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

Poster Presentations

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Identification of *Hub* genes and key pathways involved in ovarian carcinomas by integrated bioinformatics analysis

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Background: Ovarian carcinoma is one of the most aggressive cancers among women. Although the main mechanism of this cancer is not clear, several studies have revealed the fundamental role of genetic abnormalities in the pathogenesis of the disease.

Objective: This study aimed to investigate the potential genes and pathways in susceptibility to ovarian carcinomas for prognosis and developing therapeutic strategies.

Materials and Methods: The microarray data of gene expression profile for GSE66957 including 57 ovarian carcinomas and 12 ovarian normal samples based on Rosetta/Merck Human RSTA Custom Affymetrix 2.0 microarray platform was downloaded from Gene Expression Omnibus database. To identify differentially expressed genes (DEGs), GEO2R tool based on R language was applied. Then, we used Database for Anno-tation, Visualization, and Integrated Discovery online tools to perform gene ontology and kyoto encyclopedia of genes and genomes (KEGG) analyses for DEGs ($p < 0.05$ as a significant level). In the next step, the STRING database and cytoscape software were employed to construct protein-protein interaction network. This network was used to predict hub genes in the development of ovarian carcinomas considering maximal clique centrality algorithm.

Results: Our study revealed that up-regulated DEGs were enriched in the membrane (cellular component), protein binding (molecular function), regulation of the biological process, and cell adhesion molecules (KEGG pathway). Down-regulated DEGs were also enriched in the postsynaptic membrane (cellular component), sequence-specific DNA binding (molecular function), positive regulation of cell proliferation (biological process), and Neuroactive ligand-receptor interaction (KEGG pathway). In addition, PPI network analysis revealed 10 hub genes including *CDH1*, *EPCAM*, *CLDN4*, *CLDN7*, *CLDN3*, *KRT8*, *KRT5*, *CD24*, *ESRP1*, and *RAB25*, which were enriched in the lateral plasma membrane (cellular component), structural molecule activity (molecular function), cell-cell adhesion (biological process), and cell adhesion molecules (CAMs) (KEGG pathway).

Conclusion: Our bioinformatics study suggested that these ten genes might play fundamental roles in the progression of ovarian carcinomas, which pave the way for further functional studies to identify biomarkers and future treatments for the disease.

Key words: *Ovarian cancer, Microarray, Gene expression, Bioinformatics.*