PS160
Predictive value of homocysteine for depression after acute coronary syndrome: Finding from the K-DEPACS study
Running title: Homocysteine for depression in ACS
Jae-Min Kim1,*, Robert Stewart2, Hee-Ju Kang3, Kyung-Yeol Bae4, Sung-Wan Kim5, Il-Seon Shin4, Jin-Sang Yoon4
1Department of Psychiatry, Chonnam National University Medical School, Gwangju, Korea; 2‘King’s College London, Institute of Psychiatry, London, UK

Abstract
Aim: Homocysteine and the methylenetetrahydrofolate reductase (MTHFR) C677T polymorphism have been investigated as risk factors for depression and ACS separately, but not for depression comorbid with ACS. This study aimed to investigate whether homocysteine and MTHFR gene are associated with occurrence of depressive disorder in ACS.
Methods and results: A sample of 969 patients with recent ACS were recruited and 711 followed 1 year later. Depressive disorder was diagnosed according to DSM-IV criteria, and classified as baseline prevalent, and follow-up incident or persistent disorder according to status at the two examinations. Plasma homocysteine concentration and the MTHFR C677T polymorphism were assayed, and a range of demographic and clinical characteristics evaluated as covariates. A higher homocysteine concentration was independently associated with prevalent depressive disorder at baseline irrespective of MTHFR genotype; and with both incident and persistent depressive disorder at follow-up only in the presence of TT genotype. MTHFR genotype was not itself associated with depressive disorder after ACS.
Conclusions: Plasma homocysteine could be a biomarker for depressive disorder particularly in the acute phase of ACS. Focused interventions for those with higher homocysteine level and MTHFR TT genotype might reduce the risk of later depressive disorder.

PS161
Association study of polymorphism in the serotonin transporter gene promoter, methylation profiles, and expression in patients with major depressive disorder
Junichi Iga
Ehime University Graduate School of Medicine, Japan

Abstract
The serotonin transporter (SHTT) may be associated with the pathogenesis of major depressive disorder (MDD). The SHTT-linked polymorphic region (SHTTLPR) genotype may determine how levels of SHTT mRNA are influenced by promoter methylation. We examined the association of SHTT gene methylation, which influences gene expression, and the SHTTLPR genotype before antidepressant treatment and expression before and after treatment. The aims of this study were: (1) to investigate the association between SHTT methylation or expression in leukocytes and depression, and (2) to investigate a possible effect of SHTT methylation, expression, and genotype on clinical symptoms in MDD. The SHTTLPR genotype was significantly associated with mean methylation levels in patients only (patients: r = 0.40, P = 0.035, controls: P = 0.96). The mean methylation level was significantly increased in patients compared to controls (patients: 5.30 ± 0.24, controls: 4.70 ± 0.15, unpaired t test, P = 0.04). SHTT expression using real-time PCR and Taqman probes was increased in unmedicated patients compared to controls and then decreased 8 weeks after antidepressant treatment. The mean SHTT expression level was not associated with the SHTTLPR genotype in patients or controls. Increased depressive symptoms were related to decreased levels of methylation.

PS162
Genetic role of CSNK1E on circadian and childhood characteristics of the patients with major depressive disorder
Eun-Jeong Joo, Kyu Young Lee, Eui-Joong Kim
Eulji University School of Medicine, Republic of Korea

Abstract
Objectives: More evening type of circadian rhythm characteristics has been reported for MDD. Mood instability in childhood has also suggested for the patients with MDD. Here we would like to investigate a genetic role of CSNK1E on circadian and childhood characteristics in the patients with MDD. CSNK1E (Casein kinase 1 epsilon) is one of circadian genes, encoding the protein phosphorylate period, a circadian rhythm protein.
Methods: Total 164 patients with major depression were included: 49 patients with single episode and 115 patients with recurrent episodes. Circadian rhythm of current state was collected with 13 items of CSComposite scale). Childhood characteristics were collected retrospectively using 25 items of WURS(wender Utah Rating Scale). Factor analysis was done for WURS. Three factors were extracted: Impulsivity, Inattention, and Mood instability. All subjects were ethnically Korean. Genotyping was done for three SNPs of CSNK1E: rs135745(C/G), rs1534891(C/T), and rs2075984(A/C). Analysis of association was done by SPSS 12.0 for males and females separately.
Results: The mean WURS total scores of MDD were 26.89 for males and 27.08 for females. The mean CS total scores were 37.91 for males and 33.67 for females. Genetic association tests with three SNPs of CSNK1E gene found no association for WURS total score and factor scores, CS total score for both males and females.
Conclusion: We could not find association between CSNK1E gene and childhood characteristics and circadian rhythm in MDD. In this study, CSNK1E gene does not seem to play a significant role for childhood and circadian characteristics.
Keywords: MDD, childhood characteristics, circadian rhythm, CSNK1E

