Failure to confirm CNVs as of aetiological significance in twin pairs discordant for schizophrenia.
Failure to confirm CNVs as of aetiological significance in twin pairs discordant for schizophrenia

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Running title: Genomic Alterations in Monozygotic Twins for Schizophrenia
Abstract

Copy number variations (CNVs) are common structural variations in the human genome that strongly affect genomic diversity and can play a role in the development of several diseases, including neurodevelopmental disorders. Recent reports indicate that monozygotic twins can show differential CNV profiles. We searched CNVs in monozygotic twins discordant for schizophrenia to identify susceptible loci for schizophrenia. Three pairs of monozygotic twins discordant for schizophrenia were subjected to analysis. Genomic DNA samples were extracted from peripheral blood lymphocytes. We adopted the Affymetrix Genome-Wide Human SNP (Single Nucleotide Polymorphism) Array 6.0 to detect copy number discordance using Partek Genomics Suite 6.5 beta. In three twin pairs, however, validations by quantitative PCR and DNA sequencing revealed that none of the regions had any discordance between the 3 twin pairs. Our results support the hypothesis that epigenetic changes or fluctuation in developmental process triggered by environmental factors mainly contribute to the pathogenesis of schizophrenia. Schizophrenia caused by strong genetics factors including copy number alteration or gene mutation may be a small subset of the clinical population.

Keywords: CNVs, schizophrenia, genotype, monozygotic twin, epigenetic change
Introduction

Schizophrenia is a chronic, debilitating psychiatric illness with a 1% worldwide prevalence. Genetic studies have shown that schizophrenia has a high heritability with strong genetic factors involved in its etiology. Twin studies have played an important role in the elucidation of the genetic factors underlying neurodevelopmental disorders. Several twin studies have revealed that the concordance rate between monozygotic twins is 41–79% for schizophrenia, whereas the concordance rate between dizygotic twins is 0–14% (Shih et al., 2004; Kakiuchi et al., 2008). The higher concordance rate in monozygotic rather than dizygotic twins for schizophrenia suggests the contribution of genetic factors. Phenotypically discordant monozygotic twins are especially interesting resources for genetic studies, and twin studies could facilitate the identification of the causative genes of phenotypes. Kondo et al. (2002) reported that a nonsense mutation in IRF6, which is a causative gene for Van der Woude syndrome, was found in one affected individual in monozygotic phenotypically discordant twins. In relation to neurodevelopmental disorders, Bruder et al. (2008) reported that discordant monozygotic twins with parkinsonism showed different copy number variation (CNV) profiles.

CNVs are the most prevalent type of structural variations in the human genome that
largely contribute to genomic diversity. Redon et al. (2006) and Carter et al. (2007) showed that as much as 12% of the human genome and thousands of genes are variable in copy number. A great number of CNVs may not be pathogenic but simply contribute to human genome diversity not related to phenotype. Meanwhile, some CNVs have been proven a significant factor related to disease susceptibility. Recent studies reported that CNVs contribute to genetic vulnerability factors and can play an important role in the etiology of several neurodevelopmental disorders (Sebat et al., 2007, 2009). Xu et al. (2008) found that de novo copy number mutations were about eight times more frequent in patients with sporadic schizophrenia. Numerous copy number analyses in schizophrenia revealed that genes that were disrupted by CNVs, which include TBX1, ERBB4, SLC1A3, RAPGEF4, CIT, NRXN1, and 16p11.2 region, were candidate genes and regions for schizophrenia (Walsh et al., 2008; Cook et al., 2008; Merikangas et al., 2009; McCarthy et al., 2009); however, most of these are rare copy number variants and the contribution of those genes to schizophrenia is restricted to a tiny part of etiologies.

To date, numerous causative genes for schizophrenia have been identified; however, because of genetic heterogeneity, there is still a long path to the elucidation of the pathogenesis of schizophrenia. To identify causative genes for schizophrenia, we have utilized the Affymetrix Genome-Wide Human SNP Array 6.0 in 3 pairs of
monozygotic twins discordant for schizophrenia. Here, we describe the results of CNV and genotype profiles in 3 monozygotic twins.

