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Predictive value of homocysteine for depression after acute coronary syndrome: Finding from the K-DEPACS study

Running title: Homocysteine for depression in ACS

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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.

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Association study of polymorphism in the serotonin transporter gene promoter, methylation profiles, and expression in patients with major depressive disorder

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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 ± 0.19, 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.

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Genetic role of CSNK1E on circadian and childhood characteristics of the patients with major depressive disorder

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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 phosphorlyate 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 CS(Composite scale). Childhood characteristics(≥ 12Y) 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 12.0.0 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

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Serotonin Transporter Polymorphism in Severe Major Depressive Disorder in Indonesia

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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.