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NO ASSOCIATION BETWEEN CATECHOLAMINE- O-METHYLTRANSFERASE GENE POLYMORPHISM AND BIPOLAR DISORDER AND IT SUBTYPES

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Aims: The catecholamine hypothesis of affective disorders suggests that depression is associated with a functional decrease of catecholamines. There is consistent evidence that COMT gene would be a candidate gene for studies of bipolar disorder.

Methods: The study was performed on patients with bipolar disorder n=298 (male n=126, female n=172). Control subjects were blood donors n=336 (male n=130, female n=206), who were not psychiatrically assessed. The subgroup of patients with psychotic features not congruent with mood contained n=88 patients, males n=41, females n=47. The subgroup of patients with psychotic features congruent with mood contained n=89 patients, males n=47, females n=42. The subgroup of patients with melancholic depression contained n=197 patients, males n=76, females n= 121. A polymorphism was analysed by PCR-RFLP method.

Results: There were no differences in the frequency of genotypes, alleles between patients and controls in the whole group (p=0,286 for genotypes, p= 0,652 for alleles). Dividing the patients according to the gender, no differences in the frequency of either genotypes or alleles were found (p=0,298 for genotype males, p=0,456 for genotypes females). We did not find the association in the subgroup of patients with psychotic features congruent (p=0,828 for genotypes, p= 0,866 for alleles), or not congruent with mood (p=0,116 for genotypes, p= 0,673 for alleles) and with the subgroup of patients with depression with melancholic features (p= 0,758 for genotypes, p= 0,849 for alleles).

Conclusion: Results of our study suggest that the polymorphism of COMT gene is not associated with the susceptibility to bipolar disorder.

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