

LETTERS TO THE EDITOR

The human serotonin transporter gene explains why some populations are more optimistic?

Molecular Psychiatry (2009) 14, 828;
doi:10.1038/mp.2009.48

The recent report by Fox *et al.*¹ analyzed the impact of a common serotonin transporter polymorphism (5-HTTLPR) in biased attention toward positive and negative affective pictures. They found that homozygous for the 'L' variant (LL) differed significantly from the other genotype groups (Ls and ss) in terms of both their avoidance of negative material as well as their vigilance for positive material.

Their results raised an interesting question: if the human serotonin transporter gene plays a role in positive or negative affective states (such as optimism and joy as opposed to pessimism), would the LL polymorphism be more frequent among people (or in populations) with more optimistic attitude?

Recently, studies about the subjective perception of happiness across nations show that some groups are highly motivated and enthusiastic, such as Brazilians, despite the fact of living in places with a general low human development index.² Could this be explained by the differential distribution of such polymorphisms across nations?

We were able to address this question, as we have investigated, several years ago, the distribution of these polymorphisms in neuropsychiatric disorders as compared with the normal controls.³ It is interesting to note that the LL genotype was found to be 2.5 times more frequent in the Brazilian population as compared with that reported by Fox *et al.* in UK population. Among 197 normal Brazilian controls, there were 32 ss (16.2%), 87 Ls (44.2%) and 78 LL (39.6%) as compared with the following distribution among 97 normal controls reported by Fox *et al.*: 36 ss (37%), 45 Ls (46.4%) and 16 LL (16.5%). These differences are statistically significant ($\chi^2 = 23.16$, d.f. = 2, $P < 0.0001$).

Association studies between the different polymorphisms in the promoter region of the 5-HTTLPR human serotonin transporter gene and neuropsychiatric disorders, including mood disorders, have shown controversial results.^{3–7} One possible explanation is the difference of the various genotypes distribution in various populations. However, it is very interesting to observe that the LL genotype is relatively frequent in the Brazilian normal population. Although the association of this variant with personality traits should be validated in other population studies, it would provide an interesting biological explanation for being more or less optimistic.

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Role of genetic variants in the *CHRNA5–CHRNA3–CHRN4* cluster in nicotine dependence risk: importance of gene–environment interplay

Molecular Psychiatry (2009) 14, 828–830;
doi:10.1038/mp.2009.25

The *CHRNA5–CHRNA3–CHRN4* locus on chromosome 15q25.1 contains three genes encoding nicotinic acetylcholine receptor (nAChR) subunits, which lie very close to, and in strong linkage disequilibrium with, each other. A plethora of recent evidence suggests an association of this gene cluster with several nicotine dependence (ND) phenotypes. Saccone *et al.*¹ tested 348 candidate genes in a mixed gender sample of 1050 cases of European ancestry with scores ≥ 4 on the Fagerstrom test for nicotine