

Table 2. White matter DTI measurement in six fibre tracts

		FES (<i>N</i> = 9)	pre-onset patients (<i>N</i> = 10)	HS (<i>N</i> = 10)	<i>F</i>	<i>df</i>	<i>p</i>
LT_ILF	Mean FA	0.40 ± 0.02	0.39 ± 0.02	0.41 ± 0.02	2.75	2	0.082
	Range	0.37–0.44	0.36–0.42	0.38–0.44			
LT_CHP	Mean FA	0.25 ± 0.02	0.25 ± 0.02	0.25 ± 0.02	0.03	2	0.971
	Range	0.22–0.28	0.22–0.28	0.20–0.27			
LT_SLF	Mean FA	0.40 ± 0.02	0.38 ± 0.04	0.43 ± 0.03	5.78	2	0.008*
	Range	0.36–0.43	0.33–0.45	0.39–0.49			
RT_ILF	Mean FA	0.41 ± 0.02	0.41 ± 0.02	0.42 ± 0.02	1.29	2	0.293
	Range	0.39–0.45	0.38–0.43	0.38–0.45			
RT_CHP	Mean FA	0.26 ± 0.02	0.25 ± 0.03	0.26 ± 0.03	0.35	2	0.711
	Range	0.24–0.32	0.21–0.29	0.20–0.31			
RT_SLF	Mean FA	0.44 ± 0.02	0.44 ± 0.03	0.48 ± 0.02	10.31	2	0.001*
	Range	0.43–0.37	0.38–0.47	0.44–0.50			

<i>Post hoc t-test</i>		
		<i>p</i>
LT_SLF	HS	0.048*
	Pre-onset	0.002*
FES	HS	0.048*
	Pre-onset	0.239
Pre-onset	HS	0.002*
	FES	0.239
RT_SLF	HS	0.002*
	Pre-onset	<0.001*
FES	HS	0.002*
	Pre-onset	0.430
Pre-onset	HS	<0.001*
	FES	0.430

CHP, cingulum hippocampal part; FES, first-episode schizophrenia; HS, healthy subject.
**p* > 0.05 (correct).

should make it easier to understand the brain changes that will occur as the disease proceeds.

Some schizophrenia studies have shown left temporal impairment (27–29), while others indicate disruptions of the bilateral temporal area (30–32). In addition, a previous study showed that compared with healthy controls, high-risk subjects for schizophrenia showed lower FA in SLF (19). We observed a volume loss in the bilateral temporal cortices and microstructural disturbance in the bilateral SLF. Consistent with the findings of previous studies that used DTI, 3D-T1 weighted volume data and post-mortem brain study, the present study provides direct *in vivo* evidence of structural anomalies in patient groups. Anomalies of temporal regions have found in patients with schizophrenia, and are associates with delusions and hallucinations (33–36). Previous studies showed that the brain change preceded the episode of clinical symptoms (7–11). Our participants at high risk who did not show the delusion and hallucination may develop the precedent morphological change that would affect on the

delusion and hallucination. Some neuroimaging studies focussed on the prodromal state have shown temporal lobe anomalies, but the results on the localisation of disturbance were controversial. Some studies have shown left temporal impairment using DTI and volume data (8,10). However, one study indicated reduction of the bilateral temporal grey matter (11), and some papers denied the temporal change using DTI (7,9). These inconsistencies may result from that they used intake criterion for identifying participants at high risk that included so many psychotic symptoms, such as perceptual disturbance, disorganisation, delusion, hallucination and decrease in mental state or functioning. In this study, we regarded the patients who showed perceptual disturbance revealed by the Rorschach test as the high-risk group that fell under the group 1 of the PACE criteria. By using the simple intake criterion, useful information was obtained. Furthermore, structural and functional imaging studies have revealed that the high-risk group is associated with regional volumetric and functional abnormalities that are qualitatively similar to those in patients with

schizophrenia but are less severe (37). The present observations need to be replicated with a larger study population.

In this study, our participants showed the perceptual impairment. The parietal lobe is known to be an essential part of the sensory integration (38), and it could be expected that there were morphological changes of parietal regions in high risk and schizophrenic patients. However, our results did not show the change of parietal region. Previous study that intended the early-onset schizophrenia showed the parietal abnormality (39), though the other studies unlikely show the parietal change (1,3). Previous childhood-onset schizophrenic study suggested that schizophrenic brain change in parietal lobe was obvious in youth, but the changes appear to be diminished with age (40). Our results that did not show the parietal change may be because the mean age of our participants was in the middle of 20s, and the loss of parietal lobe was attenuated.

Functional, anatomical and histopathological studies provide considerable evidence that the connections between subregions of the cingulate cortex and other brain regions are disturbed in schizophrenia (41,42). Previous neuroimaging studies have shown abnormalities of ACC in schizophrenia (43). In this study, the volume loss in ACC was detected not in the high-risk patient group but in the first-episode schizophrenia group. This may result from the fact that the schizophrenic brain shrinkage progress from posterior to anterior (44). Further follow-up studies that focus on the conversion from the prodromal state into schizophrenia are needed to reveal the pattern of ACC shrinkage.

In this study, we evaluated only a few participants. Further work with the large sample size will be necessary to confirm our results.

In summary, the present study confirms that there are proceeding changes in the brains of schizophrenic patients at the pre-onset state. The findings indicate that brain impairments may be altered in patients at the pre-onset of psychosis, possibly as a result of disrupted developmental mechanisms, and, furthermore, that these pathological changes may be predictive of functional outcome. The present observations remain to be replicated with a larger study population and with follow-up of the high-risk patients.

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Glutamatergic changes in the cerebral white matter associated with schizophrenic exacerbation

Ota M, Ishikawa M, Sato N, Hori H, Sasayama D, Hattori K, Teraishi T, Nakata Y, Kunugi H. Glutamatergic changes in the cerebral white matter associated with schizophrenic exacerbation.

Objective: Glutamatergic dysfunction in the brain has been implicated in the pathophysiology of schizophrenia. This study was aimed to examine several brain chemical mediators, including Glx (glutamate + glutamine), using ^1H magnetic resonance spectroscopy (MRS) in medicated patients with schizophrenia, with and without psychotic exacerbation.

Method: ^1H MRS was acquired in 24 patients with schizophrenia, with psychotic exacerbation; 22 patients without exacerbation; and 27 age- and sex-matched healthy volunteers. The levels of metabolites were measured in the left frontal and inferior parietal white matter and compared across the three groups.

Results: The Glx level was significantly elevated in the left inferior parietal white matter in the patients with psychotic exacerbation in comparison with that in the healthy volunteers and the patients without exacerbation ($P < 0.05$). We also detected that there was a significant correlation between Positive and Negative Syndrome Scale-positive scale and Glx level in the left parietal white matter ($r = 0.51$, $P < 0.001$).

Conclusion: Higher than normal Glx levels indicate glutamatergic overactivity in the left inferior parietal white matter with schizophrenic exacerbation, a finding that is in accordance with the glutamatergic hypothesis in schizophrenia. The Glx level measured by ^1H MRS could be a biomarker for exacerbation in schizophrenia.

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Key words: glutamine + glutamate; exacerbation; magnetic resonance spectroscopy; schizophrenia

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Significant outcomes

- The Glx level was significantly elevated in the left inferior parietal white matter in patients with schizophrenia, with psychotic exacerbation.
- The Glx level in the patients with schizophrenia, with psychotic exacerbation was significantly elevated compared with that in the non-exacerbated patients.

Limitations

- The regions of interests (ROIs) were limited to the left frontal white matter and the inferior parietal white matter. Further work with other several ROIs will be necessary to confirm our results.
- The sample size was relatively small. More studies with larger sample sizes are warranted.

Introduction

N-methyl-*D*-aspartate (NMDA) receptor antagonists such as phencyclidine and ketamine induce

symptoms closely resembling schizophrenia (1). These findings have suggested the presence of altered NMDA-glutamatergic function in schizophrenia; however, the glutamatergic model of

schizophrenia cannot be fully tested without *in vivo* measures of glutamate metabolism. A previous 1.5-tesla (T) ^1H magnetic resonance spectroscopy (MRS) study found higher levels of glutamine and similar levels of *N*-acetylaspartate (NAA) in the left medial prefrontal region of never-treated patients with schizophrenia compared with healthy volunteers (2). Another study using 4.0-T ^1H MRS found increased levels of glutamine and normal levels of NAA in the left anterior cingulate and thalamic regions of never-treated, first-episode patients with schizophrenia compared with healthy volunteers (3). In addition, one study showed increased levels of γ -aminobutyric acid and Glx (glutamine + glutamate) in the medial prefrontal cortex of unmedicated patients with schizophrenia compared with controls (4). A review of ^1H MRS studies concerning the glutamate in schizophrenia showed an overall increase in glutamine levels in patients with schizophrenia at the early phase of the disease (5). In contrast, one study showed decreased levels of glutamine in the anterior cingulate of chronic schizophrenia patients (6).

Astrocyte is essential for glutamate homeostasis, and its deficit in glutamate uptake might contribute to elevated extracellular glutamate and resultant excitotoxicity to neurons and glia in subjects with schizophrenia. Ultrastructural changes in the cells responsible for myelination, namely oligodendrocytes, have been observed in postmortem and biopsy tissues of patients with schizophrenia. Oligodendrocytes are known to be vulnerable to excitotoxicity induced by hyperglutamatergic states via the overactivation of alpha-amino-3-hydroxy-5-methyl-4-isoxazolepropionic acid and kainate receptors (7, 8). The rate of transmission of information in neural networks is critical for the integration of information processing. Dysmyelination causes focal disruption of such networks and dyssynchrony in the reverberating networks that integrate perception, thought and action, which may give rise to psychotic symptoms (9). Degenerative changes have been described in the oligodendroglia and myelinated fibers in postmortem and biopsy tissues of patients with schizophrenia (10). The recent glutamatergic model of schizophrenia has suggested a possible role of glutamate-induced neurodegeneration (11, 12). However, little is known regarding changes in glutamate levels in the white matter in schizophrenia. It is worthwhile to evaluate the levels of metabolites in the left inferior parietal and middle frontal white matter regions that are regarded as the areas associated with psychopathology of schizophrenia (13) and where there are sufficient white matter volumes to put regions of interest

(ROI) large enough to get adequate signal-to-noise ratio. We hypothesized that patients with psychotic exacerbation would have higher levels of Glx compared with patients without exacerbation and healthy controls.

Aims of the study

The present study was aimed to examine brain chemical mediators, including Glx, in white matter areas using ^1H MRS in schizophrenia patients with and without psychotic exacerbation and healthy controls.