**Methods**

**Subjects**

Three pairs of monozygotic twins discordant for schizophrenia participated in this study. Ten years have passed after the onset of schizophrenia in the affected individuals in all twins. All of the twins were male, and their mean age was 53 years old. Two well-trained psychiatrists diagnosed the twins by structured clinical interview, and all affected individuals corresponded to the DSM-IV-TR criteria for the undifferentiated type of schizophrenia.

**DNA microarrays**

Ten ml of peripheral blood samples was collected after obtaining written informed consent, and genomic DNA was extracted from blood lymphocytes using QIAamp DNA Mini Kit (QIAGEN, Hilden, Germany). Experimental procedures were approved by the Committee for the Ethical Issues on Human Genome and Gene Analysis at Nagasaki University.
DNA microarray experiments were performed using Affymetrix Genome-Wide Human SNP Array 6.0 (SNP Array 6.0) (Affymetrix, Santa Clara, CA, USA). We performed a paired analysis for loss of heterozygosity (LOH) and an unpaired analysis for copy number analysis using control individuals’ data. All of the computer analyses were performed using Genotyping Console (Affymetrix) and Genomics Suite version 6.5 beta software (Partek, St. Louis, MO, USA). Genomic copy number data were analyzed with Partek Genomics Suite software using a segmentation algorithm with stringent p-value cutoff.

**Quantification of genome copy number**

We performed real-time quantitative PCR using an intercalating dye, SYTO13 (Molecular Probes, Eugene, OR, USA), which is an alternative to SYBR green I, or using Universal Probe Library (Roche Diagnostics, Mannheim, Germany) to verify copy number changes suggested by the microarray analyses. Primers and probes were designed using the website software Universal ProbeLibrary Assay Design Center (https://www.roche-applied-science.com). Real-time PCR amplification was run on a LightCycler 480 Real-Time PCR System (Roche Diagnostics, Mannheim, Germany). All samples were measured in tetraplicates.
DNA sequencing

To verify the SNP genotypes obtained by SNP Array 6.0, we performed direct sequencing of PCR-amplified genomic DNA fragments including SNPs that showed discordant allele calls in each twin pair. The amplified fragments were directly sequenced after purification with exonuclease I and NTPhosTM Thermolabile Phosphatase (Epicentre, Madison, WI, USA) using the BigDye Terminator v3.1 Cycle Sequencing Kit and run on an ABI PRISM 3130xl Genetic Analyzer (Applied Biosystems). DNA sequences were analyzed using Variant Reporter (Applied Biosystems) and ATGC version 6.0 (Software Development, Tokyo, Japan).

Results

Microarray analysis results

Quality control (QC) data obtained from the SNP Array 6.0 are summarized in Table 1. The call rate and contrast QC in SNP Array 6.0 data were >95% and >1.50, respectively, for all samples, and both values indicated experiments using the SNP Array 6.0 were done well. [insert Table 1 here] Copy number analysis of microarray data using Partek Genomics Suite showed some deleted or amplified regions in each twin pair (data not shown). Regions with discordant genotyping between twins from
microarray data are summarized in Table 2. [insert Table 2 here] Unpaired analysis of 6 individuals in comparison with ethnically-matched normal controls (HapMap-JPT) revealed that an approximately 3 kb region within the \textit{SLC25A37} gene was deleted in two of the three schizophrenia twin pairs, 11A/B and 31A/B. The deleted region (chromosome 8:23460969–23463786) was not registered in the Database of Genomic Variants (http://projects.tcag.ca/variation/).

**Quantitative PCR results**

We verified the copy number state by real-time PCR of the regions with discordant copy number, including genes, by paired analysis using SNP Array 6.0. Primers were designed for the middle position of the regions. Quantitative PCR was performed for a total of 120 regions. However, we could not reconfirm the differences between twins in all 120 tested regions. In addition, quantitative PCR within the \textit{SLC25A37} gene revealed no loss or gain of the genome in comparison with ethnically matched control individuals.

