



Behavioral and gene expression analyses of *Wfs1* knockout mice as a possible animal model of mood disorder

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Abstract

Wolfram disease is a rare genetic disorder frequently accompanying depression and psychosis. Non-symptomatic mutation carriers also have higher rates of depression and suicide. Because *WFS1*, the causative gene of Wolfram disease, is located at 4p16, a linkage locus for bipolar disorder, mutations of *WFS1* were suggested to be involved in the pathophysiology of bipolar disorder. In this study, we performed behavioral and gene expression analyses of *Wfs1* knockout mice to assess the validity as an animal model of mood disorder. In addition, the distribution of *Wfs1* protein was examined in mouse brain. *Wfs1* knockout mice did not show abnormalities in circadian rhythm and periodic fluctuation of wheel-running activity. Behavioral analysis showed that *Wfs1* knockout mice had retardation in emotionally triggered behavior, decreased social interaction, and altered behavioral despair depending on experimental conditions. *Wfs1*-like immunoreactivity in mouse brain showed a similar distribution pattern to that in rats, including several nuclei potentially relevant to the symptoms of mood disorders. Gene expression analysis showed down-regulation of *Cdc42ep5* and *Rnd1*, both of which are related to Rho GTPase, which plays a role in dendrite development. These findings may be relevant to the mood disorder observed in patients with Wolfram disease.

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1. Introduction

Wolfram disease (Online Mendelian Inheritance in Man [OMIM] 222300) is a rare autosomal recessive neurodegenerative disorder characterized by early-onset diabetes mellitus, progressive optic atrophy, diabetes insipidus, and deafness (Domenech et al., 2006); *WFS1/wolframin* has been identified as the causative gene (Strom et al., 1998; Inoue et al., 1998). Approximately, 60% of the patients with Wolfram disease have mental symptoms, such as severe depression, psychosis, impulsivity, and aggression (Swift et al., 1990). More importantly, carriers of *WFS1* mutations, who are not affected with Wolfram disease, have a 26-fold higher likelihood of

psychiatric hospitalization mainly due to depression (Swift and Swift, 2000). The *WFS1* gene locates at 4p16.1 (Strom et al., 1998; Inoue et al., 1998), a replicated linkage locus of bipolar disorder (Ewald et al., 1998, 2002; Detera-Wadleigh et al., 1999). Some studies showed that bipolar disorder with psychosis (Als et al., 2004; Cheng et al., 2006) or suicidal behavior (Cheng et al., 2006) is linked with this locus. These lines of evidence suggested the possible role of *WFS1* mutations in the pathophysiology of bipolar disorder and related phenotypes.

To date, mutation screening of the *WFS1* gene has been reported in 84 patients with bipolar disorder, 54 with major depression, 119 with schizophrenia, 100 suicide victims, 3 with schizoaffective disorder, and several other patients with other psychiatric diagnoses (Ohtsuki et al., 2000; Martorell et al., 2003; Torres et al., 2001; Crawford et al., 2002; Evans et al., 2000). However, none of these patients had mutations causing Wolfram disease.

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Despite the fact that *Wfs1* mutations may not be a frequent cause of mental disorders, the mechanism underlying how *Wfs1* mutations lead to mental symptoms in patients with Wolfram disease will shed light on the pathophysiology of mood disorders. Mice lacking the *Wfs1* gene might be useful as a genetic animal model of mood disorders.

The symptoms of Wolfram disease resemble those of mitochondrial diseases and, indeed, initial studies suggested mitochondrial dysfunction in Wolfram disease based on mitochondrial DNA (mtDNA) deletions found in patients (Rotig et al., 1993). However, the protein coded by *Wfs1* was found to be localized in endoplasmic reticulum (ER) (Takeda et al., 2001; Philbrook et al., 2005). *Wfs1* expression was induced by ER stress (Fonseca et al., 2005) or *XBP1* overexpression (Kakiuchi et al., 2006), and disruption of *Wfs1* caused a dysfunctional ER stress response (Fonseca et al., 2005; Riggs et al., 2005; Yamada et al., 2006). Recent studies have provided insight into the function of *Wfs1* protein; *Wfs1* induces cation channel activity on ER membranes (Osman et al., 2003) and regulates calcium levels in ER (Takei et al., 2006). It also plays a role in stimulus-secretion coupling for insulin exocytosis in pancreatic β cells (Ishihara et al., 2004). Disruption of *Wfs1* increased vulnerability to cell death in the knockout (KO) mice (Ishihara et al., 2004; Philbrook et al., 2005; Riggs et al., 2005; Yamada et al., 2006). In the rat brain, *Wfs1* was distributed predominantly in neurons of the so-called limbic system (Takeda et al., 2001). *Wfs1* mutations could lead to loss of *Wfs1*-expressing neurons in particular brain regions of patients with Wolfram disease, which may underlie progression of mental symptoms.

In this study, we performed behavioral analysis of *Wfs1* KO mice to characterize their behavioral abnormality. We previously developed neuron-specific mutant polymerase γ -transgenic mice (mPolg Tg mice) based on a mitochondrial dysfunction hypothesis of bipolar disorder (Kato and Kato, 2000) and demonstrated that these mice had bipolar disorder-like phenotypes, such as altered circadian rhythm and periodic fluctuation of wheel-running activity (Kasahara et al., 2006). Whether or not the *Wfs1* KO mice show such wheel-running activity was examined. A behavioral test battery was also conducted to search for other behavioral phenotypes. Distribution of *Wfs1* in the brain was examined to search for the neural basis of behavioral alteration. In addition, gene expression analysis was performed to search for the molecular basis of behavioral phenotypes of *Wfs1* KO mice.

2. Experimental procedures

2.1. Generation of *Wfs1* KO mice

The methods for the generation of *Wfs1* KO mice have been described elsewhere (Ishihara et al., 2004). In brief, a neomycin-resistance gene was inserted into exon 2 of the *Wfs1* gene in the targeting vector. The targeting vector was injected into 129Sv embryonic stem (ES) cells, and the ES cells with homologous recombination were obtained. By crossing the chimeric mice with C57BL/6J (B6) mice, *Wfs1* heterozygous KO mice were obtained. Genotyping was performed as previously described (Ishihara et al., 2004). The heterozygous KO mice were crossed with the B6 mice for at least eight generations before the

analysis. The mice were maintained in a 12-h light:12-h dark cycle, except for several specific experiments as indicated. Wild-type (WT) littermates were used for the control whenever possible. All animal experiments were approved by the local animal experiment committees of RIKEN and Behavioral and Medical Sciences Research Consortium (BMSRC) (Akashi, Japan). Animal experiments were carried out in accordance with the National Institute of Health Guide for the Care and Use of Laboratory Animals. All efforts were made to minimize the number of animals used and their suffering.

2.2. Wheel-running activity

For this analysis, 11 homozygous KO mice (*Wfs1*^{-/-}) and 9 WT littermates (*Wfs1*^{+/+}) were used. All were males aged 34 weeks at the initiation of the analysis. The groups did not differ significantly in body weight.

The methods for the analysis of wheel-running activity were described in detail elsewhere (Kasahara et al., 2006). In brief, mice were individually housed in cages (width, 24 cm; depth, 11 cm; height, 14 cm) equipped with a steel wheel (width, 5 cm; diameter, 14 cm) (O'Hara & Co., Tokyo, Japan). Wheel-running activity was monitored by measuring the rotation of the wheel (3 counts/1 rotation). Food and water were available ad libitum. The data of initial 7–10 days were omitted from the analysis. Delayed and anticipatory activity indices, referring to the wheel-running activity during the initial 3 h of a light phase and that during the last 3 h of a light phase, were calculated. The periodicity of wheel-running activity was assessed by Lomb-Scargle periodogram (Kasahara et al., 2006).

The Mann-Whitney *U*-test was used for statistical analyses. Significance levels were set at 0.05 (two-tailed; d.f., degree of freedom). The average and standard error of mean (S.E.M.) were presented for each experimental parameter in one group.

2.3. Behavioral analysis: phase I. Screening by a test battery

This analysis was performed at BMSRC (Akashi, Japan). For this analysis, 14 homozygous KO mice (*Wfs1*^{-/-}), 14 heterozygous KO mice (*Wfs1*^{+/-}), and 13 WT littermates (*Wfs1*^{+/+}) were analyzed. All were males aged 12 weeks at the initiation of the behavioral analysis. The analyses were performed in the order of open-field test, startle response and prepulse inhibition test, elevated plus maze, Morris water maze, passive avoidance learning, active avoidance learning, and forced swimming test. After the behavioral test battery, the non-fasting blood glucose level was examined to rule out the possibility that elevated blood glucose levels might affect the results of behavioral analysis. There was no significant difference among the genotypes, consistent with a previous report that there was no apparent increase in blood glucose levels in *Wfs1* KO mice on the B6 background (Ishihara et al., 2004).

2.3.1. Open-field test

A transparent cubic box without a ceiling (30 cm \times 30 cm \times 30 cm) was placed in a ventilated sound-attenuating chamber. A 40-W white lamp provided room lighting, which was approximately 110 lx on the floor of the chamber. In addition, a fan attached on the upper part of the wall at one end of the chamber presented a masking noise of 45 dB. Two infrared beams were set on each wall 2 cm above the floor with an interval of 10 cm. The total number of successive interceptions of two adjoining beams on each bank was scored as locomotion behavior. The other 12 infrared ray beams were attached 4.5 cm above the floor in 2.5-cm intervals, and the total number of vertical beam interceptions was scored as rearing behavior. Each mouse was allowed to explore freely in the open-field area for 20 min.

For statistical analysis, repeated measures analysis of variance (ANOVA) with the intrasubject factor of time (1–20 min) and the intersubject factor of genotype ($-/-$, $+/-$, and $+/+$) was applied.

2.3.2. Startle response and prepulse inhibition (PPI)

Each mouse was enclosed in a transparent acrylic box (7 cm \times 7 cm \times 10 cm). Startle response was detected as vibration of the box, using an accelerometer (GH-313A, Keyence, Osaka, Japan). The acoustic startle pulse of broadband burst (115 dB, 50 ms) and tone prepulse (85 dB, 30 ms) were presented via a speaker located in front of the box. Light prepulse (30 ms) was

applied by LED. At the beginning of the session, 40 startle pulses were presented to test for basal startle responsiveness and its habituation. The average values of eight blocks, consisting of five startle pulses each, were used for the statistical analysis. After that, three different types of tones were performed: startle pulse alone ($n = 12$), startle pulse preceded by a tone prepulse ($n = 12$), and startle pulse preceded by a light prepulse ($n = 12$). Prepulses were presented 50, 100, or 200 ms before the startle pulse. In total, six types of prepulse ($n = 4$, each) were applied. The mean interval averaged 25 s (15–45 s) throughout the session. The startle response was recorded for 200 ms with the sampling frequency of 1000 Hz. The PPI was assessed by the ratio of the mean response of trials with one type of prepulse ($n = 4$) divided by the mean response of trials without prepulse ($n = 12$). Because light prepulse did not attenuate the startle response at all, only the data of tone prepulse were presented.

2.3.3. Elevated plus maze

The maze consisted of four arms, two open arms and two closed arms, 5 cm wide and 30 cm long with a gray acrylic floor, that met at a 10 cm \times 10 cm center zone. Two closed arms had the transparent walls of 15 cm height on both sides, and the open arms had the low walls of 3 mm height on the both sides. The apparatus was mounted 75 cm above the floor of the room. The room lighting was approximately 20 lx on the maze. The video camera was placed 80 cm above the maze. A fan generated a masking noise of 45 dB. The animal was placed gently onto the center of the maze and was allowed to explore the maze freely for 10 min. Number of entries into each arm and time spent in each arm were recorded from videotapes.

