厚生労働科学研究費補助金
障害者対策総合研究事業
（精神障害分野）

Fyn チロシンキナーゼ・シグナリングを介した統合失調症分子病態の解析

平成２２年度　総括研究報告書

研究代表者　服部　功太郎

平成２３（２０１１）年５月

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研究要旨

本研究の目的は、抗精神病薬伝達機構を担うFynシグナルカスケードの統合失調症分子病態における役割を明らかにし、その臨床応用の可能性を検討することである。

本年度の研究により、統合失調症死後脳において Fyn タンパク質の量および活性型 Fyn の量が増加していることが判明した。また、血液と脳との結果の乖離から、より脳に近い臨床検体である脳脊髄液の収集を本年度より開始し、統合失調症、気分障害、健常対照者、計 99 検体を得た。

A. 研究目的

Fynチロシンキナーゼは脳に強く発現し神経細胞内のシグナル伝達を担うことで、シナプス可塑性や記憶学習、情動行動の制御に関わっている。近年、Fynはドーパミン D2受容体によるNMDA受容体機能の制御にも関わり、マウスの抗精神病薬への反応性に関わることを我々は見出した。このためFynは統合失調症の分子病態にも関与している可能性が高い。そこで、本研究においては統合失調症の血液、死後脳、脳脊髄液などの臨床検体を用いて統合失調症の分子病態におけるFynの変化を解析し、バイオマーカーとしての可能性を検討する。

B. 研究方法

(1) 死後脳におけるFynおよび関連タンパク質の解析

前年度のスタンレー研究所の60例の死後脳検体セットで得られた結果（統合失調症におけるFyn活性上昇とNMDA受容体サブユニット減少）を受け、本年度は、同研究所の105例（統合失調症、双極性障害、健常者各35例）の死後脳検体を用いブラインドで解析を行った。Fynの解析には独自に確立したSandwich ELISAを用い、NMDA受容体サブユニットなどの解析にはドットブロットを用いた。

(2) 脳脊髄液の収集とFynおよび関連タンパク質の解析

前年度までの血液を用いた解析結果（脳と異なりfyn発現は減少していた）を受け、より脳に近い脳脊髄液で解析する必要性が生まれた。そこで、当センター倫理委員会の承認を経てボランティア等に同意を得たうえで研究目的の腰椎穿刺を行った。

（倫理面への配慮）

●対象者と説明同意

本研究の参加は全くの自由であり、参加を拒否したからといって診療に不利益を受けることはない。措置入院の患者、16歳未満の患者は対象とならない。主治医が不適切であると判断した場合も対象より除外する。参加希望者には十分な説明を行い文書で同意を得る。医療保護入院患者や未成年患者に検査を行う場合は、本人だけでなく保護者や親権者にも説明し書面で同意を得る。同意はいつでも文書によって撤回できる。

●個人情報保護

試料・臨床情報については当センター、バイオリソース管理室において、個人情報管理者・補助者のみが使用できるスタンドアローンのＰＣを用いて連結可能匿名化を行い、以後、試料や臨床情報（病名・年齢・性別・投薬歴など）を記号のみで扱う。対応表や個人が特定できるような情報は個人情報管理者が上記のＰＣか金庫で管理し、研究終了後破棄する。結果の公表に際しても、個人が特定できるような形での発表は行わない。

●腰椎穿刺時の苦痛低減と安全性の確保

穿刺前に眼底検査等の神経内科的診察にてリスク要因（脳圧亢進、髄膜兆候など）を除外する。脊髄を損傷することがないようL3/4ないしL4/5にて熟練した医師が腰椎穿刺を行う。穿刺時の病原体混入を防ぐため入念に消毒を行い、苦痛を最小限にするため皮膚、および靭帯に麻酔を十分施す。穿刺針には22Gを用い穿刺時、抜去時には内針を入れることで頭痛のリスクを軽減する。

●副作用への対応と補償

外来の参加者には医師の連絡先を知らせ、24時間対応できる体制とする。副作用発生時には必要に応じ当センターにて医療補償（治療）を行う。

C. 研究結果

(1) 死後脳におけるFynおよび関連分子の解析

60検体、105検体、両方の解析系にて統合失調症群ではFynの有意な増加が認められた。またFyn関連分子のうち60検体ではNR2A, NR2Bの量が統合失調症において有意に減少していたが、105検体ではNR2Aの減少傾向のみ認められた。

(2) 脳脊髄液の収集とFynおよび関連タンパク質の解析

H22年度には統合失調症、気分障害、健常対照者、計99検体を収集した。統合失調症の未治療例は確保できていない。気分障害については電気痙攣療法前後に採取できた症例も確保できた。また、Fyn-ELISAのプロトコルを改善し、脳脊髄液での解析も行えるようになった。

D. 考察

(1) 死後脳におけるFynおよび関連タンパク質の解析

2組のコホートで盲検試験にて、統合失調症死後脳のFynタンパク発現の亢進が確認されたことから、統合失調症の前頭葉でFynが増えている可能性は極めて高いと考えられる。NMDA受容体の変化については、1組目で顕著であったNR2Bの減少は2組目では確認できず、NR2Aの減少傾向のみ共通していた。薬剤やストレスなどによる二次性の変化とともに、疾患自体による可能性も考えられるが、今後、薬剤投与動物実験などにより、この判別をすすめていきたい。

(2) 脳脊髄液の収集とFynおよび関連タンパク質の解析

検体収集は順調に進んでおり、解析に十分な症例数が集まった。ただ診断マーカーの開発に重要と思われる、未治療例の確保が果たせていないため、今後の検討課題となっている。

E. 結論

Fynが統合失調症で変化していることが確認された。特に死後脳でみられたFynの活性変化、NMDA受容体の減少は統合失調症の分子病態において重要な所見であると考えられた。脳脊髄液の収集は順調に進んでおり、Fynを含めた関連分子の解析に着手できる状況となった。

F. 健康危険情報

特になし

G. 研究発表

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2. 知的財産権の出願登録状況

なし

研究成果の刊行に関する一覧表

雑誌

発表者氏名	論文タイトル名	発表誌名	巻号	ページ	出版年
Hattori K, Tanaka H, Wakabayashi C, Yamamoto N, Uchiyama H, Teraishi T, Hori H, Arima K, Kunugi H.	Expression of Ca(2+)-dependent activator protein for secretion 2 is increased in the brains of schizophrenic patients.	Prog Neuropsychopharmacol Biol Psychiatry	Epub		2011
Furuse T, Wada Y, Hattori K, Yamada I, Kushida T, Shibukawa Y, Masuya H, Kaneda H, Miura I, Seno N, Kanda T, Hirose R, Toki S, Nakanishi K, Kobayashi K, Sezutsu H, Gondo Y, Noda T, Yuasa	Phenotypic characterization of a new Grin1 mutant mouse generated by ENU mutagenesis.	Eur J Neurosci	31	1281-91	2010

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Expression of Ca^{2+}-dependent activator protein for secretion 2 is increased in the brains of schizophrenic patients

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ABSTRACT

Ca^{2+}-dependent activator protein for secretion 2 (CADPS2), a secretory granule associate protein, mediates monoamine transmission and the release of neurotrophins including brain-derived neurotrophic factor (BDNF) which have been implicated in psychiatric disorders. Furthermore, the expression of CADPS2deltaExon3, a defective splice variant of CADPS2, has been reported to be associated with autism. Based on these observations, we examined whether expression levels of CADPS2 and CADPS2deltaExon3 are altered in psychiatric disorders. Quantitative polymerase chain reaction analysis was performed for postmortem frontal cortex tissues (BA6) from 15 individuals with schizophrenia, 15 with bipolar disorder, 15 with major depression, and 15 controls (Stanley neuropathology consortium). The mean CADPS2 expression levels normalized to human glyceraldehyde-3phosphate dehydrogenase (GAPDH) or TATA-box binding protein levels was found to be significantly increased in the brains of the schizophrenia group, compared to the control group. On the other hand, the ratio of CADPS2deltaExon3 to total CADPS2 was similar in the 4 diagnostic groups. We then analyzed CADPS2 expression in blood samples from 121 patients with schizophrenia and 318 healthy controls; however, there was no significant difference between the two groups. Chronic risperidone treatment did not alter the expression of CADPS2 in frontal cortex of mice. The observed increase in the expression of CADPS2 may be related to the impaired synaptic function in schizophrenia.

1. Introduction

Ca^{2+}-dependent activator protein for secretion (CADPS) family, which consists of two members, CADPS1 and CADPS2, is a secretory granule-associated proteins involved in Ca^{2+}-dependent exocytosis of large dense-core vesicles containing diverse array of modulators including neurotrophines, monoamines and neuropeptides (Liu et al., 2008; Sadakata et al., 2004). CADPS2 mediates the release of neurotrophins such as brain-derived neurotrophic factor (BDNF) and neurotrophin-3. Mouse CADPS2 protein is associated with BDNF-containing secretory vesicles and promotes activity-dependent release of BDNF (Sadakata et al., 2004). BDNF release is significantly reduced in cultured neurons prepared from the brain of CADPS2 deficient mice (Sadakata et al., 2007a,b).