**Sequencing results**

DNA sequencing was performed for a total of 37 regions surrounding SNPs that
had shown discordant genotype calls from microarray analysis within twin pairs. We selected one or more SNP(s) called discordant genotype in each LOH region. Sequencing revealed all of the SNPs were concordant between twin pairs (data not shown).

**Discussion**

In this study, we analyzed genomic alterations, CNVs and genotypes, in 3 pairs of monozygotic twins discordant for schizophrenia. None of the regions of copy number difference between twins shown by SNP Array 6.0 were re-vericated by quantitative PCR, and none of the genotype discordance was re-verified by sequencing. Additionally, no novel CNVs was detected in the identified CNVs between twins. To our knowledge, this is the first report verifying the data from high-density and high-resolution DNA microarrays by quantitative PCR and DNA sequencing. Our results indicate that genomic alterations including CNVs and gene mutations contribute minimally to etiologies of schizophrenia. The large genome-wide study by The Wellcome Trust Case Control Consortium (WTCCC) revealed CNVs is not main cause of bipolar disorder which is one of the neurodevelopmental disorders (WTCCC, 2010). This report have a different concept from our study because our study aimed to find copy number
alteration as a single gene disorder, however, WTCCC report could not discover the CNV contributing to the bipolar disorder. Our results may support the hypothesis that epigenetic changes (Roth et al., 2009), which can influence the expression of genes without affecting the DNA sequence, mainly contribute to the pathogenesis of schizophrenia.

SNP Array 6.0 allows us to detect different genotype or copy number neutral LOH regions. In our twin comparison, copy number neutral LOH would indicate segmental uniparental disomy (UPD) in twin pairs. Actually, UPD of the paternal allele at 11p15 in the affected twin caused discordance for hemihypertrophy in monozygotic twins (West et al., 2003). Furthermore, recent studies revealed that UPD was associated with schizophrenia. UPD on chromosome 1 and 5q32-qter in a patient with schizophrenia has been described in 2004 and 2006, respectively (Abecasis et al., 2004; Seal et al., 2006). But no genotype difference between twins was confirmed in this study.

Here, we presented no genomic discordance between twins; hereinafter, we will discuss some speculation about the relation between genetic factors and phenotypic discordance. First, it is possible that mosaicism at specific tissues (i.e., brain) because of postzygotic genomic rearrangements causes discordant phenotypes between monozygotic twins. Although we used DNA samples extracted from peripheral blood
cells in this study, mosaic genomic rearrangement could be detected in brain. It is clear that the ideal source for studies of neurodevelopmental disorders is brain tissue. Nonetheless, it is practically impossible to harvest the brain tissue of twins (Kato et al., 2005). Olfactory sensory neurons have recently been shown to be easily accessible neuronal cells that have been useful for studies on schizophrenia (Arnold et al., 2001), enabling the study of neuronal cell character including genotype and copy number state.

Second, it is possible that smaller-scale genomic aberrations below detection sensitivity influence the discordant phenotype of monozygotic twins. SNP Array 6.0 is one of the highest resolution platforms commercially available and allows us to identify CNVs much smaller than 10 kb. However, McCarroll et al. (2008) showed that the detection rate using the SNP Array 6.0 sharply diminished for CNVs <4 kb. To increase sensitivity, the use of many more detection probes is needed, and more than one experimental platform should be performed in future studies.

Bruder et al. (2009) successfully detected many copy number changes in peripheral blood using a Bacterial Artificial Chromosome (BAC)-array at mosaic state (~20%) in 9 monozygotic twins discordant for parkinsonism. All of the nine pairs had copy number discordancy in their reports. Because their results suggested copy number change could be found in the mosaic state, tissue-specific mosaicism is a possible
explanation for psychiatric disorders. We may have overlooked copy number change in a mosaic state in peripheral blood with the use of the SNP Array 6.0 instead of the BAC-array because the SNP Array 6.0 is a powerful tool to identify small regions with copy number change but is not suitable to detect copy number in a mosaic state.

