



# Behavioral and transcriptional effects of repeated electroconvulsive seizures in the neonatal MK-801-treated rat model of schizophrenia

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## Abstract

**Rationale** Electroconvulsive therapy (ECT) is an effective treatment modality for schizophrenia. However, its antipsychotic-like mechanism remains unclear.

**Objectives** To gain insight into the antipsychotic-like actions of ECT, this study investigated how repeated treatments of electroconvulsive seizure (ECS), an animal model for ECT, affect the behavioral and transcriptomic profile of a neurodevelopmental animal model of schizophrenia.

**Methods** Two injections of MK-801 or saline were administered to rats on postnatal day 7 (PN7), and either repeated ECS treatments (E10X) or sham shock was conducted daily from PN50 to PN59. Ultimately, the rats were divided into vehicle/sham (V/S), MK-801/sham (M/S), vehicle/ECS (V/E), and MK-801/ECS (M/E) groups. On PN59, prepulse inhibition and locomotor activity were tested. Prefrontal cortex transcriptomes were analyzed with mRNA sequencing and network and pathway analyses, and quantitative real-time polymerase chain reaction (qPCR) analyses were subsequently conducted.

**Results** Prepulse inhibition deficit was induced by MK-801 and normalized by E10X. In M/S vs. M/E model, *Egr1*, *Mmp9*, and *S100a6* were identified as center genes, and interleukin-17 (IL-17), nuclear factor kappa B (NF-κB), and tumor necrosis factor (TNF) signaling pathways were identified as the three most relevant pathways. In the V/E vs. V/S model, mitophagy, NF-κB, and receptor for advanced glycation end products (RAGE) pathways were identified. qPCR analyses demonstrated that *Igfbp6*, *Btf3*, *Cox6a2*, and *H2az1* were downregulated in M/S and upregulated in M/E.

**Conclusions** E10X reverses the behavioral changes induced by MK-801 and produces transcriptional changes in inflammatory, insulin, and mitophagy pathways, which provide mechanistic insight into the antipsychotic-like mechanism of ECT.

**Keywords** Electroconvulsive therapy · Schizophrenia · Immediate early genes · Nuclear factor-κB · Insulin signaling · Mitophagy

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## Introduction

Electroconvulsive therapy (ECT) is a treatment modality for various neuropsychiatric disorders, including depression and schizophrenia (Lisanby 2007; Weiner and Reti 2017). ECT is a safe and effective adjunct to antipsychotic therapy for patients with treatment-resistant schizophrenia (de Mangoux et al. 2022; Kim et al. 2018a; Petrides et al. 2015; Sanghani et al. 2018; Sinclair et al. 2019; Youn et al. 2019). ECT is particularly effective in patients with schizophrenia who exhibit catatonia or suicidal behaviors (Grover et al. 2019). This treatment can prevent relapse in schizophrenia without significant adverse effects and may improve social functioning and quality of life (Grover et al. 2019; Ward et al. 2018; Youn et al. 2019). Evidence strongly indicates that ECT has not only antidepressant but also antipsychotic effects (Ali et al. 2019; Kim et al. 2018a; Petrides et al. 2015; Sinclair et al. 2019; Ward et al. 2018), and it has become a crucial part of current clinical guidelines for the management of schizophrenia (Galletly et al. 2016; Grover et al. 2017; Lee et al. 2020).

Animal models of in vivo genetic and molecular mechanisms are a useful tool to understand the mechanism of action of ECT. Repeated treatments of electroconvulsive seizure (ECS), an animal model for ECT, induce neurogenesis, synaptic modifications, dendritic remodeling, increased spine density, increased expression of neurotrophic factors, alterations in the activity of intracellular signaling molecules, and anti-apoptotic activity (Enomoto et al. 2017; Maffioletti et al. 2021; Meyers et al. 2023; Segi-Nishida 2011; Tartt et al. 2023). Moreover, repeated ECS treatments alter the expression levels of genes related to neurotransmission and neural plasticity (Chang et al. 2018; Huang and Chen 2008; Kobayashi and Segi-Nishida 2019). However, most studies to date have been designed to examine the antidepressant activity of ECT (Maffioletti et al. 2021). The mechanisms underlying the antipsychotic action of ECT require further investigation.

The N-methyl-D-aspartic acid (NMDA) glutamate receptor hypofunction hypothesis is a leading theory for understanding the pathophysiology of schizophrenia (Bygrave et al. 2019; Kantrowitz and Javitt 2010; Nakazawa and Sapkota 2020). Neurodevelopmental animal models exhibit behavioral and molecular alterations compatible with schizophrenia (Bialon and Wasik 2022). Neuronal and synaptic development, myelination, and gliogenesis are most pronounced around postnatal day 7 (PN7), which is analogous to the third trimester of pregnancy in humans (Bolon et al. 2021; Semple et al. 2013). In this period, susceptibility to the apoptotic effects of NMDA receptor antagonism is high (Lim et al. 2012a; Ritter et al. 2002), which can cause defects in dopamine regulation

and parvalbumin neuron maturation, subsequently producing schizophrenia-like phenotypes (Abekawa et al. 2007; Belforte et al. 2010; Nakazawa et al. 2017). Administration of MK-801, a selective non-competitive NMDA receptor antagonist (Tricklebank et al. 1989), during this critical period, induces long-term behavioral and cognitive changes in rodents, such as decreased prepulse inhibition of acoustic startle responses and impairments in spatial memory (Lim et al. 2012a; Mohammadi et al. 2020; Uehara et al. 2009; Uttl et al. 2018). MK-801 injections during the neonatal period provide a useful neurodevelopmental animal model, especially for evaluating antipsychotic-like activity (Niu et al. 2020).

The present study was performed to examine the behavioral and transcriptomic changes that underlie the antipsychotic mechanism of ECT using the MK-801 model of schizophrenia. We previously reported that neonatal MK-801 treatment induces dysregulations in protein translation signal pathways in the prefrontal cortex (PFC) of developing rats (Kim et al. 2010a). In this study, the neonatal NMDA receptor antagonist was administered as in our previous study (Kim et al. 2010a), and long-term behavioral changes were evaluated during the young adult period. The PFC is one of the central brain regions of antipsychotic action (Artigas 2010; MacDonald et al. 2005), and we conducted mRNA sequencing, network, and pathway enrichment analyses of PFC samples. Quantitative real-time polymerase chain reaction (qPCR) was then conducted to confirm the findings. We demonstrated that repeated ECS treatments restored the behavioral abnormalities and induced transcriptomic changes in the PFC.

## Methods

### Animals

All animals in this study were treated in accordance with the National Institutes of Health (NIH) Guide for the Care and Use of Laboratory Animals. The experiment was approved by the animal subjects review board of Seoul National University Hospital. Female Sprague–Dawley rats (weighing 12–16 g) were housed with their mother under a 12-h light/12-h dark cycle with food and water available ad libitum. Female rats were chosen for their more conspicuous long-term behavioral changes in response to neonatal MK-801 treatment (Kim et al. 2010a).