2.3.4. Morris water maze

A round pool, with the diameter of 95 cm and the depth of 21.5 cm, was placed in the center of a 140 cm \times 130 cm room. A platform with the diameter of 11 cm was set in one of quadrants and 5 mm beneath the surface of black water maintained at 21 ± 1 °C. On the first to fifth days, five trials per day were performed for learning phase. The mouse was released on one of three quadrants of the pool without the platform, and the time to reach the platform was measured. When the mouse could not reach the platform within 60 s, the experimenter placed the mouse on the platform. On the sixth day, a probe test was performed to examine whether the mouse remembered the place of the platform. The mouse was released in the quadrant on the opposite side of the platform and its behavior for 60 s was videotaped. The time staying in the target quadrant, where the platform had been placed, and immobility time were measured.

2.3.5. Passive avoidance learning

A mouse was placed in a box, consisting of two rooms separated by a shutter, that is, light and dark compartments (10 cm \times 10 cm each). In the acquisition trial, the mouse was kept in the light compartment. Five seconds later, the door to the dark compartment was opened. When the mouse moved into the dark compartment, the shutter was closed, and 10 s later, an electrical shock (160 V, 3 s) was delivered through the grid floor. Twenty-four hours later, each mouse was placed again in the light compartment and the latency to enter the dark compartment was recorded up to a maximum of 180 s.

2.3.6. Active avoidance learning

The same apparatus with the one used for passive avoidance learning was used, but there was no shutter between the light and dark compartments. The box was set in a soundproof chamber, and illuminated by a 20 W white light set on the chamber. The ceiling of the dark room is made of a black acrylic board, and the ceiling of the light room was a transparent acrylic board.

The training was performed for 3 days. On each day, one session consisting of 50 trials was performed. In each trial, a condition stimulus (CS) of 1500 Hz sound (85 dB) was followed by an unconditioned stimulus (US) of 140-V electrical shock. The US was given 5 s after the initiation of the CS and continued until the mouse escaped to the other compartment. If the mouse did not move to the other compartment, the US lasted 15 s together with the CS. If the mouse moved within 5 s after the CS, CS was stopped and no US was given. None of the mice experienced the maximum length of the CS. The time from the CS to the escape and the number of escapes were used for the performance of learning.

2.3.7. Forced swimming test

Animals were thrown into a square pool 24 cm \times 24 cm in size. The water was maintained constant at 21 °C. On the first day, the mice were left in the pool for 20 min, and the mobility during the first 5 min recorded by videocamera was assessed. On the second day, animals were thrown into the pool for 5 min and the immobility time during the 5 min was recorded. The immobility was defined by the two criteria. (1) No movement of all legs and the tail. (2) Completely stationary state in the pool, or the movement only by inertia by the adjacent movement. The immobility was assessed by three independent raters by scrutinizing the video and the median value of the three raters was used for the analysis.

2.4. Behavioral analysis: phase II

This analysis was performed at the Support Unit for Animal Experiment, RIKEN BSI. For this analysis, 9 homozygous KO mice ($Wfs1^{-/-}$) and 11 WT littermates ($Wfs1^{+/+}$) were analyzed. All were males aged 31 weeks at the initiation of the behavioral analysis. There was no significant difference of body weight at the initiation of the behavioral tests.

The analyses were performed in the order of home cage activity, open-field test, light-dark (L-D) box test, elevated plus maze, startle response and PPI test, Morris water maze, and fear conditioning. After each trial (except the auditory startle response and the water maze), apparatuses were wiped and cleaned by 80% alcohol and damp towel. For data acquisition, the Image J program (<http://rsb.info.nih.gov/ij/>) was used after some modification.

2.4.1. Environment of behavioral laboratory and housing condition of mice

Mice were housed individually for several days before they were transferred to the behavioral laboratory. The laboratory was air-conditioned and maintained temperature and humidity within approximately 22–23 °C and 50–55%. Food and water were freely available except during experimentation. Large tweezers were used to handle mice to avoid individual differences in the handling procedure. All of the experiments were conducted in the light phase (9:00–18:00 h), and the starting times of the experiments were kept constant.

2.4.2. Home cage activity measurement

Spontaneous activity of mice in their home cage was measured using a 24-ch ABsystem 4.0 (Neuroscience, Tokyo, Japan). Cages were individually set into the compartments made of stainless steel in the negative pressure rack (JCL, Tokyo, Japan). An infrared sensor was equipped on the ceiling of each compartment and it detected movements of the mice. Home cage activity was measured for 1 week from the afternoon of the day of transferring to the behavioral laboratory (day 1) until the next day of the week (day 8). After the termination of home cage activity measurement, cages and bedding materials were changed to fresh ones and then mice were maintained in the micro-isolation rack (Allentown Inc., Allentown, PA, USA), the same as those used in breeding rooms throughout the behavioral screening.

2.4.3. Open-field test

Four days after the termination of home cage activity measurement (day 12), an open-field test was conducted. The detailed protocol is shown in the supplementary information.

2.4.4. L-D box test

The next day (day 13) after the open-field test, an L-D box test was conducted. A four-channel of the L-D box system was equipped in the same sound-proof room as the open field. Each light box was made of white plastic (20 cm \times 20 cm \times 20 cm [H]) and illuminated by LEDs (250 lx at the center of the box); a CCD camera was equipped on the ceiling. Each dark box was made of black plastic (20 cm \times 20 cm \times 20 cm [H]) and an infrared camera was equipped on the ceiling. There was a tunnel for transition on the center panel between the light box and dark box (3 cm \times 5 cm) with an automatic sliding door. In the L-D box test, mice were individually introduced into the light box, and the door of the tunnel automatically opened 3 s after the introduction of a mouse. Then mouse was allowed to move freely in the L-D box for 10 min. Total distance traveled, percent distance traveled in the light

box, percent duration staying in the light box, numbers of the transition between light and dark box, and the first latency to enter the dark box were measured as indices.

2.4.5. Elevated plus maze test

The next day (day 14) after the L-D box test, an elevated plus maze test was conducted. The detailed protocol is shown in the supplementary information.

2.4.6. Auditory startle response

The next day after the L-D box test, an auditory startle response test was conducted for 2 days. The detailed protocol is shown in the supplementary information.

2.4.7. The Morris water maze test

Three days after the termination of the auditory startle response test (day 18), a series of the Morris water maze test began. The detailed protocol is shown in the supplementary information.

2.4.8. Classical fear conditioning

Three days after the termination of the Morris water maze test (day 25), a classical fear-conditioning test was conducted. This test consisted of three parts: a conditioning trial (day 25), a context test trial (day 26), and a cued test trial (day 27). Fear conditioning was carried out on a clear plastic chamber equipped with a stainless steel grid floor (34 cm × 26 cm × 30 cm [H]). A CCD camera was equipped on the ceiling of the chamber and was connected to a video monitor and computer. The grid floor was wired to a shock generator. White noise (65 dB) was supplied from a loudspeaker as an auditory cue (CS). The conditioning trial consisted of a 2-min exploration period followed by two CS-US pairings separated by 1 min each. A US (foot-shock: 0.5 mA, 2 s) was administered at the end of the 30-s CS period. A context test was performed in the same conditioning chamber for 3 min in the absence of the white noise at 24 h after the conditioning trial. Further, a cued test was performed in an alternative context with distinct cues; the test chamber was different from the conditioning chamber in brightness (almost 0–1 lx), color (white), floor structure (no grid), and shape (triangular). The cued test was conducted 24 h after the contextual test was finished and consisted of a 2-min exploration period (no CS) to evaluate the non-specific contextual fear followed by a 2-min CS period (no foot shock) to evaluate the acquired cued fear. Rate of freezing response of mice was measured as an index of fear memory.

2.5. Behavioral analysis: phase III

This analysis was performed at the Support Unit for Animal Experiment, RIKEN BSI. For this analysis, seven homozygous KO mice ($Wfs1^{-/-}$) and eight WT littermates ($Wfs1^{+/+}$) were analyzed. All were males aged 9 weeks at the initiation of the behavioral analysis. There was no significant difference of body weight at the initiation of the behavioral tests (WT, 25.2 ± 0.6 g; KO, 25.2 ± 0.5 g).

The analyses were performed in the order of social interaction, rotarod test, sucrose preference test, tail suspension test, forced swimming test, marble burying test, hot plate test, and tail flick test. Inter-test intervals were 1 day to a week. After each trial (except the auditory startle response and the water maze), apparatuses were wiped and cleaned by 80% alcohol and damp towel. For data acquisition, the Image J program was used after some modification.

2.5.1. Social interaction test (encounter method)

Subject mice were individually put into the center of a white-colored open field (40 cm × 40 cm × 30 cm [H]). Immediately after the introduction of the subject mouse, a target mouse was also introduced into the same open field. The duration of contact behavior was measured for 60 min to assess passive contact. Contact or separation of mice was expressed as "1" or "2" by computerized image analysis. If the two mice contacted, the software return value of "1," and if separated, return value "2." Thus, smaller number means higher contact. Data were collected and analyzed using a personal computer and commercially available software (Time HC; O'Hara, Tokyo, Japan).

2.5.2. Motor coordination and motor learning test (rotarod)

Mice were individually placed on a rotating rod (O'Hara, Tokyo, Japan) and the time each animal was able to maintain its balance walking on top of the rod was measured. The speed of the rotarod was 4 rpm (on the first day) or accelerated from 4 to 40 rpm over a 4-min period and 40 rpm another 1 min (day 2 to day 5). Mice were given a trial for 2 min (day 1) or four trials with a maximum time of 300 s (inter-trial intervals were 20–30 s). Time between placement and falling or revolving around the rod was recorded manually.

2.5.3. Sucrose preference test

Mice were tested for a 3-days 24-h test and 1-day 1-h test with water deprivation. The 24-h tests were free choice between two bottles, one with sucrose (3% in filtered water) and another with filtered water. To eliminate the side preference, the position of bottles was switched every 24 h. The consumption of water and sucrose solution was assessed daily. After the choice test, mice were deprived water for 24 h and then a 1-h choice test between water and sucrose was conducted.

2.5.4. Tail suspension test

Mice were individually hung by the tail using an adhesive tape placed approximately 1.5 cm from the tip of the tail attached to a wire and 30 cm above the floor. The duration of immobility was scored and analyzed using Image J TS (O'Hara, Tokyo, Japan) for 5 min.

2.5.5. Forced swimming test

Mice were individually placed for 15 min (day 1) or 5 min (day 2) in glass cylinders (30 cm high, 10 cm in diameter) containing 10 cm of water maintained at 23–25 °C. The duration of immobility was scored and analyzed using Image J software. The immobility time during the first 5 min was assessed.

2.5.6. Marble burying test

The test was performed in the test cage identical to their home cage with a 5-cm thick layer of bedding material (TEK-FRESH, Edstrom Industries, Waterford, WI, USA). Mice were habituated to fresh bedding for 30 min and then briefly returned to their home cage; 20 glass marbles (1.5 cm in diameter) were placed evenly on the bedding. Mice were then reintroduced into the test cage and the number of buried marbles (buried into the bedding over 2/3) was analyzed 30 min later.

2.5.7. Hot plate and tail flick test

In the hot plate test (Model MK-350C, Muromachi-kikai, Tokyo, Japan), mice were individually placed on the plate (52 ± 0.5 °C) enclosed in a translucent plastic wall, and the time between placement and licking of the paws and jumping was recorded manually as the response latency. A cut-off time was 90 s. Because most of the mice did not jump, latency to licking was used for statistical analysis.

In the tail flick test (Model MK-330B, Muromachi-kikai, Tokyo, Japan), mice were individually restricted on the radiant heat meter and focused heat was applied to the surface of the tail at 2–3 cm from its tip; the latency to reflexive removal of the tail from the heat was recorded manually as the tail flick latency. A cut-off time was 10 s.

In these tests, data were obtained by two observers, and the shorter scores were adopted as the response time.

