran, Iran.*
3. *Department of Bioinformatics, Institute of Biochemistry and Biophysics, University of Tehran, Tehran, Iran.*
4. *Department of Endocrinology and Female Infertility, Reproductive Biomedicine Research Center, Royan Institute for Reproductive Biomedicine, ACECR, Tehran, Iran.*
5. *Department of Andrology, Reproductive Biomedicine Research Center, Royan Institute for Reproductive Biomedicine, ACECR, Tehran, Iran.*
6. *Human Developmental Genetics Unit, Institut Pasteur, Paris, France.*
7. *Department of Stem Cells and Developmental Biology, Cell Science Research Center, Royan Institute for Stem Cell Biology and Technology, ACECR, Tehran, Iran.*

Email: totonchimehdi@gmail.com

Background: Primary ovarian insufficiency (POI) is a complex and relatively poorly understood disorder. It affects 1% of women below the age of 40 accompanied by raised gonadotropins and estradiol deprivation. Women with POI have no antral follicles and size of ovaries are below normal.

Objective: Our objective was to identify the genetic cause of POI in affected members of a consanguineous Iranian family.

Materials and Methods: In this study, we recruited an Iranian family with 2 affected members to be studied by whole exome sequencing (WES). Validation of WES results and cosegregation analysis was performed by Sanger Sequencing. In silico analysis was used to predict the effect and pathogenicity level of the discovered variants.

Results: The proband and her affected sister tested normal for karyotype and *FMR1* CGG repeats. A final list of pathogenic variants was prepared according to WES results, and one specific variant in a conserved domain of transcription factor protein was confirmed to be mutual among the affected. The discovered variant is very rare in the gnomAD database.

Conclusion: This study supports the clinical applicability of WES for cost-effective molecular diagnosis and improves the understanding of the genetic basis of female infertility and ovarian function. Therefore, our finding provides yet another piece of evidence that Loss of function variations in transcription factors with limited expression in ovaries may be the cause of POI.

Key words: *Primary ovarian insufficiency, Familial exome sequencing, Causative mutation.*

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