Material and methods

Subjects

The subjects were 24 schizophrenia in-patients with psychotic exacerbation and 22 outpatients without exacerbation. The exacerbation group included one patient with a first episode of psychosis. Consensus diagnosis by at least two psychiatrists was made according to the Diagnostic and Statistical Manual of Mental Disorders, 4th edition, (DSM-IV) criteria (14), on the basis of unstructured interviews and information from medical records. Patients who met both of the following two criteria were defined as having exacerbation: i) symptom scores of ≥ 4 (at least moderate) on at least two of the Positive and Negative Syndrome Scale [PANSS, (15)] items of hostility, excitement, tension, uncooperativeness, and poor impulse control, and a total combined score of ≥ 17 for these items and ii) psychiatric hospitalization (16, 17). All the in-patients were admitted to an acute psychiatric ward of the National Center of Neurology and Psychiatry Hospital, Japan. Most in-patients underwent an MRS scan within 4 weeks (mean period = 14.5 ± 13.6 days) after their admission to this study. Outpatients were recruited and chosen from those patients who were treated by the authors and those who voluntarily responded to our poster announcement in the Hospital. Twenty-seven age- and sex-matched healthy subjects were recruited from the community through local magazine advertisements and our website announcement. Participants were interviewed for enrollment by research psychiatrists using the Japanese version of the Mini-International Neuropsychiatric Interview (18, 19). Participants were excluded if they had a prior medical history of central nervous system disease or severe head injury or if they met the criteria for substance abuse or dependence. Those who demonstrated no history of psychiatric illness or contact with psychiatric services were enrolled

Brain changes with schizophrenic exacerbation

Table 1. Characteristics of the study sample

	Healthy volunteers	Patients with schizophrenia	
		Exacerbation (+)	Exacerbation (–)
Male/Female	13/14	11/13	12/10
Age	42.8 ± 15.1	45.0 ± 15.4	41.3 ± 11.2
Education	14.0 ± 2.8	13.3 ± 3.1	14.1 ± 2.6
Age at onset		23.5 ± 7.4	25.7 ± 11.8
Duration of illness		20.4 ± 15.6	14.6 ± 8.8
Chlorpromazine equivalent dose of medication (mg)		838.1 ± 472.2*	354.2 ± 366.1*
PANSS positive		17.4 ± 5.2*	11.7 ± 4.7*
PANSS negative		17.5 ± 6.9	15.8 ± 6.5
PANSS general		34.3 ± 9.9	28.7 ± 9.4

PANSS; positive and negative syndrome scale.

*There were significant differences between the schizophrenia groups ($P < 0.001$).

as controls in this study. The characteristics of the participants are shown in Table 1. Daily doses of antipsychotics, including depot antipsychotics, were converted to chlorpromazine equivalents using published guidelines (20, 21).

After the study was explained to the subjects, written informed consent was obtained for participation in the study from every subject. This study was approved by the ethics committee of the National Center of Neurology and Psychiatry, Japan.

MRI data acquisition

MR imaging was performed on a Magnetom Symphony 1.5-T (Siemens, Erlangen, Germany). Spectra were acquired with a point-resolved pulse sequence ('PRESS', repetition time = 1500 ms, echo time = 30 ms, 1024 points, 1000 Hz spectral width, 160 averages water-suppressed and 30 averages without water suppression) from a $1.5 \times 1.5 \times 2.5$ cm voxel placed in the left middle frontal white matter region and a $1.5 \times 2.5 \times 1.5$ cm voxel in the left inferior parietal white matter region (see Fig. 1 for illustration of voxel placement) so as to exclude cerebrospinal fluid and gray matter contained in the ROI as much as possible. We visually checked T2 imaging and located ROIs to avoid cerebrospinal fluid. ROIs were positioned by the scanner operator based on anatomical landmarks. The scan took approximately 10 min per region. Global and local shimmings were performed before the ^1H -MRS sequence.

Magnetic resonance spectroscopy analysis

Water-suppressed spectra were analyzed using 'LCModel' (20) a fully automated, commercially

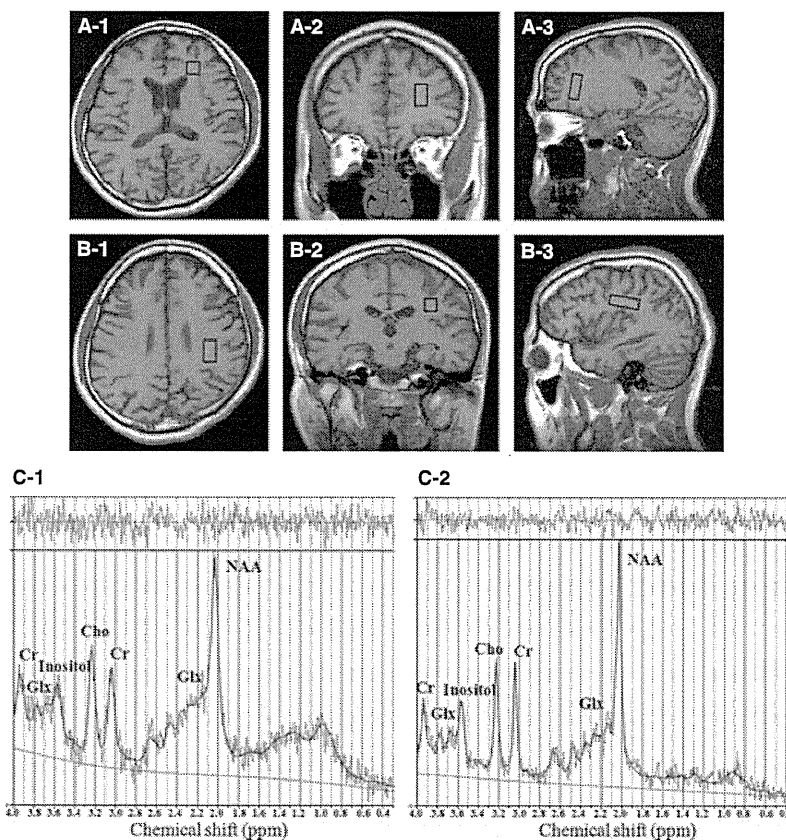


Fig. 1. Regions of interests placement in two regions of interest; left middle frontal white matter (A-1, 2, 3) and left inferior parietal white matter (B-1, 2, 3) and representative spectra of frontal white matter (C-1) and parietal white matter (C-2). Figure 1(C-1 and C-2) shows strong sharp resonances from creatine at 3.0 and 4.0 ppm, Glutamine + Glutamate (Glx) at 2.0–2.5 ppm and 3.8, Glycerophosphocholine + Phosphocholine (Cho) at 3.3 ppm, Inositol at 3.6 ppm and *N*-acetylaspartate at 2.0 ppm.

available curve-fitting software that uses a least squares analysis method for estimating metabolite concentrations in the millimolar range. LCModel was set to 0.2–4.0 ppm to cover the whole spectral region of the metabolites of interest. The quantification model included the following metabolites: aspartate, creatine, inositol, L-alanine, γ -aminobutyric acid, glucose, Glx, glycerophosphocholine + phosphocholine, guanidinoacetate, L-lactate, NAA, N-acetylaspartylglutamate, scyllo-inositol, and taurine. For each spectrum, the area under each peak was normalized to the unsuppressed water peak [corrected for water T1 relaxation (22)], yielding metabolite concentrations. The fitting quality of each spectrum is shown as percent SD, and those with SD values over 20% were excluded from analysis.

Statistical analysis

The differences in age, sex, and years of education among patients with schizophrenia, with and without exacerbation and healthy subjects were evaluated using analysis of variance (ANOVA). The differences in concentration of creatine, Glx, glycerophosphocholine + phosphocholine, inositol, and NAA, those percent SD were under 20%, in the left frontal and inferior parietal white matter in patients with schizophrenia, with and without exacerbation of psychosis and in healthy subjects were also evaluated using ANOVA. The *post hoc* test was carried out using Bonferroni's correction for multiple comparisons. The differences in age at onset, duration of illness, the chlorpromazine equivalent dose of medication, and the subscales of PANSS between the groups of schizophrenia were evaluated using a two-sample *t*-test.

The statistical correlations between the concentrations of creatine, Glx, glycerophosphocholine + phosphocholine, inositol, and NAA on the one hand and age, chlorpromazine equivalent dose of medication, and the subscales of PANSS on the other in the two patient groups were examined using Pearson's correlation analysis.

Statistical analyses were performed using SPSS Statistics for Windows 17.0 software (SPSS Japan, Tokyo, Japan).

Results

There was no statistically significant difference in age, sex, or education years across the three groups, and no difference in age at onset, duration of illness, or negative or general subscales of PANSS was found between the patient groups

with and without exacerbation. The differences in chlorpromazine-equivalent dose of medication ($t = -3.86$; $df = 44$; $P < 0.001$) and positive PANSS score ($t = -3.91$; $df = 44$; $P < 0.001$) between the two groups of patients were statistically significant. Six of the 22 patients without psychotic exacerbation and one of the 24 patients with exacerbation were medicated only by typical antipsychotics. The remaining patients were treated with the atypical or both antipsychotics.

There was a significant effect of group on the Glx concentration in the left inferior parietal white matter ($F_{2,70} = 5.5$; $P = 0.006$). *Post hoc t*-test analyses showed that the Glx level was higher in the patients with exacerbation than in the healthy subjects ($P = 0.009$, corrected) or the patients without exacerbation ($P = 0.033$, corrected) (Table 2).

There was no significant correlation of the concentration of any metabolite with age, education years, chlorpromazine-equivalent dose, or PANSS subscale scores except for a correlation between age and NAA in the left parietal white matter ($r = -0.48$, $P = 0.001$), a correlation between age and inositol in the frontal white matter ($r = 0.45$, $P = 0.002$), and a correlation between PANSS-positive scale and Glx level in the left parietal white matter ($r = 0.51$, $P < 0.001$).

Discussion

To our knowledge, this is the first study that examined the glutamatergic change in relation to the exacerbation of psychotic symptoms. Some previous studies examined glutamatergic changes in first-episode schizophrenia (2, 3, 23), chronic schizophrenia (6, 24–26), and subjects at high risk of schizophrenia (27). However, no study has thus far focused on the possible relationship between the exacerbation of psychotic symptoms and glutamatergic activity.

