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TRANSCRIPTOMIC DIFFERENCES IN MONOZYGOTIC TWINS WITH OVARIAN CANCER

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ABSTRACT

Objectives: The most significant barrier to treating epithelial ovarian cancer(EOC), is the late diagnosis and the emergence of chemotherapy resistance in the early stages.The ineffectiveness of standard treatment protocols in advanced-stage cases highlights the value of individualized EOC treatment.Even monozygotic(MZ) twins, with almost the same genotype in nature, can develop different phenotypic characteristics throughout life.

Materials-Methods: In this context, the peripheral blood and ovarian tissues of monozygotic twins who are discordant in terms of ovarian cancer and the other healthy sibling who is a BRCA1 mutation carrier were compared in the study to analyze all RNA molecules transcribed at the genome level using next-generation sequencing technology.Through analyzing the molecules transcribed in the whole genome,the genetic variations underlying the development of ovarian cancer in a high-risk family bearing the BRCA1 mutation but only one of whom was found to have ovarian cancer were examined.

Results: As a result of the transcriptomic analysis of the total RNA of 6 samples obtained from the ovarian tissues and peripheral blood samples of MZ twins with ovarian cancer and healthy sibling, the protein-encoding protein that shows expression changes in tissue and blood compared to healthy people genes,lncRNAs,precursor-miRNAs and fusion-transcripts have been identified.Filtering procedures and expression change coefficients(log2Fc) were calculated based on the expression data of identified ovarian cancer tumor markers CA125 and CA15-3.

Conclusions: According to our study the expression levels of 66 protein-coding genes,23 novel lncRNAs,9 miRNAs and,2 fusion transcripts were found to vary in three groups and,these molecules are thought to be candidate molecules associated with epithelial ovarian cancer.

Keywords: monozygotic twins, Epithelial Ovarian Cancer, RNA Sequence Analysis, Gene Expression Profiling