### Experimental procedure

This study was designed to examine the effects of repeated treatments of ECS on the long-term behavioral and cortical transcriptional changes induced by neonatal MK-801

treatment. On PN7, the rats were randomly injected with either MK-801 or vehicle (normal saline). The rats were housed with their dam until weaning on PN21. On PN50, each group was randomly divided into two subgroups and treated daily with either ECS (E10X) or sham shock (sham) for 10 days. Ultimately, the rats were divided into four subgroups: vehicle/sham (V/S), MK-801/sham (M/S), vehicle/E10X (V/E), and MK-801/E10X (M/E). After the last ECS or sham treatment, a prepulse inhibition (PPI) test and locomotor activity assessment were performed on PN59. The rats were decapitated 24 h after the last ECS or sham treatment, and the PFC was dissected and used for mRNA sequencing, network and pathway enrichment analyses, and qPCR analyses. The experimental design is summarized in Fig. 1.

### MK-801 treatment

MK-801 was administered as in our previous study (Kim et al. 2010a). We administered subcutaneous injections of either normal saline vehicle or 1.0 mg/kg MK-801 (Tocris Bioscience, Bristol, UK) dissolved in normal saline to the rats on PN7, which is within the period of high vulnerability to MK-801 (Lim et al. 2012a; Ritter et al. 2002). Among the MK-801 treatment conditions of our previous report, the protocol of two 1.0 mg/kg MK-801 injections administered 8 h apart was selected because it resulted in the most prominent molecular changes in the frontal cortex (Kim et al. 2010a). Drug injections were performed outside the cage under a heating lamp, and the pups were returned to the cage immediately after the injections.

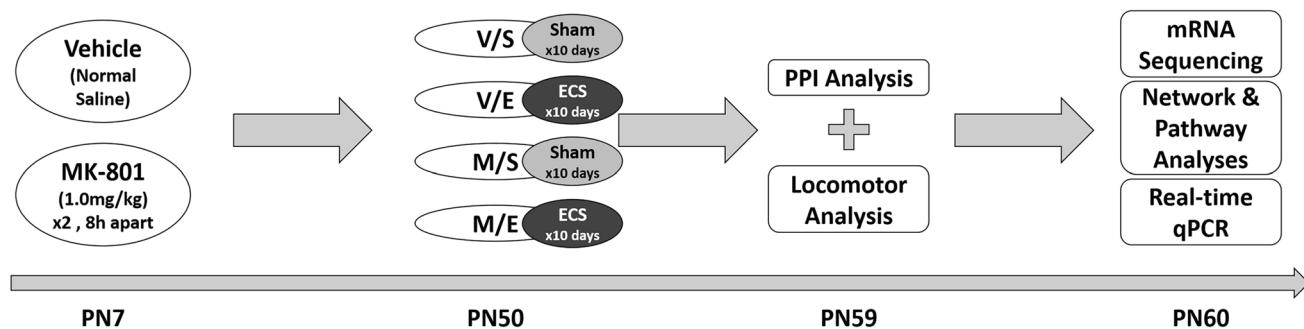
### ECS treatment

From PN50, rats that had been treated with MK-801 or vehicle on PN7 were divided into the sham group (sham shock for 10 days) and the E10X group (ECS for 10 days). Both groups were treated daily at the same time (12:00–13:00) for 10 days. As previously reported (Kim et al. 2022), ECS

was administered to the rats using ear-clip electrodes and a pulse generator (UgoBasile ECS Unit-57800-001; UgoBasile, VA, Italy) at a frequency of 100 pulses/s, with a pulse width of 0.5 ms, shock duration of 0.5 s, and current of 55 mA. These parameters were comparable to protocols of other ECS studies on psychosis model rodents (Kimura et al. 2021; Limoa et al. 2016) and settings used in clinical ECT on patients (Galletly et al. 2014; Minelli et al. 2016). Sham-treated control animals were handled in the same fashion as ECS-treated animals, but no electric current was delivered. ECS-induced seizure was validated by observing general convulsions consisting of tonic and clonic phases, and the duration of the convulsions was measured. ECS-treated animals that experienced a generalized convolution for more than 30 s were included for further analysis.

### Measurement of PPI

The PPI testing protocol used in this experiment was based on that described in previous studies (Gururajan et al. 2011; Lim et al. 2012b) with minor modifications. All rats were first acclimatized to the enclosure in the startle chamber on PN58 and exposed only to background noise (65 dB) for 30 min. On PN59, each rat underwent a PPI test of a 5-min acclimatization period (65-dB background sound) and subsequent 120-dB startle pulses of 40-ms duration that were presented with or without prepulses. The non-startling prepulses were 3, 6, or 12 dB above the background and 20 ms in duration, with an inter-stimulus interval (start of prepulse to start of pulse) of 100 ms. Background- and prepulse-only trials were also completed. Each trial type was completed 10 times in a pseudorandom order with an average inter-trial interval of 15 s. In addition, six pulse alone trials were presented at the start and end of each session. The startle magnitude was determined by taking the average of 100 1-ms samples of accelerometer startle responses immediately following the onset of the pulse. Percent PPI was computed as



**Fig. 1** Schematic outline of the experimental design. The schematic illustrates the ages of the animals and treatments applied in each group. Abbreviations: V/S, vehicle-sham shock  $\times$  10 days

(Sham) group; V/E, vehicle-ECS  $\times$  10 days (E10X) group; M/S, MK-801-Sham group, M/E, MK-801-E10X group; PN, postnatal day; PPI, prepulse inhibition; qPCR, quantitative polymerase chain reaction

[1 – (mean startle magnitude after prepulse and pulse/mean startle magnitude after pulse alone)] × 100.

### Measurement of locomotor activity

Locomotor activity was measured with video tracking software (Activity Monitor 5; MED Associates, St. Albans, VT, USA), and locomotor activity was measured during the light phase of the day (12:00–20:00) as previously reported (Kim et al. 2013, 2008). The rats were acclimated to the testing environment 1 day before the test, and the distance traveled in 30 min was measured.

### RNA isolation

On PN60, the rats were decapitated, and fresh frozen brain tissue was obtained. We defined the PFC as the cortical tissues located rostrally to the genu of the corpus callosum. The PFC was dissected and analyzed using a QuantSeq 3' mRNA sequencing kit (Lexogen, Vienna, Austria). Total RNA was isolated using a Trizol reagent (Invitrogen, Waltham, MA, USA). RNA quality was assessed by Agilent 2100 Bioanalyzer using the RNA 6000 Nano Chip (Agilent Technologies, Santa Clara, CA, USA), and RNA quantification was performed using ND 2000 Spectrophotometer (Thermo Fisher Scientific, Waltham, MA, USA).

### Library preparation and sequencing

The library of control and test RNAs was constructed using QuantSeq 3' mRNA-Seq Library Prep Kit (Lexogen) according to the manufacturer's instructions. In brief, 500 ng total RNA was prepared, an oligo-dT primer containing an Illumina-compatible sequence at its 5' end was hybridized to the RNA, and reverse transcription was performed. After degradation of the RNA template, second strand synthesis was initiated by a random primer containing an Illumina-compatible linker sequence at its 5' end. The double-stranded library was purified by using magnetic beads to remove all reaction components. The library was amplified to add the complete adapter sequences required for cluster generation. The finished library was purified from PCR components. High-throughput sequencing was performed as single-end 75-bp sequencing using a NextSeq 500 system (Illumina, San Diego, CA, USA).