2.5.8. Statistical analysis

For statistical analysis of behavioral analyses phases I–III, the Student's *t*-test, one-way ANOVA, and repeated measures ANOVA (RMANOVA) were used. When a significant effect was found by one-way ANOVA, Tukey post hoc comparisons were applied. When sphericity was rejected by the Mauchly test before the application of RMANOVA, the Greenhouse-Geisser estimate was used. Paired *t*-test and two-sample *t*-test were also used for post hoc analysis when necessary. These statistical analyses were performed using SPSS 11.0 for Windows (SPSS Japan, Tokyo, Japan). Significance levels were set at 0.05 (two-tailed); d.f., degree of freedom. Average and standard error of mean (S.E.M.) were presented for each experimental parameter in one group.

2.6. Immunohistochemistry

Because several computer programs predicted that mouse *Wfs1* protein would be cleaved around position 36, we used the following amino acid sequence, Glu³⁹–Gly⁵³ as an antigen. A hexadecapeptide (CEPPRAPRPQADP-SAG) was synthesized, purified using high-performance liquid chromatography, and conjugated to keyhole limpet hemocyanin (KLH). Five Balb/c mice were injected intraperitoneally with the KLH-conjugated peptide emulsified in complete Freund's adjuvant. Antiserum was obtained 1 week after boosting with the same antigen. We performed Western blot analysis to selected sensitive antiserum specific to *Wfs1* protein.

For immunohistochemical analysis using *Wfs1* antibody, wild-type B6 mice aged 20–22 weeks were used. The mouse brain was fixed by perfusion of paraformaldehyde and embedded with paraffin. Coronal or sagittal sections with the thickness of 8 μ m were sliced from paraffin-embedded mouse brain.

After deparaffinization and hydration, the slices were incubated for 10 min at 95 °C in sodium citrate buffer. Endogenous peroxidase activity was quenched by H₂O₂/methanol treatment. For blocking, 0.8% Block Ace (Dainippon Sumitomo Pharma, Osaka, Japan) in phosphate-buffered saline (PBS) was used. Anti-*Wfs1* antiserum was used by 2500 \times dilution. For second antibody, biotinylated anti-mouse IgG (Vector Laboratories, Burlingame, CA, USA) was used. Peroxidase/DAB staining was performed by Vectastain Elite ABC kit (Vector Laboratories).

2.7. DNA microarray analysis

DNA microarray analysis was performed in two developmental stages, 12 and 30 weeks old. Eight homozygous *Wfs1* KO mice and 8 WT littermates were sacrificed at the age of 12 weeks. Seven homozygous *Wfs1* KO mice and five WT littermates were also analyzed at the age of 30 weeks.

The hippocampus was rapidly dissected, and total RNA samples were extracted from the hippocampi using TRIzol reagent (Invitrogen, Carlsbad, CA, USA). Microarray analysis was performed according to the manufacturer's protocol (Affymetrix, Santa Clara, CA, USA). Briefly, 5 μ g total RNA of each sample was reverse-transcribed into cDNA, and biotinylated cRNA was synthesized from the cDNA by in vitro transcription. DNA microarray experiments were performed using Mouse Genome 430 2.0 GeneChips (Affymetrix). The hybridization signal on the chip was scanned by a GeneArray scanner and processed by GeneSuite software (Affymetrix). The probe sets labeled as "present" in 8 of 16 samples at 12 weeks old (24703/45101 probe sets) or in 5 of 12 samples at 30 weeks old (24455/45101 probe sets) were selected. The raw data were analyzed using MASS (Affymetrix) and then imported into GeneSpring 7.3 software (Silicon Genetics, Redwood, CA). The signal intensity

of each probe set on the microarray was divided by its median value using GeneSpring 7.3 software.

For statistical analysis, the Mann–Whitney *U*-test was performed between the KO mice and their WT littermates, and $P < 0.05$ was considered statistically significant.

The probe sets were classified based on the information from GeneOntology (<http://www.geneontology.org/>) using GeneSpring software. For the GeneOntology analysis, the differentially expressed probes were selected. The categories showing overrepresentation at the level of $P < 0.05$ and containing 10 or more probe sets were selected.

2.8. Real-time quantitative polymerase chain reaction (RT-PCR) analysis

The representative probe sets that showed altered expression in the DNA microarray analysis of mouse brains were verified by RT-PCR. The cDNA used for the DNA microarray analysis was used. Primers and probes for *Gapdh*, *cdc42ep5*, *Rnd1*, *Wnt2*, and *Garn1* were commercially available by the Assay-on-Demand service (Applied Biosystems, Foster City, CA). The assays were carried out according to the protocols supplied by the manufacturer using 7900HT real-time PCR systems (Applied Biosystems). The relative values were calculated by measuring $\Delta C_t = C_t$ (each gene) – C_t (*Gapdh*) for each sample in quadruplicate. For statistical analysis, one-tailed Mann–Whitney *U*-test was applied, and $P < 0.05$ was considered statistically significant.

3. Results

3.1. Wheel-running activity

To assess whether or not the *Wfs1* KO mice show bipolar disorder-like behavioral phenotypes, wheel-running activity of the *Wfs1* KO mice and WT littermates was recorded for a period up to 2 months. The levels of wheel-running activity and the circadian rhythm were assessed using male mice that were 34 weeks old at the initiation of this analysis (KO, $n = 11$; WT, $n = 9$). Average wheel-running activity per day of *Wfs1* KO mice during 28 days under the L–D condition did not differ from that of WT littermates (Fig. 1a; WT, 221.3 ± 64.7 [mean \pm S.E.M.] counts; KO, 142.2 ± 57.6 counts, d.f. = 18, $U = 29$, $P = 0.21$ by Mann–Whitney *U*-test). Delayed activity

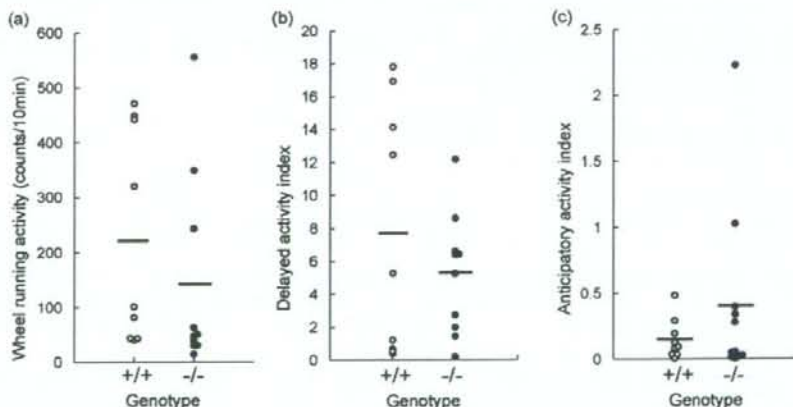


Fig. 1. Long-term wheel-running activity analysis. (a) Wheel-running activity. (b) Delayed activity index. Delayed activity index is defined as a percent of the wheel-running activity during the first 3 h of the light period with the total activity during the previous dark period (12 h). (c) Anticipatory activity index, the wheel-running activity in the last 3 h of light phase in comparison with the activity during dark phase. +/+, WT mice; -/-, *Wfs1* homozygous KO mice. Bars indicate averages. Each circle represents the datum of a mouse.

index (WT, 7.70 ± 2.50 ; KO, 5.29 ± 1.16 , d.f. = 18, $U = 42$, $P = 0.84$) and anticipatory activity index (WT, 0.14 ± 0.05 ; KO, 0.34 ± 0.21 , d.f. = 18, $U = 41$, $P = 0.78$) did not differ between the KO mice and WT littermates (Fig. 1a–c).

There was no abnormality of free running period measured at the constant dark condition in *Wfs1* KO mice (average 23.7 h, $n = 6$). None of female KO mice showed significant periodicity in wheel-running activity with the duration of 4–5 days (data not shown). These results show that the behavioral phenotypes of *Wfs1* KO mice are different from the mPolg Tg mice that exhibit altered circadian rhythm of wheel-running activity (Kasahara et al., 2006).

3.2. Behavioral analysis: phase I. Screening by a test battery

To screen the behavioral abnormality of *Wfs1* KO mice, we performed a conventional behavioral test battery using 14 homozygous KO mice, 14 heterozygous KO mice, and 13 WT littermates. The results of behavioral tests are summarized in Table 1.

3.2.1. Open-field test

Although a significant effect of time was found for both locomotor activity (d.f. = 8.6, $F = 3.0$, $P = 0.002$) and rearing (d.f. = 11.0, $F = 9.7$, $P = 0.000$), no significant effect of genotype was found for locomotor activity (d.f. = 2, $F = 0.70$, $P = 0.49$) and rearing (d.f. = 2, $F = 0.57$, $P = 0.56$). There was no significant interaction between time and genotype (locomotor, d.f. = 17.3, $F = 21.1$, $P = 0.57$; rearing, d.f. = 22.0, $F = 0.80$, $P = 0.71$) (Fig. 2a and b).

3.2.2. Startle response and prepulse inhibition

When RMANOVA was applied for the data of startle response, significant effect of blocks was found (d.f. = 5.12, $F = 7.80$, $P < 0.001$). However, no significant effect of genotype (d.f. = 2, $F = 0.664$, $P = 0.52$) or genotype \times block interaction (d.f. = 10.2, $F = 1.30$, $P = 0.22$) was found (Fig. 2c). No significant effect of genotype was found for the PPI ratio regardless of the interval of prepulse (50 ms, d.f. = 2, $F = 0.38$, $P = 0.68$; 100 ms, d.f. = 2, $F = 0.65$, $P = 0.52$; 200 ms, d.f. = 2, $F = 0.41$, $P = 0.66$, one-way ANOVA) (Fig. 2d).

3.2.3. Elevated plus maze

The number of entry into the open arms ($F = 0.31$, d.f. = 2, $P = 0.72$, one-way ANOVA) (Fig. 2e) and the time spent in the open arms ($F = 2.05$, d.f. = 2, $P = 0.14$) (Fig. 2f) were not significantly different among the genotypes. A significant effect of genotype was found for the total number of boluses ($F = 7.16$, d.f. = 2, $P = 0.002$) (Fig. 2g). The Tukey honest significant difference (HSD) test showed that homozygous KO mice had a significantly lower number of fecal boluses (2.7 ± 0.3 [mean \pm S.E.M.]) compared with heterozygous KO mice (4.8 ± 0.5 , $P = 0.01$) and WT mice (5.2 ± 0.5 , $P = 0.004$).

Table 1
Summary of findings in behavioral tests

Test battery	Findings
Wheel-running activity (34 weeks, 11 KO, 9 WT)	
Periodicity	NS
Diurnal activity rhythm	NS
Phase I (12 weeks, 13 KO, 14 Hetero, 13 WT)	
Open field	NS
Startle/PPI	NS
Elevated plus maze	NS
Morris water maze	NS
Passive avoidance test	Longer latency to move
Active avoidance test	Reduced number of escape at day 3
Forced swimming test	Reduced immobility on the second day
Phase II (31 weeks, 9 KO, 11 WT)	
Home cage activity	NS
Open field	NS
Light-dark box	NS
Elevated plus maze	NS
Startle/PPI	NS
Morris water maze	Increased escape latency without the change of distance traveled
Fear conditioning	Enhanced freezing during conditioning and before the cue at the cue test
Phase III (9 weeks, 7 KO, 8 WT)	
Social interaction	Decreased interaction
Rota-rod	NS
Sucrose preference	NS
Tail suspension test	NS
Forced swimming test	Reduced immobility on the second day
Marble burying test	NS
Hot plate test	NS
Tail flick test	NS

KO, *Wfs1* (−/−); Hetero, *Wfs1* (−/+); WT, *Wfs1* (+/+). PPI: prepulse inhibition test, NS, non-significant.