A number of findings suggest that BDNF action is impaired in psychiatric disorders including schizophrenia, bipolar disorder and depression. Several studies have shown decreased levels of BDNF or its receptor, TrkB, in the postmortem brains of patients with schizophrenia (Hashimoto et al., 2005; Iritani et al., 2003; Weickert et al., 2003), although there are contradictive reports (Chen et al., 2001; Dunham et al., 2009; Durany et al., 2001; Takahashi et al., 2000). The contribution of BDNF in depression has been suggested from animal studies that demonstrated stressful environments decrease, and antidepressive treatments increase BDNF levels in the brain (Duman and Monteggia, 2006; Martinowich et al., 2007). Also, centrally administered BDNF has an antidepressant-like effect in rat models (Siuciak et al., 1997). Thus, the molecules that contribute to the trafficking and release of BDNF may be a culprit of these disorders.

CADPS family also mediate monoamine transmission. Both CADPS1 and CADPS2 mediate the refilling of catecholamine to the releasable vesicles, and catecholamine secretion is significantly suppressed in the CADPS1/2 double deficient cells. (Liu et al., 2008). Another study supports that CADPS family are involved in monoamine storage as antibodies against CADPS1 or 2 inhibit monoamine

Abbreviations: ANCOVA, Analysis of covariance; BDNF, Brain-derived neurotrophic factor; CADPS2, Ca^{2+}-dependent activator protein for secretion 2; CCK, Cholecystokinin; DSM–IV, Diagnostic and Statistical Manual of Mental Disorders, 4th edition; FST, Freezer storage time; M.I.N.I., Mini-International Neuropsychiatric Interview; NT, Neurotensin; PCR, Polymerase chain reaction; PMI, Postmortem interval; SD, Standard deviation; TBP, TATA-box binding protein.

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sequestration by synaptic vesicles from mice brain (Brunk et al., 2009).

Dysregulation of monoamine neurotransmission has been hypothesized to play a central role in the etiology of psychiatric disorders including schizophrenia and mood disorders. In schizophrenia, not only classical evidence that dopamine agonists induce and dopamine D2 receptor antagonists ameliorate psychoses but also brain imaging studies on drug naïve patients have suggested that dopamine transmission is affected in this disorder (Lyon et al., 2011). In major depression, reduced monoamine transmission hypothesis was derived from the finding that most anti-depressants increase monoamine levels in the synaptic cleft and that reserpine, a monoamine-depleting drug, worsen depressive symptoms in a subset of patients with mood disorder (Krishnan and Nestler, 2008), although imaging, postmortem, or cerebrospinal fluid studies have yet to find the definitive evidence for altered monoamine neurotransmission in this disorder (Belmaker and Agam, 2008; Nikolaus et al., 2009).

While, to our knowledge, CADPS2 expression in schizophrenia or mood disorders have not yet been examined, aberrant splicing of CADPS2 mRNA was reported in autism (Sadakata et al., 2007b). In this study, an exon-3 skipped isoform, CADPS2ΔExon3, was detected in the bloods of several autistic patients but not in those of healthy controls. They also showed that CADPS2ΔExon3 was deficient in proper axonal transport, which results in the loss of local synaptic BDNF release. Though the CADPS2ΔExon3 expression in the brains of patients with autism is unclear, the aberrant splicing of CADPS2 could contribute to susceptibility to autism by affecting neurotrophin release.

Based on above findings, the present study was aimed to examine whether the expression of CADPS2 transcripts is altered in the frontal cortex of patients with psychiatric disorders including schizophrenia, major depression and bipolar disorder. The CADPS2 expression levels in the blood of schizophrenia were also examined.

2. Materials and methods

2.1. Brain samples

Frozen postmortem samples of frontal cortex (BA6) were obtained from the Stanley Foundation Neuropathology Consortium (Torrey et al., 2000). The collection consists of 60 subjects: 15 with schizophrenia, 15 bipolar disorder, 15 major depression and 15 unaffected controls. All groups were matched for age, sex, race, pH and hemispheric side (Table 1), although postmortem interval (PMI) and freezer storage time differed across the groups. The brain tissues obtained were coded. Once our blind study was complete, we sent the data to the Stanley Foundation who then returned the codes, demographic and clinical data. In a cold-room, each frozen brain tissue was broken into powder in the plastic bag using dry-ice block and dry-ice-cold hammer. The powder was then transferred and kept in dry-ice-cold tubes. Temperature of the tubes and instruments that directly contacted to the samples was frequently measured by infrared-thermometer (AD-5613A, A&D Company, Japan) and kept under −20 °C. Then, 30 to 40 mg of brain powder was used for cDNA synthesis. RNA was extracted using RNAqueous (Applied biosystems, Foster City, CA) according to manufacturer's instructions with a slight modification, i.e., after homogenization, samples were washed twice with 500 μl of chloroform, and then applied to the spin-column. Extracted RNA was quantified by optical density reading at 260 nm using NanoDrop ND-1000 (Thermo Scientific, Rockford, IL). Then, the obtained RNA (14 μl) was used for cDNA synthesis using SuperScript VILO cDNA Synthesis Kit (Invitrogen, Carlsbad, CA).

Table 1
Demographic information on brain specimens of Stanley Neuropathology Consortium.

	Control	Schizophrenia	Bipolar disorder	Major depression
Age (years)	48.1 (29–68)	44.2 (25–62)	42.3 (25–61)	46.4 (30–65)
Gender (M/F)	9/6	9/6	9/6	9/6
Race	14 C, 1 AA	13 C, 2 A	14 C, 1 AA	15 C
PMI (hours)	23.7 (8–42)	33.7 (12–61)	32.5 (13–62)	27.5 (7–47)
pH	6.3 (5.8–6.6)	6.1 (5.8–6.6)	6.2 (5.8–6.5)	6.2 (5.6–6.5)
Side of brain frozen (R/L)	7/8	6/9	8/7	6/9
Freezer storage time (months)	11.3 (1–26)	20.7 (2–31)	20.7 (7–28)	14.5 (3–31)

AA, African American; A, Asian; C, Caucasian; F, female; M, male; and PMI, postmortem interval.

2.2. Blood samples

Subjects were 121 patients with schizophrenia (84 males and 37 females; age 44.1 ± 13.7 (mean ± SD) years) and 318 controls (90 males and 228 females; age 43.1 ± 15.3 years). All subjects were biologically unrelated Japanese and recruited from the same geographical area (Western part of Tokyo Metropolitan). Consensus diagnosis by at least two psychiatrists was made for each patient according to the Diagnostic and Statistical Manual of Mental Disorders, 4th edition (DSM–IV) criteria (American Psychiatric Association, 1994) on the basis of unstructured interviews and information from medical records. The controls were healthy volunteers recruited from the community, through advertisements in free local magazines and our website announcement. Control individuals were interviewed by the Japanese version of the Mini-International Neuropsychiatric Interview (M.I.N.I.) (Otsubo et al., 2005; Sheehan et al., 1998) and those who had a current or past history of psychiatric treatment were not enrolled in the study. After the nature of the study procedures had been fully explained, written informed consent was obtained from all subjects. The study was conducted in accordance with the Declaration of Helsinki and approved by the ethics committee of the National Center of Neurology and Psychiatry, Japan.

Blood collection and RNA isolation were performed using the PAXgene blood RNA system (Qiagen, Valencia, CA). Blood samples were collected around 11 A.M. Extracted RNA was quantified as described above. Samples that contained more than 40 ng/μl of total RNA were used for analysis; 8 μl from each sample was reverse transcribed using SuperScript VILO cDNA Synthesis Kit (Invitrogen, Carlsbad, CA).

2.3. Chronic risperidone treatment to mice

C57BL/6J male mice aged 10 weeks were purchased from Crea Japan. Chronic oral risperidone treatment was performed according to Belforte et al., (Belforte et al., 2010). In brief, 2.5 mg/kg/day of risperidone (Rispadal liquid, Janssen Pharmaceutical, Tokyo, Japan) in drinking water freshly made every 72 h had been administered continuously for 3 weeks. Control mice received solvent (1.4 mM tartaric acid neutralized to pH 6–7). All experimental procedures were in accordance with the guidelines of the United State's National Institutes of Health (1996) and were approved by the Animal Care Committee of the National Institute of Neuroscience, NCNP.

2.4. Quantitative real-time polymerase chain reaction

Polymerase chain reaction (PCR) amplifications were performed in triplicate (5 μl volume) on 384-well plates using ABI prism 7900HT (Applied Biosystems, Foster City, CA). Each reaction contained 0.28 μl of cDNA sample, qPCR QuickGoldStar Mastermix Plus (Eurogentec, Seraing, Belgium) and a primer of the target, i.e. human CADPS2 (Hs01095968_m1 at Exon 4–5 on NM_017954.9), mouse CADPS2 (Mm00462577_m1), human CADPS2ΔExon3 (Forward primer: GTAGCTGACGAAGCATTTTGCA,

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Reverse Primer: TGATCTGGGCTGCTTGTTCAT, Reporter: CTGCGTTATC-CAGCTCAT) and a primer of the housekeeping gene human glyceraldehyde-3phosphate dehydrogenase (GAPDH, 4326317E), mouse GAPDH (4352339E) and human TATA-box binding protein (TBP, Hs99999910_ml) all purchased from Applied Biosystems (Foster City, CA). Negative control reactions were carried out with "no RNA" samples. The real time PCR reactions ran at 50 °C for 2 min, at 95 °C for 10 min and in 40 or 45 cycles changing between 95 °C for 15 s and 60 °C for 1 min. A standard amplification curve was made by serial dilution of a "standard" pooled cDNA sample in each plate. The mean value of triplicate of each sample was normalized to the standard curve. Then, the values of CADPS2 and CADPS2ΔExon3 from each sample were normalized to those of GAPDH.