### Transcriptomic analyses

QuantSeq 3' mRNA-Seq reads were aligned using Bowtie 2 (SourceForge, San Diego, CA, USA) (Langmead and Salzberg 2012). Bowtie 2 indices were generated from either the genome assembly sequence or the representative transcript sequences for alignment to the genome and

transcriptome. The alignment file was used for assembling transcripts, estimating their abundances, and detecting differential expression of genes. Differentially expressed genes (DEGs) were determined based on counts from unique and multiple alignments using coverage in BEDTools (SourceForge) (Quinlan et al. 2010). The read count data were processed based on the quantile normalization method using edgeR in the R environment (R Development Core Team, 2016) via Bioconductor (Gentleman et al. 2004). Gene classification was based on searches of the DAVID database (<https://david-d.ncifcrf.gov/>) and Medline database (<https://www.ncbi.nlm.nih.gov/>).

### Network and pathway analyses

DEGs that met the following criteria were considered for the network analysis: false discovery rate (FDR) of < 0.05 in the model that compared all four groups separately as well as in the model of interest, and an absolute value of log<sub>2</sub> value of fold change (log<sub>2</sub>FC) of > 0.5. Gene regulatory networks in these DEGs were discovered via NetworkAnalyst with reference to SIGnaling Network Open Resource 2.0 (SIGNOR 2.0). Only the subnetworks with the most nodes were analyzed. The resulting interactome depicted a subnetwork that maximally connected the seeds (Zhou et al. 2019). The degree and betweenness distribution of nodes were calculated. To identify the relevant biological pathways, the identified DEGs were compared to the Kyoto Encyclopedia of Genes and Genomes (KEGG) database for enrichment analysis. Molecular pathways with at least 3 hits, a *P*-value < 0.0001, and an FDR of < 0.05 were included.

### qPCR analyses

Among the identified DEGs, qPCR analysis was conducted on genes with a log<sub>2</sub>FC of > 1 or log<sub>2</sub>FC of < -1 and genes that code proteins with degree of ≥ 3 in the gene regulatory network. Genes with no corresponding human gene or no annotations in Ensembl were excluded. The analysis mostly followed previously described procedures (Park et al. 2014). Total RNA was extracted from the rodent PFC, and 1 µg of the total RNA was used to produce the corresponding complementary DNA using Superscript II Reverse Transcriptase (Invitrogen). Next, qPCR was performed using an ABI PRISM 7500 Real-Time PCR System (Applied Biosystems, Waltham, MA, USA). Relative amounts of mRNA were calculated by the comparative cycle threshold (Ct) method. The average fold change of each gene was normalized to the Ct value of beta-actin. The primer sequences for the qPCR analysis are shown in Supplementary Table 1.

## Statistical analyses

At each prepulse stimulus intensity, PPI was analyzed by three-way analysis of variance (ANOVA) using drug and shock as the independent variables, followed by post hoc Tukey's test. Two-way ANOVA tests were conducted on locomotor activity and the qPCR results. All results are in means  $\pm$  standard error of the mean (SEM). All statistical tests and corresponding graphs were generated using GraphPad Prism for Windows (ver. 10.0.1.; GraphPad Software, La Jolla, CA, USA), and  $P$ -values of  $<0.05$  were considered statistically significant.

## Results

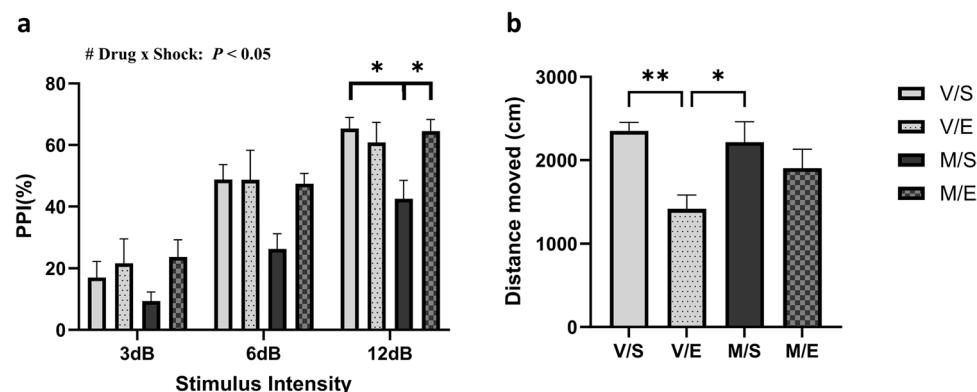
### PPI assay

PPI deficit is a reliable behavioral phenotype in animal models of schizophrenia (Lim et al. 2012b; Zhao et al. 2013). Previous studies have reported that early postnatal administration of NMDA receptor antagonists in rodents induces PPI deficits in the adolescent and adult periods (Garcia-Mompo et al. 2020; Lim et al. 2012b). In this study, MK-801 or vehicle was injected into rats on PN7, and ECS or sham shock was then administered daily for 10 days (PN50–PN59). On PN59, PPI was measured to examine the psychotomimetic effects of early postnatal MK-801 in the young adult period and the effects of repeated ECS treatments. Three-way ANOVA demonstrated a significant main effect of E10X ( $P=0.049$ ,  $F(1, 20)=4.400$ ) and a significant interaction effect between E10X and MK-801 ( $P=0.049$ ,  $F(1, 20)=4.385$ ). A

significant interaction effect between E10X and MK-801 ( $P=0.018$ ,  $F(1, 20)=6.591$ ) was observed at the prepulse stimulus intensity of 12 dB, whereas no such effect was found at 3 or 6 dB. Post hoc analyses demonstrated that at the prepulse stimulus intensity of 12 dB, the PPI value was significantly lower in M/S than in V/S ( $P=0.025$ ) and significantly higher in M/E than in M/S ( $P=0.033$ ) (Fig. 2a). These findings indicated that neonatal MK-801 treatment on PN7 induced PPI deficits in young adult rats and that these deficits were normalized by repeated ECS treatments.

### Locomotor activity test

Locomotor activity is reportedly affected by early postnatal NMDA receptor antagonism; however, the findings have varied depending on the experimental conditions (Gururajan et al. 2011; Hlavacova et al. 2023; Li et al. 2023; Lim et al. 2012a). In this study, locomotor activity was tested on PN59 to elucidate the effects of neonatal MK-801 on locomotion and to determine whether repeated ECS treatments could normalize the MK-801-induced changes. The total distance traveled during the 30-min test session was 2350, 1415, 2217, and 1904 cm in V/S, M/S, V/E, and M/E, respectively. Two-way ANOVA revealed that E10X had a significant main effect on the locomotor activity of the rodents ( $P=0.003$ ,  $F(1, 48)=10.068$ ), while neonatal MK-801 treatment showed no significant main effect (Fig. 2b). Post hoc analyses revealed that the distance traveled was significantly shorter in V/E than in V/S ( $P=0.009$ ) and M/S ( $P=0.034$ ).