3.2.4. Morris water maze

The time to reach the platform during the 5-day learning phase became shorter than the first day, shown by a significant effect of day by RMANOVA (d.f. = 4, $F = 19.1$, $P < 0.001$) (Fig. 2h). However, there was neither significant effect of genotype (d.f. = 2, $F = 0.56$, $P = 0.57$) nor significant interaction of day and genotype (d.f. = 2, $F = 0.53$, $P = 0.94$). The time spent in the target quadrant (d.f. = 2, $F = 0.10$, $P = 0.90$, one-way ANOVA) and immobility time (d.f. = 2, $F = 0.58$, $P = 0.56$) at the probe test performed on day 6 did not show a significant difference among the genotypes (Fig. 2i).

3.2.5. Passive avoidance test

The latency to escape at the conditioning phase was significantly different among the genotypes (d.f. = 2, $F = 4.70$, $P = 0.015$, one-way ANOVA). Multiple comparison showed that the latency in homozygous KO mice was significantly longer than that in WT mice ($P = 0.02$) (Fig. 3a). There was no significant difference in escape latency at the test session (d.f. = 2, $F = 0.81$, $P = 0.92$, one-way ANOVA).

3.2.6. Active avoidance test

The time course of mean escape latency was examined during 3-days' training, consisting of 5 blocks in each day

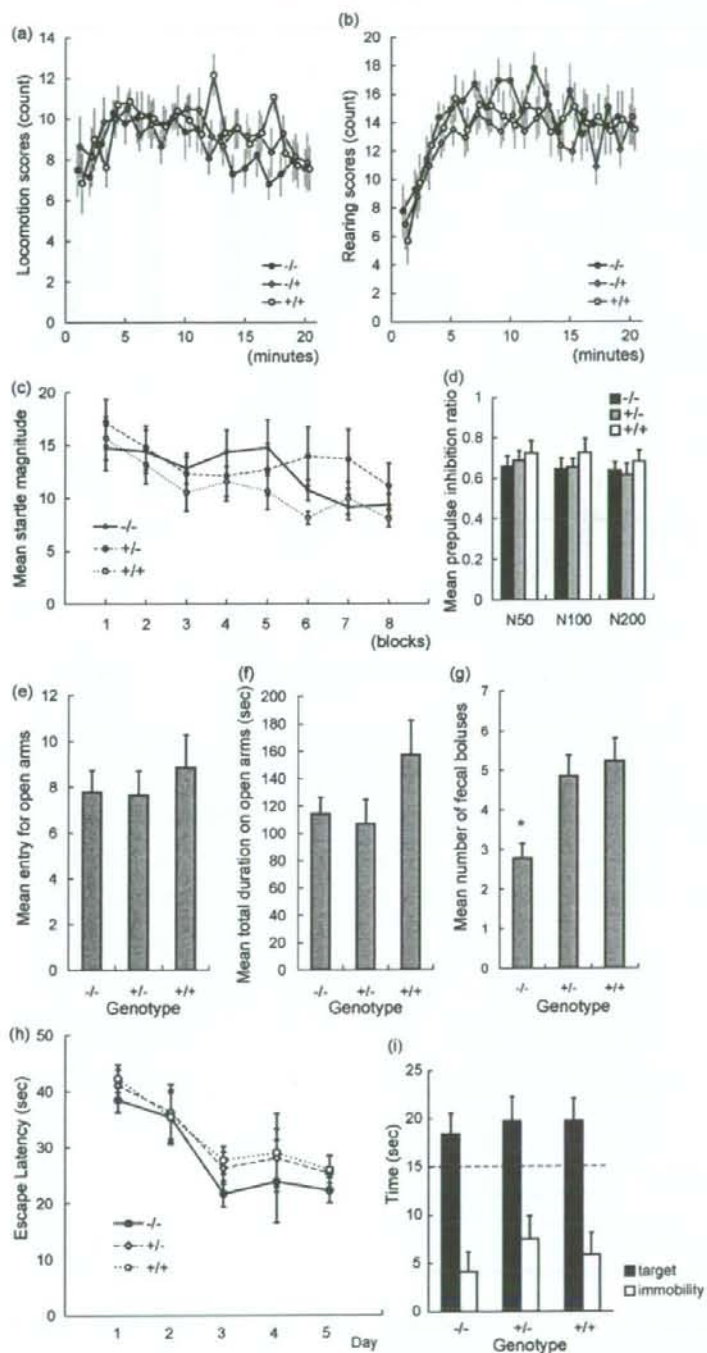


Fig. 2. Behavioral screening (1). (a–b) Open-field test. Locomotion scores (a) and rearing scores (b). Bars indicate the standard errors. (c) Startle response. (d) Prepulse inhibition test. N50 means the prepulse 50 ms before the startle pulse. (e–g) Elevated plus maze test. (h–i) Morris water maze test. Time course of escape latency during 5-days training (h), and time spent in the target quadrant during the 60-s session. Error bars represent standard error of mean. The dotted line represents the chance level. *+/+*, WT mice; *+/-*, *Wfs1* heterozygous KO mice; *-/-*, *Wfs1* homozygous KO mice. * $P < 0.05$.

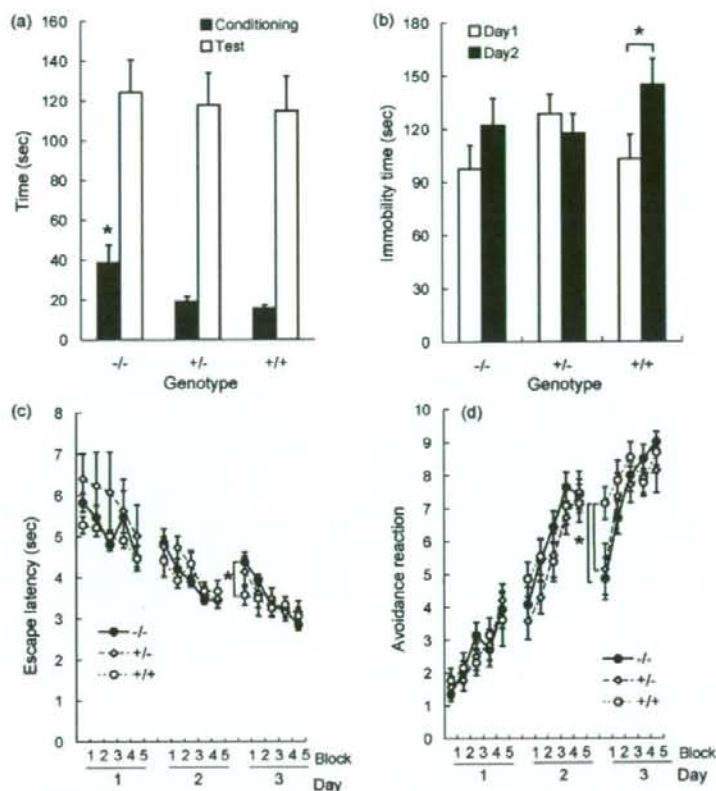


Fig. 3. Behavioral screening (2). (a) Passive avoidance test. (b) Forced swimming test performed on two sequential days. (c–d) Active avoidance test. +/+, WT mice; +/-, *Wfs1* heterozygous KO mice; -/-, *Wfs1* homozygous KO mice. Error bars represent standard error of mean. * $P < 0.05$.

(Fig. 3c). In the three-way RMANOVA with the within-group factors of day and block and the between-group factor of genotype, although no significant effect of genotype was found (d.f. = 2, $F = 0.75$, $P = 0.47$), there was a significant interaction between genotype and block (d.f. = 1.75, $F = 2.94$, $P = 0.007$). No other two-way or three-way interactions were statistically significant. This significant interaction may be caused by longer escape latency of KO mice only at the first block. A post hoc analysis showed that the escape latency of the homozygous KO mice at the first block on day 3 was significantly longer than that in WT mice (d.f. = 25, $t = 2.34$, $P = 0.027$, with no correction for multiple comparison).

Similar interaction between genotype and block was also seen for the numbers of avoidance (d.f. = 6.3, $F = 3.25$, $P = 0.004$) (Fig. 3d). Both homozygous and heterozygous KO mice showed significantly lower numbers of avoidance at the first block on day 3 (homozygotes, d.f. = 25, $t = -2.82$, $P = 0.009$; heterozygotes, d.f. = 25, $t = -2.15$, $P = 0.04$).

3.2.7. Forced swimming test

When the immobility time was analyzed by RMANOVA, a significant effect of day (d.f. = 1, $F = 5.5$, $P = 0.024$) and a significant interaction of day and genotype (d.f. = 2, $F = 3.8$,

$P = 0.031$) were found, whereas no significant effect of genotype was found (d.f. = 2, $F = 0.48$, $P = 0.61$) (Fig. 3b).

In the WT mice, immobility time was significantly longer on the second day (144.6 ± 53.0 s) compared with the first day (103.0 ± 48.3 s, d.f. = 12, $t = -3.45$, $P = 0.005$, paired t -test), possibly reflecting the learned despair (Parra et al., 1999). On the other hand, such a significant increase of immobility time on the second day was not observed for heterozygous (day 1, 128.5 ± 39.4 s; day 2, 117.5 ± 39.4 s; d.f. = 12, $t = 1.11$, $P = 0.28$) and homozygous (day 1, 97.4 ± 50.6 s; day 2, 122.0 ± 57.0 s; d.f. = 13, $t = -1.44$, $P = 0.17$) KO mice (Fig. 3b).

3.2.8. Summary of the phase I behavioral analysis

The results of the phase I behavioral analysis are summarized as follows.

- (1) There was no abnormality in open field, elevated plus maze, PPI, and Morris water maze. However, it cannot be ruled out that the mice develop behavioral phenotypes at later age because depression is an adult-onset disease.
- (2) The passive avoidance test showed the longer latency to enter the other chamber in *Wfs1* KO mice. This could be

explained either by low anxiety or retardation, that is slow movement or delayed onset of motion. However, it is also possible that mice could have been just busy exploring the first box, or they had some kind of place neophobia.

- (3) The active avoidance test showed longer escape latency and lower numbers of avoidance at the first block on day 3 in *Wfs1* KO mice. This might suggest that the emotional memory is impaired in the *Wfs1* KO mice. It cannot be excluded, however, that *Wfs1* KO mice have impairment of pain sensitivity.
- (4) Altered response to serial forced swimming test. This may suggest that the *Wfs1* KO mice tend to be resistant to behavioral despair.

3.3. Behavioral analysis: phase II

To further characterize the behavioral phenotypes of *Wfs1* KO mice, additional behavioral analysis was performed.

3.3.1. Open-field, elevated plus maze, PPI tests, and Morris Water Maze at 31 weeks

At first, four of behavioral tests were repeated in the mice aged 31 weeks to assess the effect of age. There were no significant difference between WT mice and *Wfs1* KO mice for three of these behavioral tests: open-field, elevated plus maze, and PPI tests (data not shown).

On the other hand, the Morris water maze test showed longer escape latency. Two-way RMANOVA showed significant effects of genotype (d.f. = 1, $F = 9.04$, $P = 0.008$) and day (d.f. = 3, $F = 8.45$, $P < 0.001$) (Fig. 4a). The *Wfs1* KO mice showed longer escape latency than controls. There was no significant interaction between genotype and day (d.f. = 3, $F = 0.60$, $P = 0.61$). On the other hand, there was no significant effect of genotype on the distance (d.f. = 1, $F = 0.38$, $P = 0.54$) (Supplementary Fig. 1a). Effect of day was significant (d.f. = 3, $F = 25.2$, $P < 0.001$), but the interaction between genotype and day was not significant (d.f. = 3, $F = 0.71$, $P = 0.54$). To assess the speed of swimming, a new index, swimming speed index = (total distance)/(latency to reach platform) was calculated. Two-way RMANOVA showed no significant effects of day (d.f. = 1.77, $F = 2.57$, $P = 0.09$) and genotype (d.f. = 1, $F = 0.04$, $P = 0.83$). There was no significant day \times genotype interaction (d.f. = 1.77, $F = 0.33$, $P = 0.69$) (Supplementary Fig. 1b). Spatial memory cannot be assessed because no significant difference was found between the time spent in the target quadrant and that in the other three quadrants, suggesting that the probe test did not work properly even for wild-type mice (data not shown).