2.5. Statistical analyses

Data analyses were performed with SPSS software (Version 11, SPSS Japan, Tokyo, Japan). Effect of age, brain pH, postmortem interval (PMI), and freezer storage time on each brain analysis was assessed by Pearson's correlations (Table 2). Variables showing significant correlations were included as covariates in the main analysis. Levene's test was used to assess the equality of variances across diagnostic group. Analysis of covariance (ANCOVA) was used to identify overall effects of diagnosis and significant main effects of diagnosis were investigated by planned post hoc contrasts. In the blood sample analyses, CADPS2 expression levels were converted to 10-log scale before statistical analysis in order to obtain a normal distribution (Castensson et al., 2005). The effect of diagnosis on blood CADPS2 expression was assessed by ANCOVA with sex and age as covariates after Levene's test. The effect of diagnosis on blood CADPS2ΔExon3 expression was assessed by logistic regression, controlling for sex and age as covariates. The effect of risperidone on CADPS2 expression in mice brain was assessed by student's *t*-test after F-test.

3. Results

3.1. CADPS2 expression levels in the postmortem brain (BA6)

We first analyzed the effects of age, brain pH, postmortem interval (PMI), and freezer storage time (FST) on each expression analysis (Table 2). Brain pH was significantly correlated with GAPDH expression levels or raw CADPS2 expression levels. PMI also tended to be correlated with GAPDH expression levels or raw CADPS2 expression levels. If the effects were analyzed separately within each diagnostic group, no significant correlation was detected.

CADPS2 expression levels normalized to GAPDH expression levels (CADPS2/GAPDH) in each sample are shown in Fig. 1A. ANCOVA with brain pH as covariates detected a significant effect of diagnosis on CADPS2/GAPDH levels ($F=3.4$, $df=3$, $p=0.025$) and post hoc test detected a significant difference between schizophrenia and control groups ($p=0.03$). Even if PMI was added as another covariate, the difference was significant ($p=0.002$). There was no significant difference between bipolar disorder and controls or between depression and controls. There was no significant correlation between CADPS2/GAPDH levels and lifetime dose of antipsychotic drugs (data not shown). There was a significant effect of diagnosis on GAPDH expression levels ($F=3.4$, $df=3$, $p=0.023$, Fig. 1B). GAPDH levels in the control group was significantly higher than that of schizophrenia ($p=0.012$), bipolar disorder ($p=0.009$) or major depression group ($p=0.013$). Raw CADPS2 levels did not differ among the diagnostic groups ($F=1.0$, $df=3$, $p=0.38$, Fig. 1C). There was a significant correlation between GAPDH expression levels and raw CADPS2 expression levels (Pearson's correlation 0.69, $p<0.001$, Fig. 1D).

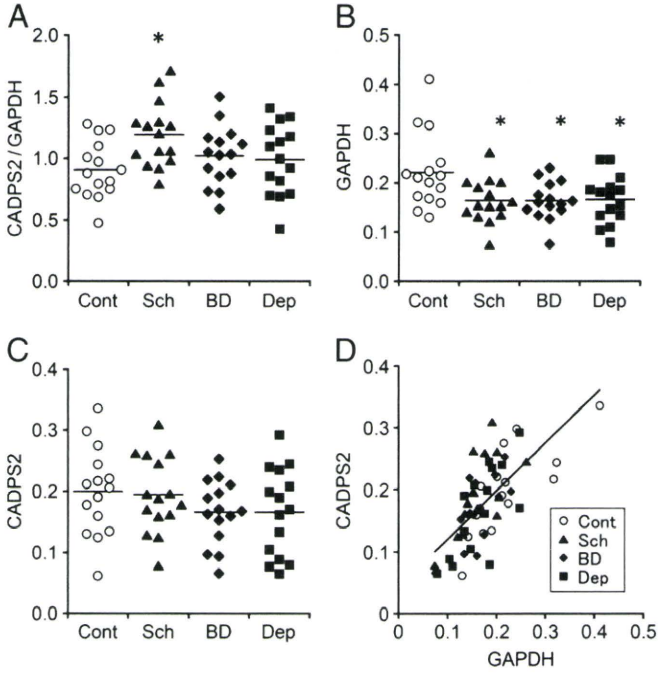

Fig. 1. CADPS2 expression levels in the postmortem brains of psychiatric disorder. (A) CADPS2 expression levels normalized by GAPDH levels. Scatter plots display the variability and differences in the CADPS2 mRNA expression levels normalized by each GAPDH expression levels. A crossbar on each scatter plot represents mean expression levels for each group. (B) GAPDH expression levels (C) Raw CADPS2 expression levels. (D) Correlation between GAPDH levels and raw CADPS2 levels. Cont, control; Sch, schizophrenia; BD, Bipolar Disorder; and Dep, Depression. *, statistically significant difference ($p<0.05$).

We compared relative CADPS2 expression levels among diagnostic groups using another endogenous control, TATA-box binding protein (TBP), and obtained similar result (Fig. S1, this experiment was done after uncode the sample). ANCOVA with brain pH as covariates detected a significant effect of diagnosis on CADPS2/TBPlevels ($F=3.3$, $df=3$, $p=0.027$) and post hoc test detected a significant

Table 2
The effect of age, pH, postmortem interval, and freezer storage time on each brain expression analysis.

		GAPDH	CADPS2	ΔExon3	CADPS2/GAPDH	ΔExon3/G APDH	ΔExon3/C ADPS2
Age	Pearson's	0.013	−0.13	0.19	−0.18	0.088	0.27
	P	0.92	0.34	0.37	0.16	0.51	0.041
pH	Pearson's	0.36	0.26	0.25	0.031	0.12	0.090
	p	0.005	0.048	0.058	0.81	0.38	0.50
Post mortem Pearson's interval (hours)	−0.23	−0.22	−0.13	−0.040	0.039	0.15	
	P	0.076	0.098	0.30	0.76	0.77	0.25
Freezer storage time (months)	Pearson's	−0.22	−0.034	−0.041	0.21	0.12	0.052
	P	0.092	0.80	0.75	0.11	0.36	0.69

ΔExon3, CADPS2ΔExon3; and Pearson's, Pearson's correlation.

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difference between schizophrenia and control groups ($p=0.019$). Even if PMI was added as another covariate, the difference was significant ($p=0.012$).

With respect to CADPS2ΔExon3/GAPDH level (Fig. 2A), the effect of age was detected in the control group (Pearson's correlation 0.58, $p=0.023$) and the effect of pH was detected in the bipolar disorder group (Pearson's correlation 0.60, $p=0.018$). ANCOVA with age and brain pH as covariates detected the marginal effect of diagnosis ($F=2.8$, $df=3$, $p=0.050$) and the mean expression level was significantly increased in the schizophrenia group, compared to the control group ($p=0.030$). When the ratio of CADPS2ΔExon3 to raw (total) CADPS2 expression levels was compared, the ratio was similar in the 4 diagnostic groups ($F=1.1$, $df=3$, $p=0.36$, Fig. 2B). Neither the effect of diagnosis on raw CADPS2ΔExon3 levels was observed ($F=1.9$, $df=3$, $p=0.15$, Fig. 2C). There was a significant correlation between GAPDH expression levels and raw CADPS2ΔExon3 expression levels (Pearson's correlation 0.66, $p<0.001$, Fig. 2D).

3.2. Cortical CADPS2 expression after chronic antipsychotic treatment in mice

To see whether antipsychotics alter the mRNA expression of CADPS2, we measured the CADPS2 levels in the frontal cortex of mice, following chronic treatment with an antipsychotic risperidone. Oral administration of risperidone (2.5 mg/kg, $n=15$ for the controls and 16 for the risperidone group) for 3 weeks did not alter CADPS2 expression ($F=1.5$, $df=29$, $p=0.61$).

3.3. CADPS2 expression in blood sample

Since we observed increased expression of CADPS2 in postmortem brains of schizophrenia patients, we then examined whether such an alteration exists in peripheral blood samples. The CADPS2/GAPDH expression levels were converted to 10-logarism before statistical analyses to obtain normal distribution. The mean (Standard deviation) CADPS2 expression level was 0.17 (1.29) in the control group and 0.32 (1.46) in the schizophrenia group. ANCOVA controlling for age and sex did not detect the significant effect of diagnosis on CADPS2/GAPDH level ($F=1.67$, $df=1$, $p=0.20$). We also measured CADPS2ΔExon3 levels in the blood samples. Compared to brain samples, the expression levels were quite low and could not detect in the majority of samples. Thus, we defined "expressed" when at least 2 tubes in triplet analyses of each sample were detected until 45 cycles. CADPS2ΔExon3 expression was detected in 36 of 318 control samples (ratio = 0.11), and 21 of 121 schizophrenia samples (ratio = 0.17). There was no significant effect of diagnosis on CADPS2ΔExon3 expression by the logistic regression analysis controlling for age and sex (odds ratio 1.51, [95% CI 0.80–2.86], $p=0.21$). Even when men and women were examined separately, there was no significant difference between the patients and controls for each sex (data not shown).