**Fig. 2** Behavioral effects of MK-801 and repeated ECS treatments on rats. The figure shows **a** PPI and **b** locomotor activity of the animals. PPI (%) was calculated as percent of  $[1 - (\text{mean startle magnitude after prepulse and pulse}/\text{mean startle magnitude after pulse alone})] \times 100$ . PPI data were organized according to the prepulse stimulus intensity. Locomotor activity was measured as the distance moved in centimeters in an open field during a 30-min test session.

Bars represent mean  $\pm$  SEM of each behavioral assay. \* $P<0.05$  and \*\* $P<0.01$  (significant differences between groups). # $P<0.05$  (significant interactions between MK-801 treatment and electroconvulsive shock). Abbreviations: V/S, vehicle-sham shock  $\times$  10 days (Sham) group; V/E, vehicle-ECS  $\times$  10 days (E10X) group; M/S, MK-801-Sham group; M/E, MK-801-E10X group; PPI, prepulse inhibition; dB, decibels

## Transcriptomic analyses of PFC samples

We used PFC samples from four animals in each group and obtained high-quality RNA (mean RNA integrity number: 8.7; range: 7.1–9.3) for mRNA sequencing analysis. With strict adherence to the procedures in the “[Methods](#)” section to ensure the quality of the mRNA, an average of 16,348,154 trimmed reads ( $SEM = 207,628$ ) were processed to yield an average of 15,791,396 mapped reads per sample ( $SEM = 204,919$ ) (Supplementary Table 2), to the reference genome, rn6, from the University of California, Santa Cruz genome database. The scatterplots of the gene expression levels between the two samples were drawn (Supplementary

[Fig. 1](#)). A total of 17,048 genes were detected. The raw expression level results for each gene are also presented in the supplementary material.

In the analysis of the gene expression profile of M/E compared with M/S, performed to demonstrate the effect on neonatal MK-801-induced changes, 53 genes were identified as DEGs. The five most upregulated genes were *Crabp1*, *Mmp9*, *Sprrla*, *Igfbp6*, and *Aqp1*, and the five most downregulated genes were *Harb1l*, *Fos*, *Fosb*, *Ptgds*, and *Egr2* (Table 1a, b). Next, the gene expression profile of V/E was compared with that of V/S to examine the effects of E10X. In total, 34 DEGs were identified. The five most upregulated genes were *Crabp1*, *Calm14*, *Aqp1*, *Timp1*, and *Masp1*, and

**Table 1** Top five DEGs based on mRNA-Seq analysis ranked by fold change

Gene name	Ensembl gene ID	Log2FC	P value	FDR
(a) Upregulated in M/E, compared to M/S				
Crabp1	ENSRNOG00000023633	2.173655772	4.43E-19	1.65E-15
Mmp9	ENSRNOG0000017539	2.089660053	7.47E-08	4.19E-05
Sprrla	ENSRNOG0000024028	1.769602671	9.90E-10	8.77E-07
Igfbp6	ENSRNOG0000010977	1.767518236	4.21E-06	1.37E-03
Aqp1	ENSRNOG0000011648	1.674059167	4.60E-08	2.95E-05
(b) Downregulated in M/E, compared to M/S				
Harb1l	ENSRNOG0000043204	-1.722559975	1.52E-07	7.87E-05
Fos	ENSRNOG0000008015	-1.326977137	2.96E-29	5.51E-25
Fosb	ENSRNOG0000046667	-1.238502853	9.33E-14	1.58E-10
Ptgds	ENSRNOG0000015550	-1.179094976	2.05E-07	9.52E-05
Egr2	ENSRNOG0000000640	-1.09628899	5.40E-11	5.58E-08
(c) Upregulated in V/E, compared to V/S				
Crabp1	ENSRNOG0000023633	2.851953953	3.45E-13	6.43E-09
Calm14	ENSRNOG0000038202	2.524179642	5.24E-05	3.05E-02
Aqp1	ENSRNOG0000011648	1.812551855	1.00E-05	9.34E-03
Timp1	ENSRNOG0000010208	1.277733088	1.18E-05	9.98E-03
Masp1	ENSRNOG0000001827	0.953378862	2.90E-06	3.60E-03
(d) Downregulated in V/E, compared to V/S				
Cox6a2	ENSRNOG0000019851	-1.263626858	7.70E-05	3.95E-02
Fos	ENSRNOG0000008015	-1.088532153	1.61E-09	7.25E-06
Pdyn	ENSRNOG0000026036	-1.023465337	9.75E-08	2.02E-04
Fosb	ENSRNOG0000046667	-1.013057495	3.24E-06	3.78E-03
Egr4	ENSRNOG0000015719	-1.006908967	6.84E-10	4.25E-06
(e) Upregulated in M/S, compared to V/S				
Mx2	ENSRNOG0000001963	2.464436765	4.19E-09	7.79E-05
Hspa2	ENSRNOG0000006472	0.665163188	4.21E-05	3.48E-02
(f) Downregulated in M/S, compared to V/S				
Igfbp6	ENSRNOG0000010977	-2.273219315	2.08E-08	1.93E-04
Pde4a	ENSRNOG0000020828	-1.641666343	1.41E-05	2.01E-02
H2az1	ENSRNOG0000010306	-1.553003106	2.06E-06	4.26E-03
Btf3	ENSRNOG0000016912	-1.548191245	1.28E-05	1.97E-02
Lmo2	ENSRNOG0000009401	-1.080952282	4.99E-07	1.86E-03

(a) and (b) M/E versus M/S models, (c) and (d) V/E versus V/S models, and (e) and (f) M/S versus V/S models. For each gene, the Ensembl gene ID, log2FC, P-value, and FDR are listed. Abbreviations: V/S, vehicle-sham shock×10 days (Sham) group; V/E, vehicle-ECS×10 days group (E10X); M/S, MK-801-Sham group; M/E, MK-801-E10X group

the five most downregulated were *Cox6a2*, *Fos*, *Pdyn*, *Fosb*, and *Egr4* (Table 1c, d). Finally, the gene expression profile of M/S was compared with V/S to investigate the long-term effects of neonatal MK-801 treatment, and 16 DEGs were identified. The two upregulated genes were *Mx2* and *Hspa2*, and the five most downregulated genes were *Igfbp6*, *Pde4a*, *H2az1*, *Btf3*, and *Lmo2* (Table 1e, f). The complete list of DEGs and their respective log2FC, *P* value, and FDR are shown in Supplementary Table 3.

