## 9<sup>th</sup> Yazd International Congress and Student Award on Reproductive Medicine with 4<sup>th</sup> Congress of Reproductive Genetics

## **Poster Presentations**

## **P-98**

The relationship between *FOXR2* gene expression profile and epithelial ovarian cancer

Asadollahi S<sup>1, 2</sup>, Mazaheri Nacini M<sup>1, 3</sup>, Karimi Zarchi M<sup>4, 5</sup>, Fesahat F<sup>6, 7</sup>.

- 1.Departments of Medical Genetics, Faculty of Medicine, Shahid Sadoughi University of Medical Sciences, Yazd, Iran.
- 2. Diabetes Research Center, Shahid Sadoughi University of Medical Sciences, Yazd, Iran.
- 3. Mother and Newborn Health Research Center, Shahid Sadoughi University of Medical Sciences, Yazd, Iran.
- 4. Department of Obstetrics and Gynecology, Iran University of Medical Sciences, Tehran, Iran.
- 5. Endometriosis Research Center, Iran University of Medical Sciences, Tehran, Iran.
- 6.Reproductive Immunology Research Center, Shahid Sadoughi University of Medical Sciences, Yazd, Iran.

7.Department of Advanced Medical Sciences and Technologies, School of Paramedicine, Shahid Sadoughi University of Medical Sciences, Yazd, Iran.

Email: mazaheri54@yahoo.com

**Background:** Several factors have been evaluated for their competency as applied biomarkers regarding diagnosis and therapy of ovarian cancer as one of the most causes of death due to gynecologic malignancies. However, some Fox-factors have been shown to modulate cancer progression primarily by their impacts on the proliferation of the cells, the expression and potential function of *FOXR2* (Forkhead Box R2), newly identified as a probable oncogene in a few human cancers, remains undecided in ovarian cancer. **Objective:** The aim was to evaluate the *FOXR2* and some epithelial-mesenchymal transition (EMT) related genes expression profiles in epithelial ovarian cancer (EOC) tissues and their healthy samples as well as an ovarian cancer cell line (SKOV-3).

**Materials and Methods:** In this observational study, twenty epithelial ovarian adenocarcinoma (case group) and their marginal samples (controls), obtained from 20 patients with EOC, besides SKOV-3, were investigated for the relative gene expression levels of *FOXR2*, *CDH1* (encoding E-cadherin), and *FN1* (fibronectin-1) in two groups using qualitative real-time PCR (qRT-PCR) technique.

**Results:** The findings demonstrated a significant upregulation of *FOXR2* and *FN1* despite the *CDH1* down-regulation in case samples compared to controls (p < 0.05). There was a significant correlation between *FOXR2* gene expression profile and EMT-related markers in high-grade tumors. Furthermore, the biomarker index of 0.772 was obtained for *FOXR2* gene expression levels.

**Conclusion:** The findings indicated that the expression levels of *FOXR2* have a significant association with ovarian cancer as far as it can be used as a diagnostic and therapeutic molecular biomarker in ovarian cancer.

*Key words:* FOXR2, Gene expression, Ovarian cancer, Epithelial-Mesenchymal transition.

## The original full text of this abstract has been published in<br/>KlinickáOnkologie2020:201.https://doi.org/10.14735/amko2020201.

How to cite to this article: Asadollahi S, Mazaheri Naeini M, Karimi-Zarchi M, Fesahat F. The relationship of FOXR2 gene eExpression profile with epithelial-mesenchymal transition Related markers in epithelial ovarian cancer. Klinická Onkologie 2020: 201.