

28. ULUSAL PATOLOJİ KONGRESİ

27-30 Ekim 2018

Ankara Üniversitesi Tıp Fakültesi
Morfoloji Yerleşkesi



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PL Sözel Sunum

Nöropatoloji

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The relationship between positive symptoms of schizophrenia and its epigenetic modifications

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Objectives:

Schizophrenia is a complex and enigmatic psychiatric disorder which is characterized by defects in the frontal and temporal lobes. It has positive and negative symptoms, such as delirium, hallucinations, disorganized speech and impairment in social/occupational functioning. It is usually seen between the age of 18-25 years and the symptoms start at the early age are more severe. It is thought to be neurodevelopmental and physiopathological factors on the basis of its etiology but it is more likely to be emerged as a consequential mechanism which is oligogenic, polygenetic or epigenetic. Recent studies have focused on the role of epigenetic changes in complex psychiatric, autistic, and neurodegenerative disorders. Knowledge about the effect of epigenetic modification in the schizophrenia's development is very limited. In the literature, there are just five studies about the DNA methylation profiles of schizophrenia patients.

Materials and Methods:

In this study, the GSE21935 gene's microarray data were downloaded from the "Gene Expression Omnibus (GEO)" database to investigate the association of positive symptoms with epigenetic modifications. Differences in gene expression level were generated by re-analyzing the mRNA transcripts of the Affymetrix Human Genome U133 Plus 2.0 Array platform from tissues obtained from postmortal superior temporal cortices (Brodmann Area 22, BA22) associated with positive symptoms of 23 schizophrenia and 19 control patient groups. "Biobase", "Limma" and "Geoquery" libraries were obtained with bioinformatics analysis and R program. In comparing the expression profiles of transcripts, "log2 fold change > 1" and $P \leq 0.05$ were considered statistically significant.

Results:

Statistically significant differences were found in genes related to DNA methylation and histone modifications (acetylation, methylation, phosphorylation) as a result of functional association DAVID (Database for Annotation, Visualization and Integrated Discovery).

Conclusions:

Although schizophrenia is treatable, complete recovery is not possible in most patients. There is a need

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for more comprehensive genetic studies to be done in the future, considering environmental factors.

Anahtar Kelimeler :Schizophrenia, Epigenetic modification, Bioinformatic