## Network analyses of the transcriptomic data

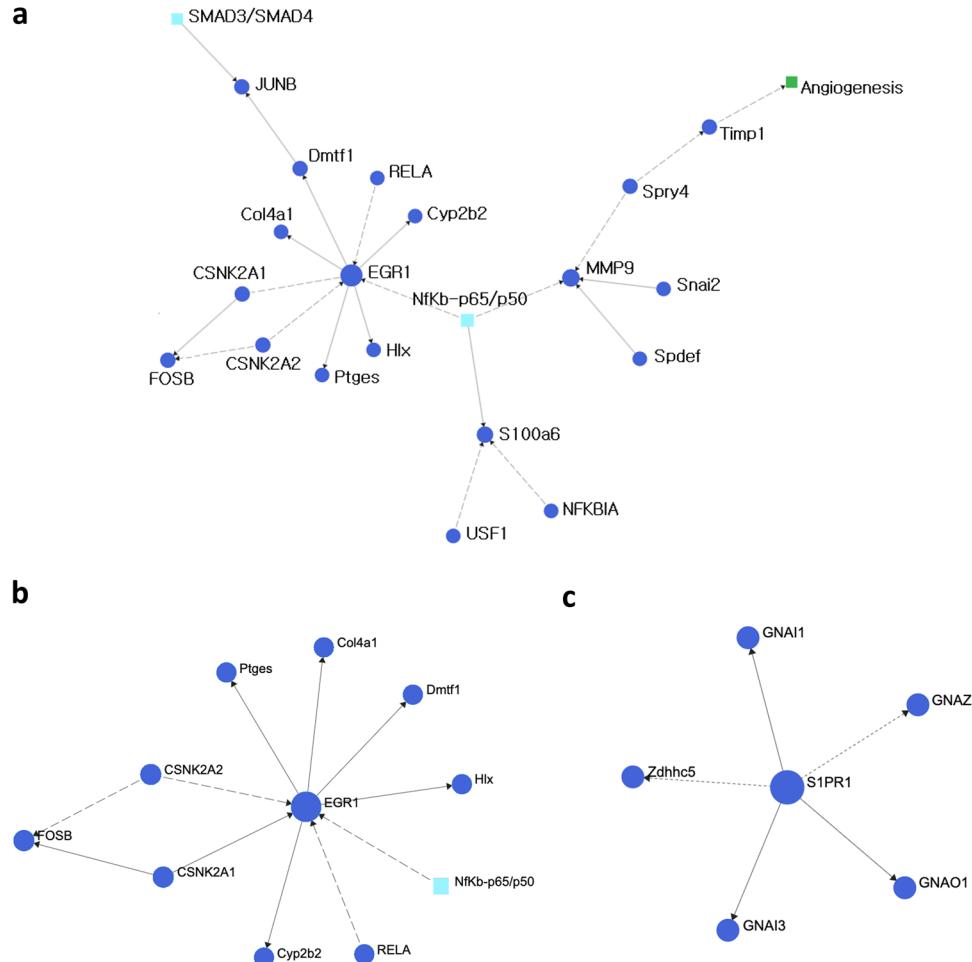
We then produced a gene regulatory network of co-expressed genes using the transcriptomic data for each set of DEGs (see Methods section). In the network of DEGs of M/E compared with those of M/S, the *NfKb-p65/p50* complex was found to be located in the center and connected to *Egr1*, *S100a6*, and *Mmp9* (Fig. 3a). Pathway analysis using the KEGG database showed that the three most relevant pathways as interleukin (IL)-17 signaling, nuclear factor kappa B (NF-κB) signaling, and tumor necrosis factor (TNF) signaling (Table 2a). In the network of DEGs of V/E compared with those of V/S,

*Egr1* (degree = 9, betweenness = 42.5) was located in the center, directly connecting 9 other genes (Fig. 3b). The three KEGG pathways most relevant to DEGs of M/S vs. V/S were mitophagy, NF-κB signaling, and advanced glycation end products (AGE)–receptor for advanced glycation end products (RAGE) signaling (Table 2b). Finally, in the network of DEGs of M/S compared to V/S, *S1pr1* (degree = 5, betweenness = 10) was in the center, directly connecting 5 other genes (Fig. 3c). The three KEGG pathways most relevant to DEGs of M/S vs. V/S were long-term depression, GABAergic synapse, and morphine addiction (Table 2c).

## qPCR analyses

As described in the “Methods” section, the genes with a log2FC of  $> 1$  or  $< -1$ , and the genes coding the proteins with degree of  $\geq 3$  in the gene regulatory network, were included in the qPCR analyses. In total, 29 genes were targeted for qPCR analyses. The expression levels relative to actin and corresponding *P*-values are shown in Supplementary Table 4.

**Fig. 3** Gene regulatory networks of DEGs. The figure illustrates gene regulatory networks of DEGs in **a** M/E versus M/S model, **b** V/E versus V/S model, and **c** M/S versus V/S model. Arrows show the direction from an upstream regulator to a downstream target. Shapes and colors are denoted as follows: circles = proteins, squares = complexes, blue = proteins, teal = complexes, and green = phenotypes. Abbreviations: V/S, vehicle-sham shock  $\times 10$  days (Sham) group; V/E, vehicle-ECS  $\times 10$  days (E10X) group; M/S, MK-801-Sham group; M/E, MK-801-E10X group



**Table 2** Annotation results of the top three KEGG pathways enriched in the gene regulatory network

KEGG pathway	Hits	Expected	P value	FDR
(a) Network based on DEG between M/E and M/S				
IL-17 signaling pathway	4	0.141	8.72E-06	1.70E-03
NF-kappa B signaling pathway	4	0.152	1.16E-05	1.70E-03
TNF signaling pathway	4	0.165	1.62E-05	1.70E-03
(b) Network based on DEG between V/E and V/S				
Mitophagy	3	0.0596	2.15E-05	6.74E-03
NF-kappa B signaling pathway	3	0.0935	8.31E-05	8.95E-03
AGE-RAGE signaling pathway	3	0.0944	8.55E-05	8.95E-03
(c) Network based on DEG between M/S and V/S				
Long-term depression	4	0.0355	1.15E-08	3.60E-06
GABAergic synapse	3	0.0527	1.12E-05	8.20E-04
Morphine addiction	3	0.0533	1.15E-05	8.20E-04

(a) DEGs between M/E and M/S, (b) DEGs between V/E and V/S, and (c) DEGs between M/S and V/S. For each pathway, the pathway name, number of hits, expected number of genes, P-value, and FDR are listed. Abbreviations: *DEG*, differentially expressed genes; *IL-17*, interleukin-17; *NF*, nuclear factor; *TNF*, tumor necrosis factor; *AGE-RAGE*, advanced glycation end products-receptor for advanced glycation end products; *V/S*, vehicle-sham shock  $\times$  10 days (Sham) group; *V/E*, vehicle-ECS  $\times$  10 days group (E10X); *M/S*, MK-801-Sham group; *M/E*, MK-801-E10X group

Twenty genes were selected for qPCR analysis in the comparison of M/E and M/S (*Crabp1*, *Mmp9*, *Sprrla*, *Igfbp6*, *Aqp1*, *Cd74*, *Lgals3*, *Ecell*, *S100a6*, *Timp1*, *Dusp6*, *Egr1*, *Nr4a3*, *Junb*, *Egr4*, *Egr2*, *Ptgds*, *Fosb*, *Fos*, and *Harb1l*, from highest to lowest fold change). Eight upregulated genes (*Crabp1*, *Mmp9*, *Sprrla*, *Igfbp6*, *Cd74*, *Lgals3*, *Ecell*, and *S100a6*, from highest to lowest absolute fold change magnitude) and four downregulated genes (*Harb1l*, *Fos*, *Fosb*, and *Egr2*, from highest to lowest absolute fold change magnitude) showed significant differences in qPCR (Fig. 4a). Among the three central genes in the corresponding regulatory network, *Egr1* expression was significantly lower, and *S100a6* and *Mmp9* expression was significantly higher, in M/E than in M/S.