In our ^1H MRS study, a significant increase in the Glx level was observed in the left inferior parietal white matter region in schizophrenia patients with exacerbation compared with healthy subjects and patients without exacerbation. As the majority of physiologically active glutamate is derived from glutamine (28), the higher level of Glx indicates greater glutamatergic activity, which is consistent with the previously described glutamatergic model of schizophrenia (11, 29, 30). Released glutamate is taken up by astrocytes, where it is converted to glutamine, transported back to the presynaptic neuron, and reconverted to glutamate (28). Our findings are in the same direction as those reported in previous studies. A study of first-episode never-medicated

Brain changes with schizophrenic exacerbation

Table 2. Characteristics of the metabolites using magnetic resonance spectroscopy

	Patients with schizophrenia					
	Healthy volunteers		Exacerbation (+)		Exacerbation (-)	
	Lt FW	Lt PW	Lt FW	Lt PW	Lt FW	Lt PW
Creatine* (mean \pm SD)	3.4 \pm 0.4	3.5 \pm 0.4	3.7 \pm 0.5	3.7 \pm 0.4	3.5 \pm 0.6	3.6 \pm 0.3
Mean % SD (mean \pm SD)	6.0 \pm 1.0	5.7 \pm 0.8	6.1 \pm 1.2	5.4 \pm 0.8	6.1 \pm 2.0	5.3 \pm 0.8
Number of subjects	N = 27	N = 27	N = 22	N = 23	N = 22	N = 22
NAA* (mean \pm SD)	5.0 \pm 0.7	5.7 \pm 0.8	4.9 \pm 0.6	5.6 \pm 0.6	4.9 \pm 0.6	5.7 \pm 0.6
Mean % SD (mean \pm SD)	6.4 \pm 2.1	6.8 \pm 2.0	6.7 \pm 2.3	6.7 \pm 1.3	7.0 \pm 2.5	6.8 \pm 1.8
Number of subjects	N = 27	N = 27	N = 21	N = 24	N = 21	N = 22
Glutamine + Glutamate* (mean \pm SD)	7.1 \pm 1.3	6.5 \pm 0.9 \ddagger	7.2 \pm 1.3	7.2 \pm 0.8 \ddagger \dagger	7.3 \pm 1.0	6.6 \pm 0.7 \ddagger
Mean % SD (mean \pm SD)	11.0 \pm 2.9	10.4 \pm 2.5	12.0 \pm 4.0	9.2 \pm 2.2	10.0 \pm 2.2	9.8 \pm 2.2
Number of subjects	N = 26	N = 27	N = 22	N = 24	N = 20	N = 22
Glycerophosphocholine + Phosphocholine* (mean \pm SD)	1.2 \pm 0.2	1.2 \pm 0.2	1.3 \pm 0.1	1.3 \pm 0.2	1.3 \pm 0.2	1.3 \pm 0.1
Mean % SD (mean \pm SD)	5.8 \pm 1.1	5.5 \pm 0.8	5.7 \pm 1.0	5.1 \pm 0.8	5.9 \pm 2.5	5.0 \pm 0.7
Number of subjects	N = 27	N = 27	N = 22	N = 24	N = 21	N = 22
Inositol* (mean \pm SD)	3.2 \pm 0.7	3.2 \pm 0.6	3.4 \pm 0.7	3.1 \pm 0.6	3.6 \pm 0.9	3.2 \pm 0.6
Mean % SD (mean \pm SD)	8.3 \pm 2.2	8.1 \pm 1.9	8.5 \pm 2.9	7.9 \pm 2.0	7.4 \pm 2.5	7.2 \pm 1.5
Number of subjects	N = 27	N = 27	N = 22	N = 24	N = 21	N = 22

Lt FW, left frontal white matter; Lt PW, left inferior parietal white matter; NAA, *N*-acetyl-aspartate; SD, standard deviation.

*Metabolites are presented in institutional values.

Analysis of variance with Bonferroni's correction for *post hoc* test: \dagger There was a significant difference between the schizophrenia groups ($P < 0.05$)

Analysis of variance with Bonferroni's correction for *post hoc* test: \ddagger There was a significant difference between the inpatients with schizophrenia and healthy volunteers ($P < 0.05$).

acute-phase schizophrenia showed elevated glutamine levels in the anterior cingulate and thalamus (3). In contrast, reduced glutamine levels were observed in the anterior cingulate of chronic stable-phase schizophrenia patients (6). Other previous studies found elevated glutamate or Glx/creatine in the frontal white matter of both medication-naïve and treated patients with schizophrenia (24, 25). Because these first two studies focused on glutamine, whereas the latter two assessed glutamate or Glx/creatine, it is difficult to compare these results directly. However, these results imply a pronounced dysfunction in the glutamate–glutamine homeostasis. Our results are also consistent with a recent report of increased glutamine in healthy participants administered a low dose of ketamine, a drug known to produce schizophrenia-like symptoms (31), and with a report of increased glutamatergic metabolites in adolescents at high risk of developing schizophrenia (27).

Hyperglutamatergic states (and subsequent hypoglutamatergic states) have been suggested to be relevant to the process of schizophrenia (2, 22, 32). Among glial cells, oligodendroglia, which are responsible for myelination, are particularly vulnerable to glutamate-mediated glial cell damage (7). Disruption of the speed of neurotransmission throughout the web of reverberating myelinated networks within the brain may desynchronize and disrupt elements of perception, attention, complex processing of information, and behaviour in schizophrenia. Herein, we provide evidence of

changes in such myelin-containing white matter associated with psychosis exacerbation.

Our results showed that there was no difference in the concentration of Glx in the frontal white matter region between the two groups of patients. A previous study showed that during the development of schizophrenia in early adolescent subjects, a dynamic wave of gray matter loss occurred, starting in the parietal association cortices and proceeding frontally to envelop the dorsolateral prefrontal cortex and temporal cortices, including the superior temporal gyri (33). Our results also indicated that disruption of the parietal region with psychotic exacerbation may account for psychotic impairment.

There are several limitations to this study. First, the regions of interest were limited to the left frontal white matter and inferior parietal white matter. Therefore, we obtained no data on metabolic changes in other brain regions that could be related to psychotic exacerbation. In particular, temporal regions were regarded as the areas associated with positive symptoms of schizophrenia (34). We put the relatively large ROIs purely on white matter not to mix the data derived from gray matter and white matter, then it is difficult to put rectangle large ROI in temporal region. Further work with the high magnetic field that adds the high signal-to-noise ratio will be necessary. Secondly, all patients were medicated, and the doses of antipsychotic medication in the patients with exacerbation were significantly higher than those

in the patients without exacerbation. Although using chlorpromazine equivalents to compare dosages of antipsychotic medication is controversial because the conversion of the atypical antipsychotics to chlorpromazine equivalents might not be the same as for the typical antipsychotics (35), one might suspect that the differential dose may account for the difference in Glx between the two groups. However, Theberge et al. (23) showed that glutamine and glutamate levels did not significantly decrease in participants with schizophrenia whose symptoms were stabilized with medication for 10 months, suggesting that medication does not have a major effect on glutamine and glutamate levels. A more recent study by 4T ¹H-MRS has also found no changes in NAA, Gln/Glu or any of the other metabolites in any of the regions of interest after antipsychotic treatment in early schizophrenia (36). Moreover, in the present study, chronic patients without exacerbation who received antipsychotic medication showed Glx concentrations similar to those of the controls. Thus, the observed increase in Glx level in the exacerbated group is unlikely to be attributable to the higher dose of antipsychotic medication.

Thirdly, the sample size of the present study was relatively small. Replication studies in larger samples are clearly required.

Our ¹H MRS study showed a significantly increased level of Glx in the left inferior parietal white matter region in patients with schizophrenia, with exacerbation compared with healthy subjects and patients without exacerbation. These results suggest that glutamatergic dysfunction in the parietal white matter is involved in psychotic exacerbation. If our results are replicated, the quantification of the brain metabolites using MRS could be used as a good biomarker for exacerbation and could provide valuable hints to the brain pathology underlying the exacerbation of schizophrenia.

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Declaration of interests

None.

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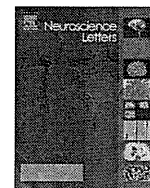
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Cortical neurons from intrauterine growth retardation rats exhibit lower response to neurotrophin BDNF

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ABSTRACT

Intrauterine growth retardation (IUGR) is putatively involved in the pathophysiology of schizophrenia. The animal model of IUGR induced by synthetic thromboxane A2 (TXA2) is useful to clarify the effect of IUGR on pups' brains, however, analysis at the cellular level is still needed. Brain-derived neurotrophic factor (BDNF), which plays a role in neuronal survival and synaptic plasticity in the central nervous system (CNS), may also be associated with schizophrenia. However, the possible relationship between IUGR and BDNF function remains unclear. Here, we examined how IUGR by TXA2 impacts BDNF function by using dissociated cortical neurons. We found that, although BDNF levels in cultured neurons from the cerebral cortex of low birth weight pups with IUGR were unchanged, TrkB (BDNF receptor) was decreased compared with control-rats. BDNF-stimulated MAPK/ERK1/2 and PI3K/Akt pathways, which are downstream intracellular signaling pathways of TrkB, were repressed in IUGR-rat cultures. Expression of glutamate receptors such as GluA1 and GluN2A was also suppressed in IUGR-rat cultures. Furthermore, in IUGR-rat cultures, anti-apoptotic protein Bcl2 was decreased and BDNF failed to prevent neurons from cell death caused by serum-deprivation. Taken together, IUGR resulted in reductions in cell viability and in synaptic function following TrkB down-regulation, which may play a role in schizophrenia-like behaviors.

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Schizophrenia is a chronic, severe and disabling brain disease, of which neuropathological basis has remained elusive [18]. Growing evidence has suggested neurodevelopmental impairments in the pathogenesis of schizophrenia [13]. Importantly, obstetric complications play a role in such impairments [8,24,35]. Among various obstetric complications, low birth weight is a strong risk factor for schizophrenia [25].

Intrauterine growth retardation (IUGR) induced by synthetic thromboxane A2 (TXA2) was associated with a delay in postnatal neurological development and learning disabilities in rats in which the neuronal density in the cortical plate was lower than that of control rats [31]. Interestingly, mRNA expression of neurotrophins such as BDNF and NT-3 (neurotrophin-3) was suppressed in the cerebral cortex of TXA2-induced IUGR-rats [14].

BDNF has critical roles in neuronal survival and synaptic plasticity [7,32] through activation of TrkB, and consequent stimulation of downstream signaling including mitogen-activated protein/extracellular signal-regulated kinase (MAPK/ERK), phosphoinositide 3-kinase/Akt (PI3K/Akt) and phospholipase C γ (PLC γ) pathways. Recently, we reported important regulatory roles of BDNF in synaptic functions via these pathways [23,26,27]. Remarkably, altered serum levels of BDNF and its expression in the postmortem brain of schizophrenia patients have been reported [10,21,33]. Furthermore, forebrain-specific TrkB knockout mice showed schizophrenia-like behaviors, including hyperlocomotion, stereotyped behaviors and cognitive impairments [36].

