Data in Brief

Gene expression profiling in peripheral blood mononuclear cells of early-onset schizophrenia

Li Sun a, Zaohuo Cheng a,*, Fuquan Zhang a, Yong Xu b

a Wuxi Mental Health Center of Nanjing Medical University, Wuxi, Jiangsu Province, China
b Department of Psychiatry, First Hospital of Shanxi Medical University, Taiyuan, China

Abstract

Schizophrenia (SZ) is a severe chronic psychiatric disorder with wide prevalence and high morbidity. We know little about SZ’s etiology and pathophysiology at present. The study of gene expression profile is useful for us to identify potential biomarkers at molecular level and explain possible pathogenesis of SZ. Therefore we recently compared gene expression profiles in PMBCs from EOS cases and healthy controls using microarrays. Here we will describe in detail the contents and quality control of the microarray experiment. The raw microarray data are accessible through GEO series accession number GSE54913.

1. Direct link to deposited data

http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE54913.

We paid attention to this period and speculate that the altered gene expression in these patients may be associated with the disease process. Peripheral blood mononuclear cells (PBMCs) have represented an accessible tissue source for gene expression, as it is easily collected from patients. There already have many gene expression profiling studies using PBMCs, a consistent conclusion about the expression alteration of schizophrenia is lacked [3,4].

2. Experimental design, materials and methods

We recently collected blood samples from 18 EOS cases and 12 controls. Then we generated whole-genome gene expression profiles on PBMCs from these samples by using microarray. 17,200 valid probes detected in our experiment were used to identify altered gene expressions.

1.1. Study population

A total of 18 first-onset SZ patients (8 males and 10 females, aged 14.78 ± 1.70 years) were included in our study. They were untreated and drug-naïve patients diagnosed by at least two experienced psychiatrists independently according to the Diagnosis and Statistical Manual of Mental Disorders Fourth Edition (DSM-IV) criteria for SZ. 12 healthy controls (6 males and 6 females, aged 14.75 ± 2.14 years) were recruited into the study. Teenagers with a history of other mental health or neurological diseases were enrolled into our study. All participants

* Corresponding author. Wuxi Mental Health Center of Nanjing Medical University 156 Qianrong Road, Wuxi, Jiangsu Province, 214151, China. Tel.: +86 13358118908. E-mail address: zaphuocheng@sina.com (Z. Cheng).

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were unrelated Han Chinese recruited from the north of China. And both the participants and their parents signed the informed consent before participation. The study was approved by Medical Research Ethics Committee of Shanxi Medical University.

2.2. Microarray and quality control

Peripheral blood was collected. NanoDrop ND-1000 was used to quantify total RNA after RNA extraction, and RNA integrity was assessed by standard denaturing agarose gel electrophoresis. Agilent Array platform was employed to perform the microarray analysis. Following RNA amplification, hybridization and image scanning, signal intensities were normalized in the quantile method using GeneSpring GX v11.5.1 (Agilent Technologies), and low intensity mRNAs were filtered (mRNAs that at least 20 out of 30 samples have flags in Present or Marginal were chosen for further analysis). R [5] was used to perform the data processing and analyses of mRNA data. The sample preparation and microarray hybridization were performed based upon the manufacturer’s standard protocols with minor modifications.

Log2-ratios were used by quantile normalization. The distributions of the intensities after normalized among all samples were shown in Fig. 1, identification of differentially expressed genes between SZ cases and controls was made using R package genefilter [6]. We identified 84 differentially expressed genes through fold change and P value filtering (FC ≥ 2 and P_{adjusted} < 0.05) listed in Table 1.

3. Discussion

All the participants in our study were teenagers with similar age (<18 years), and their brains were still developing. The SZ cases were neither under medication nor had a history of pharmacotherapy. We mainly described a dataset about gene expression profiles of the 30 samples measured by Arraystar.

Among the 84 DE genes listed above, SLC18A1 has been reported to be associated with SZ [7,8]. In addition, CTLA4 was also identified showing a high expression level in SZ [9] which is consistent with the results from our study. Through our description above, we believe that this dataset will be useful for the exploration of SZ’s pathogenesis in the future.

Conflict of interest

The authors have no conflicts of interest.

Acknowledgments

We would sincerely thank the patients, their families and the healthy volunteers for their participation. Equal gratitude will be dedicated to all the authors contributing to this paper and medical staff involved in the study.

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