palate. In this study, we investigated the association between coding region single nucleotide polymorphisms (cSNPs) of ADAMATS20 gene and schizophrenia in a Korean population.
Methods: Six cSNPs (rs10506226, rs10880473, rs7310011, rs7297737, rs7302446 and rs11182088) in 276 schizophrenia patients and 406 control subjects were genotyped using Sequenom iPLEX-Gold assay. The associations of SNPs were analyzed based on logistic regression using multiple inheritance models (log-additive, dominant and recessive models).
Results: In our study, significant associations between rs7302446, rs7297737 and rs7310011 and schizophrenia were shown in the dominant models (p = 0.0057, OR = 1.72, 95% CI = 1.17–2.52 for rs7302446; p = 0.0043, OR = 1.75, 95% CI = 1.19–2.58 for rs7297737; p = 0.006, OR = 1.71, 95% CI = 1.17–2.52 for rs7310011). We also found a significant association between rs11182088 and schizophrenia in the log-additive (p = 0.004, OR = 1.44, 95% CI = 1.12–1.85) and dominant models (p = 0.048, OR = 1.57, 95% CI = 1.15–2.16). Additionally, in the analysis of haplotypes, the ATGCTG, ATGCTA and CCATAA haplotypes consisting six cSNPs were associated with schizophrenia (p = 0.0006, 0.044, and 0.020, respectively).
Conclusion: These results suggest that the ADAMTS20 gene contributes to the susceptibility of schizophrenia.

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Investigation of maternal effects, maternal-fetal interactions and parent-of-origin effects (imprinting), using mothers and their offspring with schizophrenia

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Abstract
Objective: Many complex genetic effects, including epigenetic effects, may be expected to operate via mechanisms in the interuterine environment. A popular design for the investigation of such effects, including effects of parent-of-origin (imprinting), maternal genotype, and maternal-fetal genotype interactions, is to collect DNA from affected offspring and their mothers (case/mother duos) and to compare with an appropriate control sample. We investigate the effects of estimation of maternal, imprinting and interaction effects using multimodal modeling using parents and their offspring with schizophrenia in Korean population.
Methods: We have recruited 27 probands(with schizophrenia) with their parents and siblings whenever possible. For best estimation of diagnosis, we have used medical records and a Korean version of DIGS (Diagnostic Interview for Genetic Studies) & FIGS (Family Interview for Genetic Studies). We have used lifetime dimensions of psychosis scale(LDPS) for measuring psychotic features. We analyzed 96 SNPs of 17 functionally only relevant genes and 21 neuronal genes in chromosome 18 for DNA samples that was checked for the data quality and genotype error. We used EMIM analysis program for the estimation of maternal, imprinting and interaction effects using multimodal modeling
Summary of results: Of analyzed 96 SNPs, significant SNP(rs 324420) will be suggested in EMIM analysis for child genetics effects($p = 1.5 \times 10^{-4}$) (and child genetic effects allowing for maternal genetic effects: $p = 5.3 \times 10^{-4}$) with very stringent multiple comparison Bonferroni correction. Additionally, analysis results for maternal genetic effects (and maternal genetic effects allowing for child genetic effects) will be presented.
Conclusions: Epigenetics and gene-environment interactions are represented underlying statistical genetics. Our results are the pilot study for investigating epigenetic mechanism in the cause of schizophrenia. And it will help to understand and use the EMIM statistical genetics analysis program with many limitations including small pedigree numbers.

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Hot genes in schizophrenia: case-control, pharmacogenetics and exploratory analyses in two independent samples

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Abstract
We investigated the effects of genetic variants within PPP3CC, RORA, SP4, ST8SIA2 and ZNF804A genes in a Korean sample of 176 SCZ patients and 326 healthy controls and an Italian sample of 83 SCZ patients and 194 healthy controls. The PANSS was used to assess psychopathological severity and antipsychotic response (AR). Several clinical features were recorded in both samples. In the Korean sample RORA rs10438338 was associated with SCZ (p=0.03) as well as haplotype rs2282888-rs2237304-rs10272006-rs12673091 within SP4 gene (p=0.02). In the Italian sample 3 PPP3CC variants (rs11780915 p=0.006; rs10108011 p=0.01; rs2249098 p=0.0004), ZNF804A rs1344706 (p=0.02) and SP4 rs12673091 (p=0.02) were associated with SCZ. The haplotype rs11780915-rs10108011-rs2249098 within PPP3CC gene and the haplotype rs7603001-rs1344706 within ZNF804A gene were associated with SCZ as well (respectively p=0.03 and p=0.02). Further, several RORA variants were associated with AR (Korean sample: rs1871858 p=0.02; rs12900122 p=0.06, rs17204440 p=0.02, haplotype rs1020729-rs1871858 p=0.01; Italian sample: rs12900122 p=0.003). In the Italian sample also 2 SP4 variants (rs2282888 p=0.02; rs10272006 p=0.02) and ST8SIA2 rs4777989 (p=0.04) were associated with AR. Exploratory analyses suggested that: 1) PPP3CC, ST8SIA2 and SP4 genes may be implicated in the develop and severity of psychotic symptoms, 2) RORA gene may play a role in AR, particularly of negative symptomatology, as well as ZNF804A gene. Considering limitations linked to the sample size and candidate genes approach, our results further support a role for these gene in SCZ, as well as in AR. Analyses in well phenotyped samples could help researchers to refine the role of these genes for further, focused investigations.

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Effects of olanzapine, clozapine, risperidone and sertindole on FGF2, synapsin and NGF expression in the hippocampus of naive mice

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Abstract
Some atypical antipsychotic drugs have unique actions,which may contribute to enhanced neurogenesis. Fibroblast growth