Though both IUGR and dysfunction of BDNF-TrkB signaling may contribute to the pathogenesis of schizophrenia, the possible change in the BDNF-TrkB signaling in Central Nervous System (CNS) neurons of IUGR has not yet been clarified. Here, we found that cortical neurons from IUGR-rats exhibited lower levels of TrkB, Bcl2, and glutamate receptors. Interestingly, neurons from IUGR-rats showed a decreased response to BDNF when survival was examined.

Female Long-Evans rats (Institute for Animal Reproduction, Ibaraki, Japan) were purchased at 8 days of pregnancy and kept

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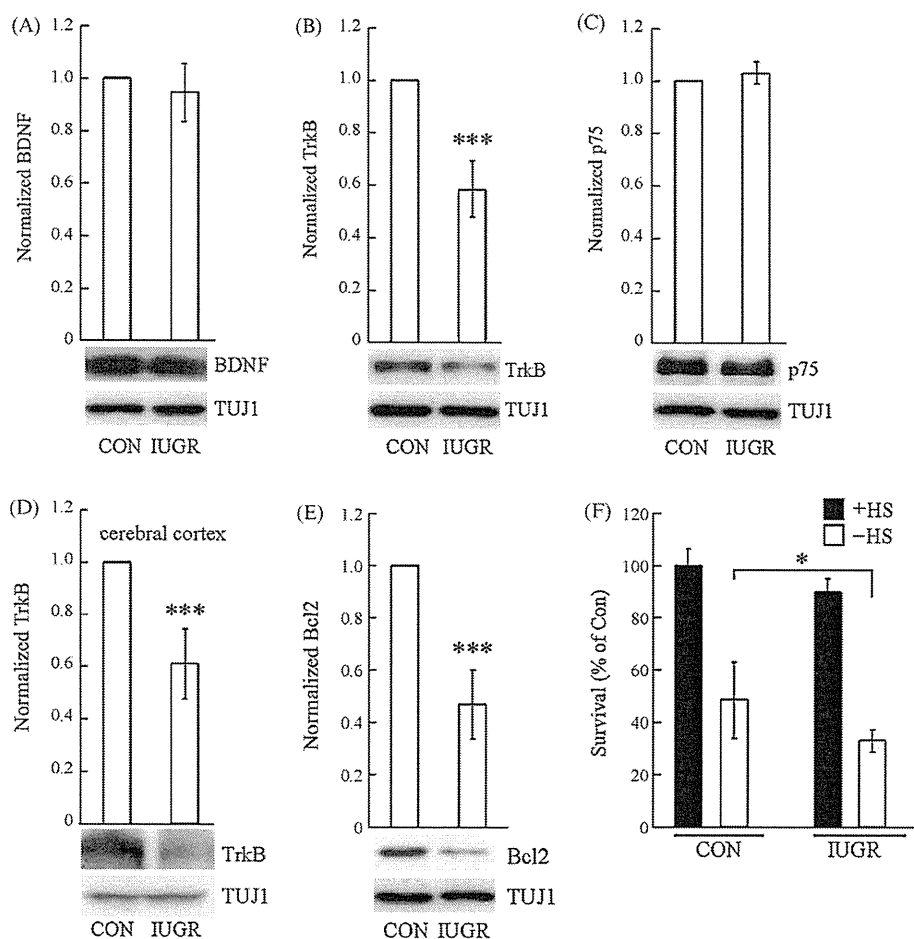


Fig. 1. Reduction in levels of TrkB, Bcl2, and cell viability in cortical cultures prepared from the cerebral cortex of low weight newborn rats with TXA2-induced IUGR. The levels of BDNF (A), TrkB (B), and p75 (C) were examined in 5DIV cortical cultures from IUGR-rats or from control-rats. TrkB was reduced in IUGR-rat neurons. Quantification was carried out after immunoblotting. Normalization to a level in control was performed. Data represent mean \pm SD ($n=6$), *** $P<0.001$. IUGR: intrauterine growth retardation. (D) TrkB down-regulation was observed in homogenates from the cerebral cortex of IUGR-rats, *** $P<0.001$ ($n=4$). (E) Reduction in Bcl2 expression in cultures from IUGR-rats. Data represent mean \pm SD ($n=7$), *** $P<0.001$. The three independent series of cultures were used for each set of immunoblotting experiments. TUJ1 levels are shown as controls in each representative blot. (F) Decrease in cell viability of cortical neurons from IUGR-rats. To induce neuronal cell death, serum-deprivation was performed. Cell survival was determined by MTT assay. Data represent mean \pm SD ($n=8$, n indicates the number of wells of a plate for each experimental condition), * $P<0.05$. To confirm reproducibility, the three independent series of cultures were used.

in individual cages under a standard laboratory environment (12L:12D, light on at 15:30; 21–24 °C temperature; free access to food and water). IUGR was induced by TXA2 analog (9,11-dideoxy-9 a, 11a-methanoepoxy-prosta-5Z, 13E-dien-1-oic acid; Cayman Chemical, MI, USA) application on mother rats according to previous studies [20]. Briefly, an osmotic pump (2ML1, Alzet Corp., Palo Alto, CA, USA) containing 2 ml of TXA2 solution (12.5 μ g/ml) or PBS for control rats was implanted into the lower portion of the peritoneal cavity under sodium pentobarbital (31.5 mg/kg b.w.) anesthesia on 13 days of pregnancy. Rats were allowed to deliver spontaneously, and pups were fed by their own mothers. Brains of pups were removed at postnatal day 1 (P1) and used for dissociated cultures. To check levels of TrkB in homogenates from the cerebral cortex, the brains were removed from the deeply anesthetized P1 IUGR- or control-rats. All the experiments were approved by the Ethics Review Committee for Animal Experimentation of the National Institute of Neuroscience, Japan.

Cultures were prepared as previously reported [28]. Dissociated cortical neurons were plated on polyethyleneimine-coated culture dishes or 48-well plates (Corning, NY, USA). The cell density was 5×10^5 /cm², respectively. Neuronal cultures from cerebral cortex of pups of control or of IUGR were maintained with 1:1 mixture

of Dulbecco's modified Eagle's medium and Ham's F-12 medium containing 5% fetal bovine serum and 5% heated-inactivated horse serum for 5 days before the survival assay or collecting samples for immunoblotting. To induce cell death, the culture media was replaced with a serum-free fresh media for 24 h. Then, to determine the cell viability, a mitochondrial-dependent conversion of the tetrazolium salt (MTT) assay was performed [30]. When glial cell contribution was checked, arabinosylcytosine (1.0 μ M, SIGMA, MO, USA) was applied at 24 h after cell plating. BDNF (100 ng/ml) was applied 20 min before serum-deprivation. LY294002 (1.0 μ M, Calbiochem-Novabiochem, CA, USA) was added 20 min before BDNF application.

MAP2 immunostaining was conducted [27]. Cells were fixed in 4% paraformaldehyde at room temperature for 20 min. After blocking with PBS containing 10% goat serum and 0.2% Triton X-100 for 30 min, anti-MAP2 (1:1000, SIGMA) antibody was incubated overnight at 4 °C. Alexa Fluor 594-conjugated anti-mouse IgG (1:200, Invitrogen, CA, USA) was used as a secondary antibody.

Cells were lysed in SDS lysis buffer (1% SDS, 20 mM Tris-HCl (pH 7.4), 5 mM EDTA (pH 8.0), 10 mM NaF, 2 mM Na₃VO₄, 0.5 mM phenylarsine oxide, and 1 mM phenylmethylsulfonyl fluoride). The protein concentration was quantified using a BCA Protein Assay Kit

