



ASSESSMENT OF *DRD2* DOPAMINE RECEPTOR GENE RS6277 IN PEDIATRIC OBESITY: A CASE-CONTROL STUDY



Renata M. Pinto, Nygell S Alves, Jakeline S Fortes, Rúbia V Monteiro, Lysa B Minasi, Aparecido D. da Cruz
Department of Biology, Replicon Research Center, Catholic University of Goiás, Goiânia, GO, Brazil; Department of Pediatrics, Federal University of Goiás, Goiânia, GO, Brazil

INTRODUCTION

Genetic variants associated with BMI in children can exert their effects by affecting eating behavior, as is the case with single nucleotide polymorphisms (SNP) of the *DRD2* gene. Patients who have the risk variation are more likely to have binge eating and hedonic disorders.

The presence of the risk allele (G) of the rs6277 polymorphism of the *DRD2* gene leads to a reduction in the affinity of *DRD2* receptors for dopamine, and in adults, it is associated with: related psychiatric disorders, higher sugar consumption and increased BMI from eutrophic to overweight/ obesity.

Our objective was to evaluate the allele and genotypic frequencies of the SNP rs6277 of the *DRD2* gene in a pediatric population with obesity and their eutrophic controls.

METHODS

The case-control study enrolled 218 pediatric patients aged 5 to 16 years, 118 obese, and 100 eutrophics. In addition to the clinical evaluation, all participants underwent biochemical tests to measure the levels of fasting lipids, blood glucose, and insulin to calculate HOMA IR. DNA samples were extracted and genotyped by the real-time polymerase chain reaction method (real-time PCR).

RESULTS

The risk allele (G) and the homozygous GG genotype were present in 57.6% and 36.4% of obese individuals and 54% and 29% of eutrophic individuals. Although the chi-square test was not significant for the distribution of the *DRD2* polymorphism rs6277 genotypes among eutrophic and obese subjects, the Z-score for proportions of two populations was significant (0.00001; CI = 0, 05), indicating a tendency of the homozygous genotype for the risk allele (GG) to focus on the sample of the obese population.

Children who had 2 or more cardiovascular risk factors were considered metabolically unhealthy. In this way, the groups were subdivided into: Obese Metabolically Unhealthy (OMU), Obese Metabolically Healthy (OMH), Eutrophic Metabolically Unhealthy (EMU) and Eutrophic Metabolically Healthy (EMH)

The comparison of the allelic and genotypic distribution carried out between the Metabolically Sick (OMD) and Obese Metabolically Healthy (WHO) subgroups were significantly different for the distribution of the genotypes, with a predominance of the GG genotype among the OMD. Table 1.

The Odds Ratio was estimated for two or more cardiovascular factors between the groups, which resulted in an OR of 2.65 (CI = 1.016 to 3.682; p = 0.031) when the genotypes contained the risk allele.

RESULTS

Table 1. Genotypic and Allelic Distribution of the *DRD2* gene in the Groups: OML (Obese Metabolically Unhealthy), OMH (Obese Metabolically Healthy), EMU (Eutrophic Metabolically Unhealthy) and EMH (Eutrophic Metabolically Healthy). Risk Allele: G

<i>DRD2</i> gene rs6277	OMU N (%)	OMH N (%)	EMU N (%)	EMH N (%)	X ²	p
Genotypes						
GG	28 (35.9)	15 (37.5)	7 (30.4)	22 (28.6)	7.53	*0.053
AG	38 (48.7)	12 (30)	12 (52.2)	38 (49.4)		
AA	12 (15.4)	13 (32.5)	4 (17.4)	17 (22)		
GG + AG	66 (84.6)	27 (67.5)	19 (82.6)	60 (88)	4.88	*0.031
AA	12 (15.4)	13 (32.5)	4 (17.4)	17 (22)		
Total	78 (100)	40 (100)	23 (100)	77 (100)		
Alleles						
G	94 (60.3)	42 (52.5)	26 (56.5)	82 (53.2)	2.02	0.567
A	62 (39.7)	38 (47.5)	20 (43.5)	72 (46.8)		
Total	156 (100)	80 (100)	46 (100)	154 (100)		

Legend: * - p comparison between OMU and OMH

CONCLUSION

The allelic and genotypic distribution proved to be significantly different from the distribution of the genotypes, with a predominance of GG among the metabolically ill obese.

The A allele can be correlated with a protective effect in eutrophic individuals, despite its variation.

REFERENCES

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