P69

WHOLE GENOME MIRNA PROFILES IN PATIENTS WITH HIGH RISK OVARIAN CARCINOMA

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Introduction - Purpose : Ovarian cancer is a major cause of gynecological cancer mortality. It is the second most common gynecologic cancer with high malignancy and mortality rate among gynecological cancer types. BRCA1 gene mutations are associated with 44% of ovarian-cancer development in high risk hereditary families. MicroRNAs, a subset of the non-coding RNAs, that are single-stranded, untransformed to protein, and are thought to regulate cleavage of target mRNAs post-transcriptionally and translationally repressed RNA molecules. A number of studies have reported differences in miRNA expression levels on ovarian-cancer. There is no data about miRNA profiles of whole genome in patients with high risk ovarian cancer having BRCA1 mutation

Methods - Tools : In our study, miRNA array analysis of whole genome was performed on members of high-risk ovarian-cancer family including monozigotic twins who were healthy and diagnosed with ovarian carcinoma and the rest of family members.

Findings : The expression level of several miRNAs such as miR-1260a, miR-1260b, miR-26b-5p, miR-4286, miR-5100, miR-7977, let-7a-5p were found highly expressed and associated with BRCA1 mutation. The expression level of miRNAs such as miR-126-3p, miR-4428, miR-1225-5p, miR-142-3p, miR-26a-5p, miR-5p, miR-451a were significantly found decreased in patients with high risk ovarian cancer.

Discussion : Total of 14 high and low expressed miRNAs, can be used for the ethiogenesis, diagnosis and prognosis of ovarian carcinoma. But, it will be needed further research in large cohort whether they have a potential to be a biomarkers. Note to the Scientific Committee: The project was supported by the scientific research department of Istanbul University with TDK2016/20140 project number and approved by Ethics Committee of Istanbul University: Approval number:01/08.01.2016