receptor abnormalities in schizophrenia may help explain prior epidemiologic data relating the risk for this illness to altered rates of autoimmune disorders, prenatal infection and familial leukemia. Colony stimulating factor 1 receptor (CSF1R) gene encodes a tyrosine kinase growth factor receptor for CSF1, the macrophage and monocyte specific growth factor. CSF1R gene is located at chromosome 5q32, a region that was suggested to be linked to childhood onset schizophrenia. CSF1R gene mutation has been associated with microglial development. In this study, we investigated the genetic association between schizophrenia and single nucleotide polymorphisms (SNPs) of the CSF1R gene.

**Methods:** 219 Korean schizophrenia patients and 379 control subjects were enrolled for this study. We genotyped four SNPs (rs216138, rs10079250, rs2228422 and rs1986027) of the CSF1R gene by direct sequencing. All patients were evaluated by the Operational Criteria Checklist for Psychotic Illness. Multiple logistic regression models (that is, co-dominant, dominant, and recessive) were performed to generate odds ratios, 95% confidence intervals, and p values.

**Results:** The genotype frequencies of rs1986027 showed significant association between schizophrenia and control groups (p=0.011 in the co-dominant model [T/T vs. C/C]; p=0.003 in the recessive model [T/T vs. C/C + C/T]). For the SNP rs10079250, significant association was found in the recessive model [(C/C vs. T/T + C/T); p=0.035]. There was no significant association between other two SNP polymorphisms and schizophrenia.

**Conclusions:** Our study is the first to report an association of the CSF1R gene polymorphisms with schizophrenia. We found significant association between CSF1R polymorphism and schizophrenia in Korean population.

**Key Words:** CSF1R, cytokine, schizophrenia, association.

**PM454**

Association analysis between (AAT)n repeats in the cannabinoid receptor 1 (CNR1) gene and smooth pursuit eye movement (SPEM) abnormality in Korean patients with schizophrenia.

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**Abstract**

**Objective:** According to previous studies, the cannabinoid receptor 1 (CNR1) gene could be an important candidate gene for schizophrenia which is located on chromosome 6q14-q15. The association between CNR1 polymorphisms and schizophrenia is actively being investigated, and some studies have linked the AAT-trinucleotide repeats in CNR1 gene with the risk of schizophrenia. Meanwhile, smooth pursuit eye movement (SPEM) has been regarded as one of the most consistent endophenotype of schizophrenia.

In this study, we investigated the association between the AAT-trinucleotide repeats in CNR1 gene and smooth pursuit eye movement abnormality in Korean patients with schizophrenia.

**Methods:** We measured SPEM function in 187 Korean patients with schizophrenia (84 male, 83 female) and they were divided according to SPEM function into two groups, good and poor SPEM function groups. We also investigated allele frequencies of AAT-repeat polymorphisms on CNR1 gene in each group. A logistic regression analysis was performed to find the association between SPEM abnormality and AAT-trinucleotide repeats in each group.

**Results:** The natural logarithm value of signal/noise ration (Ln S/N ratio) of good SPEM function group was 4.34±0.29 and that of poor SPEM function group was 3.21±0.70.

In total, 7 types of trinucleotide repeats were identified, each containing 7, 10, 11, 12, 13, 14, and 15 repeats, respectively. (AAT)n allele was most frequently observed, with a frequency of 30.5%. The frequencies of the other repeat alleles (in the decreasing order) were as follows: (AAT)n, 30.5%, (AAT)n, 24.3%, (AAT)n, 19.8%, and (AAT)n, 11.1%.

**Conclusions:** No significant associations were found between the number of AAT-repeat polymorphisms of the CNR1 gene and SPEM function.

**PM455**

Genetic variants in Chromogranin B is associated with the Risk of Schizophrenia in Korean male population

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**Abstract**

Schizophrenia is a devastating mental disorder with high heritability estimate up to 80%. Secretory pathway of peptide hormones and neuropeptides in brain is regulated by chromogranin proteins. Chromogranin B (CHGB), a member of chromogranin family gene, is proposed as one of the candidate genes for the risk of schizophrenia. In a genome wide association study performed in a Japanese population, genetic variant (microsatellite: D20S95) near CHGB could be a potential genetic marker for the schizophrenia development.

