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## Lack of association between a polymorphism of the norepinephrine transporter gene and schizophrenia in a Brazilian sample

Dear Editor,

Post-mortem studies found increased levels of norepinephrine in the nucleus accumbens of patients with paranoid schizophrenia (SCZ). In chronic schizophrenic patients, the level of norepinephrine in the cerebrospinal fluid was increased. Medication-free relapsing patients also showed higher levels of norepinephrine and its metabolites in the cerebrospinal fluid.[1] The norepinephrine turnover was increased during acute psychotic episodes.[2] Early relapse of psychotic symptoms in patients with SCZ after neuroleptic (haloperidol) withdrawal was predicted by an increased noradrenergic activity during the treatment.[3]

Since SCZ has a genetic compound on its etiology[4] and the noradrenergic system may be involved in the pathophysiology of the disorder, the norepinephrine transporter (NET) gene is a candidate for genetic studies on this disorder. NET is a 617-amino acid protein and its gene is located on chromosome 16 (16q12), consisting of 14 exons (protein coding regions). We performed a study using a silent mutation, 1287 A/G, located in the exon 9 to verify its association with SCZ. This variant is unlikely to have any functional effect. We compared the allelic and genotypic distributions between 211 DSM-IV schizophrenic patients and 283 healthy controls.

Genomic DNA was extracted from venous blood samples and the exonic silent polymorphism (1287 A/G) was analyzed in the Lab as described by Leszczynska-Rodziewicz et al.[5] The $X^2$ test was applied to verify differences in allelic and genotypic distributions between patients with SCZ and controls. A two-tailed type I error rate of 5% was chosen for the statistical analysis.

The genotypic distributions were in Hardy-Weinberg equilibrium (SCZ: $p=0.41$; controls: $p=0.77$). We did not find differences in the allelic or genotypic distribution (Table 1). Our results, which are in concordance with Stöber et al[6] and Leszczynska-Rodziewicz et al,[5] studies, do not support the association between the 1287 A/G polymorphism in the NET gene with SCZ in our Brazilian sample.

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**Table 1 – Allelic and genotypic distributions**

| | SCZ | Controls | $X^2$ | *p* value |
|---|---|---|---|---|
| **Alleles** | | | 0.22 | 0.63 |
| A | 318 (75.35) | 419 (74.02) | | |
| G | 104 (24.64) | 147 (25.97) | | |
| Total | 422 (100) | 566 (100) | | |
| **Genotypes** | | | 0.40 | 0.81 |
| AA | 122 (57.82) | 156 (55.12) | | |
| AG | 74 (35.07) | 107 (37.81) | | |
| GG | 15 (7.10) | 20 (7.06) | | |
| Total | 211 (100) | 283 (100) | | |

This article has received corrections in agreement with the ERRATUM published in Volume 27 Number 1.