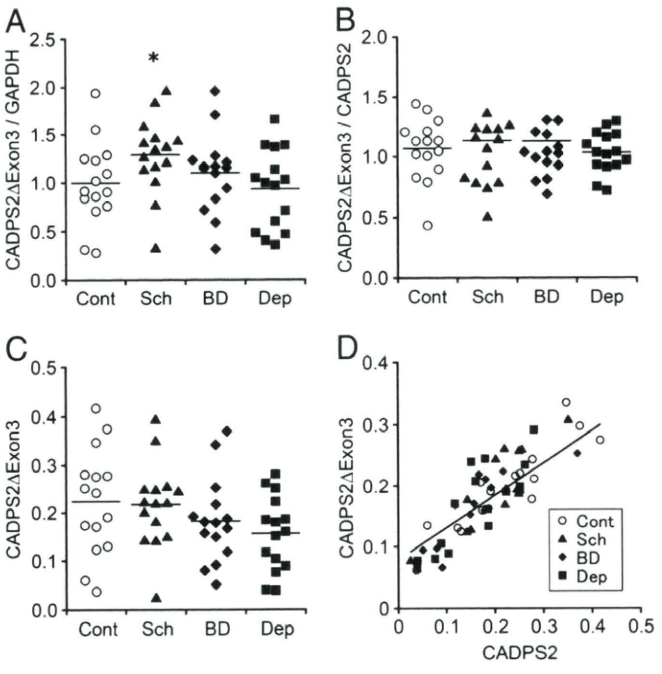

Fig. 2. CADPS2ΔExon3 expression levels in the postmortem brains of psychiatric disorder. (A) CADPS2ΔExon3 expression levels normalized by GAPDH levels. Scatter plots display the variability and differences in the CADPS2ΔExon3 mRNA expression levels normalized by each GAPDH expression levels. A crossbar on each scatter plot represents mean expression levels for each group. (B) CADPS2ΔExon3 levels normalized to each total CADPS2 expression levels. (C) Raw CADPS2ΔExon3 expression levels. (D) Correlation between GAPDH expression levels and raw CADPS2ΔExon3 expression levels. Cont, control; Sch, schizophrenia; BD, Bipolar Disorder; and Dep, Depression. *, statistically significant difference ($p<0.05$).

4. Discussion

4.1. Main findings

In the present study, we analyzed the expression of CADPS2 mRNA in the postmortem brains (BA6) of psychiatric patients (schizophrenia, major depression and bipolar disorder) and controls. A significant increase in the CADPS2 expression was detected in the brains of the schizophrenia group, compared to the control group. No change was detected in other disease groups. While a CADPS2 splice variant, CADPS2ΔExon3 showed a non-significant increase in the schizophrenia group, its ratio to the total CADPS2 levels was not different from the control group. Chronic risperidone treatment did not alter the CADPS2 levels in mice brain. We also analyzed CADPS2 or CADPS2-ΔExon3 expression levels in the blood samples of schizophrenia and control subjects; however, the levels were not significantly different between the two groups.

4.2. Brain analysis

4.2.1. Drug effect

A large number of gene expressions in the brain are affected by antipsychotic treatments (Girgenti et al.,; Mehler-Wex et al., 2006; Thomas, 2006). Therefore, the observed increase in CADPS2 mRNA in the schizophrenia group could be the result of antipsychotic treatment. However, our results did not support this assumption because the CADPS2 levels did not correlate to life-time antipsychotic dose and chronic risperidone treatment in mice did not alter CADPS2 expression on their cortices, although caution is required for the interpretation of those results because we don't have data for the latest dose before death and other drugs such as chlorpromazine, haloperidol and clozapine might be used in the patients.

4.2.2. Possible relevance to BDNF secretion, dopamine transmission, and neuropeptide release

Considering that defective BDNF signaling has been suggested in schizophrenia and mood disorders (Angelucci et al., 2005) and that CADPS2 mediates BDNF release in neurons (Sadakata et al., 2004), we initially expected that CADPS2 levels would be decreased in frontal cortex in patients with these psychiatric disorders. However, in our results, CADPS2 levels were not altered in mood disorders but increased in schizophrenia. In addition, the relative levels of defective CADPS2 isoform, CADPS2ΔExon3 were not altered in those disorders. Thus, it is unlikely that altered CADPS2 expression might be a cause of BDNF deficits in schizophrenia. It may be rather a compensatory consequence of reduced BDNF signaling.

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CADPS2 also promotes monoamine storage in neurons (Brunk et al., 2009; Liu et al., 2008). CADPS2 is highly expressed in the dopamine-rich brain areas such as ventral tegmental area and substantia nigra of mice brain (Sadakata et al., 2006) and it is reported to interact with dopamine D2 receptor (Binda et al., 2005). Growing evidence has demonstrated increased presynaptic dopamine levels in the striatum of schizophrenia patients (Lyon et al., 2009). If the observed increase in the expression of CADPS2 occurs in the subcortical regions including striatum and midbrain as well as frontal cortex, it might be the cause of hyper-dopamine transmission that reflects psychotic state (Howes et al., 2009).

Furthermore, large dense-core vesicles contain not only neurotrophins and monoamines but also neuropeptides (Salio et al., 2006). Neuropeptides such as endorphins, cholecystokinin (CCK), neurotensin (NT), somatostatin, Neuropeptide Y and neuregulin 1 have been implicated in schizophrenia (Caceda et al., 2007). Especially reduced levels of CCK and NT have been repeatedly reported in the disorder (Caceda et al., 2007), which may have caused compensatory increase in the CADPS2 expression in schizophrenia.

4.3. CADPS2 expression in the blood

4.3.1. CADPS2 expression and diagnosis

Following the report that 4 of 16 patients with autism expressed CADPS2ΔExon3 in peripheral bloods but none in 24 normal subjects (Sadakata et al., 2007b), another group reported that they detected CADPS2ΔExon3 in some control subjects (Eran et al., 2009). Thus we assumed that the ratio of CADPS2ΔExon3 to total CADPS2 rather than whether CADPS2ΔExon3 exists or not is important and therefore we applied quantitative real-time PCR to measure their expression. The pilot experiment in the present study indicated that our quantification method using SuperScript VILO and random-hexamer, was 4 to 8 fold more sensitive than one step real-time PCR using gene specific primers and could detect l0 to 100 clones of CADPS2 or CADPS2-ΔExon3 sequence-containing vector. Compared with the brains, CADPS2 expression was 32 to 128 fold lower in the blood. Unlike in the brain, CADPS2ΔExon3 could not be detected in most blood samples. So we performed qualitative analysis for each subject. As a result, we didn't detect any significant difference in the expression of CADPS2ΔExon3 in the blood between patients with schizophrenia and controls. The CADPS2ΔExon3 was abundantly expressed in the brain and the levels were unchanged across the diagnostic groups. Thus, it is unlikely that the expression or the splicing balance should relate to diseases we analyzed.

5. Conclusion

In conclusion, we found increased mRNA expression of CADPS2 in the postmortem frontal cortex of schizophrenia patients which might have some relevance to dysregulation in the release of dopamine, neurotrophins, and/or neuropeptides in the disorder. This increase was unlikely to be attributable to antipsychotic medication. We also analyzed the CADPS2ΔExon3 in human brains and found that it is abundantly present in the frontal cortex in any diagnostic group. We obtained no evidence for the specific role of the splice variant in schizophrenia or mood disorders. Future research should include the evaluation of CADPS2 expression in other brain areas, and basic studies on the cause and consequence of increased CADPS2 expression.

Supplementary materials related to this article can be found online at doi:10.1016/j.pnpbp.2011.05.004.

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BEHAVIORAL NEUROSCIENCE

Phenotypic characterization of a new *Grin1* mutant mouse generated by ENU mutagenesis

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Keywords: animal model, behavior, D,l-methylphenidate, NMDA receptor

Abstract

In the RIKEN large-scale *N*-ethyl-*N*-nitrosourea (ENU) mutagenesis project we screened mice with a dominant mutation that exhibited abnormal behavior in the open-field test, passive avoidance test and home-cage activity test. We tested 2045 progeny of C57BL/6J males treated with ENU and untreated DBA/2J females in the open-field test and isolated behavioral mutant M100174, which exhibited a significant increase in spontaneous locomotor activity. We identified a missense mutation in the *Grin1* gene, which encodes NMDA receptor subunit 1, and designated the mutant gene $Grin1^{Rgsc174}$. This mutation results in an arginine to cysteine substitution in the C0 domain of the protein. Detailed analyses revealed that $Grin1^{Rgsc174}$ heterozygote exhibited increased novelty-seeking behavior and slight social isolation in comparison with the wild type. In contrast to other *Grin1* mutant mice, this mutant exhibited no evidence of heightened anxiety. These results indicate that this is a unique behavioral *Grin1* gene mutant mouse that differs from the known *Grin1* mutant mice. The results of immunohistochemical and biochemical analyses suggested that impaired interaction between the glutamatergic pathway and dopaminergic pathway may underlie the behavioral phenotypes of the $Grin1^{Rgsc174}$ mutant.

