Identification and functional analysis of circulating extrachromosomal circular DNA in schizophrenia implicate its negative effect on the disorder

Xiang, Xi; Pan, Xiaoguang; Lv, Wei; Chen, Shanshan; Li, Jinguang; Zhang, Haoran; Liao, Yanhui; Yu, Jiaying; Li, Jing; Dang, Yonghui; You, Zifan; Wang, Liangliang; Chen, Wei; Han, Peng; Tang, Jinsong

Published in:
Clinical and Translational Medicine

DOI:
10.1002/ctm2.1488

Publication date:
2023

Document version
Publisher's PDF, also known as Version of record

Document license:
CC BY

Citation for published version (APA):
Identification and functional analysis of circulating extrachromosomal circular DNA in schizophrenia implicate its negative effect on the disorder

Dear Editor,

Extrachromosomal circular DNA (eccDNA) is a circular DNA molecule derived and free from linear chromosomes,1 and its characteristics and potential function in schizophrenia (SCZ) remain unclear. In this study, we explored the characteristics of plasma-derived eccDNAs from 10 chronic SCZ patients and 17 healthy controls (Table S1), utilizing the Circle-seq approach. Then the molecular role of SCZ over-represented eccDNAs carrying genic segments (eccGene) was investigated by both bioinformatical and experimental analysis.

The workflow of SCZ plasma sampling, eccDNA purification, sequencing and bioinformatic analysis is conducted as previously described2,3 and is illustrated in Figure 1A. Especially, given that only the eccDNA carrying a certain length of gene segment can express potential regulatory RNA molecules,4 eccDNAs with > 60 bp overlap of certain gene loci were defined as “eccGenes” in this study. The NGS information of the two groups is listed in Table S2. In total, a median number of 7717 and 7423 eccDNA loci were identified in healthy control and SCZ plasma samples, respectively. Both the absolute number (Figure 1B) and the eccDNA counts per million mapped reads (Figure 1C) were comparable between the two groups. The length of most eccDNAs was less than 2 kb with four predominant peaks at around 197 bp, 363 bp, 555 and 747 bp (Figure 1D,E). GC content of these eccDNAs was higher than that of the average genomic distribution (Figure 1F), suggesting the generation of circulating eccDNAs was not random. Meanwhile, the generation frequency of eccDNA in each chromosome of the two groups was comparable. However, the tendency of eccDNA generation was varying in different chromosomes (Figure 1G).

EccGenes showed the potential to transcribe RNAs2,5 and produce functional si-like RNA which leads to suppression of their host genes.4 In the study, we identified 26 differential eccGenes in the healthy control group and 211 differential eccGenes in the chronic SCZ group (Table S3). Figure 2A shows the existing frequency of these eccGenes in the two groups with p-value < .03. Through comparing the 211 SCZ over-represented eccGenes with the combination of two reported SCZ high-risk gene (HRG) sets (104 and 67 HRGs) inferred from the worldwide SCZ GWAS data,6,7 we identified the TAOK2 gene, whereas no overlapped gene was found in the healthy control-specific eccGene set (Figure 2B). Reads distribution of eccTAOK2 exhibited by the Integrative Genomics Viewer showed that three of the five detected eccTAOK2 in SCZ were derived from intron-1 of the TAOK2 gene, while the other two were from intron-8 (Figure 2C). Intriguingly, we found that the full length of the TAOK2 gene showed a very high degree of conservation in sequence in animals such as horses, cows, dogs, pandas, rats and dolphins, but not in the birds, Sarcopterigii or fish (Figure S1). Given that TAOK2 expresses broadly in many organs, the highly conserved TAKO2 gene suggests that not only the TAOK2 coding sequence but also its introns may play a critical role in the overall development of mammals. At last, we verified the existence of SCZ over-represented eccGenes in corresponding samples, including four eccTAOK2, one eccDNMT3B, two eccJAG1 and two eccSIRT5, by both outward polymerase chain reaction (PCR) (Figure 2D and Table S4) and Sanger sequencing of the eccDNA junction sites (Figure 2E).

Furthermore, the Human Phenotype Ontology (HPO) analysis (http://www.webgestalt.org/option.php) was conducted on the 211 SCZ over-represented eccGenes. The term “Intellectual disability, progressive” (IDP) was enriched significantly with FDR < 0.05 (Figure S1A, upper), while no significant term was found upon the healthy control-specific eccGenes (Figure S1A, below). Six genes contributed to the IDP term (6 of 48 genes, enrichment ratio = 11.682), including DDB2, ERCC3, PTS, UBE3A, UROC1 and XPA (Figure S2B). The existence frequency of the six eccGenes in the chronic SCZ group

This is an open access article under the terms of the Creative Commons Attribution License, which permits use, distribution and reproduction in any medium, provided the original work is properly cited.