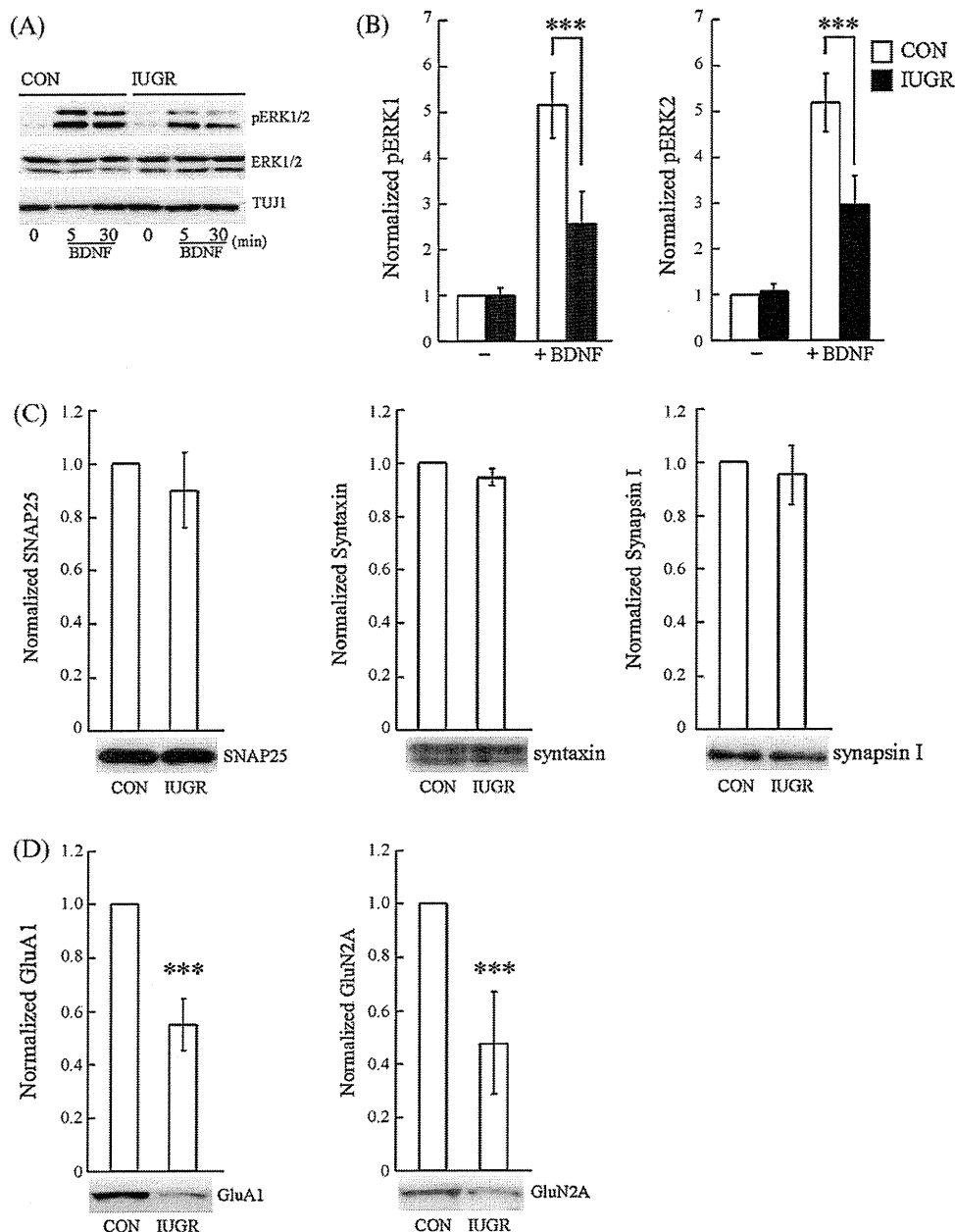


Fig. 2. Decrease in BDNF-stimulated ERK1/2 and in levels of glutamate receptors in IUGR-rat cultures. (A) and (B) Levels of activated ERK1/2 (pERK1/2) in IUGR- or control-rat cultures were examined at 5DIV. Cultured neurons with IUGR- or control-rats were stimulated by BDNF (100 ng/ml) for 0 min, 5 min, or 30 min. pERK1/2 stimulated by BDNF (5 min) was suppressed in IUGR-rat cultures. To quantify the pERK1/2 (BDNF 5 min), normalization to a level in control was performed. Data represent mean \pm SD ($n=5$), *** $P<0.001$. Total ERK1/2 was unchanged. TUJ1 is shown as a control. (C) Presynaptic proteins including SNAP25, syntaxin, and synapsin I were unchanged in IUGR-rat cultures. Data represent mean \pm SD (SNAP25, $n=6$, syntaxin, $n=6$, synapsin I, $n=6$). (D) Postsynaptic glutamate receptor (GluA1 and GluN2A) levels in IUGR-rat neurons were reduced. Data represent mean \pm SD (GluA1, $n=6$, GluN2A, $n=5$). *** $P<0.001$. The four independent series of cultures were used for each set of experiments.

(PIERCE, IL, USA), and equivalent amounts of protein were applied for each immunoblotting. Antibodies were used at the following dilutions: anti-Akt (1:1000, Cell Signaling, MA, USA), anti-pAkt (1:1000, Cell Signaling), anti-ERK (1:1000, Cell Signaling), anti-pERK (1:1000, Cell Signaling), anti-GluN2A (NR2A) (1:500, SIGMA), anti-GluA1 (GluR1) (1:1000, CHEMICON, CA, USA), anti-SNAP25 (1:1000, Synaptic Systems, Gottingen, Germany), anti-syntaxin (1:10000, SIGMA), anti-synapsin I (1:2000, CHEMICON), anti-Bcl2 (1:1000, BD Biosciences, CA, USA), anti-TUJ1 (1:5000, Berkeley Antibody Company, CA, USA), anti-p75 (1:1000, Promega, WI, USA), anti-TrkB (1:1000, BD Biosciences), and anti-BDNF (1:200, Santa Cruz Biotechnology Inc., CA, USA) antibodies. The immunoreactiv-

ity was quantified by using Lane & Spot Analyzer software (ATTO Corporation, Tokyo, Japan).

Data shown are presented as mean \pm standard deviation (SD). Statistical significance was evaluated using a one-way ANOVA followed by Tukey's test in SPSS ver11 (SPSS Japan, Tokyo, Japan). Probability values less than 5% were considered statistically significant.

Initially, we examined the possible change in levels of endogenous BDNF and associated receptors in 5 days in vitro (5DIV) neurons prepared from the cerebral cortex of low weight pups with TXA2-induced IUGR (IUGR-rats). Birth weight was decreased by approximately 16% due to IUGR (control rats: 7.76 ± 0.25 g;

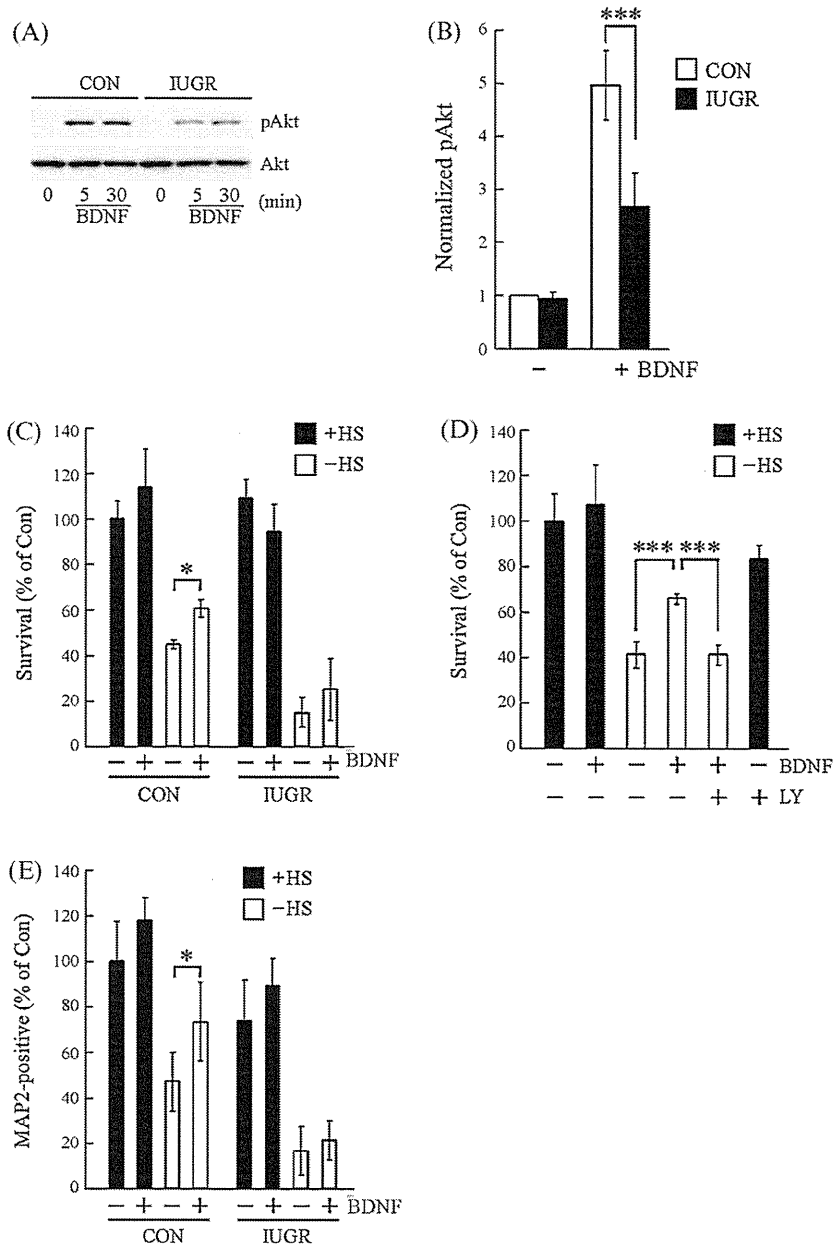


Fig. 3. Cortical neurons from IUGR-rats demonstrated a weakened response to BDNF measured through activation of the PI3K/Akt pathway and neuronal survival. (A) and (B) BDNF-stimulated Akt, a component of the PI3K pathway, was diminished in IUGR-rat cultures at 5DIV. BDNF (100 ng/ml) was applied for the indicated number of minutes. Activated Akt (pAkt, BDNF 5 min) was quantified. Normalization to a level in control was performed. Data represent mean \pm SD ($n = 5$, n indicates the number of wells of a plate for each experimental condition), $***P < 0.001$. Three independent series of cultures were used for experiments. (C) The survival-promoting effect of BDNF was lost in IUGR-rat cultures. Cell viability was determined by MTT assay. Data represent mean \pm SD ($n = 5$, n indicates the number of wells of a plate for each experimental condition), $*P < 0.05$. To confirm reproducibility, the three independent series of cultures were used. (D) BDNF-dependent survival was blocked by LY294002 (1 μ M), an inhibitor for PI3K. Data represent mean \pm SD ($n = 6$, n indicates the number of wells of a plate for each experimental condition), $***P < 0.001$. To confirm reproducibility, the three independent series of cultures were used. (E) Neuronal survival was determined by MAP2 immunostaining. The number of MAP2-positive cells was counted. The lower response to BDNF was confirmed in IUGR-rat cultures. Data represent mean \pm SD ($n = 11$, n indicates the number of wells of a plate for each experimental condition), $*P < 0.05$.

IUGR-rats: 6.54 ± 0.40 g, $n = 6$ for each). As shown in Fig. 1A, BDNF levels in neurons from IUGR-rats were unchanged compared with those from normally weighed rats (control-rats). In contrast, TrkB, a high affinity receptor for BDNF, was significantly decreased in neurons from IUGR-rats (Fig. 1B). A low affinity common receptor for neurotrophins, p75, was unchanged in cultures from IUGR-rats (Fig. 1C). Such down-regulation of TrkB was confirmed in homogenates from the cerebral cortex of IUGR-rats (Fig. 1D), suggesting that the change observed in TrkB levels in culture is not specific to culture conditions. TUJ1 (class III β -tubulin, a neuronal

marker) levels are shown as a control (Fig. 1A–D). As BDNF/TrkB signaling is important for expression of Bcl2 [4], we determined the Bcl2 levels and found marked reduction in IUGR-rat cultures, though TUJ1 was unchanged (Fig. 1E), raising a possibility that IUGR makes cortical neurons vulnerable to death-inducible stimuli. Cell viability of cultures from both IUGR- and control-rats was decreased after serum-deprivation (Fig. 1F). Expectedly, the level of decrease in cell viability of IUGR-rat neurons was larger than that of control-rats. We observed a clear reduction of TrkB and Bcl2 levels in 8DIV cultures (Supplementary Fig.S1), implying that down-

regulation of TrkB and Bcl2 proteins due to IUGR is sustained during neuronal maturation. Furthermore, decreased viability of 8DIV neurons from IUGR-rats was confirmed (Supplementary Fig.S1).

Next, activation of intracellular signaling stimulated by BDNF was examined. Activation of ERK1/2 (phosphorylated ERK1/2, pERK1/2) 5 min after BDNF application was reduced in IUGR-rat cultures while total ERK1/2 and TUJ1 levels were unchanged (Fig. 2A and B). In the presence of arabinosylcytosine, which prevents glial cell proliferation, the reduced pERK1/2 in IUGR-rat cultures when BDNF was added was also observed (Supplementary Fig.S2), suggesting that this suppression of ERK1/2 activation is a neuronal, and not glial, response. We previously reported that ERK1/2 regulates synaptic protein expression [23,26]. In the current study, the expression levels of SNAP25, syntaxin, and synapsin I were unchanged in IUGR-rat neurons compared with control (Fig. 2C). Interestingly, ionotropic glutamate receptors (GluA1 and GluN2A) in IUGR-rat cultures were down-regulated (Fig. 2D). It is possible that the decreased activity of the ERK1/2 pathway via IUGR results in down-regulation of glutamate receptors.