Introduction

N-ethyl-*N*-nitrosourea (ENU) is an effective chemical mutagen that introduces single base-pair changes into genomic DNA (Kohler *et al.*, 1991; Provost & Short, 1994). The point mutations that are induced by ENU can result in a large variety of aberrations ranging from complete or partial loss-of-function to gain-of-function. Several large-scale saturation ENU mutagenesis projects have been undertaken in order to generate large numbers of mutants that will allow gene functions to be systematically investigated *in vivo* (Justice *et al.*, 1999; Hrabe de Angelis *et al.*, 2000; Nolan *et al.*, 2000). The aim of our RIKEN mutagenesis project is to generate mouse models of human diseases, including diabetes, hypertension and cancer, and deformities. We have been screening dominant mutant mice for visible, clinical biochemical, and hematological abnormalities and have succeeded in establishing unique models of human disease (Inoue *et al.*, 2004; Masuya *et al.*, 2005, 2007). In 2007, Keays *et al.* (2007) reported finding that a mouse with ENU-induced mutation that exhibited hyperactivity in the open-field test and abnormal neuronal migration carried a missense mutation in alpha-tubulin (Tuba1a). The Tuba1a mutant mouse displayed phenotypic similarity to lissencephaly patients, and Keays *et al.* (2007) identified *de novo* mutations in *TUBA3*, the human homolog of Tuba1. As these findings indicated that ENU mutagenesis might be useful as a means of generating models of various psychiatric diseases, we have conducted behavioral screening that included the open-field test, passive avoidance test and home-cage activity test.

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Materials and methods

Animals and production of ENU mutant mice

All animal studies were carried out in accordance with the guideline issued by the RIKEN Bioscience Technology Center in the 'Outline for conducting animal experiments' (August 1999, revised October 2001). The study was approved by the ethics committee of the RIKEN Tsukuba Institute. A large-scale mouse ENU mutagenesis was conducted as described previously (Masuya *et al.*, 2005) with some modifications. C57BL/6J (B6) and DBA/2J (D2) mice were purchased from a commercial supplier (CLEA Japan, Inc., Tokyo, Japan). The following outline strategy is given in more detail in Supporting information, Fig. S1. B6 males were treated with ENU (150–250 mg/kg) by intraperitoneal (i.p.) injection and crossed with D2 females. The progeny generated by this cross were designated G1 mice (supporting Fig. S1A). To obtain control data for genetic mapping and to confirm phenotypic transmission, D2 females and (D2 × B6) F1 mice were crossed. This cross yield D × DB mice (supporting Fig. S1B). G1 mice were then backcrossed with D2 mice six times for inheritance testing, gene mapping and elimination of other ENU-induced mutations (supporting Fig. S1C). In order to eliminate the effects of the D2 genetic background, an N6 mouse was backcrossed to B6 at least 10 times, and naive backcrossed progeny were used for all behavioral tests except the resident–intruder paradigm (supporting Fig. S1D). The F1 mice from the cross between N6 mice and B6 mice were used for the resident–intruder paradigm (supporting Fig. S1D). Male mice that had never undergone inheritance testing or linkage analysis were used in the behavioral tests in order to eliminate any influence of the female estrous cycle and previous handling.

Phenotype screening and gene mapping

We used locomotor activity in the open field as an index of abnormal behavior. The G1 mice were screened for abnormal open-field activity at 9 weeks of age. Mice that showed high or low activity (> mean ± 3 SD of the G1 population) were classified as behavioral phenodeviants and crossed with wild-type D2 mice to test for phenotypic transmission and genetic mapping. A total of 229 N2–6 mice (supporting Fig. S1C) between 10 and 12 weeks of age were collected and tested for spontaneous locomotor activity in the open field. A genome-wide scan was conducted as described previously (Masuya *et al.*, 2005) with some modifications. Single nucleotide polymorphism (SNP) markers spaced at 10 cm were chosen from the Mouse SNP database (http://www.broad.mit.edu/snp/mouse/) and used for genome-wide scanning (supporting Table S1). We used microsatellite or SNP markers for a detailed linkage analysis. Candidates for the causative gene located near the mapped locus were identified by searching the positional cloning assistant database Positional MEDLINE (PosMed, http://omicspace.riken.jp/PosMed/; Kobayashi & Toyoda, 2008). The genomic structures of the candidates were determined with the mouse Ensembl database (http://www.ensembl.org/Mus_musculus/index.html), and coding regions were directly sequenced. The accession numbers of all of these genes are listed in Table 1.

TABLE 1. List of candidate causative genes

Gene name	No. of exons sequenced	No. of exons	MGI accession no.
Hnmt	7	7	2153181
Cacna1b	47	48	88296
Ehmt1	23	26	1924933
Arrdc1	7	8	2446136
Zmynd19	5	6	1914437
NM_026044	9	9	1914478
Q9CQN7	2	2	1333816
Nelf	14	15	1861755
Entpd8	10	10	1919340
Noxa1	6	12	2449980
NM_026624	7	7	3605773
Grin1	18	20	95819
Npdc1	8	9	1099802
Clic3	6	7	1916704
Ptgds	6	7	99261

Candidate genes for the mutant line from founder mouse M100174 obtained by a search of the PosMed database are listed. Accession numbers of genes used for primer design are listed on the right side of the table. MGI, Mouse Genome Informatics (http://www.informatics.jax.org/). The genomic sequences and exon/intron structures of each gene were retrieved from the Ensembl Mouse database (http://www.ensembl.org/Mus_musculus/index.html) by entering MGI accession numbers. Sequencing of 191 of the 210 exons in these 18 genes was performed.

Mutation analysis of the Grin1 gene

The C-to-T point mutation in exon 18 of *Grin1* was identified by using the allele-specific primer–polymerase chain reaction (ASP-PCR) and direct sequencing. ASP-PCR was performed with the following primers: forward primer for wild-type and mutant alleles, tgctgagggtccctcacag; reverse primer for the wild-type allele, agctgcatctgcttcctagg; reverse primer for the mutant-type allele, agctgcatctgcttcctaga.

Homology search and accession number of the amino acid sequence

The accession number of the amino acid sequence used for alignment was A2AI21.

Open-field test

Each mouse was placed in the corner of an open-field apparatus (400 wide × 400 long × 300 high; O'Hara & Co., Ltd., Tokyo, Japan) made of white polyvinyl chloride. The distance traveled by each animal in the open field was recorded for 20 min with a video imaging system (Image OF9; O'Hara & Co., Ltd.).

Home-cage activity test

Each mouse was placed alone in a testing cage (227 × 329 × 133 mm) under a 12-h light–dark cycle (light on at 08:00 h) and had free access to both food and water. After 1 day of acclimation, spontaneous activity in the cage was measured for 5 days (starting at 08.00) with an infrared sensor (AB system 4.0; Neuroscience Co., Ltd., Tokyo, Japan).

Object exploration test

We used the procedure described previously (Glenn *et al.*, 2008; Tomihara *et al.*, 2009) with some modifications. Each mouse was placed in the open-field apparatus without the novel object for 20 min of acclimation before testing. A transparent acrylic tube (bottom diameter, 66 mm; top diameter, 44 mm; height, 154 mm) containing marbles was placed in the center of the open field. The total time spent exploring the object and the frequency of exploration during a 10-min period were determined with a video imaging system purchased from a commercial supplier (O'Hara & Co., Ltd.). Exploration was defined as the state when the distance between the object and the mouse was < 1 cm.

