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Data in Brief

Gene expression profiling in rats with depressive-like behavior

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ABSTRACT

Individual differences indicate stronger phenotypes than model animals especially in behavioral studies, and some animals show unexpected behaviors in control and animal model groups. High-throughput analysis including cDNA microarray analysis are more affected by individual differences, because more samples are needed to reduce the difference in multiple factor analysis than single factor analysis such as real-time PCR. We measured the depressive-like behavior of over 100 normal rats in the forced swimming test and selected the rats for control and depression group from them to minimize the individual difference using data of force swimming test. Here, we provided the detail of methods and quality control parameters for the cDNA microarray data. This dataset can reflect the increase of depressive-like behavior. The dataset is deposited in the gene expression omnibus (GEO), series GSE63377.

Specifications	
Organism/cell line/tissue	Wistar rats/cerebellum and prefrontal cortex
Sex	Male
Sequencer or array type	SurePrint G3 Rat Gene Expression 8 × 60 K Microarray Kit
Data format	Normalized
Experimental factors	Immobility ratio in forced swimming test
Experimental features	We selected rats with average depressive-like behavior and ones with increasing depressive-like behavior from 106 rats using results of forced swimming test.
Consent	
Sample source location	

1. Direct link to deposited data

The expression dataset was deposited in the gene expression omnibus (GEO) under series accession number GSE63377 (http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE63377).

2. Experimental design, materials and methods

2.1. Animals

Animal preparation was written [1] and a brief method of preparation was cited below. The immobility ratios of 106 male Wistar rats were measured in the forced swimming test. We selected the rats with immobility ratio from −1 to +1 SD from the mean as control group and rats with immobility ratio from +1 to +2 SD above the mean as depressive group. Collection of brain tissues for preparing RNA samples was performed one week after the forced swimming test.

2.2. RNA sample preparation

Under isoflurane anesthesia, the brain was perfused with cold phosphate-buffered saline through the heart using a syringe with cannula. Coronal brain sections (1 mm thick) were prepared on ice, using a brain slicer (Muromachi Kikai, Tokyo, Japan). The prefrontal cortex was sliced 3.2 to 4.2 mm anterior to the bregma, and the cerebellum 9.8 to 10.8 mm posterior to the bregma. Total RNA was isolated immediately from these tissue samples using an RNeasy kit (Qiagen, Hilden, Germany).

2.3. Microarray analyses

Four rats were randomly selected from each group, and an equal amount of RNA from four rats per group was pooled. The quality of purified RNA was assessed using a NanoDrop 2000c (Thermo Fisher Scientific, Waltham, MA) and an Agilent 2100 Bioanalyzer with an RNA 6000 Nano Labchip kit (Agilent Technologies, Palo Alto, CA, USA) (Table 1). Total RNA (400 ng per group) was first reverse transcribed using a T7 sequence-conjugated oligo dT primer, using a One Color RNA Spike-In Kit (Agilent) for internal positive controls. Production of complementary RNA (cRNA) with Cy3 dye were performed according to the manufacturer's protocols. Prepared cRNA was hybridized with a SurePrint G3 Rat Gene Expression 8 × 60 K Microarray Kit (Agilent) at 65 °C for 17 h. Fluorescence intensity was measured using a scanner (G2565BA; Agilent). The signal intensities were quantified and analyzed

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Table 1
Quality of RNA samples.

Sample name	Accession no.	A260/A280	A260/A230	RIN
Cerebellum_Control	GSM1547703	2.10	1.95	8.8
PrefrontalCortex_Control	GSM1547704	2.09	1.90	8.3
Cerebellum_Depression	GSM1547705	2.11	2.09	8.3
PrefrontalCortex_Depression	GSM1547706	2.11	2.07	7.9

Table 2
Agilent spike-in concentration-response statistics and liner range statistics.

Sample name	Low relative concentration	High relative concentration	Slope	R^2 value
Cerebellum_Control	1E+1.67	1E+6.61	1.01	0.99
PrefrontalCortex_Control	1E+1.60	1E+6.51	1.02	0.99
Cerebellum_Depression	1E+1.96	1E+6.59	1.03	0.99
PrefrontalCortex_Depression	1E+1.64	1E+6.64	1.01	0.99

by subtracting background fluorescence using Feature Extraction software (Agilent). Linier range statistics showed that a value representing linearity between signal intensities and concentration of positive control if signal intensities were more than 92 (Table 2).

Normalization among data was performed by GeneSpring 12.0 software (Agilent). There were no differences of number of detectable probes among data (Table 3).

Table 3
Number of detectable probes.

Sample name	Detected probe	Compromised probes	Not detected probe
Cerebellum_Control	23,237	2	7128
PrefrontalCortex_Control	22,711	2	7654
Cerebellum_Depression	21,782	4	8581
PrefrontalCortex_Depression	22,959	2	7406

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Reference

[1] Y. Yamamoto, T. Ueyama, T. Ito, Y. Tsuruo, Down-regulation of growth hormone 1 gene in the cerebellum and prefrontal cortex of rats with depressive-like behavior. Physiol. Genomics 47 (5) (2015 May) 170–176. http://dx.doi.org/10.1152/physiolgenomics.00119.2014.