The activation of Akt, a component of the PI3K pathway (well-known as a survival promoting pathway), was also determined. BDNF-stimulated activation of Akt (phosphorylated Akt, pAkt) was reduced in IUGR-rat neurons with or without arabinosylcytosine treatment (Fig. 3A and B, and Supplementary Fig.S2). To test whether the PI3K/Akt pathway is involved in neuronal survival [9], we examined the BDNF-dependent protection of cortical neurons from cell death caused by serum-deprivation. MTT assay revealed that BDNF inhibited the cell death in control-rat cultures, however, the protection by BDNF was not observed in IUGR-rat cultures (Fig. 3C). In control cultures, BDNF upregulated Bcl2, an anti-apoptotic protein (Supplementary Fig.S3). We confirmed that LY294002, a PI3K inhibitor, blocked BDNF-dependent survival in control cultures (Fig. 3D). Furthermore, immunostaining with anti-MAP2 (microtubule-associated protein 2, neuronal marker) antibody revealed that, though the number of MAP2-positive surviving cells was reduced after serum-deprivation in both IUGR- and control cultures, a lower response to BDNF was confirmed in IUGR-rat neurons compared with control (Fig. 3E). Taken together, it is possible that the survival-promoting effect of BDNF was weakened in IUGR-rat neurons.

We found that TrkB (not BDNF) was significantly decreased in cortical cultures from IUGR-rats. Consistent with the reduction of TrkB, BDNF-stimulated MAPK/ERK1/2 and PI3K/Akt pathways were diminished in IUGR-rat cultures compared with control. Bcl2, a survival promoting protein, was also down-regulated in IUGR-rat cultures. We also found a significant decrease in synaptic protein (GluA1 and GluN2A) levels in IUGR-rat cultures. Interestingly, cortical neurons from IUGR-rats showed vulnerability to cell death as well as a weakened response to the survival-promoting effect of BDNF.

Impairment of BDNF and TrkB functions has been implicated in the pathogenesis of schizophrenia [6,11], as well as other neuropsychiatric diseases such as depression [5]. A recent study demonstrated a reduction in BDNF in the dorsolateral prefrontal cortex of schizophrenics [34], suggesting that BDNF down-regulation may affect the functions of intrinsic cortical neurons, afferent neurons, and target neurons. Remarkably, an animal model of IUGR by TXA2 showed decreased BDNF and NT-3 mRNA in the cerebral cortex [14]. In our system, TrkB was decreased by IUGR, although BDNF levels were not altered. In addition to ligand (BDNF), a change in the expression of receptor (TrkB) may contribute to neuronal dysfunction due to IUGR.

Perhaps the down-regulation of TrkB in IUGR-rat neurons occurred as a result of post-transcriptional modifications. Ernst et al. reported that TrkB.T1 (one of the truncated types of TrkB) is down-regulated in the frontal cortex in a subset of suicide vic-

tims compared with controls and that this down-regulation is associated with methylation at specific CpG dinucleotides proximal to the coding region [12]. Indeed, several susceptibility genes for schizophrenia are subject to changes in transcriptional activity due to histone modifications and DNA methylation [15]. To date, most studies exploring DNA methylation changes in schizophrenia postmortem brain were focused on the cerebral cortex, primarily its prefrontal areas [3]. Various degrees of aberrant CpG hyper- or hypomethylation have been reported in regulatory sequences of promoters of genes involved in the cortical dysfunction of schizophrenia, including the glycoprotein *REELIN*, *COMT*, and *SOX10* [1,2,3,16,22]. Thus, TrkB reduction via IUGR in our models may be due to DNA methylation, although further studies are required to confirm this possibility.

In IUGR-rat cultures, the expression of postsynaptic proteins, GluA1 and GluN2A, was decreased. In the hippocampus of schizophrenia postmortem brains, reduced expression of subunits for ionotropic glutamate receptors (including NMDA, AMPA, and kainate type receptors) was reported [17]. Recently, we found that intracellular signaling, including the MAPK/ERK pathway, has an important role in the maintenance of synaptic proteins and is involved in schizophrenia [19,23,26,29]. The decrease of TrkB expression may lead to the reduction in postsynaptic proteins as observed in patients with schizophrenia.

TrkB down-regulation may cause reduced activation of the MAPK/ERK and PI3K/Akt pathways in response to BDNF. These pathways are critical for synaptic protein expression and neuronal survival. We confirmed that cortical neurons from IUGR-rats were vulnerable to cell death by serum-deprivation. Bcl2 expression and survival-promoting effects of BDNF were also decreased in IUGR-rat cultures. Increased vulnerability of neurons to neurotoxic damage caused by inadequate neurotrophic support is thought to be involved in the etiology of psychiatric disease [6]. In summary, our results suggest that impairment of BDNF-TrkB signaling caused by IUGR and the resultant decrease in viability of neurons and expression of glutamate receptors may be responsible, at least in part, for the cortical dysfunction observed in schizophrenia-like behaviors. We demonstrated that our *in vitro* system may offer a useful model for studies to investigate the cellular mechanisms of schizophrenia.

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Appendix A. Supplementary data

Supplementary data associated with this article can be found, in the online version, at doi:10.1016/j.neulet.2010.03.082.

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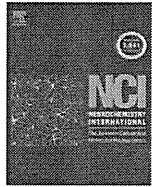
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Review

MicroRNA function and neurotrophin BDNF

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ABSTRACT

MicroRNAs (miRs), endogenous small RNAs, regulate gene expression through repression of translational activity after binding to target mRNAs. miRs are involved in various cellular processes including differentiation, metabolism, and apoptosis. Furthermore, possible involvement of miRs in neuronal function have been proposed. For example, miR-132 is closely related to neuronal outgrowth while miR-134 plays a role in postsynaptic regulation, suggesting that brain-specific miRs are critical for synaptic plasticity. On the other hand, numerous studies indicate that BDNF (brain-derived neurotrophic factor), one of the neurotrophins, is essential for a variety of neuronal aspects such as cell differentiation, survival, and synaptic plasticity in the central nervous system (CNS). Interestingly, recent studies, including ours, suggest that BDNF exerts its beneficial effects on CNS neurons via up-regulation of miR-132. Here, we present a broad overview of the current knowledge concerning the association between neurotrophins and various miRs.

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1. Introduction

miRs regulate the expression of target genes and ultimately affect translation. Through this process, multiple mechanisms are impacted, including differentiation, cell death, and cell metabolism in plants and animals (Bartel, 2004; Chapman and Carrington, 2007; Pillai et al., 2007). Recent evidence suggests that brain-specific miRs may be involved in the regulation of neuronal function. For instance, miR-132 is important for neurite outgrowth, while miR-134 negatively regulates the spine size in neurons (Vo et al., 2005; Schratt et al., 2006). Furthermore, change in expression and/or function of some miRs may be associated with several brain diseases such as schizophrenia (Mellios et al., 2009), panic disorder (Muiños-Gimeno et al., 2010), and Rett syndrome (Wu et al., 2010), etc. Additionally, regulation of neurodegeneration-related toxic molecules by miRs has been suggested (Eacker et al., 2009). Taking these findings together, an extensive examination of the basic functioning of miRs and their relationship with brain disease pathophysiology is very important.

Many studies discuss the involvement of BDNF, a critical neurotrophic factor, in brain function. On a cellular level, it is well-

established that BDNF influences proliferation, maturation, survival, and synaptic function via activation of intracellular signaling cascades including mitogen-activated protein kinase/extracellular signal-regulated protein kinase (MAPK/ERK), phospholipase C γ (PLC γ), and phosphatidylinositol 3-kinase (PI3K) pathways (Huang and Reichardt, 2003; Minichiello, 2009; Russo et al., 2009; Numakawa et al., 2010a). As expected, alteration in expression/function of BDNF is involved in the pathophysiology of several brain diseases including neurodegenerative diseases and mental disorders (Karege et al., 2005; Numakawa et al., 2011). As both miRs and BDNF affect neuronal processes, the crosstalk between these molecules is very interesting. In the present review, we focus on the current relationship between miRs and BDNF in neurons, in addition to giving a broad overview of the basic functioning of miRs.

2. Biogenesis of microRNA and its basic function

The first miR, *lin-4*, was initially discovered as a direct target when researchers were performing genetic analysis of defects in post-embryonic development of *Caenorhabditis elegans* (Chalfie et al., 1981; Ambros, 1989). *Lin-4* encodes a 22-nucleotide non-coding RNA that binds to the 3'UTR of *lin-14* mRNA, which serves to regulate protein translation (Wightman et al., 1991; Lee et al., 1993). The second miR to be identified was *let-7* (Reinhart et al., 2000). The *let-7* miR encodes a 21-nucleotide RNA that binds to the 3'UTR of *lin-41* and *hbl-1* (*lin-57*) in order to inhibit translation (Slack et al., 2000; Abrahante et al., 2003; Lin et al., 2003; Vella

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et al., 2004). Both *let-7* and its target *lin-41* are evolutionarily conserved throughout a wide range of animal species, including vertebrate, ascidian, hemichordate, mollusc, annelid and arthropod, suggesting a general role of small RNA molecules in developmental regulation. As a result of the above findings, extensive analysis and identification of new miRs were triggered (Pasquinelli et al., 2000). Since this time, several hundred miRs have been identified in various organisms such as viruses, worms, flies, fish, frogs, mammals and plants (Lagos-Quintana et al., 2001, 2003; Lau et al., 2001; Lee and Ambros, 2001; Llave et al., 2002; Reinhart et al., 2002; Lim et al., 2003; Pfeffer et al., 2005; Watanabe et al., 2005). The miR database now lists over 15,000 miR gene loci in over 140 species, and over 17,000 distinct mature miR sequences (Kozomara and Griffiths-Jones, 2011).

Generally, miR genes are transcribed by RNA polymerase II as primary miRs (pri-miRs are hundreds to thousands of nucleotide-length transcripts) containing cap structures and poly (A) tails (Cai et al., 2004; Lee et al., 2004; Parizotto et al., 2004, and see

Fig. 1). At this point, known transcription factors engage in the transcriptional control of miR genes. For instance, the myogenic transcription factors, such as Myogenin and MyoD, bind to regions upstream of miR-1 and miR-133 loci and are likely to regulate their expression during myogenesis (Rao et al., 2006). HBL-1, a protein product of *hbl-1* and one of *let-7*'s targets, is responsible for inhibiting the transcription of *let-7* temporarily in seam cells, vulval precursor cells, and the hypodermal syncytium 7. This negative feedback mechanism between *let-7* and HBL-1 has been identified and characterized by researchers (Roush and Slack, 2009). Epigenetic control also contributes to miR gene expression. For example, the miR-203 gene locus is hypermethylated in several hematopoietic tumors, including chronic myelogenous leukemia and some acute lymphoblastic leukemias (Bueno et al., 2008).