© 2023 The Authors. Clinical and Translational Medicine published by John Wiley & Sons Australia, Ltd on behalf of Shanghai Institute of Clinical Bioinformatics.
**FIGURE 1** General features of the plasma-derived extrachromosomal circular DNAs (eccDNAs). (A) Workflow of the study. (B) Detected eccDNA number in the healthy control and chronic schizophrenia (SCZ) groups. (C) Normalized eccDNA counts: eccDNA number per million mapped reads (EPM) in the two groups. (D) Length distribution of plasma-derived eccDNA in the two groups. (E) Percentage of eccDNA with different lengths in total detected eccDNAs in each sample of the two groups. (F) GC content of SCZ, healthy control, in silico and their upstream and downstream regions with equivalent length. (G) Normalized density (ratio of EPM) of eccDNA in the 24 human chromosomes.
FIGURE 2 Determination of the differential eccGenes in either the schizophrenia (SCZ) or healthy control group. (A) Detection frequency of differential eccGenes in the two groups (Wilcoxon’s rank-sum test, p-value < .03). The row indicates the extrachromosomal circular DNA (eccDNA) carrying a certain genic segment; The column represents a sample within the given group. The blue block represents the eccGene detected in the corresponding sample. (B) Comparison of SCZ over-represented eccGenes with the SCZ high-risk gene sets and the healthy-specific eccGenes by GeneVenn. (C) Length and reads coverage presentation of the five eccTAOK2 detected in SCZ patients. S211, S226, S238, S239 and S245 indicate the sample of SCZ patients. S1–S20 indicate healthy people. Blue lines and bars below represent the intron and exon distribution of the TAOK2 gene. (D) Polymerase chain reaction (PCR) assay and gel visualization of the junction sites of several eccGenes by outward PCR. (E) Sanger sequencing of the junction sites of 8 eccGenes detected in SCZ.
was significantly higher compared to the healthy control (Figure S2C). Furthermore, both outward PCR (Figure S2D) and Sanger sequencing of the junction regions (Figure S2E) verified the presence of the six IDP-related eccGenes in SCZ samples.

To further study the regulatory function of eccTAOK2, we synthesized two eccDNAs carrying the segments of either the TAOK2 intron 1 or intron 8 (Table S5) using the ligase-assisted mini-circle accumulation (LAMA) strategy (Figure 3A left). Both the exonuclease
Transfection of the artificial eccTAOK2 dysregulated the immune-related biological processes in U-251MG cells. (A) Volcano plot of the differentially expressed genes (DEGs) after artificial eccTAOK2#1 transfection in U-251MG cells. Blue and red spots indicate the down- (n = 46 DEGs) and up-regulated (n = 65 DEGs) DEGs with p-adjust value < .05 and |Log2(FoldChange)| > 0.5, respectively. (B) Top 20 of the biological processes enriched by GO enrichment analysis upon the 111 DEGs. The y-axis indicates the term of the biological processes and the x-axis represents the gene percentage in each category. The number on the right of each bar indicates the enriched gene number in each cluster and the p-adjust value is in parenthesis. (C) Top 20 KEGG pathways enriched in the 111 DEGs. (D) KEGG enrichment network plot of the enriched signalling pathways.

(Figure 3A right) and the single restriction endonuclease digestion (Figure 3B) demonstrated the circular structure and high purity of the LAMA-produced artificial eccTAOK2s. Transfection of the two eccTAOK2s (Figure 3C) resulted in down-regulation of TAOK2 mRNA level in both the SH-SY5Y (Figure 3D) and U-251MG cell lines (Figure 3E). Renilla luciferase gene containing the full length of eccTAOK2#1 and #2 sequence at the 3′UTR (Table S6) were co-transfected with the artificial eccTAOK2 for dual-luciferase assays in U-251MG cells (Figure 3F). EccTAOK2#1 and eccTAOK2#2 repressed the renilla luciferase carrying their intron-origin sequences by 48.5% and 69.1%, respectively (Figure 3G). These results suggested that eccTAOK2 carrying intronic sequence was able to repress TAOK2 mRNA expression, in which the process might be dependent on the production of regulatory RNAs which target the intronic portion of pre-mRNA.