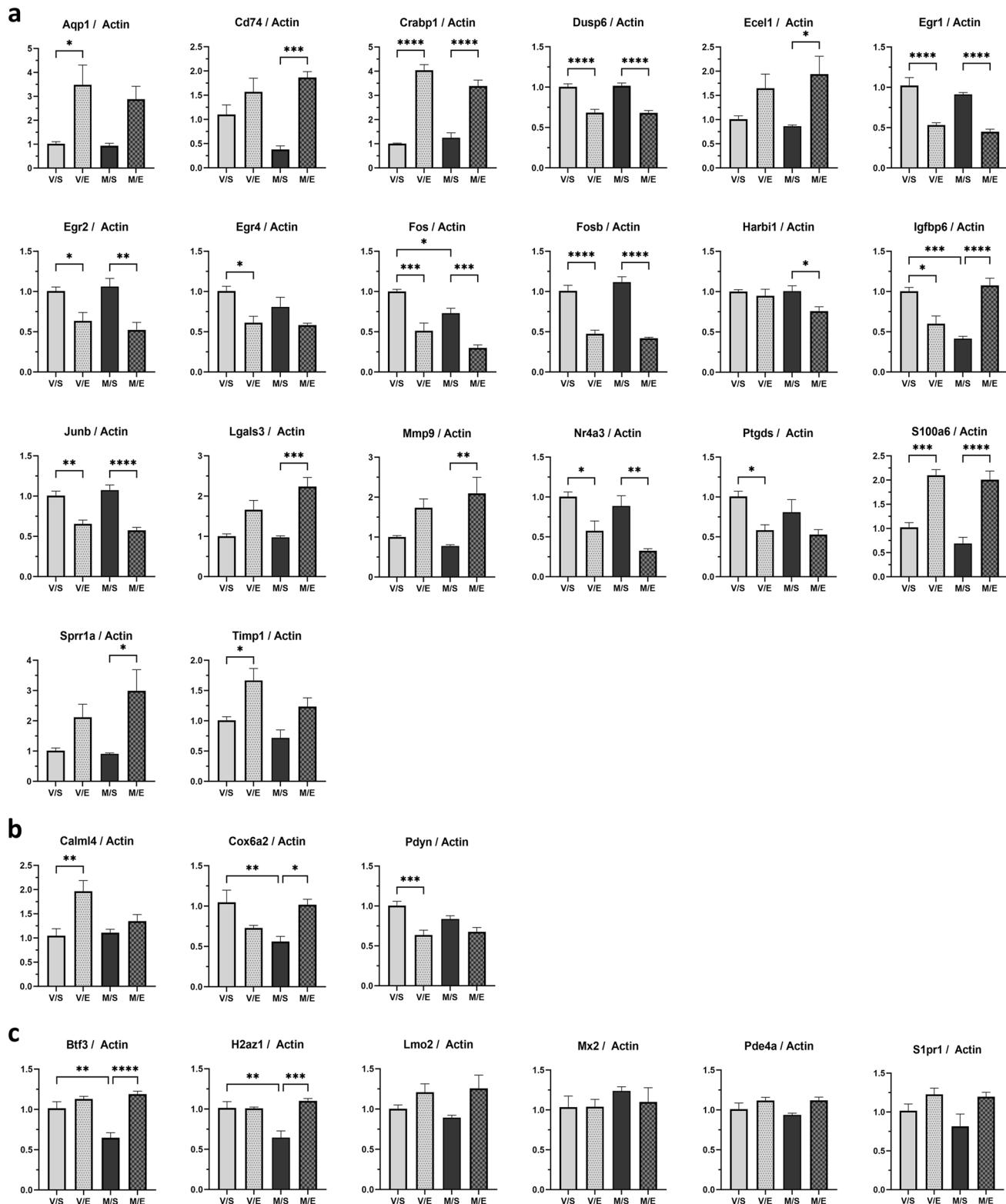
Twelve genes were selected for qPCR analysis in the comparison of V/E and V/S (*Crabp1*, *Calml4*, *Aqp1*, *Timp1*, *Egr1*, *Nr4a3*, *Ptgds*, *Egr4*, *Fosb*, *Pdyn*, *Fos*, and *Cox6a2*, from highest to lowest fold change). Four upregulated genes (*Crabp1*, *Calml4*, *Aqp1*, and *Timp1*, from highest to lowest absolute fold change magnitude) and four downregulated genes (*Fos*, *Pdyn*, *Fosb*, and *Egr4*, from highest to lowest absolute fold change magnitude) showed significant differences in qPCR (Fig. 4b). *Egr1*, the central gene in the corresponding regulatory network, had a significantly lower expression level in V/E than in V/S.

Seven genes were selected for qPCR analysis in the comparison of M/S and V/S (*Mx2*, *S1pr1*, *Lmo2*, *Btf3*, *H2az1*, *Pde4a*, and *Igfbp6*, from highest to lowest fold change). Although *Mx2*, an upregulated gene, did not show a significant difference, three downregulated genes (*Igfbp6*, *H2az1*, and *Btf3*, from highest to lowest absolute fold change magnitude) showed significant differences in qPCR (Fig. 4c). *S1pr1*, the central gene in the corresponding regulatory network, showed no significant difference.

## Discussion

The present study examined the behavioral and transcriptomic effects of repeated ECS in an animal model of schizophrenia. Neonatal treatment of MK-801 induced PPI deficits in young adult rats, confirming the relevance of this treatment for establishing a neurodevelopmental animal model. Repeated ECS treatments normalized the MK-801-derived PPI deficits and induced significant alterations in the PFC transcriptome of MK-801-treated animals. Comparison of the transcriptomes between M/E and M/S, showing the effects of repeated ECS on neonatal MK-801-treated animals, revealed 53 DEGs. The network analysis of DEGs identified *Egr1*, *Mmp9*, and *S100a6* as central genes of the regulatory network, and KEGG pathway enrichment analyses showed that IL-17, NF- $\kappa$ B, and TNF signaling were the three most relevant pathways in this comparison. Among the downregulated genes in the MK-801-treated group, *Igfbp6*, *Btf3*, *Cox6a2*, and *H2az1* recovered their respective expression level with repeated ECS treatments. The findings demonstrate that repeated ECS treatments confer antipsychotic-like benefits in the animal models of psychosis and imply that such an effect likely involves gene networks that regulate insulin, and mitophagy pathways.