3.3.2. Home cage activity

To assess the general activity level, home cage activity was recorded for 8 days. When RMANOVA was applied, a significant effect of day (d.f. = 5, $F = 5.95$, $P < 0.001$) was found. There was no significant effect of genotype (d.f. = 1, $F = 0.61$, $P = 0.44$) and genotype \times day interaction (d.f. = 5, $F = 0.53$, $P = 0.75$) (Fig. 4b).

3.3.3. Anxiety-like behavior

Next, the level of anxiety-like behavior was further assessed by the L-D box. The marble burying test was also performed in the 9-week-old mice in the phase III behavioral analysis.

In the L-D box test, no significant difference was found in the time spent in the light box (WT, $39.2 \pm 9.0\%$, KO, $37.1 \pm 9.8\%$, d.f. = 18, $t = 0.50$, $P = 0.61$). There was no significant difference in the number of marbles buried (WT 16.0 ± 0.8 , KO 17.1 ± 0.7 , $t = 1.0$, $P = 0.33$). These findings suggest that longer latency to escape at the passive avoidance test was not due to lower anxiety-like behavior.

3.3.4. Emotional memory

To test the hypothesis that emotional memory is impaired in the *Wfs1* KO mice, the fear conditioning test was performed.

During the conditioning phase, two-way RMANOVA revealed significant effect of genotype (d.f. = 1, $F = 4.47$, $P = 0.049$) and time (d.f. = 3.54, $F = 22.1$, $P < 0.001$). No significant period \times genotype interaction was found (d.f. = 3.54, $F = 1.73$, $P = 0.16$). The *Wfs1* KO mice showed significantly longer time of freezing during the conditional stimuli (periods 5 and 7) and at the final period (Student's *t*-test, $P < 0.05$) (Fig. 4c).

For the cue test, two-way RMANOVA was applied to the data set before and after the cue, separately. For the data of freezing before the cue, a slight tendency of the effect of genotype (d.f. = 1, $F = 2.9$, $P = 0.10$) was seen, whereas there was significant effect of time (d.f. = 3, $F = 5.93$, $P = 0.001$) and no interaction between genotype and time (d.f. = 3, $F = 0.30$, $P = 0.82$). The *Wfs1* KO mice spent a significantly longer time for freezing ($t = 2.48$, $P < 0.01$) (Fig. 4d). However, no significant effect of genotype was found after the cue (effect of genotype, d.f. = 1, $F = 1.48$, $P = 0.23$; effect of time, d.f. = 3, $F = 1.60$, $P = 0.19$; genotype \times time interaction, d.f. = 3, $F = 0.40$, $P = 0.75$). There was no significant effect of genotype at the context test (Fig. 4e).

These findings suggested that memory of emotion is not impaired in the *Wfs1* KO mice.

3.4. Behavioral analysis: phase III

3.4.1. Pain sensation

As noted above, it cannot be excluded that *Wfs1* KO mice have impairment of pain sensitivity. To rule out such possibility, the hot plate test and tail flick test were performed. No difference in the latency to licking (WT, 10.3 ± 1.2 s; KO, 9.9 ± 0.9 s, $t = 0.219$, d.f. = 12, $P = 0.83$, by Student's *t*-test) was found between the *Wfs1* KO mice and WT mice by the hot plate test. There was no significant difference in the latency to flick the tail (WT, 3.5 ± 0.2 s; KO, 3.4 ± 0.2 s, d.f. = 12, $t = 0.29$, $P = 0.77$).

3.4.2. Motor function

As noted above, many of the positive findings in behavioral tests can be interpreted as reflecting retardation. Such findings can be explained by altered motor functions, such as impairment in muscle contraction, voluntary movement, or

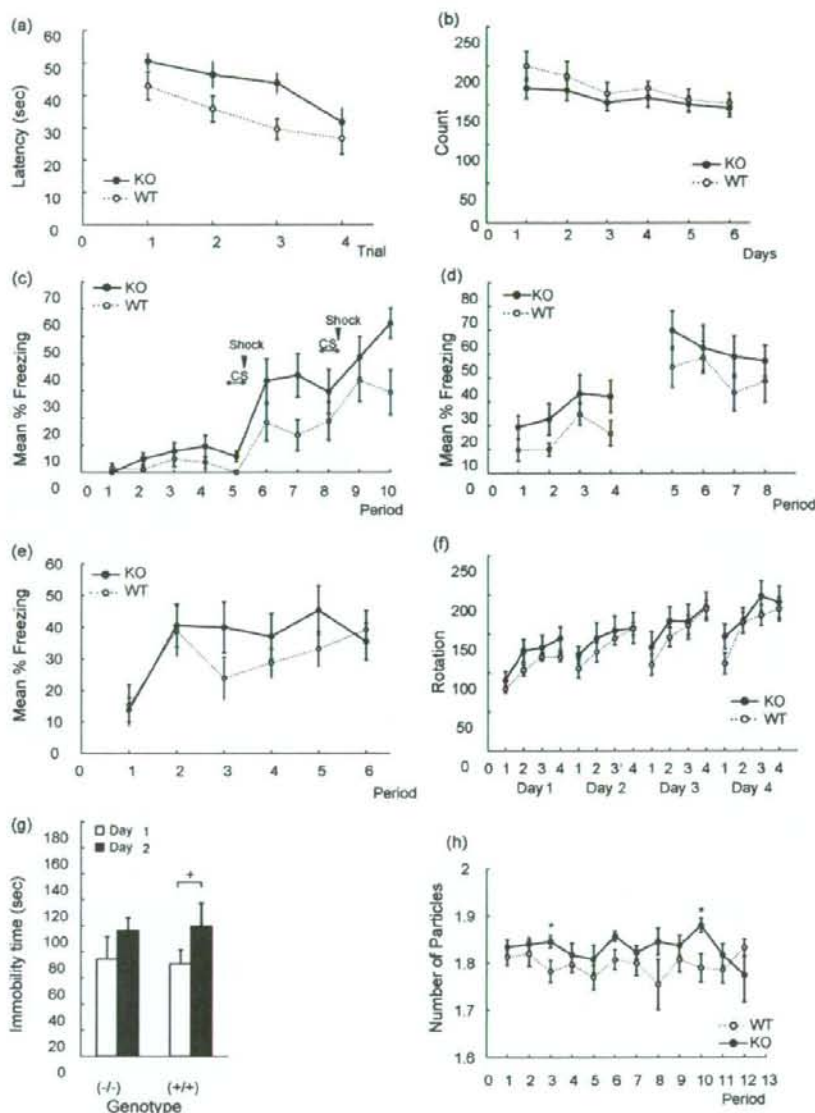


Fig. 4. Further characterization of behavioral phenotypes of *Wfs1* KO mice. (a) Morris water maze test. (b) Home cage activity. (c and d) Fear conditioning test. One time period is 30 s. (c) Conditioning phase. Conditional stimuli (tone) and unconditional stimuli (foot shock) were applied during periods 5 and 8. (d) Cue test. Cue was applied between the time periods 4 and 5. (e) Context test. (f) Rotarod test. (g) Forced swimming test. (h) Social interaction test. Note that high number of particles indicates lower levels of social interaction.

motor coordination. To test this possibility, the rotarod test was performed. Three-way RMANOVA with the intra-individual factors of day and trial and inter-individual factor of genotype showed no significant effect of genotype (d.f. = 1, $F = 1.02$, $P = 0.33$). Whereas significant effects of day (d.f. = 3, $F = 15.6$, $P < 0.001$) and trial (d.f. = 3, $F = 51.0$, $P < 0.001$) were found, no significant two-way or three-way interactions were detected except for a trend of interaction between day and trial (d.f. = 3, $F = 2.54$, $P = 0.07$) (Fig. 4f).

3.4.3. Behavioral despair

As noted above, *Wfs1* KO mice showed altered response to the serial forced swimming test. To further confirm this finding, the forced swimming test was performed again.

RMANOVA revealed a tendency of effect of day (d.f. = 1.0, $F = 3.83$, $P = 0.07$). There was no significant effect of genotype (d.f. = 1, $F = 0.18$, $P = 0.67$) and day \times genotype interaction (d.f. = 1.0, $F = 0.17$, $P = 0.68$).

Although no day \times genotype interaction was found in this analysis, the paired *t*-test was applied similarly to the first experiment (Fig. 4g). Immobility time tended to be longer on the second day (99.7 ± 17.4 s) compared with the first day (71.0 ± 10.55 s, $r = 0.68$, $P = 0.064$, paired *t*-test) in WT mice, whereas no significant difference was found in *Wfs1* KO mice (day 1, 74.5 ± 17.1 s; day 2, 96.2 ± 10.0 s, $r = 0.50$, $P = 0.24$). This analysis showed a similar tendency to the first experiment.

The other test of behavioral despair, the tail suspension test, was also performed. There was no significant difference in the immobile time between the *Wfs1* KO mice and WT mice (WT, $9.0 \pm 2.8\%$; KO, $9.4 \pm 3.0\%$, $t = 0.09$, $P = 0.92$).

3.4.4. Other aspects of depression

Some of these noted findings in the *Wfs1* KO mice can be explained by the retardation in emotionally triggered motion. This could not be explained by abnormalities in instrumental motor functions. Such findings seem to be similar to "psychomotor retardation" seen in human depressive patients. Though the findings in the forced swimming test and tail suspension test are equivocal, behavioral despair is not always a valid depression model. Thus, we further examined the other aspects of depression.

The sucrose preference test is an established test for anhedonia, one of the core symptoms of depression. In the choice test for 3 days, there was no significant effect of genotype (d.f. = 1, $F = 0.95$, $P = 0.34$) by two-way RMANOVA (WT, day 1, $44.2 \pm 16.7\%$, day 2, $94.1 \pm 5.2\%$, day 3, $84.5 \pm 9.7\%$; KO, day 1, $37.3 \pm 12.9\%$, day 2, $97.3 \pm 1.7\%$, day 3, $60.2 \pm 16.0\%$). A significant effect of trial (d.f. = 2, $F = 10.7$, $P = 0.001$) and no significant interaction of genotype \times trial was found (d.f. = 2, $F = 0.68$, $P = 0.51$). The 1-h choice test after 24-h water deprivation did not show a significant difference between genotypes (WT $90.2 \pm 1.7\%$, KO $86.3 \pm 5.3\%$, $U = 28$, NS).

The social interaction test is an established test for anxiety-like behavior (File and Seth, 2003). However, its response to drugs is different from elevated plus maze, and it is more sensitive to serotonergic drugs. Recently, this test is also applied to animal models of schizophrenia (Miyakawa et al., 2003) and autism, and to genetic models of anxiety and depression (Overstreet et al., 2003). Thus, social behavior of the *Wfs1* KO mice was examined by this test. Two-way RMANOVA revealed no significant effect of genotype (d.f. = 1, $F = 2.0$, $P = 0.17$) and time (d.f. = 11, $F = 0.93$, $P = 0.51$). There was a trend of genotype \times time interaction (d.f. = 11, $F = 1.67$, $P = 0.08$) (Fig. 4h). The *Wfs1* KO mice showed significant decrease of social interaction at the periods 3 and 10 (Student's *t*-test, $P < 0.05$) shown by the higher number of particles observed.

3.5. *Wfs1* immunohistochemistry

To determine the molecular basis of behavioral abnormality in *Wfs1* KO mice, we verified whether the distribution of *Wfs1* protein in the brains of WT B6 mice is similar to that in rats (Fig. 5a–f) (Takeda et al., 2001). We verified that no staining

was observed in *Wfs1* KO mice, suggesting the specificity of the anti-*Wfs1* antibody (Fig. 5g).