PS163
Serotonin Transporter Polymorphism in Severe Major Depressive Disorder in Indonesia
Wulandari Arlisa1, Purnomowati Augustine2, Wahmurti Tuti2, Achmad Tri Hanggono2
1Jenderal Achmad Yani University, Indonesia, 2Padjadjaran University, Indonesia

Abstract
Background: A functional polymorphism in the promoter region of the serotonin transporter (5-HTT) gene-linked polymorphic region (5-HTTLPR) of the human serotonin gene (SLC6A4), alters its transcription. Short allele (S/S) variation decreases the transcriptional efficacy of serotonin, is associated with increased risk of major depressive disorder (MDD) in response to stressful life events. The aim of this study was to identify the genotype distribution for the serotonin transporter polymorphism (5-HTTLPR) in a sample of severe major depressive disorder patients in Bandung, Indonesia.
Methods: Data were available from a sample of 40 severe MDD patients defined by DSM-IV diagnostic criteria. 19 (47.5%) men and 21 (52.5%) women, ages 17–54 years was assessed through Structured Clinical Interview For DSM-IV Axis I Disorders and have a 17-item Hamilton Depression Rating Scale of 18 or higher. The 5-HTTLPR variant was genotyped according to published protocols. Three allele variants of the gene polymorphism were identified based on the PCR fragment sizes: short (S; 486bp, 14 repeats), long (L; 529bp, 16 repeats), or extra-long (XL; 612bp, 20 repeats).

Results: The HDRS score was 21.42±1.920. This study exhibits high frequency of S/S genotype (50%), lower frequency of L/S genotype (30%), L/L genotype (17.5) and L/XL (2.5%) in severe MDD patients.

Conclusions: These results support the possibility of serotonin transporter polymorphism role in the etiology of MDD.

Key Words: Severe Major Depressive Disorder, Serotonin Transporter, SLC6A4, Indonesia

PS164
Concomitant Use of Benzodiazepine Hypnotics and Alcohol in Patients with Schizophrenia, Depression and Insomnia: A Preliminary Finding
Takahito Uchida1, Aki Endo1, Masura Mimura1, Ai Otani1, Masaki Shinfuku1, Takefumi Suzuki1, Hiroyuki Uchida1, Fumihiko Ueno1
1 Department of Neuropsychiatry, Keio University School of Medicine, Tokyo, Japan, 2 Department of Neuropsychiatry, Kurihama Medical and Addiction Center, Japan, 3 Department of Psychiatry, Seoul Metropolitan Government-Seoul National University Boramae Medical Center, Seoul, Republic of Korea

Abstract
Objective: Concomitant use of benzodiazepines and alcohol seems prevalent in general clinical settings; however, previous studies have not focused solely on psychiatric patients. The objectives of this study were two-fold: (1) to investigate the prevalence of concomitant use of benzodiazepine hypnotics and alcohol in outpatients with mixed psychiatric diagnoses and (2) to examine the extent of awareness on the side of their psychiatrists about the concomitant use.

Methods: A questionnaire survey was carried out for outpatients with schizophrenia, depression and primary insomnia (ICD-10) who were receiving benzodiazepine hypnotics at Kawasaki Municipal Hospital, Kanagawa, Japan. After providing informed consent, participants were asked to fill in a sleeping diary for seven days in which use of alcohol and hypnotics was also recorded, if any. In addition, their treating psychiatrists were asked as to whether or not they thought the patients were using them concomitantly.