It seems most likely that epigenetic changes between monozygotic twins influence the phenotypic discordance of monozygotic twins. Several recent studies indicate that epigenetic changes contribute to the etiology of schizophrenia. Rett syndrome and Fragile X syndrome are neurodevelopmental disorders caused by a single gene defect and dysregulation of DNA methylation very early in life (Amir et al., 1999; Das et al., 1997). Kaminsky et al. (2009) have shown that differences in DNA methylation profiles increase in monozygotic twins along with aging. Because the onset of schizophrenia is later than Rett syndrome and Fragile X syndrome, it is possible that cumulative epigenetic modifications could be one cause of schizophrenia development. Furthermore, a recent study by Roth et al. (2009) suggested that DNA methylation and histone modification triggered by influence of environmental factors is responsible for the difference in onset age between these disorders. Akbarian et al. (2005) indicated that histone modification contributes to the pathogenesis of prefrontal dysfunction in patients with schizophrenia based on the finding that the level of H3-(methyl)arginine

12
17 in patients with schizophrenia exceeded control values by 30%. Thus, genome-wide DNA methylation and genome-wide histone modification studies for monozygotic twins discordant for phenotypes may be promising techniques in future twin studies. In fact, Baranzini et al. (2010) reported genomic sequence and epigenetics (methyl-cytosine) analysis of monozygotic twin discordant for multiple sclerosis using next generation sequencer. They could not find reproducible differences between twins, but these comprehensive analyses including genome and epigenome sequence are just started. As Crow (2002) discussed, it is important to analyze the genetic and epigenetic influence to the species-specific characteristics. Comprehensive genetic and epigenetic analysis of discordant monozygotic twins will be advanced using next generation technologies.

In summary, we did not detect genomic alterations including CNVs and gene mutations between twins discordant for phenotype. Our results indicate that schizophrenia caused by genomic alterations may be a small subset of the clinical population and may support the hypothesis that epigenetic mechanisms triggered by the influence of environmental factors are associated with the etiology of schizophrenia. Experimental investigations of epigenetic mechanisms such as expression analysis, methylation site sequence and histone modification studies using DNA samples
extracted from olfactory sensory neurons are needed to identify the differences responsible for discordant phenotypes in future studies.
Acknowledgments

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Table 1
Summary of Twin Samples and Affymetrix GeneChip Genotyping Results.

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<tr>
<th>Samples</th>
<th>Sex</th>
<th>Phenotype</th>
<th>SNP call rate</th>
<th>Contrast QC*</th>
</tr>
</thead>
<tbody>
<tr>
<td>11A / B</td>
<td>male</td>
<td>Schizophrenia / unaffected</td>
<td>99.444 / 99.516</td>
<td>2.38 / 2.48</td>
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<tr>
<td>21A / B</td>
<td>male</td>
<td>Schizophrenia / unaffected</td>
<td>98.974 / 99.175</td>
<td>1.88 / 2.22</td>
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<tr>
<td>31A / B</td>
<td>male</td>
<td>Schizophrenia / unaffected</td>
<td>99.199 / 99.179</td>
<td>2.26 / 1.60</td>
</tr>
</tbody>
</table>

*Contrast QC (Quality Control) is per sample Quality Control test metric for SNP Array
6.0 intensity data. In high-quality data sets, the Contrast QC metric is higher than the
0.4 threshold according to user manual provided by the manufacturer.
Table 2  
List of loss of heterozygosity regions derived from microarray data.

<table>
<thead>
<tr>
<th>chr.</th>
<th>Physical position</th>
<th>twin #</th>
<th>validated SNPs</th>
<th>overlapping genes</th>
</tr>
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<td>start</td>
<td>end</td>
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<td></td>
</tr>
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<td></td>
</tr>
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<td>twin #</td>
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Chr. # means the number of chromosome.