Wfs1-like immunoreactivity (*Wfs1*-IR) localized mostly to neurons and its regional distribution was mostly similar to that in rats (Fig. 5a). *Wfs1*-IR was most abundant in the hippocampal CA1 pyramidal neurons (Fig. 5b), and strong in the layer II pyramidal neurons of the cerebral cortex (Fig. 5c). Similar to rats, *Wfs1*-IR was also rich in the striatum, nucleus accumbens, thalamus, cerebellar Purkinje cells, amygdala, and bed nucleus of the stria terminalis (Fig. 5d). In addition, *Wfs1*-IR was observed in several hypothalamic nuclei, such as the paraventricular nucleus and supraoptic nucleus (SCN) in mice (Fig. 5e). In the adjacent region of SCN, sub-paraventricular zone, some cell bodies showed *Wfs1*-IR. The ventromedial nucleus and arcuate nucleus also showed *Wfs1*-IR (Fig. 5f). *Wfs1*-IR was also found in the locus coeruleus and cochlear nucleus (data not shown).

3.6. DNA microarray analysis

To examine what sort of functional impairment occurs in the neurons of *Wfs1* KO mice, we performed gene expression analysis using DNA microarray. Because *Wfs1*-IR was most abundant in hippocampus, we performed DNA microarray analysis in the hippocampus of the *Wfs1* KO mice. A total of 1012 probe sets were changed at the age of 12 weeks. To narrow down the gene list, we repeated the experiment at the age of 30 weeks. We assumed that the true gene expression difference observed at age 12 weeks should be replicated at age 30 weeks. At the age of 30 weeks, 3508 probe sets showed significant differences. The genes altered in the same direction at both the ages of 12 and 30 weeks, and the fold change higher than 1.2 are shown in Table 2.

GeneOntology (GO) analysis showed that genes related to ribosome biogenesis (GO:3735: structural constituent of ribosome, GO:7046: ribosome biogenesis, GO:3723: RNA binding) or other basic cellular functions (GO:5622: intracellular, GO:44249: cellular biosynthesis, GO:15399: primary active transporter activity, GO:5623: cell, GO:7028: cytoplasm organization and biogenesis) were commonly up-regulated at the age of 12 and 30 weeks (Supplementary Tables 1 and 2). The major difference between the weeks 12 and 30 is the inclusion of neurodevelopment-related genes at the age of 30 weeks (GO:48666: neuron development, GO:30182: neuron differentiation, GO:7409: axonogenesis, GO:48667: neuron morphogenesis during differentiation, and GO:31175: neurite morphogenesis) (Supplementary Table 2).

3.7. RT-PCR analysis

To test whether the findings by DNA microarray analysis are chance findings, RT-PCR analysis was performed. For this purpose, two down-regulated genes, *cdc42ep5* and *Rnd1*, as well as two up-regulated genes, *Wnt2* and *Garn1*, were examined using *Gapdh* as a reference.

The level of *cdc42ep5* and *Rnd1* tended to be lower at 12 weeks but not at 32 weeks. On the other hand, *Wnt2* and *Garn1*

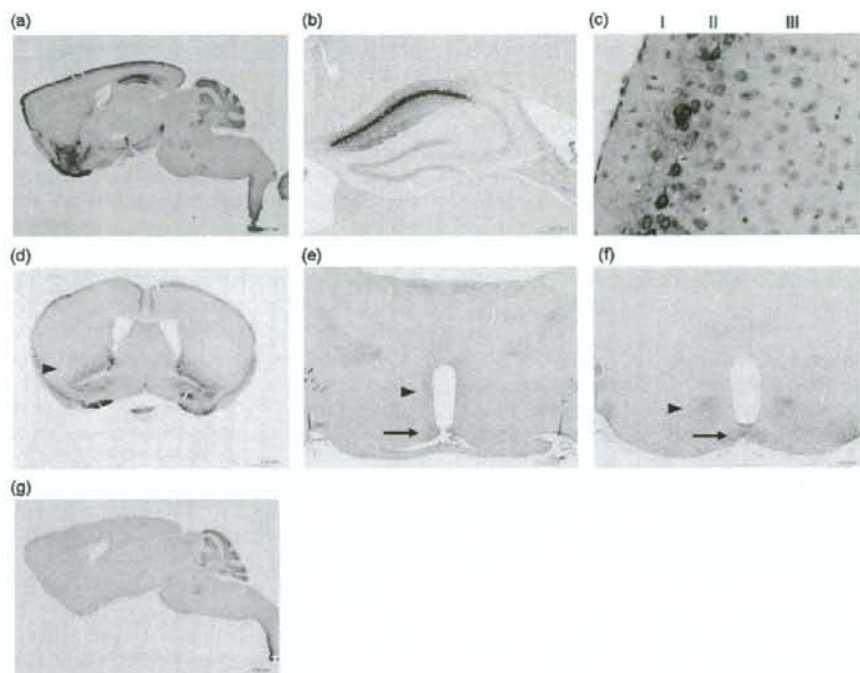


Fig. 5. Localization of *Wfs1*-like immunoreactivity in mouse brain. Immunohistochemistry analysis of mouse brain using anti-*Wfs1* antiserum. Coronal sections are shown except for panel a. (a) Sagittal section of the whole brain. (b) Hippocampus. CA1 (corpus ammon 1) region is selectively stained. (c) Cerebral cortex. Layer II pyramidal neurons are stained. (d) Coronal section at the level of bed nucleus of striata terminalis (BNST). At this level, the regions with intense *Wfs1*-IR looked as if they are surrounding the internal capsule (arrowhead). (e and f) Hypothalamus. Suprachiasmatic nucleus and sub-paraventricular zone are indicated by an arrow and an arrowhead, respectively (e). Arcuate nucleus and ventromedial nucleus are shown by an arrow and an arrowhead, respectively (f). (g) Immunohistochemistry analysis of the brain of a *Wfs1* KO mouse using anti-*Wfs1* antiserum. No staining is detected.

were significantly up-regulated at 32 weeks but not at 12 weeks (Table 3).

4. Discussion

4.1. Behavioral analyses

We recently reported that mPolg Tg mice show bipolar disorder-like behavioral phenotypes, such as altered circadian rhythm in both males and females and periodic fluctuation of wheel-running activity in females (Kasahara et al., 2006). Based on previous reports suggesting that patients with Wolfram disease are frequently affected with depression or bipolar disorder, we speculated that the *Wfs1* KO mice might also show these bipolar disorder-like phenotypes, which were seen in the mPolg Tg mice. However, *Wfs1* KO mice did not show similar phenotypes (Fig. 1).

Thus, we next examined the possibility that *Wfs1* KO mice show other types of behavioral phenotypes. At first, a battery of established behavioral tests was applied. There was no marked difference found in most of conventional behavioral tests, such as the open-field test, startle response, prepulse inhibition test, and elevated plus maze. The lack of marked difference in these tests was replicated in the mice aged 31 weeks. On the other

hand, several tests in the initial test battery showed equivocal findings. In the passive avoidance test, the mice showed longer latency to move into the dark compartment at the training phase (Fig. 3a). The active avoidance test showed subtle differences between the KO and WT mice. On the third day of training, WT mice kept the same level of escape latency and number of avoidance reactions as the final block of the second day. Although, *Wfs1* KO mice seemed as if they forget the previous memory of escape training (Fig. 3c and d), it is unlikely considering the fact that there were no differences in the day 2 of the active avoidance test and in the contextual testing of the fear conditioning test. Otherwise, they may remember the events, but could not take the adequate action under the situation for some other reasons. For example, a possibility is that they showed retardation or increased behavioral despair without any problems in memory retention. In the forced swimming test performed for two sequential days, WT mice showed an increase of immobility time on the second day (Fig. 3d). This is in accordance with a previous study showing that mice became immobile on the second day of the sequential forced swimming test (Parra et al., 1999). This phenomenon was not observed in the homozygous and heterozygous KO mice (Fig. 3d). Although statistical analysis did not show the same difference, a similar tendency was observed in the second

Table 2

Probe sets commonly altered both at 12 and 30 weeks

Probe set ID	P-value		Fold change		Gene symbol chromosome	Gene title
	12W	30W	12W	30W		
Down						
1433815 at	0.0008	0.0074	-2.24	-1.72	Jakmip1	5qB3 ^a Janus kinase and microtubule interacting protein 1
1448411 at	0.0008	0.0045	-2.10	-2.00	<i>Wfs1</i>	5qB3 ^a Wolfram syndrome 1
1419744 at	0.0357	0.0424	-1.45	-1.44	H2-DMb2	17qB1 Histocompatibility 2, class II, locus Mb2
1442241 at	0.0357	0.0424	-1.41	-1.49	Srpk2	5qA3 ^a Serine/arginine-rich protein specific kinase 2
1425620 at	0.0157	0.0284	-1.39	-1.22	Tgfb β 3	5qE5 ^a Transforming growth factor, beta receptor III
1418712 at	0.0274	0.0284	-1.36	-1.47	Cdc42ep5	7qA1 CDC42 effector protein (Rho GTPase binding) 5
1441317 x at	0.0011	0.0045	-1.34	-1.71	Jakmip1	5qB3 ^a Janus kinase and microtubule interacting protein 1
1455197 at	0.0357	0.0424	-1.26	-1.29	Rnd1	15qF1 Rho family GTPase 1
Up						
1418148 at	0.0087	0.0074	2.03	1.68	Abhd1	5qB1 ^a Abhydrolase domain containing 1
1431328 at	0.0046	0.0424	1.50	1.21	Ppp1cb	5qB1 ^a Protein phosphatase 1, catalytic subunit, beta isoform
1459714 at	0.0157	0.0284	1.35	1.57	-	4qE1 -
1449425 at	0.0357	0.0074	1.28	1.28	Wnt2	6qA2 Wingless-related MMTV integration site 2
1457532 at	0.0357	0.0185	1.27	1.35	Garn1	12qC1 GTPase activating RANGAP domain-like 1
1416569 at	0.0274	0.0118	1.25	1.24	Act16a	3qA3 Actin-like 6A
1446406 at	0.0460	0.0424	1.24	1.20	Paqr8	1qA4 Progesterin and adipoQ receptor family member VIII
1446815 at	0.0357	0.0424	1.23	1.29	Dph4	2qE3 DPH4 homolog (JJJ3, <i>S. cerevisiae</i>)
1456328 at	0.0460	0.0284	1.22	1.33	Bank1	3qG3 B-cell scaffold protein with ankyrin repeats 1

^aThe probe sets on the chromosome 5.

forced swimming test. In addition, the other test for behavioral despair, the tail suspension test, did not show any significant difference. On the other hand, the longer escape latency of the KO mice without the difference of the distance traveled in the Morris water maze might reflect the longer time for immobility during the session. Thus, the *Wfs1* KO mice might show

enhanced or attenuated behavioral despair depending on experimental conditions.

As described above, it was speculated that longer latency to move at the passive avoidance test can be explained either by low anxiety or retardation of *Wfs1* KO mice. The former possibility was not supported by two established tests for anxiety-like behavior, the L-D box test, and the marble burying test.

Wfs1 KO mice also showed longer escape latency and lower numbers of avoidance during the active avoidance test. This was not due to decreased pain sensitivity. This cannot be explained by the impairment of emotional memory, because there was no significant abnormality in fear conditioning test. This test instead showed increased freezing during conditioning phase. Freezing was also increased during the cue test, not after the cue but before the cue.

The *Wfs1* KO mice did not show impairment in fundamental motor functions that can explain these findings.

In summary, the following findings were obtained.

- (1) Longer latency to move in passive avoidance test.
- (2) Diminished avoidance reaction during active avoidance test.
- (3) Longer escape latency in Morris water maze.
- (4) Increased freezing during conditioning.
- (5) Normal sensorimotor function and anxiety-like behavior.