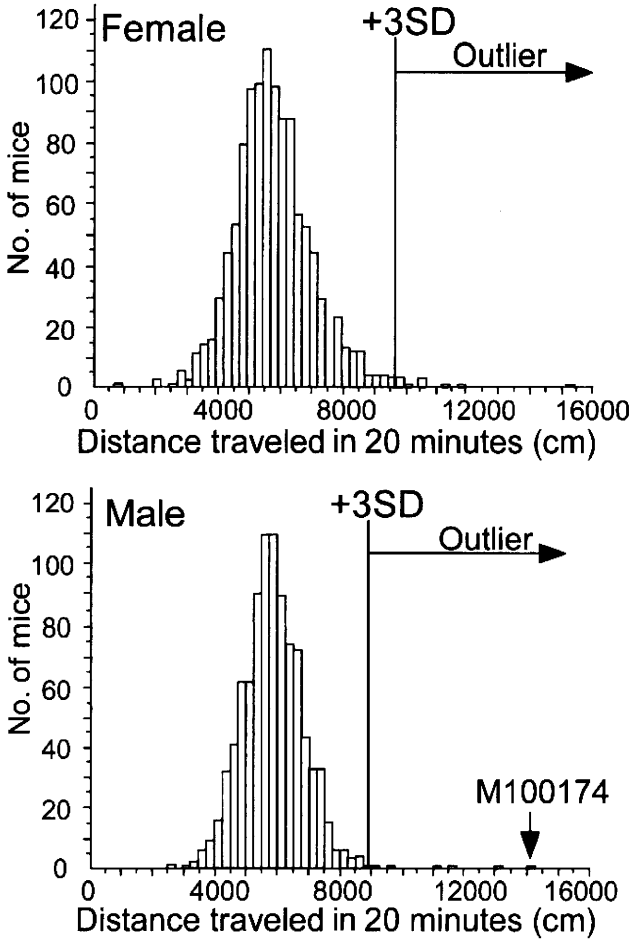

FIG. 1. Histograms of the open-field activity of G1 mice. The ordinate and abscissa indicate the number of mice and the distance traveled, respectively. The vertical line in the histograms indicates the population > 3 SD above the mean. Spontaneous activity during the open-field test was normally distributed. Mice whose activity level was > 3 SD above the mean (the mean was 9734.9 cm for G1 females and 8984.9 cm for G1 males) were isolated as mutant candidates. The vertical arrow indicates the activity level of the M100174 mouse.

Effect of D,L-methylphenidate hydrochloride (MPH) on spontaneous locomotor activity in the open-field

Each mouse was acclimated to the open field as above described for 1 h. Mice were injected intraperitoneally with saline or a 30 mg/kg dose of MPH (SIGMA-ALDRICH, St. Louis, MO, USA). The free base of methylphenidate was calculated as 108 μmol/kg dose. Locomotor activity in the open-field apparatus was measured as described above for 20 min, beginning at 80 min after the injection (Gainetdinov *et al.*, 1999). To assess the dose- and time-dependence of the effect of MPH, small pilot experiments were carried out in which various doses were given (supporting Appendix S1 and Fig. S2).

Measurement of NMDA-induced changes in intracellular calcium levels in mouse primary cortical neurons

Dissociated cerebral cortical cells were prepared from embryonic day (E) 14–15 mice as described in supporting Appendix S2. Pregnant female mice were killed by cervical-vertebrae dislocation and isolated embryos were killed by decapitation before removing the brain. The cells were stimulated with 10 μM *N*-methyl-D-aspartate (NMDA) and 100 μM glycine at 37°C, and fluorescence (excitation wavelength,

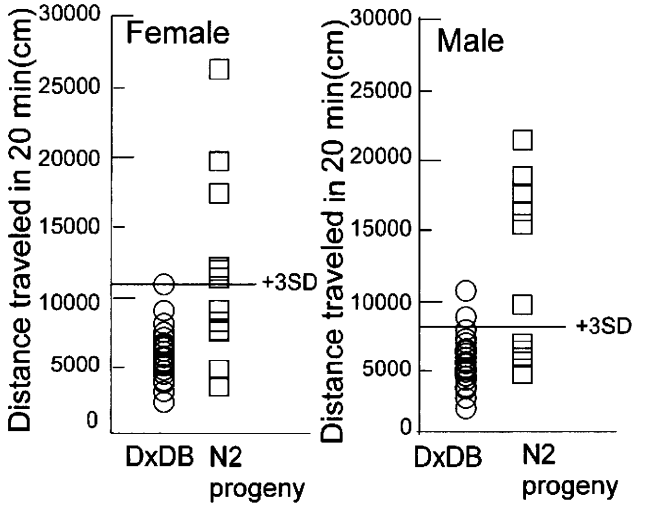

FIG. 2. Distribution of the locomotor activity of the N2 progeny of the M100174 founder mouse and the control mice (D × DB). Locomotor activity of D × DB (females, n = 68; males, n = 74) and the N2 progeny of M100174 (females, n = 12; males, n = 10) in the open-field test. Open circles, D × DB; open squares, N2 progeny of M100174. The horizontal line indicates the locomotor activity criterion that divides wild-type mice and mutant mice (3 SD above the mean in the D × DB population).

480 nm; emission wavelength, 540 nm) was measured with an FDSS6000 fluorimeter (Hamamatsu Photonics, Hamamatsu, Japan).

Immunoblotting of NMDA receptor (NMDAR) subunits

The brain tissue samples were prepared as described previously (Bajo *et al.*, 2006) with a slight modification (supporting Appendix S3). Mice were killed by cervical-vertebra dislocation. The blotted membranes were blocked with Starting Block TBS-T (Pierce, Rockford, IL, USA) for 10 min and probed with the following primary antibodies: mouse antineuronal class III β-tubulin (Covance, Berkeley, CA, USA) and rabbit anti-*GRIN1*, anti-GRIN2A and anti-GRIN2B (Frontier Science Ishikari, Hokkaido, Japan). After washing three times with Tris-buffered saline (TBS; pH 7.5) containing 0.1% Tween 20 (TBS-T), the membranes were incubated with horseradish peroxidase-labeled secondary antibody, and signals were detected with SuperSignal West Femto (Pierce) and LAS1000 mini (Fujifilm, Tokyo, Japan).

Immunoblotting of extracellular signal-regulated kinase (ERK2) and phospho-ERK2 (pERK2) proteins

At 90 min after i.p. injection of saline or MPH 30 mg/kg, the nucleus accumbens was prepared as reported previously (Hattori *et al.*, 2006; supporting Appendix S4). Mice were killed by cervical-vertebra dislocation. The proteins were transferred onto membranes, and ERK proteins were probed and signals detected as described above [primary antibodies, 1 : 50 000 dilution for anti-pERK antibody and 1 : 20 000 for anti-ERK antibody (Cell Signaling Technology, Danvers, MA, USA), horseradish peroxidase-labeled secondary antibody and anti-rabbit IgGs, 1 : 5000 dilution for pERK and 1 : 2000 dilution for ERK (Pierce)].

General histology and Nissl staining

Mice were deeply anesthetized by i.p. pentobarbital injection and then fixed by transcardiac perfusion with a solution of 4%

paraformaldehyde and 0.5% picric acid in PBS. The brains were removed, and coronal or parasagittal sections (70 μm thick) were prepared with a vibratome. Sections were stained with NeuroTrace 500/525 (fluorescent Nissl stain; Invitrogen, Carlsbad, CA, USA) according to the manufacturer's instructions. Fluorescence images were obtained directly with a confocal laser-scanning microscope (LSM5 Pascal; Zeiss, Oberkochen, Germany).

Immunohistological study of c-Fos expression

Two hours after i.p. injection of saline or MPH 30 mg/kg, mouse brains were perfusion-fixed and removed, and sections were prepared as described above. The sections were postfixed in the same fixative for 2 h at 4–8°C and then rinsed with PBS. c-Fos immunostaining and quantification of c-Fos-positive neurons were performed as reported previously (Hattori *et al.*, 2001). Brain regions that were responsive to MPH treatment were selected as described in the literature (Yano & Steiner, 2005).

Statistical analysis

Two-way (genotype and experimental factor: between-subjects) or three-way (genotype, sex, and experimental factor: between- or within-subjects) ANOVA with Fisher's PLSD *post hoc* analysis and Student's *t*-test were used for statistical analysis. Differences were considered to be statistically significant at *P*-values < 0.05.

Results

Isolation of a mutant with increased locomotor activity and identification of a missense mutation in the Grin1 gene

We used the total distance traveled during the open-field test to screen locomotor activity in a population of 2045 (female, $n = 1124$; male, $n = 921$) G1 mice in a large-scale ENU mutagenesis program conducted at the RIKEN Genome Science Center. Mouse M100174 exhibited the highest locomotor activity among the male G1 population (Fig. 1), and this founder mouse was backcrossed with D2 females, and 22 offspring of the backcrossed mice (N2 progeny)