Sensorimotor gating dysfunction is a central mechanism in the pathogenesis of schizophrenia (San-Martin et al. 2020; Swerdlow and Light 2018). Because PPI can be used to quantitatively measure sensorimotor gating function in both humans and animals (Garcia-Mompo et al. 2020; Miller et al. 2021; San-Martin et al. 2020; Tsivion-Visbord et al. 2020), PPI has been utilized as a standard behavioral measure in animal models of psychosis (Bialon and Wasik 2022; Khan and Powell 2018; Swerdlow and Light 2018). PPI deficits induced by perinatal antagonism of NMDA receptors have been demonstrated repeatedly (Li et al. 2016; Lim et al. 2012b; Phensy et al. 2017; Uehara et al. 2009) and were confirmed in the present study. ECS has been demonstrated to normalize PPI in rats selectively bred for high and low PPI (John et al. 2016), in rats with methamphetamine-induced psychotomimetic conditions (Chao et al. 2012), and in Gunn rats with schizophrenia-like behaviors (Limoa et al. 2016). This study also confirmed the antipsychotic effect of



**Fig. 4** Real-time qPCR analysis results. qPCR graphs of **a** genes included in DEGs between M/E and M/S, **b** genes included in DEGs between V/E and V/S, and **c** genes included in DEGs between M/S and V/S are shown. Genes already listed in **a** are not shown in **b** or **c**. The relative mRNA expression level of each gene was normalized to actin with the comparative Ct method, with the expression level

of V/S set as 1.0. In each group, the graphs are organized in alphabetical order of gene names. \* $P < 0.05$ , \*\* $P < 0.01$ , \*\*\* $P < 0.001$ , and \*\*\*\* $P < 0.0001$  (significant differences between groups). Abbreviations: V/S, vehicle-sham shock  $\times$  10 days (Sham) group; V/E, vehicle-ECS  $\times$  10 days (E10X) group; M/S, MK-801-Sham group; M/E, MK-801-E10X group

repeated ECS treatments, which normalized the sensorimotor deficits produced by the neonatal MK-801 treatment.

The long-term effects of MK-801 on spontaneous locomotor activity of rodents are mixed: the activity level increases, does not significantly change, or decreases depending on the experimental conditions (Akosman et al. 2021; Guneri et al. 2021; Kawabe and Miyamoto 2019; Lim et al. 2012a; b; Murueta-Goyena et al. 2018). In this study, neonatal MK-801 injection induced no significant effect on the locomotor activity level on PN59, and repeated ECS treatments led to a decreasing trend in the activity level. Systemic treatment of NMDA receptor antagonists induces dose-dependent changes in the locomotor activity level of rodents. In adult rodent models, a lower dose of MK-801 induces hyperactivity, while a higher dose induces either no changes or hypoactivity (Ahn et al. 2006; Gururajan et al. 2011; Kawabe and Miyamoto 2019; Liljequist et al. 1991). In the present study, MK-801 was injected twice daily at an 8-h interval using a dose of 1.0 mg/kg, which is higher than the doses of 0.1 mg/kg (Xiao et al. 2019), 0.2 mg/kg (Kraeuter et al. 2020), and 0.3 mg/kg (Cui et al. 2022) that produced hyperlocomotion in rodents. Although there is no clear relationship between the administered dose of the perinatal NMDA receptor antagonist and adult locomotor activity (Lim et al. 2012a), the MK-801 dose that affects the activity level in the adult period requires further clarification. Moreover, based on the two-hit hypothesis (Khan and Powell 2018; Lim et al. 2012b), additional stimuli during the adult period (after the early life manipulation) may induce more prominent psychotomimetic changes, such as hyperlocomotion, in rodent animal model (Lim et al. 2012b; Zhao et al. 2013). In this study, no additional stimulus was applied after the prenatal treatment, which may explain the lack of changes in locomotor activity. The repeated ECS treatments in this study reduced the activity level of rats, as reported in previous literature (Batterman et al. 2019; Park et al. 2011). Further investigation using a different MK-801 dose or an additional provocation will be needed to confirm the effects of repeated ECS on rodent hyperactivity.

*Egr1*, *NFKb-p65/p50*, *Mmp9*, and *S100a6* were identified as central genes in the network model of the effects of repeated ECSs in the psychosis animal model. *Egr* family genes, which are zinc finger transcriptional regulators involved in synaptic plasticity and memory, are implicated in schizophrenia (Cheng et al. 2012; Kim et al. 2010b; Yamada et al. 2007). Accordingly, a biological pathway that integrates NMDA receptors, *Egr* family genes, and long-term depression has been suggested as a possible explanation for the pathophysiology of schizophrenia (Marballi and Gallitano 2018). Especially, *Egr1* has been shown to be a key gene in schizophrenia in expression studies (Cattane et al. 2015; Li et al. 2022c; Pouget et al. 2016; Xu et al. 2016). In the central nervous system, *Egr1* exhibits unique roles

in synaptic plasticity regulation (Duclot and Kabbaj 2017; Pouget et al. 2016), dopamine signaling during social interactions (Tallafuss et al. 2022), and memory formation (Gallo et al. 2018; Marballi and Gallitano 2018; Veyrac et al. 2014). Downregulation of immediate early genes (IEGs) including *Egr1* by repeated seizures has been demonstrated in several studies (Calais et al. 2013; Kalinina et al. 2022; Tsankova et al. 2004). We previously reported that repeated ECS treatments downregulated the expression of IEGs, such as *Egr1*, *Egr2*, and *c-Fos*, and inhibited the cocaine-induced increase of these genes in the rat frontal cortex (Park et al. 2011) and that this process was mediated by the histone deacetylase 2 (Park et al. 2014). IEGs including *Egr1* are important modulators of antipsychotic-induced neuroplasticity as well (de Bartolomeis et al. 2017; Verma et al. 2006). Considering that IEGs were enriched in the network analysis of DEGs between samples of schizophrenia patients before and after electroconvulsive therapy (Peng et al. 2021), focusing on IEGs such as *Egr1* holds promise for future research into the mechanisms underlying the antipsychotic effects of ECT.

In our pathway analysis, the IL-17, NF- $\kappa$ B, and TNF signaling pathways were identified as key enriched KEGG pathways in the regulatory network of repeated ECS treatments in psychosis animal models. NF- $\kappa$ B, a central pro-inflammatory transcription factor, induces several inflammatory cytokines, activates immune cells, and regulates inflammasomes; however, its dysregulation leads to inflammatory diseases and tumorigenesis (Liu et al. 2017; Yu et al. 2020). In the central nervous system, NF- $\kappa$ B plays important roles in synaptic plasticity and neurogenesis and protects neurons from injury; however, inducible NF- $\kappa$ B in glia causes neuronal damage that can lead to various neuroinflammation-associated pathogenesis (Shih et al. 2015). Neuroinflammation plays a critical role in schizophrenia, as numerous studies have reported an association between the two (Bae et al. 2023; Pandurangi and Buckley 2020; Rahman et al. 2022; Zhu et al. 2021). Patients with schizophrenia show elevated concentrations of plasma inflammatory markers, including NF- $\kappa$ B (de Bartolomeis et al. 2022; Kartalci et al. 2016; Miller and Goldsmith 2020; Muller et al. 2015), as well as upregulated NF- $\kappa$ B transcripts in the PFC (Murphy et al. 2021). Consequently, neuroinflammation is increasingly becoming the focus in terms of the pathogenesis of schizophrenia, as well as a therapeutic target (Messina et al. 2023; Miller and Goldsmith 2020; Mongan et al. 2020). NF- $\kappa$ B deserves particular attention because of cortical immune activation (Volk et al. 2019) and its involvement in the dysregulation of susceptible genes in schizophrenia (Long et al. 2022). Antipsychotics are known to reduce inflammation by attenuating cytokine expression (Dutheil et al. 2023; Patlola et al. 2023), including NF- $\kappa$ B (Al Abadey et al. 2022; Zhu et al. 2019). We have previously reported that the antipsychotic agent clozapine exerts