These findings together suggest that the *Wfs1* KO mice might show retardation in the emotionally triggered motion. We could not discriminate whether this feature of the *Wfs1* KO mice reflects the slow movement, longer time to initiate movement, or mixture of both. Psychomotor retardation, that is, slow voluntary movement and thoughts and/or taking longer

Table 3

Validation study of gene expression using RT-PCR

Gene	Genotype	N	Average	S.E.M.	P-value
12w					
cdc42ep5	WT	8	0.68	0.02	0.088*
	KO	8	0.63	0.02	
Rnd1	WT	8	0.42	0.01	0.070*
	KO	8	0.39	0.02	
Wnt2	WT	8	0.42	0.01	0.227
	KO	8	0.44	0.02	
Garn1	WT	8	15.30	0.37	0.180
	KO	8	14.62	0.61	
32w					
cdc42ep5	WT	5	0.63	0.01	0.225
	KO	7	0.66	0.03	
Rnd1	WT	5	0.58	0.04	0.235
	KO	7	0.54	0.04	
Wnt2	WT	5	0.40	0.01	0.041**
	KO	7	0.44	0.02	
Garn1	WT	5	12.95	0.16	0.049**
	KO	7	14.37	0.64	

The gene expression levels were normalized by *Gapdh*. Each value represents the gene/*Gapdh* ratio $\times 10^{-2}$. P-values were calculated by Mann-Whitney U-test (one tailed).

* $P < 0.10$ ** $P < 0.05$.

time to initiate movement, is one of the characteristic symptoms of melancholic depression. The observed retardation of the *Wfs1* KO mice resembled such a characteristic symptom of depression. Thus, other aspects of depression were also examined. Although, the sucrose preference test did not show any difference, the social interaction test showed decreased social interaction in *Wfs1* KO mice.

Together these results suggest that *Wfs1* KO mice have some similarity to patients with depressive disorder. It should be noted, however, that the observed difference in the social interaction test might also reflect the retardation noted above. The *Wfs1* KO mice did not show marked abnormalities in the conventional behavioral despair paradigm, such as the forced swimming test and tail suspension test. These tests are established as screening tests for compounds having tricyclic antidepressant-like properties. However, its construct validity as a depression model is questioned (Crawley, 2007).

Taken together, the *Wfs1* KO mice show behavioral alterations at least partly mimicking the symptoms of depression. Further studies to examine the effects of antidepressive agents would be extremely interesting.

4.2. Morphological analyses

Immunohistochemistry demonstrated that the distribution of *Wfs1*-IR was similar to that in rats (Fig. 5) (Takeda et al., 2001). In addition, we found that *Wfs1*-IR is also present in the hypothalamus. The presence of *Wfs1*-IR in the arcuate nucleus seems to be in accordance with diabetes insipidus, the major symptom of Wolfram disease. In a similar way, *Wfs1*-IR in the cochlea nucleus may be relevant to deafness in patients with Wolfram disease. It is also interesting that *Wfs1*-IR is found in the locus coeruleus and substantia nigra, from which noradrenergic and dopaminergic fibers originate. In *Wfs1* KO mice, however, we did not observe marked morphologic alterations in these regions using hematoxylin–eosin staining and Klüver-Barrera staining (data not shown).

4.3. Gene expression analysis

The fact that *Wfs1* itself is included in the list of altered genes (Table 2) supports the validity of our experiment and data analysis. Among the eight down-regulated and nine up-regulated genes, six other genes in addition to *Wfs1* itself were on the chromosome 5. This is possibly caused by residual genomic region derived from the 129Sv mice. Thus, only a part of these changes can be attributable to the absence of *Wfs1* itself. The present result is in accordance with a previous report that there were only small differences in expression profiles seen in fibroblasts obtained from patients with Wolfram disease (Philbrook et al., 2005).

Among the three down-regulated genes outside chromosome 5, two (*Cdc42ep5* and *Rnd1*) were related to Rho GTPase. Down-regulation of *Rnd1* was validated at the age of 12 weeks but not at 32 weeks.

Cdc42ep5 encodes CDC42 effector protein. CDC42 plays a role in dendrite development (Threadgill et al., 1997).

Cdc42ep5 is one of the targets of CDC42 (Joberty et al., 1999), but its function in neurons is not known yet. *Rnd1* also plays a role in activity-dependent dendrite development (Ishikawa et al., 2006). A recent fine mapping analysis of 13q33 in bipolar disorder revealed the linkage with DOCK9, an activator of Cdc42 (Detera-Wadleigh et al., 2007). This finding also suggested the possible role of Rho GTPase in mood disorder. Together with the GO analysis showing altered neural development related genes at age 30 weeks, these findings may suggest that dendrite development may be impaired in *Wfs1* KO mice. Although, we did not observe morphologic difference between *Wfs1* KO mice and WT littermates using hematoxylin–eosin staining and Klüver-Barrera staining, dendrite morphology cannot be assessed using these methods. Further analysis by Golgi staining or other methods might be promising.

Up-regulation of two genes were validated at 32 weeks but not at 12 weeks. Up-regulation of *Wnt2* is potentially interesting because Wnt signaling plays a role in neural plasticity and is implicated in the molecular pathology of bipolar disorder (Gould and Manji, 2002; Matigian et al., 2007).

Up-regulation of ribosome-related genes at both 12 and 30 weeks revealed by gene ontology analysis might be in accordance with the putative role of *Wfs1* in ER stress response (Fonseca et al., 2005; Yamada et al., 2006).

4.4. Phenotypic discordance between *Wfs1* KO mice and patients with Wolfram disease

In this study, *Wfs1* KO mice did not show marked sensorimotor and general health problems that are seen in patients with Wolfram disease. This is in accordance with the lack of spontaneous diabetes mellitus in *Wfs1* KO mice on the B6 background (Ishihara et al., 2004). Although, we detected some behavioral phenotypes in KO mice, it cannot be ruled out that some of detected behavioral alterations in *Wfs1* KO mice could be explained by the residual genomic region derived from 129Sv mice (Mouse Phenome Database, <http://phenome.jax.org/pub/cgi/phenome/mpdcgi?rtm=docs/home>).

It is possible that the symptoms in patients with Wolfram disease are the combination of the loss of function of *Wfs1* and the dominant-negative effect of the mutations. Meta-analysis of genotype–phenotype correlation in Wolfram disease suggested that nonsense or frame-shift mutations caused more severe phenotypes compared with missense mutations (Cano et al., 2007). The *Wfs1* KO mice we analyzed in this study are *Wfs1*-null mice. On the other hand, another line of *Wfs1* KO mice, in which the exon 8 of *Wfs1* is deficient, was reported to show striking behavioral phenotypes (European Patent EP1353549). These findings suggest the possibility that the symptoms of Wolfram disease are accelerated by the aberrant proteins truncated around exon 8. Because function of *Wfs1* has not been well established yet, it is difficult to conclude which mechanism, loss of function or dominant-negative effect, is more influential. Further studies will be necessary to make draw a conclusion.

In summary, we studied the behavior and gene expression patterns in *Wfs1*-null mice. The *Wfs1* KO mice showed several

behavioral features, such as retardation in emotionally triggered motion, decreased social interaction, and enhanced or attenuated behavioral despair depending on experimental conditions. These findings might be relevant to the neuropsychiatric phenotypes reported in patients with Wolfram disease.

Appendix A. Supplementary data

Supplementary data associated with this article can be found, in the online version, at doi:10.1016/j.neures.2008.02.002.

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Aberrant endoplasmic reticulum stress response in lymphoblastoid cells from patients with bipolar disorder



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Abstract

Impaired endoplasmic reticulum (ER) stress response has been suggested as a possible pathophysiological mechanism of bipolar disorder (BD). The expression of ER stress-related genes, spliced form or unspliced form of XBP1, GRP78 (HSPA5), GRP94 (HSP90B1), CHOP (DDIT3), and calreticulin (CALR), were examined in lymphoblastoid cells derived from 59 patients with BD and 59 age- and sex-matched control subjects. Basal mRNA levels and induction by 4 h or 12 h of treatment with two ER stressors, thapsigargin or tunicamycin, were examined using real-time quantitative reverse transcription-polymerase chain reaction. Induction of the spliced form of XBP1 as well as total XBP1 by thapsigargin was significantly attenuated in patients with BD. Induction of GRP94 by thapsigargin was also decreased in the BD group. A haplotype of GRP94, protective against BD, exhibited significantly higher GRP94 expression upon ER stress. This report confirms and extends earlier observations of impaired ER stress response in larger samples of lymphoblastoid cell lines derived from BD patients. Altered ER stress response may play a role in the pathophysiology of BD by altering neural development and plasticity.

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Introduction

Bipolar disorder (BD) is a severe mental illness characterized by recurrent episodes of mania and depression that affects about 1% of the population (Goodwin and Jamison, 2007). Although genetic factors contribute to the onset of this illness, genetic risk factors or causative genes have not been elucidated (Kato, 2007). Studies of action mechanisms of mood stabilizers revealed that both lithium and valproate have direct actions on neurons, including protection of neurons from cell death or enhancement of neurogenesis (Chuang, 2005; Manji and Duman, 2001). Among the findings obtained from neuroimaging studies of BD, increased incidence of white-matter

hyperintensity is one of the most replicated findings (Altshuler et al., 1995); a meta-analysis showed that 9 out of 10 studies supported this finding (Videbech, 1997). Because this finding is a non-specific finding and there is no specific brain region, the infarction of which causes bipolar disorder, it would be more reasonable to assume that the hyperintensity lesion is not a causative factor but that brain cells of patients with bipolar disorder are more vulnerable to mild hypoxia. Decreased levels of *N*-acetylaspartate in the brain also suggest impaired integrity of neurons of BD patients (Stork and Renshaw, 2005). A study using olfactory neuroepithelium showed that cells derived from BD patients were more vulnerable to cell death (McCurdy et al., 2006). Studies of peripheral blood cells showed increased levels of calcium in platelets, lymphocytes and lymphoblastoid cells (reviewed by Warsh et al., 2004). These findings together suggest that BD patients have some vulnerability or impaired resilience at the cellular level (Kato, 2008; Shaltiel et al., 2007).

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However, the actual mechanism of such cellular impairment, if any, has not been elucidated. Suggested mechanisms for the effects of mood stabilizers on neurons include, among others, depletion of inositol (Williams et al., 2002), up-regulation of bcl-2 on mitochondrial outer membrane (Chen et al., 1999b), up-regulation of endoplasmic reticulum (ER) chaperones (Chen et al., 2000), and inhibition of GSK-3 β (Chen et al., 1999a) effects on the extracellular signal-regulated kinase (ERK) pathway (Yuan et al., 2001). It is still unknown which of these mechanisms has the most important effect on BD and it remains to be clarified what signal cascade is impaired in the cells of BD patients.

To address this question systematically, we previously used DNA microarray analysis of lymphoblastoid (LB) cells derived from two pairs of monozygotic twins discordant with respect to BD and found down-regulated expression of *XBPI* and *GRP78* (*HSPA5*) in both affected twins (Kakiuchi et al., 2003). Because both of these genes are related to the ER stress response pathway, we focused on this pathway as a possible molecular cascade responsible for BD.

ER is a site of synthesis, folding, and modification of secretory and cell surface proteins (Yoshida, 2007), and this organelle is widely distributed throughout neurons (Murakami et al., 2007). Various cellular insults or increased demands of protein synthesis cause accumulation of unfolded proteins in the ER lumen. This condition is designated as ER stress. Unfolded protein response (UPR) is one of the adaptive responses by which cells protect themselves from ER stress. UPR consists of four signalling cascades: (1) induction of ER chaperones, e.g. *GRP78* (also named *HSPA5* or BiP), *GRP94* (*HSP90B1*), calreticulin (*CALR*), which promotes the folding of unfolded proteins; (2) inhibition of protein synthesis; (3) induction of an ER-associated degradation pathway; and (4) induction of *CHOP*, a transcription factor implicated in ER stress-induced apoptosis.

XBPI is a pivotal transcription factor that plays a crucial role in the induction of ER chaperones such as *GRP78* and *GRP94* (Lee et al., 2002; Yoshida et al., 2001). With ER stress, *IRE1 α* , an endoribonuclease on ER membranes, cleaves a 26-nt fragment from an unspliced form of *XBPI* mRNA (*XBPI μ*), inducing a frame shift of the open reading frame of the message. *XBPI* protein encoded by the spliced mRNA (*XBPI ν*) is a potent transcription factor inducing the expression of ER chaperone genes.