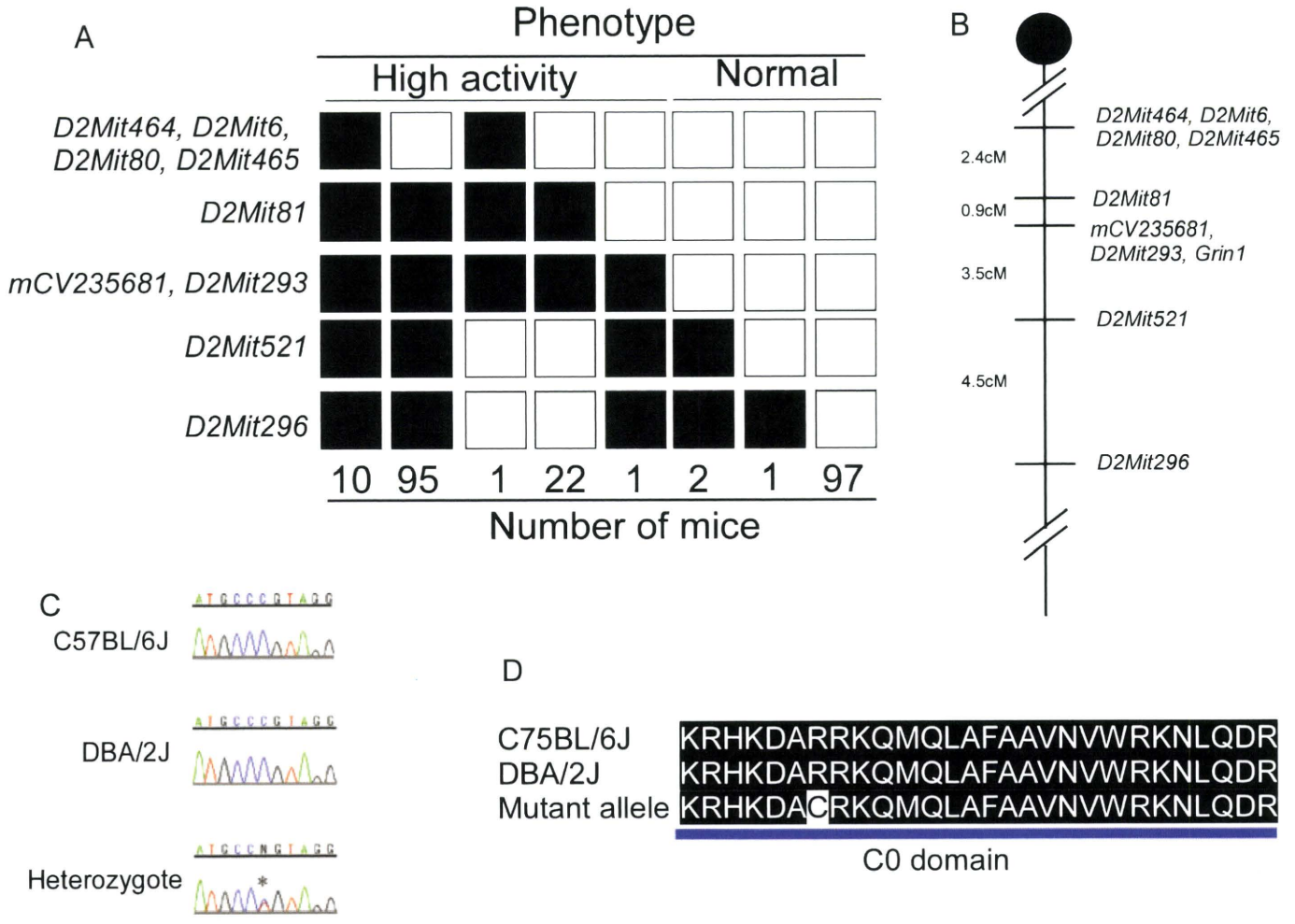

FIG. 3. Mutant mouse line M100174 carries a missense mutation in *Grin1*, which encodes NMDAR1. (A) Haplotype analysis of backcrossed progeny of M100174. Genetic markers are listed on the left side of the panel. The black boxes represent the heterozygote of C57BL/6J and DBA/2J, and the white boxes represent the homozygote of DBA/2J. The numbers of progeny that inherited each haplotype are shown at the bottom. (B) Genetic map of M100174 constructed from the backcrossed progeny of G1 mice. Genetic markers are listed on the right. (C) Sequence trace from a heterozygote. The C-to-T substitution is highlighted with an asterisk and corresponds to a point mutation in exon 18 of *Grin1*. (D) Alignment of the C0 domain of wild-type NMDAR1 with that of the mutant allele. Conserved amino acids sequences are highlighted in black. The C-to-T mutation results in an amino acid substitution in the C0 domain of NMDAR1.

TABLE 2. Numbers and percentages of wild-type, heterozygous and homozygous pups obtained by intercrossing heterozygote

	Grin1 gene genotype: number of pups (and %)				
Age	Wild	Hetero	Homo	Total	Genetic background
E14	15 (22)	34 (50)	19 (28)	68 (100)	N9 × N9
E17–18	25 (41)	28 (46)	8 (13)	61 (100)	N10 × N10
P4w	11 (35)	19 (62)	1 (3)	31 (100)	N5 × N5

Pups were generated by mating heterozygous females and males. The parents of the pups were generated by backcrossing M100174 with DBA/2J or C57BL/6J. The genetic background of the parents is indicated by the backcross generation. The proportions of offspring according to genotypes were examined at embryonic day 14 (E14), embryonic day 17–18 (E17–18), and 4 weeks after birth (P4w). Wild, +/+; Hetero, $Grin1^{Rgsc174}$/+; Homo, $Grin1^{Rgsc174}/Grin1^{Rgsc174}$.

were generated for the inheritance test. Based on their level of open-field activity the N2 progeny were divided into a normal group and an increased locomotion group by scoring the animals relative to the mean open-field activity of D × DB mice (Fig. 2). A total of 229 mice from generations N2–N6 were collected and used for a linkage analysis. The causative locus was mapped to a region between D2Mit81 and D2Mit521 (Fig. 3A and B).

A search of the Ensembl mouse genome database revealed that 172 genes were located between D2Mit81 and D2Mit521, and these candidates were investigated with PosMed. Based on a list of keywords related to behavior, PosMed narrowed the number down to 18 candidate genes (Table 1), and one of them, *Grin1* (glutamate receptor, ionotropic, NMDA1), was a strong candidate. *Grin1* encodes NMDAR1 protein, and analysis of the *Grin1* sequence revealed a C-to-T mutation in exon 18 of the gene (Fig. 3C). This mutation results in a substitution of arginine for cysteine at residue 844. We designated the *Grin1* mutant allele $Grin1^{Rgsc174}$ (where 'Rgsc' indicates RIKEN Genome Science Center).

$Grin1^{Rgsc174}$ homozygotes exhibited perinatal lethality, but heterozygotes were histologically normal

$Grin1^{Rgsc174}$ heterozygotes of both sexes mated naturally and were fertile. At E14, wild-type, heterozygous ($Grin1^{Rgsc174}$/+) and homozygous ($Grin1^{Rgsc174}/Grin1^{Rgsc174}$) fetuses were present in the uterus. The number of homozygous pups gradually decreased from E17/E18 to 4 weeks postnatally (Table 2). No obvious morphological defects were detected in Nissl-stained tissue sections of the brains of the heterozygote ($Grin1^{Rgsc174}$/+; supporting Fig. S3).

Altered NMDAR function in $Grin1^{Rgsc174}$ heterozygote without any reduction in GRIN protein expression

To investigate the effect of the $Grin1^{Rgsc174}$ allele on NMDAR function, primary cultured cortical neurons were prepared from homozygous, heterozygous and wild-type pups, and transient calcium influx was measured by fluorescence imaging after 10 μM NMDA stimulation. ANOVA showed a significant effect of genotype on the maximum calcium influx after NMDA stimulation and on its duration at half-maximal calcium levels ($T_{1/2max}$). The maximum calcium influx level in the homozygote was significantly higher than in the wild type (Fig. 4A), and $T_{1/2max}$ was significantly longer in the homozygote than in either the wild type or the heterozygote (Fig. 4B). GRIN1, GRIN2A and GRIN2B protein levels were determined in the adult cingulate cortex by immunoblotting, but no differences were found between the heterozygous and wild-type mice (Fig. 5A and B).

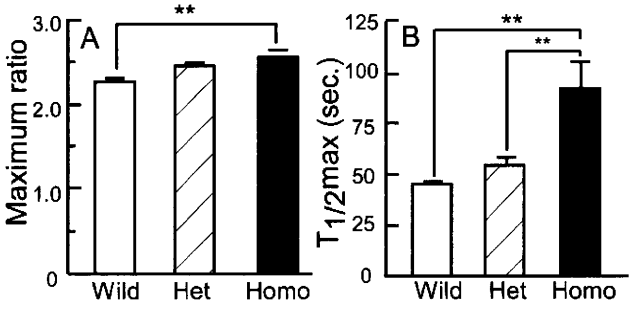

FIG. 4. Fluorescence imaging of transient NMDA-induced calcium influxes in primary cultured cortical neurons from E14 mouse embryos. (A) Maximum calcium influx after stimulation with 10 μM NMDA relative to baseline intracellular calcium levels. ANOVA, effect of genotype, $F_{2,32} = 5.4$, $P < 0.013$. $^{**}P < 0.004$, Fisher's PLSD. (B) Duration at half-maximal calcium level ($T_{1/2max}$) after 10 μM NMDA. ANOVA, effect of genotype, $F_{2,32} = 8.4$, $P < 0.002$; $^{**}P < 0.01$, Fisher's PLSD. White columns, wild type; hatched columns, $Grin1^{Rgsc174}$/+; black columns, $Grin1^{Rgsc174}/Grin1^{Rgsc174}$. Error bars represent the SEM; $n = 5$ of each genotype.