In the current study, 15 SNPs of CHGB were genotyped in 310 schizophrenia patients and 604 healthy controls to investigate the association with the schizophrenia susceptibility. Statistical analysis has revealed that four genetic variants (rs446659, rs6133278 (D145N), rs910122 (R178Q), rs2821) were associated with the reduced risk of schizophrenia (OR=0.72–0.78, p=0.002–0.02). In the subgroup analysis, five genetic variants (rs236141, rs446659, rs6085323, rs910122 (D178Q), rs2821) and haplotype (ht3) showed more protective effect on the schizophrenia in male subjects (OR=0.52–0.74, p=0.002–0.05), but not in female subjects.

Our results demonstrated that genetic variants in CHGB showed gender-specific effect to the reduced risk of schizophrenia, which could be a useful preliminary result for further study.

**Keywords:** Single nucleotide polymorphisms (SNPs), Chromogranin B (CHGB), schizophrenia, gender-specific marker, male

**PM456**

Aberrant cortico-cerebellar connectivity of the default mode network in individuals at ultra-high risk for psychosis: a resting-state fMRI study

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Abstract
Dysfunction of the cerebellum in schizophrenia is established as the concept of ‘cognitive dysmetria,’ which suggests impairments in sensorimotor and mental coordination resulting in perceptual disturbance, disorganized thoughts and speech, and cognitive dysfunction. It has become evident that cerebellar dysfunction is already present in individuals at ultra-high risk (UHR) for psychosis. We investigated functional connectivity of cortico-cerebellar circuits focusing on the default mode network (DMN) during rest in UHR individuals to figure out neurofunctional correlates of disease-related vulnerability.
Thirty-three UHR individuals (including 8 converters during follow-up) and 56 healthy controls underwent fMRI scanning during rest at baseline. Seed-based functional connectivity analysis was performed using two cerebellar seeds in bilateral crus I, previously known to be associated with the DMN. We conducted a statistical comparison of cortico-cerebellar functional connectivity in the DMN between three groups; converters, non-converters, and healthy controls.
Converters showed significantly decreased connectivity in several frontal regions as compared with both non-converters and healthy controls. The ventromedial prefrontal cortex (vmPFC) was particularly decreased in converters. Non-converters and healthy controls showed no significant difference in functional connectivity.
This result suggests that aberrant cortico-cerebellar connectivity in the DMN is evident prior to the development of psychotic symptoms in UHR individuals who later become overt psychosis. The cerebellum, as an internal-model control system, may play an important role in developing psychosis and give some clues to identify ‘true’ UHR individuals for psychosis.
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PM458
Altered Frontal and Temporal Microstructure in Patients with First-Episode Psychosis: Diffusion Kurtosis Study
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Abstract
The reports of microstructural disruption in schizophrenia gray matter from post-mortem studies showed various abnormalities such as reduced somal size, dendritic arborization and length. However, it has been difficult to infer to the timing, pattern and location of the microstructural changes due to the limitations of the post-mortem method. To clarify this gap in knowledge and to extend it to in vivo, microstructural complexity of cortex in subjects diagnosed with first episode psychosis (FEP) was compared to healthy controls with diffusion kurtosis imaging (DKI) technique.
A total of 37 FEP and 36 matched healthy controls underwent DKI and T1-weighted magnetic resonance imaging (MRI) to examine the microstructural complexity in cortex. Mean kurtoses in cortical gray matter regions of interests (ROIs) were compared between groups. We also investigated the relationship between the microstructural complexity and symptom severity. Mean kurtosis that represents microstructural complexity, was significantly reduced bilaterally in frontal and temporal cortex and right occipital cortex in FEP compared to healthy controls. Our result not only highlight the location and pattern of microstructural changes in schizophrenia using MRI, it specifically points out that the microstructural anomaly already exists and detectable in FEP.

Keywords: psychosis, MRI, diffusion, kurtosis imaging, gray matter