Following this, Drosha, an RNase III enzyme, cleaves the pri-miRs into approximately 70 nucleotide stem-loop structures as precursor miRs (pre-miRs) (Lee et al., 2003, and see Fig. 1). In plants, instead of Drosha protein, Dicer-like protein 1 (DCL1) acts to convert pri-miRs to pre-miR duplexes (Papp et al., 2003; Xie et al., 2004). Then, the excised approximately 70 nucleotide fold-back double-strand RNA (dsRNA) precursors are exported from the nucleus to the cytoplasm by the protein Exportin5 (Yi et al., 2003). In the cytoplasm, the pre-miRs are cleaved by the RNase III enzyme, Dicer, generating approximately 22 nucleotide siRNA-like complexes (miR/miR*) loaded onto Argonaute (Ago) protein (Hutvagner et al., 2001; Maniataki and Mourelatos, 2005, and see Fig. 1). Specifically, the stem of pre-miR has an imperfectly double-stranded structure, and the region of RNA duplex is essentially the same as siRNA. The mature miR is partially paired to the miRNA* and the small RNA resides on the opposite side of the pre-miR stem. One strand of the duplex remains in Ago as a mature miR, while the other strand (miR*) is degraded (Schwarz et al., 2003; Du and Zamore, 2005, and see Fig. 1).

Following Dicer cleavage, the resultant approximately 22 nucleotide RNA duplex is loaded onto Ago protein so as to generate an effector complex of the RNA-induced silencing complex (RISC) recruited by trans activator RNA (TAR)-binding protein (TRBP) and PACT (Protein activator of PKR; dsRNA activated protein kinase) (Chendrimada et al., 2005; Haase et al., 2005; Lee et al., 2006). GW182 proteins are also crucial for the miR-mediated gene silencing in animal cells. GW182 family proteins interact directly with Ago. The middle and C-terminal regions act as an autonomous domain in repressive function and the function is independent of both the interaction with Ago and of P-body (Processing body) localization (Ding et al., 2005; Eulalio et al., 2009). Translationally repressed mRNAs are collected in discrete cytoplasmic foci as P-bodies (Pillai et al., 2005; Eulalio et al., 2007; Parker and Sheth, 2007).

Many studies indicate that miRs repress post-transcriptional activity. In *C. elegans*, *lin-4* negatively regulates *lin-14* via repressing its translation without inhibiting *lin-14* mRNA biogenesis and translation initiation (Olsen and Ambros, 1999). Bantam binds to the 3'UTR of the pro-apoptotic gene *hid* to exert a negative effect on its translation in *Drosophila* (Brennecke et al., 2003). Most animal miRs inhibit the translation of target mRNAs (Fig. 2). In plants, most miRs mediate the stabilization of target mRNAs (Hake, 2003, and see Fig. 2). Plant miRs pair with mRNA almost perfectly and their complementary sites are located throughout the transcribed region of the target, not limited to the 3'UTR region. The Epstein-Barr virus (human herpesvirus) has been shown to encode miRs, though viral miRs do not have close homologs in other viral or host genomes. Viral miRs are expressed individually or in clusters from either polymerase or promoters, and regulate both viral and host genes (Pfeffer et al., 2004). In the fly and animal, miRs pair with their targets through limited 2–7 nucleotides of its 5' region (called the seed region), to prohibit translation and direct degradation of

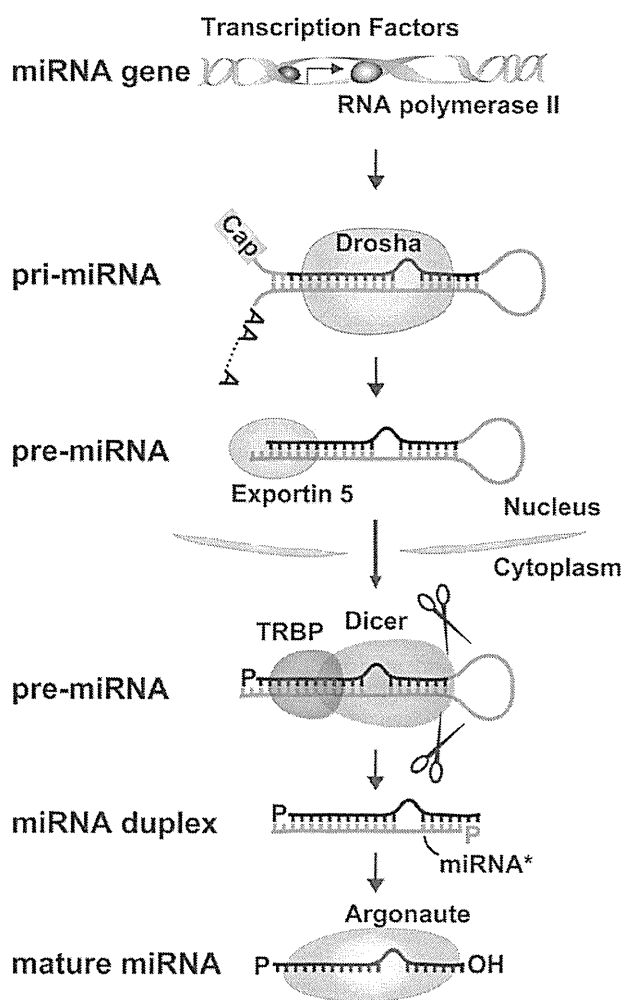


Fig. 1. MicroRNA biogenesis. An miRNA (miR) gene is generally transcribed by RNA polymerase II as primary miR (pri-miR). At this point, some transcription factors engage in the transcriptional control of miR genes. In the nucleus, the RNase III endonuclease Drosha cleaves the pri-miR to produce an approximately 70 nucleotide stem loop structure as precursor miR (pre-miR). Exportin5 transports the pre-miR into the cytoplasm, where it is cleaved by another RNase III endonuclease, Dicer, together with the trans activator RNA (TAR)-binding protein (TRBP), generating approximately 22 nucleotide miRNA/miRNA* duplex. One strand of the duplex remains Argonaute as a mature miR, while the other strand (miR*) is degraded.

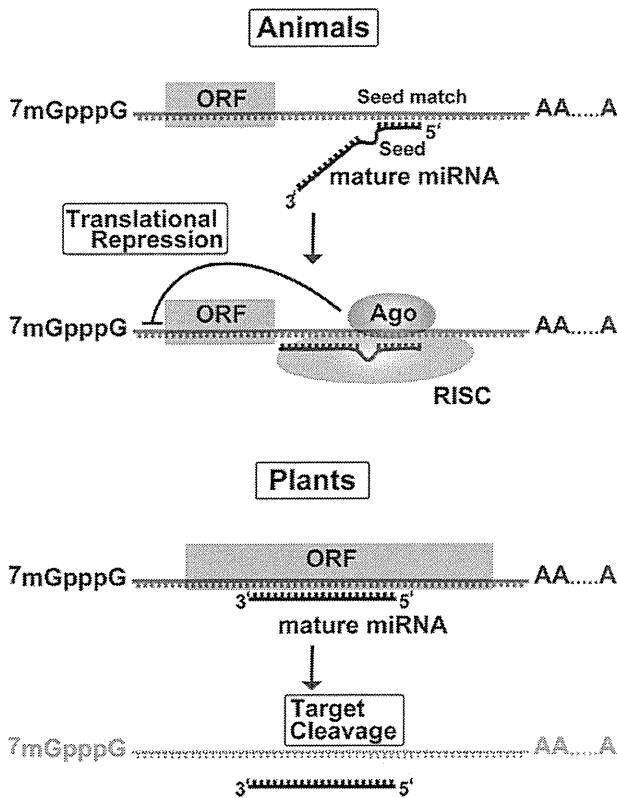


Fig. 2. MiR targeting in animal- and plant-cells. Most animal miRs recognize partially complementary binding sites, which are generally located in 3'UTRs. In the fly and animal, miRs pair with their targets through limited 2–7 nucleotides of its 5' region (called the seed region), to prohibit translation and direct degradation of target mRNAs. Plant miRs pair with target mRNA almost perfectly and their complementary sites are located through the transcribed region of the target mRNA, not limited to the 3'UTR region, and direct endonucleolytic mRNA cleavage within the base-paired region.

target mRNAs (Fig. 2). Considering that the seed region is so short, miRs are predicted to regulate a huge number of genes. In fact, human miRs may regulate as many as one-third of all protein-coding genes (Lewis et al., 2003, 2005; Xie et al., 2005).

3. miR expression in brain

miRs play a role in various cellular processes, including apoptosis and metabolism in both plants and animals. Recently, miRs that affect neuronal function in the brain have been reported. Characterization of the expression profiles of 119 miRs in mouse and human organs indicate that these miRs are phylogenetically conserved, organ-enriched and organ-specific. Interestingly, 13 of these miRs are enriched in the brain. Moreover, eight brain miRs are induced during neuronal differentiation of human and mouse EC cells after retinoic acid application, suggesting that there may be a conserved role in mammalian neuronal development (Sempere et al., 2004). Indeed, several studies indicate a relationship between miR and neuronal development. For example, miR-124a, which is perfectly conserved at the nucleotide level from worms to humans, is expressed throughout the embryonic and adult CNS (Lagos-Quintana et al., 2002). miR-124 plays an important role in neuronal differentiation and function, as overexpression of miR-124 in differentiating mouse P19 cells promotes neurite outgrowth, while blockade of miR-124 function decreases neurite outgrowth and levels of acetylated α -tubulin (Yu et al., 2008). Interestingly, miR-18 and -124a reduce glucocorticoid

receptor (GR)-mediated events in addition to decreasing GR protein levels by binding to the 3' untranslated region of GR (Vreugdenhil et al., 2009). Glucocorticoid is a stress hormone and putatively involved in the pathophysiology of mental disorders such as depression (see Sections below). Furthermore, expression of miR-9 is also found in the CNS and the knockdown of the miR results in inhibition of neurogenesis along the anterior–posterior axis (Bonev et al., 2011). miR-134 is also localized in the dendritic compartment of hippocampal neurons (Schratt et al., 2006). In midbrain dopamine neurons, miR-133b specifically expresses and regulates neural maturation and function via a negative feedback circuit that includes Pitx3, a paired-like homeodomain transcription factor (Kim et al., 2007). Recently, it was shown that overexpression of miR-137 promotes the proliferation of adult neuronal stem cells, whereas a reduction of miR-137 results in enhancement in differentiation (Szulwach et al., 2010). Taken together, all these studies indicate that brain-specific miRs have multiple roles in neuronal function. In the following section, we focus specifically on the relationship between miR function and the neurotrophin BDNF, which is well known as a critical mediator in synaptic plasticity.