Several lines of evidence support the involvement of UPR dysfunction in the pathophysiology of BD. Pharmacological studies suggested that ER chaperones such as *GRP78*, *GRP94*, and *CALR* are target

Table 1. Characteristics of the subjects

	Control	Bipolar disorder		
		Total	BP I	BP II
n	59	59	43	16
Gender	34 M, 25 F	35 M, 24 F	31 M, 12 F	4 M, 12 F
Age, yr (mean \pm s.d.)	47.9 \pm 1.6	46.1 \pm 1.6	45.5 \pm 2.0	47.6 \pm 3.6

genes of the mood stabilizers valproate (Chen et al., 2000) and lithium (Shao et al., 2006). The antimalarial drug mefloquine, which is known to cause BD in susceptible individuals, causes ER stress (Dow et al., 2003). Serotonergic stimulation or immobilization stress activates *XBPI* splicing (Toda et al., 2006). Frequent comorbidity of mood disorders has been reported in Wolfram syndrome (Swift and Swift, 2000) caused by mutations of *WFS1* that encodes an ER stress-related protein (Fonseca et al., 2005) regulated by *XBPI* (Kakiuchi et al., 2006).

We found that up-regulation of *XBPI* and *GRP78* in response to ER stress caused by thapsigargin treatment was attenuated in the cells derived from BD patients and identified that a single nucleotide polymorphism (SNP), '-116C>G' on the promoter region of *XBPI* (rs2269577) that removes the *XBPI*-binding sequence significantly attenuated this response (Kakiuchi et al., 2003). The attenuated *XBPI* response was partially rescued by valproate treatment. Although we initially reported that this SNP (rs2269577) was significantly associated with BD, this association was not replicated by subsequent studies (Cichon et al., 2004; Hou et al., 2004). We also reported that genetic variants of *GRP78* (*HSPA5*) (Kakiuchi et al., 2005) and *GRP94* (*HSP90B1*) (Kakiuchi et al., 2007) were associated with BD in Japanese individuals.

Recently, So and colleagues reported that LB cells derived from BD patients showed a striking decrease in the response of *XBPI* and *CHOP* to two ER stressors, thapsigargin and tunicamycin (So et al., 2007). The induction of *GRP78* did not differ from controls. To confirm and extend this finding in a relatively small number of samples (20 patients with bipolar I disorder and 10 healthy controls), we measured the induction of major UPR-related genes, spliced or unspliced forms of *XBPI*, *GRP78*, *GRP94*, *CHOP*, and *CALR* in response to ER stress, in more than 100 LB cells (obtained from 59 healthy individuals and 59 BD patients).

Methods

Subjects

The study included 59 unrelated BD patients [43 with bipolar I disorder (BD I) and 16 with bipolar II disorder (BD II)] and 59 age- and sex-matched unrelated healthy controls (Table 1). Patients were diagnosed according to the DSM-IV criteria by the consensus of at least two psychiatrists. Structured interviews were not used for the diagnosis, although we began to use a structured interview, the Mini-International Neuropsychiatric Interview (MINI) (Sheehan et al., 1998) for recently recruited patients ($n=22$). Family history was obtained by an interview of the patient and available family members. Nineteen of the patients had a family history of mood disorder within first-degree relatives. Eleven of the patients had a history of psychotic features. Average age at onset was 32.2 yr (s.d. = 14.2, range 15–85). Controls were selected from students, nurses, office workers, and doctors at participating institutes along with their friends. A senior psychiatrist interviewed them and assessed them as healthy. Written informed consent was obtained from all participants. Although diabetes mellitus was not an exclusion criterion, none of the subjects had diabetes mellitus. Family history of diabetes mellitus was not assessed in the subjects. The Research Ethics Committee of RIKEN approved the study.

Cell cultures and drug treatment

Lymphocytes were separated from the peripheral blood and transformed by Epstein-Barr virus. LB cells were cultured in RPMI 1640 (Sigma; St Louis, MO, USA) containing 10% fetal bovine serum (FBS) as described previously (Kato et al., 2003). All LB cells were used after two rounds of freezing and reculturing.

For induction of ER stress, we incubated LB cells with thapsigargin (0.3 μM) or tunicamycin [2.38 μM (2 $\mu\text{g}/\text{ml}$)] for either 4 h or 12 h. We selected these time-points because 4 h is the peak of *XBPI* splicing and *XBPIu* expression, and 12 h is the peak of *GRP78* expression. Thapsigargin inhibits the sarcoplasmic/ER Ca^{2+} ATPase (SERCA) leading to a rise in the cytosolic Ca^{2+} level and reduction in the ER Ca^{2+} level (Treiman et al., 1998). Tunicamycin prevents the glycosylation of newly synthesized proteins in the ER, causing the accumulation of unfolded proteins in the ER (Tordai et al., 1995). The same quantity of dimethylsulfoxide in the medium was added as vehicle control (0.5 ml in 10 ml medium). All experimental procedures and data analyses were performed blindly to the diagnosis or any other clinical variables.

RNA extraction and real-time quantitative reverse transcription-polymerase chain reaction (RT-PCR)

Total RNA was prepared from LB cells using TRIzol reagent (Invitrogen, San Diego, CA, USA), followed by DNase I (Takara Bio, Shiga, Japan) treatment to exclude genomic DNA. The SuperScriptII first-strand synthesis system with oligo(dT) (Invitrogen) was used to synthesize cDNA according to the manufacturer's instructions. Resulting cDNAs were subjected to a TaqMan RT-PCR assay (Applied Biosystems, Foster City, CA, USA) for the quantification of mRNA levels. The primer sequences were as follows: (sense) 5'-GGTCCAAGTTGTCCAGAATGC-3' [spliced form of *XBPI*, (*XBPIs*)], 5'-CTCAGACTACGTGCACCTCTGC-3' [unspliced form of *XBPI*, (*XBPIu*)]; (antisense) 5'-GCCAGTGGCCGGGTCT-3' (*XBPIs*), 5'-AGTCAATACCGCCAGAATCCAT-3' (*XBPIu*); (FAM-labelled probe): 5'-CCTGCACCTGCTGCCGACTCAGC-3' (*XBPIs*), and 5'-CAGGTGCAGGCCAGTTGTACAC-3' (*XBPIu*). To validate the *XBPI* variant specificity of each probe set, an external control standard curve was determined by PCR with the serial dilution of pcDNA/human *XBPIs* or pcDNA/human *XBPIu* plasmid as template. To test the degree of cross-reaction, we also performed quantitative PCR with the *XBPIs* plasmid template and *XBPIu*-specific probe, or with the *XBPIu* plasmid template and *XBPIs*-specific probe. These standard curves displayed a linear relationship between C_t values and the logarithm of the input plasmid amounts (Figure S1, see Supplementary Online Appendix). Although PCR efficiency of the undesirable cross-reaction was considerably less than the specific reaction, the contribution of the cross-reaction was subtracted from the absolute value estimated by the specific reaction. All other assays were performed using the Assay-on-Demand service (Applied Biosystems); *GRP94* (Assay ID, Hs00427665_g1), *GRP78* (Hs00607129_gH), *CALR* (Hs00189032_m1), *CHOP* (Hs00358796_g1), and *GAPDH* (Hs99999905_m1). We measured the $\Delta C_t = C_t$ (each gene) - C_t (*GAPDH*) for each sample in quadruplicate. The relative expression level was calculated by $2^{-\Delta C_t}$. The fold change was defined by the ratio of the relative expression level after stimulation by thapsigargin or tunicamycin to the basal relative expression level.

Genotyping of *XBPI*, *GRP78*, and *GRP94*

Genomic DNA was extracted from LB cells using standard protocols. Polymorphisms of *XBPI* (rs2269577), *GRP78* (*HSPA5*) (rs391957, rs17840761, and rs16927997), and *GRP94* (*HSP90B1*) (rs1165681 and rs17034977)

Table 2. Levels of unfolded protein response related genes at baseline

	Control (n=59)		Bipolar disorder (n=59)		p value
	Mean	s.d.	Mean	s.d.	
<i>XBPIs</i>	0.038	0.016	0.042	0.017	0.197
<i>XBPIu</i>	0.088	0.037	0.105	0.063	0.071
<i>XBPIt</i>	0.125	0.052	0.148	0.074	0.089
Ratio of <i>XBPIs</i> / <i>XBPIu</i>	0.428	0.057	0.425	0.060	0.761
<i>GRP78</i>	0.059	0.020	0.055	0.015	0.211
<i>CHOP</i>	0.00080	0.00034	0.00080	0.00021	0.527
<i>GRP94</i>	0.022	0.010	0.022	0.009	0.892
<i>CALR</i>	0.153	0.040	0.145	0.041	0.392

All genes were normalized by GAPDH.

p value: Comparison of two groups by Mann-Whitney U test.

were genotyped by commercially available TaqMan SNP genotyping assays.

In our previous paper, a haplotype (CGCTT) of five SNPs, rs1165687, rs1882019, rs17034977, rs703657, and rs2293618, in the *GRP94* gene was reported as a protective haplotype against BD. This haplotype was divided into two haplotypes based on the other upstream SNP (rs1165681), C-CGCTT and T-CGCTT. C-CGCTT was more strongly associated with BD ($p=0.0000037$, in comparison with the association with entire CGCTT, $p=0.00094$) (C. Kakiuchi et al., unpublished observations). In this study, we genotyped two SNPs, rs1165681 and rs17034977, to determine this 6-marker haplotype. This haplotype associated with BD (C-CGCTT) was named 'haplotype C-3'.

Genotyping was performed by ABI7900HT according to the protocol recommended by the manufacturer (Applied Biosystems).

Statistical analysis

The Mann-Whitney U test and Kruskal-Wallis test were used because these tests are robust to deviation from the normal distribution; $p < 0.05$ was considered as significant. Multiple statistical analysis was not corrected because this study is based on a hypothesis and intended to replicate the previously reported findings. For the analysis of the effect of clinical variables, Spearman's coefficient of correlation was also used.

To test the effect of confounding factors, two-way analysis of covariance (two-way ANCOVA) with factors of diagnosis (d.f.=1, BD or control) and sex (d.f.=1), and a covariance of age was applied. To test the interactions between the genotype and other factors, three-way ANCOVA with the factors of

genotype (d.f.=2 for *XBPI* -116C/G polymorphism and d.f.=1 for *GRP94* haplotype), diagnosis (d.f.=1), sex (d.f.=1), and a covariant of age was applied. When a significant interaction between genotype and diagnosis was found, one-way ANOVA was applied to each group (BD or control). When a significant effect of genotype was found by one-way ANOVA, multiple comparison by Bonferroni correction was applied. These statistical analyses were performed by SPSS for Windows version 11.0 (SPSS Japan, Tokyo).

Results

Baseline

At baseline, no differences in the mRNA levels of *XBPIt* (total *XBPI*), *XBPIs*, *XBPIu*, *GRP94*, *GRP78*, *CALR*, and *CHOP* were found between BD patients and controls (Table 2). A significant effect of sex was found for *XBPIs*, *XBPIu*, *XBPIt*, ratio of *XBPIs*/*XBPIu*, *CHOP*, and *GRP94* using two-way ANOVA (Tables S1, S2, online). No other main effects and interactions were statistically significant.

XBPI

The up-regulation of ER stress-related genes in response to thapsigargin and tunicamycin was examined by real-time RT-PCR. In the presence of thapsigargin or tunicamycin, expression of *XBPIt* increased by approximately 150% after 4 h of drug application and increased expression continued, to a lesser degree, at 12 h.

The thapsigargin-induced increase of *XBPIt* at 12 h was significantly lower in the BD group than in the control group (Figure 1a,d; $p=0.019$ in