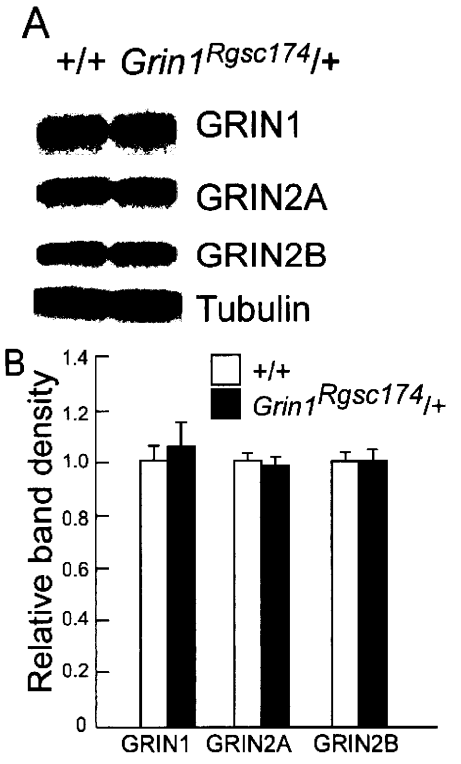

FIG. 5. Expression of NMDAR subunits in the cerebral cortex of wild-type and $Grin1^{Rgsc174}$/+ mice. (A) Protein fractions prepared from the cerebral cortex of adult +/+ and $Grin1^{Rgsc174}$/+ mice were subjected to immunoblotting. A representative immunoblot for GRIN1, GRIN2A and GRIN2B NMDAR subunits and an internal control (neuronal class III β-Tubulin) is shown. (B) Quantification of NMDAR subunit expression. The average expression level of each subunit relative to tubulin (neuronal class III β-Tubulin) is shown. There were no significant differences between the levels of expression in $Grin1^{Rgsc174}$/+ and +/+ mice. Error bars represent the SEM. Male mice, $n = 5$ of each genotype. Student's *t*-test, *GRIN1*: $t_8 = 0.652$, $P > 0.5$; GRIN2A: $t_8 = -0.678$, $P > 0.5$; GRIN2B: $t_8 = -0.244$, $P > 0.8$.

Behavioral abnormalities of $Grin1^{Rgsc174}$ mice

$Grin1^{Rgsc174}$ heterozygotes exhibited increased locomotor activity in the open-field test (Fig. 6A), and $Grin1^{Rgsc174}$/+ mice displayed increased locomotor activity in their familiar home cage (Fig. 7A) as a

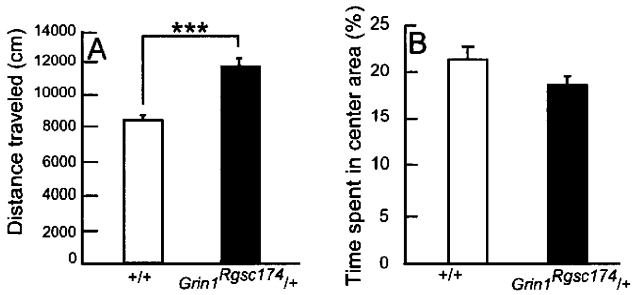

FIG. 6. Locomotor activity of +/+ and *Grin1*^{Rgsc174}/+ mice in the open-field test. (A) Distance traveled in the open field during a 20-min period. Student's *t*-test, $t_{18} = -6.3$, ***$P < 0.0001$. (B) Time spent in the center (30% of the open-field arena). Student's *t*-test, $t_{18} = 1.9$, $P > 0.6$. Error bars represent the SEM. Male mice, $n = 10$ in each group at 8 weeks of age.

result of an increase during the dark period (Fig. 7B and C). The heterozygote exhibited normal rest–activity cycles in their home cage under a standard light–dark cycle (Fig. 7D).

The novelty-seeking behavior of heterozygote was assessed by measuring time spent exploring a novel object placed in the center of the open field. *Grin1*^{Rgsc174}/+ mice spent a longer time exploring the tube filled with marbles than did the wild-type mice (Fig. 8A), and they also explored the tube more frequently (Fig. 8B). However, the time spent in exploring the object by the heterozygous and wild-type mice during each visit (mean duration) was almost the same (Fig. 8C).

In the social interaction test (supporting Appendix S5), the frequency of interaction with another subject of same genotype by heterozygote was similar to that of the wild type (supporting Fig. S4A) but, as the heterozygote spent a shorter time during each interaction with the other subject (supporting Fig. S4B), the total interaction time with the other subject in the open-field area was shorter than it was for the wild type (supporting Fig. S4C). In the resident–intruder paradigm (supporting Appendix S6), the numbers of resident heterozygous mice and wild-type mice that attacked the intruder, either by mounting or biting, were similar (supporting Table S2). Heterozygotes did not display increased anxiety in the light–dark transition test (supporting Appendix S7 and Fig. S5), and

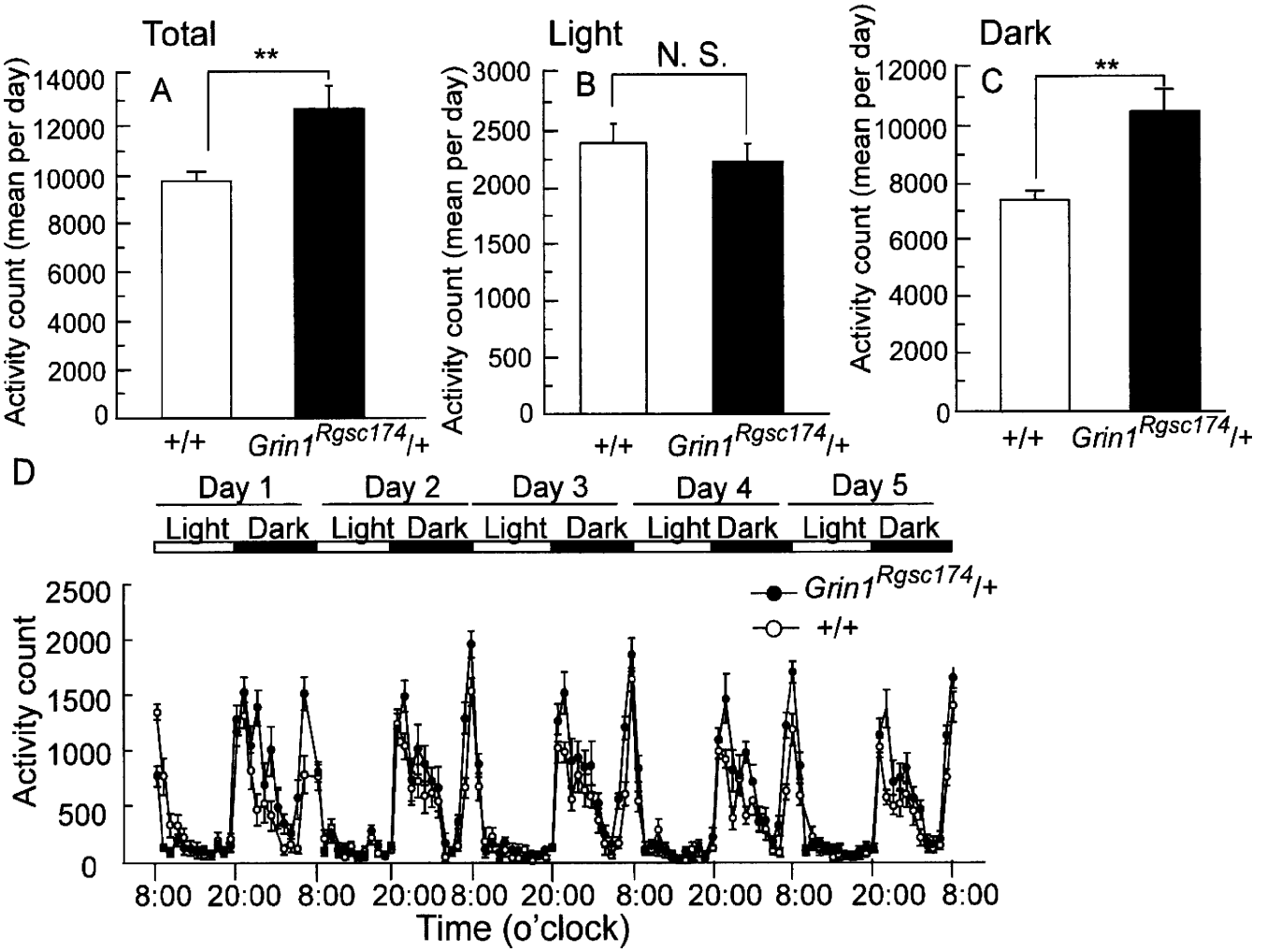

FIG. 7. Locomotor activity of +/+ and *Grin1*^{Rgsc174}/+ mice in their home cages. (A) Mean daily locomotor activity in the home cage. Student's *t*-test, $t_{18} = -3.3$, **$P < 0.01$. (B) Mean locomotor activity in the home cage during the light period. N.S. indicates no significant difference between the two groups, Student's *t*-test, $t_{18} = 0.68$, $P > 0.5$. (C) Mean locomotor activity in the home cage during the dark period. Student's *t*-test, $t_{18} = -0.39$, **$P < 0.01$. (D) Locomotor activity patterns of +/+ and *Grin1*^{Rgsc174}/+ mice during the light/dark cycle. ANOVA, effect of genotype, $F_{1,18} = 15.51$, $P < 0.003$. Error bars represent the SEM. Male mice, $n = 10$ of each genotype at 10–12 weeks of age.