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Poster Presentations

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

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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 up-regulation 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.*

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