FC02-01

BIPOLAR AND UNIPOLAR MAJOR DEPRESSION ARE NOT ASSOCIATED WITH THE P2RX7-GENE (SNP RS2230912) IN AN EUROPEAN CASE-CONTROL SAMPLE

M. Grigoroiu-Serbanescu[1], S. Herms[2], A. Georgi[3], J. Hauser[4], P. Czerski[5], C.C. Diaconu[6], G. Babadjanova[7], R. Abou Jamra[8], M. Rietschel[9], M.M. Noethen[10,11], S. Cichon[10,11]

[1]Psychiatric Genetics Research Unit, Alexandru Obregia Psychiatric Hospital, Bucharest, Romania, [2]Dept. Genomics, Life & Brain Center, Rheinische Friedrich-Wilhelms University, Bonn, [3]Dept. Genetic Epidemiology in Psychiatry, Central Institute of Mental Health, Mannheim, Germany, [4]Dept. Psychiatry, University of Medical Sciences,, [5]Dept. Psychiatry, University of Medical Sciences, Poznan, Poland, [6]Institute of Virology, Bucharest, Romania, [7]Dept. Psychiatry, Russian State Medical University, Moscow, Russia, [8]Institute of Human Genetics, Rheinische Friedrich- Wilhelms University, Bonn, [9]Dept. Genetic Epidemiology in Psychiatry, Central Institute of Mental Health, Mannheim, [10]Institute of Human Genetics, Rheinische Friedrich-Wilhelms University, [11]Dept. Genomics, Life & Brain Center, Rheinische Friedrich- Wilhelms University, Bonn, Germany

Background: In two recent studies the SNP rs2230912 (Gln460Arg) located in exon 13 of P2RX7-gene (chromosome 12q24) provided the strongest evidence of association with bipolar disorder (BP) (Barden et al,2006; McQuillin et al, 2008) and in one study with the unipolar major depression (Mdd-UP) (Lucae et al, 2006).

Objective: In the present study we investigated the involvement of the SNP rs2230912 in BPI in four European samples from Germany, Poland, Romania and Russia and in the combined sample (N=1445) in comparison with a combined sample of 2006 normal controls. Additionally, a Mdd-UP sample (N=640) from Germany was studied.
Method: All patients were diagnosed according to DSM-IV-R. The BPI sample consisted of 802 females (55.5%) and 643 males (44.5%); the mean AO was 26.9 (SD=10.6); the mean age-at-interview was 42.7 (SD=12.5). The control sample had a mean age of 39.74 (SD=11.22) [1113 females (55.5%); 893 males (44.5%)]. Genotyping of all national samples was performed at Bonn University using the Mass ARRAY system on a Sequenom Compact MALDI-TOF-device. The single marker analysis was performed with FAMHAP software.

Results: There was no allelic association between the G-allele of the SNP rs2230912 and either BPI or Mdd-UP both in the national samples and in the combined sample. The genotypic analysis also indicated no significant results. Our samples of patients and controls had genotypic distributions similar to those of the previously published studies and even in these studies there were no significant differences in genotype frequencies between BPI patients and controls.

https://doi.org/10.1016/S0924-9338(09)70451-1 Published online by Cambridge University Press