To evaluate the impact of SCZ-derived eccDNA on nerve cells, the artificial eccTAOK2 was transfected in U-251MG cells and we performed the RNA-seq analysis afterwards. A total of 111 differentially expressed genes (DEGs)
(46 downregulated and 65 upregulated genes) were identified in the eccTAOK2#1 transfection group (Figure 4A and Table S7). GO enrichment analysis highlighted the immune-related biological processes (Figure 4B and Table S8) and KEGG analysis showed these DEGs were enriched in two major signalling pathways: “TNF signalling pathway” and “cytokine-cytokine receptor interaction” (Figure 4C,D and Table S9). These results indicated that eccTAOK2 can dysregulate the immune-related biological processes in nerve-derived cells, suggesting a potential negative effect of eccDNA on the SCZ brain.

In summary, this study delineated the circulating eccDNAs profile of SCZ and highlighted the regulatory function of eccTAOK2 and its impact on cellular immune processes, underscoring the eccDNA biology and its potential role as a noninvasive biomarker for diagnosis and monitoring of SCZ.

AUTHOR CONTRIBUTIONS
Conception and Planning of the study: X.X., P.H. and J.T.; Acquisition and interpretation of the data: X.X., P.H., J.T., X.P., W.L., S.C., J.L., H.Z., Y.L., J.Y., J.L., Y.D., Z.Y., L.W. and W.C.; Writing and revision of the manuscript: X.X., P.H. and J.T.; Supervision of the study: X.X., P.H. and J.T.; All authors read, edited and approved the manuscript.

ACKNOWLEDGEMENTS
National key R & D plan of China (Grant No. 2022YFE0103700), National Natural Science Foundation of China (Grant No. 82171495 and 81871057), the Research Start-up Fund of The Seventh Affiliated Hospital, Sun Yat-sen University (Grant No. 592026), the Shenzhen Science and Technology Innovation Commission (Grant No. JCYJ20220530145014033). Fundamental Research Funds for the Central Universities, Sun Yat-sen University (Grant No. 2023KYPT02). Joint Funds of the Zhejiang Provincial Natural Science Foundation of China (Grant No.LBD23H090001).

CONFLICT OF INTEREST STATEMENT
The authors declare no conflict of interest.

DATA AVAILABILITY STATEMENT
The circulating eccDNA NGS data is deposited in the genome sequence archive of the Beijing Institute of Genomics, National Center for Bioinformation, Chinese Academy of Science. The accession number for the eccDNA sequencing data in this study is HRA004251.

ETHICS STATEMENT
All the participate in this study have signed an informed consent form proved by the Institutional Review Board (IRB) of Zhejiang University. This study was approved by the Ethics Committee of Sir Run Run Shaw Hospital School of Medicine Affiliated with Zhejiang University (IRB number: 20210205-35).

Xi Xiang1
Xiaoguang Pan2
Wei Lv3
Shanshan Chen4
Jinguang Li5
Haoran Zhang6
Yanhui Liao4
Jiaying Yu1
Jing Li6
Yonghui Dang6
Zifan You4
Liangliang Wang4
Wei Chen4
Peng Han2
Jinsong Tang7

1Scientific Research Center, The Seventh Affiliated Hospital of Sun Yat-sen University, Shenzhen, China
2Department of Biology, University of Copenhagen, Copenhagen, Denmark
3College of Life Sciences, University of Chinese Academy of Science, Beijing, China
4Department of Psychiatry, Sir Run Run Shaw Hospital, Zhejiang University School of Medicine, Hangzhou, China
5Research Center for Mental Health and Neuroscience, Wuhan Mental Health Center, Wuhan, China
6College of Medicine and Forensics, Xi’an Jiaotong University Health Science Center, Xi’an, China
7Department of Psychiatry, Sir Run Run Shaw Hospital, School of Medicine, Key Laboratory of Medical Neurobiology of Zhejiang Province, Hangzhou, China

Correspondence
Xi Xiang, Scientific Research Center, The Seventh Affiliated Hospital of Sun Yat-sen University, Shenzhen, Guangdong 518107, China.
Email: xiangx25@mail.sysu.edu.cn

Peng Han, Department of Biology, University of Copenhagen, Copenhagen 2200, Denmark.
Email: hanpeng@genomics.cn

Jinsong Tang, Department of Psychiatry, Sir Run Run Shaw Hospital, Zhejiang University School of Medicine, Hangzhou, Zhejiang 310001, China.
Email: tangjinsong@zju.edu.cn

Xi Xiang, Xiaoguang Pan, Wei Lv and Shanshan Chen contributed equally to this work.
REFERENCES


SUPPORTING INFORMATION
Additional supporting information can be found online in the Supporting Information section at the end of this article.