4. miRs and BDNF

4.1. BDNF and synaptic function

In addition to BDNF, a member of the neurotrophin family, nerve growth factor (NGF), neurotrophin-3 (NT-3), and NT-4/5 are found mainly in mammals. As high-affinity tropomyosin-related kinase (Trk) receptors, TrkA (for NGF), TrkB, and TrkC (for NT-3) are essential for proper neurotrophin functioning. In the brain, it is well known that expression of both BDNF and its receptor TrkB is very strong, as this ligand–receptor complex is responsible for multiple neuronal functions. Via stimulation of TrkB, BDNF initiates activation of various intracellular signaling cascades such as MAPK/ERK, PLC γ , and PI3K pathways. BDNF/TrkB signaling is essential for cell differentiation and survival, neurite outgrowth, and synaptic function (Huang and Reichardt, 2003; Reichardt, 2006; Minichiello, 2009; Russo et al., 2009; Numakawa et al., 2010a). BDNF is critical in glutamatergic functioning, contributing to the maintenance of both NMDA and AMPA receptors as well as glutamate-mediated synaptic plasticity (Caldeira et al., 2007a, 2007b; Yoshii and Constantine-Paton, 2010). We also demonstrated a BDNF-dependent increase in levels of glutamate receptor subunits including NR2A, NR2B, and GluR1, in addition to presynaptic synapsin I and synaptotagmin (Matsumoto et al., 2006; Kumamaru et al., 2008, and see Fig. 3). In the upregulation of synaptic proteins, activation of MAPK/ERK signaling was required (Matsumoto et al., 2006; Kumamaru et al., 2008). A recent study showed that unsupervised learning (*in vivo*) and theta burst stimulation (with hippocampal slices) increases the number of postsynaptic densities co-localized with activated TrkB in the hippocampus. The potentiation of the co-localization was inhibited by a scavenging extracellular BDNF or NMDA receptor antagonist (Chen et al., 2010), suggesting that ligand BDNF and stimulation of glutamate receptors are both involved in the learning process. In general, it is believed that an increase in intracellular Ca²⁺ concentration contributes to the activity-dependent synaptic secretion of BDNF. An increase in Ca²⁺ via voltage-gated Ca²⁺ channels (VDCC), internal Ca²⁺ stores, and NMDA receptors was, in fact, demonstrated (Hartmann et al., 2001; Kuczewski et al., 2009; Lessmann and Brigadski, 2009). Taken together, an intimate relationship exists between BDNF and synaptic function. A detailed investigation of the mechanisms underlying BDNF-mediated changes in synaptic plasticity is paramount, and the possible

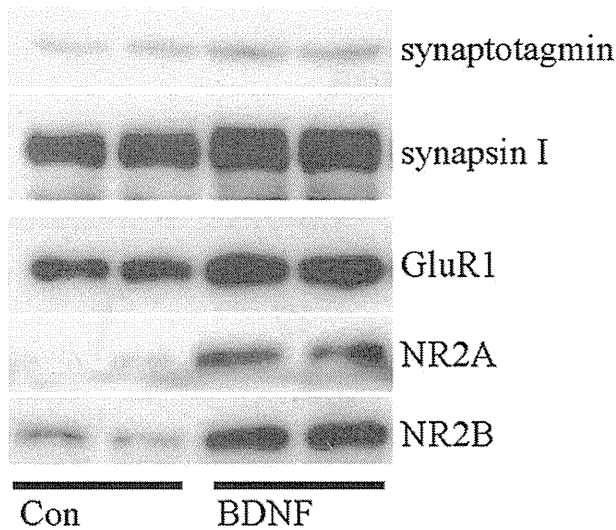


Fig. 3. BDNF increased expression of synaptic proteins including synaptotagmin, synapsin I, GluR1, NR2A, and NR2B. Cultured cortical neurons were prepared from postnatal 2 day-old rats. Six-hours after cell plating, BDNF (100 ng/ml) was added. After an additional 5-day culture, the cells were lysed for immunoblotting.

association of these mechanisms with brain-specific miRs is a topic of increased interest.

4.2. Neuronal function of miRs and BDNF

Brain-specific miRs play a role in synaptic function. In addition, BDNF is also a key player in synaptic plasticity in CNS neurons. Indeed, the interaction between BDNF and brain-specific miRs is an area of recent focus. Remarkably, after the loss of brain-specific miRs, enhanced learning and memory is observed in mice (Konopka et al., 2010). After deletion of the *Dicer1* gene in mouse forebrain, a whole set of brain miRs (including miR-124, -132, -137, -138, -29a, and -29c) was significantly decreased. In *Dicer1* mutant mice, the efficacy at hippocampal synapses and translation of BDNF was higher than in controls (Konopka et al., 2010). As mentioned above, Schrott et al. reported involvement of miR-134 in BDNF-regulated dendritic spine size in hippocampal neurons (Schrott et al., 2006). The miR-134 is localized in dendrites, and negatively regulates the spine size via repressing the translation of *Limk1* mRNA (LIM kinase 1), which is known to regulate dendritic structures (Bamburg, 1999; Meng et al., 2004). They demonstrate that BDNF relieves suppression of *Limk1* translation caused by miR-134 (Schrott et al., 2006). The current study shows that miR-134 regulates memory and neuronal plasticity (Gao et al., 2010). It is possible that the mammalian Sir2 homolog SIRT1 promotes synaptic plasticity via mediating expression of CREB by miR-134, as mutant mice lacking SIRT1 catalytic activity showed reduction in both CREB and BDNF proteins and upregulation of miR-134. A knockdown of miR-134 reversed the hippocampal long-term potentiation in SIRT1 mutant mice (Gao et al., 2010). In the cell differentiation of SH-SY5Y cells, a human neuroblastoma cell line, possible involvement of miR-125b has been reported (Le et al., 2009). miR-125b was significantly upregulated after all-trans-retinoic acid and BDNF application, and ectopic expression of miR increased differentiated SH-SY5Y cells with neurite outgrowth (Le et al., 2009). miR-375 also plays a role in regulation of neurite differentiation. Though exposure to BDNF increased neurite outgrowth in human neuroblastoma BE(2)-M17 cells, the miR-375 overexpression diminished BDNF action. Interestingly, BDNF-promoted neurite outgrowth was inhibited by silencing HuD (neuronal RNA-binding protein) or overexpressing miR-375, suggesting that miR suppresses neurite outgrowth via

decreasing the HuD levels. Indeed, reporter analysis revealed that miR-375 decreased HuD expression through targeting the HuD 3'UTR (Abdelmohsen et al., 2010).

miR-132 contributes to the action of BDNF. In cultured cortical neurons, BDNF induces upregulation of miR-132 (Vo et al., 2005). Interestingly, overexpression of miR-132 increases the outgrowth of primary neurites, and transfection of an antisense RNA for miR-132 results in a substantial decrease in neurite outgrowth (Vo et al., 2005). Recently, we also reported that BDNF induced a marked increase in miR-132 levels in cultured cortical neurons (Kawashima et al., 2010, and see Fig. 4). miR-132 upregulation may be a direct result of the BDNF in neurons, as the other miRs such as miR-9, -124, -128a, -128b, -134, -138, and -16 (as a control) were unchanged. While BDNF increased the expression of synaptic proteins including NR2A, NR2B and GluR1 (Fig. 3), transfection of double strand-miR-132 also upregulated these glutamate receptors (Kawashima et al., 2010, and see Fig. 4). Antisense RNA to inhibit endogenous miR-132 function decreased the number of BDNF-increased glutamate receptors. Interestingly, we found that blockade of the MAPK/ERK pathway suppressed BDNF-increased miR-132 levels (Fig. 4). As described above, we previously showed an important role of ERK signaling in the maintenance of glutamate receptor expression (Matsumoto et al., 2006; Kumamaru et al., 2008; Tuerxun et al., 2010). Taken together, it is possible that an increase of miR-132 via ERK activation is required for upregulation of glutamate receptors after BDNF stimulation. Furthermore, Remenyi et al. reported upregulation of miR-212/132 by BDNF stimulation in cultured cortical neurons (Remenyi et al., 2010). In their system, miRs were regulated by the ERK pathway, specifically via downstream MSK1 (mitogen- and stress-activated kinase 1) and CREB signaling.

Importantly, we found that the BDNF-increased ERK1/2 activation, miR-132 expression, and postsynaptic proteins were all diminished following chronic treatment with glucocorticoids, suggesting that treatment with chronic glucocorticoids caused suppression in BDNF-dependent neuronal function via reducing miR-132 expression (Kawashima et al., 2010, and see Fig. 5). Interestingly, increased blood levels of glucocorticoids (cortisol in humans, and corticosterone in rodents), which are stress hormones released from the adrenal glands, are putatively associated with the pathophysiology of mental disorders including depression (McEwen, 2005; Kunugi et al., 2010). Prolonged exposure to glucocorticoids as a result of stressful conditions may cause depression via damaging vital neuronal functions, as many studies suggest that downregulation of expression/function of BDNF is also closely related to the onset of depression (Altar, 1999; Nestler et al., 2002; Knable et al., 2004; Gervasoni et al., 2005; Karege et al., 2005; Numakawa et al., 2010b). We recently found a functional interaction of glucocorticoids with BDNF in cortical neurons. In cortical cultures, GR expression and an interaction between the GR and TrkB were decreased after exposure to glucocorticoids. The BDNF-evoked release of glutamate was also reduced because the GR-TrkB interaction is important for glutamate release induced by BDNF (Numakawa et al., 2009). Considering that BDNF affects levels of miRs, and glucocorticoids impact the level/function of BDNF negatively, further investigation into the relationship between glucocorticoids and miRs expression is warranted. It was reported that miR-18 and -124a decreased GR-mediated events in addition to reducing GR expression levels (Vreugdenhil et al., 2009). Both miRs suppressed levels of glucocorticoid-induced leucine zipper expression induced by DEX, a GR-selective glucocorticoid, and the reporter assays indeed revealed that miR-124a putatively bound to the 3'UTR of GR (Vreugdenhil et al., 2009). As the expression of miR-124a is restricted to the brain (Lagos-Quintana et al., 2002), further study of the neuronal role of miR-124a is needed.