Results: Forty-four patients (mean±SD age = 54.9±13.4 years; 19 females) were included: schizophrenia (n=16), depression (n=15) and primary insomnia (n=13). The prevalence rates of concomitant use of benzodiazepine hypnotics and alcohol were 56.3% (9/16) in schizophrenia, 33.3% (5/15) in depression and 66.7% (8/12) in primary insomnia. In contrast, the rates of suspicion regarding the concomitant use by their treating psychiatrists were 55.6% (5/9), 20.0% (1/5) and 33.3% (2/6), respectively. No differences in the severity of sleep-related symptoms or insomnia were observed between concomitant users and others. In participants with depression, concomitant users tended to receive more antidepressants than nonusers (Defined Daily Dose, 1.1 vs 0.7, p=0.052) although symptom severity was not significantly different.

Conclusions: Nearly half of psychiatric patients concomitantly used benzodiazepine hypnotics and alcohol, which raises a serious safety concern. Although these preliminary findings need to be confirmed by further investigations, they emphasize the need of closer attention to those hazardous combinations.

PS165
Association of cerebral amyloidosis, systolic blood pressure, and regional neuronal injury with late-life onset depression
Min Soo Byun, M.D.1, Young Min Choe, M.D.2, Bo Kyung Sohn, M.D.3, Dahyun Yi, Ph.D.1, Ji Young Han, M.A.1, Jinsook Park, Ph.D.4, Ho Jung Choi, M.D.1, Hyewon Baek M.D.1, Jun Ho Lee, M.D.1, Hyun Jung Kim, M.D.1, Yu Kyeong Kim, M.D.1, Eun Jin Yoon, M.S.1, Cheul-Ho Sohn, M.D.4, Jong In Woo, M.D.3, Dong Young Lee, M.D.1
1 Department of Neuropsychiatry, Seoul National University Hospital, Seoul, Republic of Korea. 2 Department of Neuropsychiatry, Ulsan University Hospital, Ulsan, Republic of Korea. 3 Department of Neuropsychiatry, Seoul Metropolitan Government-Seoul National University Boramae Medical Center, Seoul, Republic of Korea. 4 Department of Biomedical Engineering, Hanyang University, Seoul, Republic of Korea. 5 Department of Nuclear Medicine, Seoul Metropolitan Government-Seoul National University Boramae Medical Center, Seoul, Republic of Korea. 6 Department of Radiology, Seoul National University Hospital, Seoul, Republic of Korea. 7 Neuroscience Research Institute, Medical Research Center Seoul National University, Seoul, Republic of Korea. Corresponding author: Department of Neuropsychiatry, Seoul National University Hospital, Republic of Korea.

Abstract
Objective: Previous studies suggested that Alzheimer's disease (AD) process may possibly contribute to late-life onset depression (LLOD). We aimed to investigate whether LLOD is associated with cerebral amyloidosis and regional cortical atrophy, the two key brain changes in AD process, considering vascular risks together.

Methods: Twenty-nine non-demented individuals who first experienced major depressive episode (MDE) after age of 60 years were recruited as LLOD subjects, and 27 non-demented elderly individuals who had no life-time experience of MDE were included as normal controls (NC). All participants received a comprehensive clinical assessment including vascular risks evaluation, magnetic resonance imaging, 11C-labeled Pittsburgh Compound B (PiB) positron emission tomography and plasma beta-amyloid (Aβ) peptides level assessment.

Results: Among LLOD subjects, 48% of them had comorbid mild cognitive impairment (MCI) diagnosis, while none of NC subjects did. In VBM analysis, LLOD, irrespective of comorbid MCI diagnosis, was associated with prominent prefrontal cortical atrophy (FWE corrected p<0.05, k=100). LLOD with comorbid MCI (LLOD/MCI) subgroup showed increased cerebral PiB retention (p=0.036) and plasma Aβ40 (p=0.006) and Aβ42 peptides (p=0.03), as measures of cerebral amyloidosis, compared to NC, while overall LLOD group and LLOD without MCI (LLODw/oMCI) did not. LLOD individuals had higher systolic blood pressure (SBP) than NC subjects (p=0.017), particularly in subjects with LLODw/oMCI (p=0.026). Multiple logistic regression analysis including diagnostic group (LLOD vs. NC) as a dependent variable showed that prefrontal cortical atrophy was significantly associated with LLOD diagnostic state (p=0.002), while cerebral PiB retention and SBP did not after controlling age, gender, and education.

Conclusion: Our findings suggest that AD process probably contributes to LLOD occurrence via prefrontal neuronal injury from MCI stage, while vascular process, high SBP in particular,