Clock genes polymorphisms associations with suicide attempts in bipolar patients.

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Background

Almost one million people die every year due to suicide. Suicide attempts are made 10 to 20 times more often than suicide is committed. The average global mortality rate due to suicide equals 16/100000. Bipolar disorder is considered a heritable neuropsychiatric disorder associated both with high risk of suicide and with disrupted circadian rhythms [1]. Many genes are involved in etiopathogenesis of the disorder, but their role is unclear [2]. The results of current studies suggest many risk factors (genetic, clinical, psychological) to be related with suicide risk and indicate genetic predisposition both to psychiatric illness and suicide. Genetic risk factors for suicidal behavior are still wanted. To date there have been 21 suicide-related genes identified in humans. In mammals the most important genes are as follows: CLOCK (circadian locomotor output cycles kaput; 4q12), ARNTL (aryl hydrocarbon receptor nuclear translocator-like; 11p15), TIMELESS (TIM; 12p12-q13), PER3 (period; 1p36.23), NR1D1 (nuclear receptor subfamily 1, group d, member 1; 17q11.2), CRY1 (cryptochrome 1; 12p23-q42.1). The aim of this study was looking for possible association between selected candidate clock genes and suicide behavior in bipolar disorder sample.

Sample analysed

We analyzed total sample of 441 bipolar patients and 563 controls from Wielkopolska region of Poland. The bipolar (BP) diagnosis was based on DSM-IV criteria (two psychiatrists using SCID-I). We used data on lifetime suicide attempts from SCID and additional interview (method, family history of patients with history of suicide attempts, n=183) were divided into two sub-groups, depending on the exact method of the attempt. The first group n=61 consisted of persons, who engaged in the violent or life-threatening attempts (hanging oneself, jumping from heights, throwing oneself under a vehicle, shooting, bleeding, drowning) [3].

Statistical analyses

Kruskal-Wallis test was used to compute association between single SNPs and given trait of interest. We checked pairwise comparison between groups using Mann-Whitney U test with FDR adjustment for multiple testing.

References


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