anti-inflammatory actions via the NF-κB signaling pathway (Jeon et al. 2018). Likewise, repeated ECT treatments attenuate inflammation in the long term (Gammon et al. 2021; Maffioletti et al. 2021; Yrondi et al. 2018). ECT reduces the concentrations of inflammatory cytokines (Xu et al. 2016; Yrondi et al. 2018) and NF-κB in patients with severe mental disorders, including schizophrenia (Bioque et al. 2019; Xu et al. 2016). Because the change in inflammatory biomarkers likely predicts the ECT response, the involvement of inflammation-related mechanisms in the therapeutic action of ECT has been suggested (Dogaru et al. 2022; Kruse et al. 2018). The findings from the previous studies and this study suggest that inflammatory signaling pathways can mediate the antipsychotic effects of ECT.

Other important genes identified as the central genes in this study are *Mmp9* and *S100a6*. Matrix metalloproteinase-9 (MMP-9) in the central nervous system regulates dendritic and synaptic dynamics (Li et al. 2022b), maintains NMDA-dependent long-term potentiation (Beroun et al. 2019), and regulates neuroinflammation by focally activating chemokines (Hannocks et al. 2019). MMP-9 is also implicated in the pathophysiology of schizophrenia (Beroun et al. 2019; Keshri and Nandeesha 2023; Lepeta and Kaczmarek 2015). Reduced activity of MMP-9 in the brain induces schizophrenia-like behaviors in mice (Vafadari et al. 2019). MMP-9 was also found to be elevated in patients with clozapine-treated schizophrenia (Yamamori et al. 2013). Consistent with previous literature, the present study showed that repeated ECS treatments upregulate MMP-9 (Girgenti et al. 2011). Therefore, the therapeutic action of repeated ECS treatments may involve the regulation of MMP-9.

*S100A6*, a member of the calcium-binding protein family, is involved in cellular repair and regeneration (Lesniak and Filipek 2023) and attenuates inflammatory responses via the PI3K/Akt pathway (Zhang et al. 2021). *S100A6* is increased in status epilepticus (Jurewicz et al. 2013) and neurodegenerative disorders (Filipek and Lesniak 2020), whereas it is decreased under chronic stress (Bartkowska et al. 2017). Although the present study suggests that repeated ECS treatments upregulate *S100* proteins (Huang and Chen 2008), future studies are needed to confirm this finding. In our pathway analysis, the AGE-RAGE signaling pathway was a key enriched pathway in repeated ECS treatments. This pathway, which is involved in impaired downstream insulin signaling (Khalid et al. 2022), can interact with *S100* proteins and plays pivotal roles in immunity (Rouhiainen et al. 2013; Yatime et al. 2016).

This study illustrated the downregulation of *Igfbp6* induced by MK-801 and subsequent normalization by repeated ECS treatments. Schizophrenia is associated with abnormalities in insulin signaling (Agarwal et al. 2020a), and antipsychotics affect central insulin signaling, which may be related to therapeutic mechanism (Agarwal et al.

2020b; Kowalchuk et al. 2019). Insulin-like growth factor binding protein (IGFBP) family proteins modulate insulin growth factor receptor signaling (Baxter 2023); its member protein, IGFBP-6, regulates apoptosis and cell migration in the central nervous system (Bei et al. 2017; Dai et al. 2017). Schizophrenia is associated with decreased levels of IGFBP family proteins (Weissleder et al. 2021; Yang et al. 2020). Moreover, antipsychotic use upregulates circulating levels of an IGFBP (Fernandez-Pereira et al. 2022). The present study is the first to show that repeated ECS treatments rescue IGFBP-6 expression altered by a psychotomimetic condition, indicating that the therapeutic action of repeated ECS may involve IGFBP-6-induced modulation of insulin signaling.

Mitophagy, a selective degradation autophagy process of damaged mitochondria (Li et al. 2022a), was another key enriched pathway in the repeated ECS treatments of the present study. In the central nervous system, mitophagy plays key roles in synapse regulation and parvalbumin interneuron alterations (Khadimallah et al. 2022; Palikaras and Tavernarakis 2020). Mitophagy is linked to NF-κB through the p62-mitophagy pathway, which serves as a self-regulatory mechanism for NF-κB (Zhong et al. 2016). Schizophrenia is a neuropsychiatric disorder with disrupted mitophagy or autophagy processes (Merenlender-Wagner et al. 2015; Panda and Singh 2023; Yang and Xu 2020). Conversely, antipsychotics induce autophagy by stimulating related cellular pathways and may reduce neuronal dysfunction in schizophrenia (Kim et al. 2018b; Otreba et al. 2023; Vucicovic et al. 2018; Yang and Xu 2020; Zhu et al. 2019). We and others previously reported that repeated ECS treatments stimulated autophagy signaling and related pathways, such as the adenosine monophosphate-activated protein kinase pathway (Huh et al. 2023; Kim et al. 2022; Otabe et al. 2014). The present findings suggest the importance of mitophagy and autophagy in the therapeutic action of repeated ECS treatments and indicate the need for more studies to elucidate this relationship.

Other genes normalized by repeated ECS treatments in this animal model of psychosis include *Cox6a2*, *Btf3*, and *H2az1*; however, data on the relationship of these genes to schizophrenia are limited. The level of COX6A2 was reduced in an animal model of schizophrenia and displayed potential as a schizophrenia biomarker (Khadimallah et al. 2022). BTF3, along with other molecules, contributes to mitochondrial fusion and neuroprotection (Zeng et al. 2021). H2A.z supports normal neuronal differentiation and dendrite structure, and its absence causes behavioral abnormalities (Shen et al. 2018). Our results suggest that these proteins serve important roles in the antipsychotic action of repeated ECS treatments. Considering their above-described roles in the central nervous system, these proteins will be of particular interest for future studies.

In conclusion, this study illustrated the molecular mechanism underlying the antipsychotic-like action of repeated ECS treatments in an MK-801 schizophrenia animal model. In our experimental condition, the PPI deficit caused by neonatal MK-801 treatment was normalized with repeated ECS treatments, whereas locomotor activity remained unaffected. Thus, the transcriptomic alterations observed in this study may be associated with the changes in sensorimotor gating in psychosis model rodents, but their direct relationship requires further investigation. The sequencing analysis and subsequent pathway analysis revealed that the therapeutic mechanism of ECS likely involves the modulation of molecular pathways related to neuroinflammation, IEGs, insulin signaling, and mitophagy processes. Key genes in these analyses were confirmed by qPCR analysis. Additional studies, especially those investigating the therapeutic potential of the promising genes identified in this study, are needed to validate the present findings and shed light on clinical correlations.

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## Declarations

**Conflict of interest** The authors declare no competing interests.

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