MIGRAINE WITH AURA IN THE POPULATION OF BUENOS AIRES, ARGENTINA: ASSOCIATION ANALYSIS OF 6 SNPS

GONZÁLEZ R. [1], J.A. GIGLIO[2,3], S. MIRANDA[4], M. NOWIK[1], C.I. CATANESI[1,5]

[1] Instituto Multidisciplinario de Biología Celular IMBICE (CONICET-UNLP-CIC), La Plata, Buenos Aires, Argentina; [2] Hospital Interzonal General de Agudos "Prof. Dr. Rodolfo Rossi" ; [3] Instituto de Neurología y Neurocirugía "Fundación Dr. César R. Burry" La Plata, Buenos Aires, Argentina; [4] Instituto Central de Medicina, La Plata, Buenos Aires, Argentina; [5] Facultad de Cs. Naturales y Museo (UNLP), La Plata, Buenos Aires, Argentina.
gonzalezrebe85@gmail.com

INTRODUCTION

Migraine with aura is a complex disabling neurological disorder that manifests with episodic and recurrent attacks. It has a high prevalence and socioeconomic impact. Its causes are both environmental and genetic, and the latter are relevant for prevention and treatment. In Argentinian population, the variation of genetic markers related to pain perception have showed certain differences with other populations of the world. However, genetic variants related to migraine have not been analyzed in the population of Argentina.

OBJECTIVES

The objective of this study is to characterize migraine with aura in the population of Buenos Aires, through the analysis of genetic variants previously reported for other populations in association to this disorder.

MATERIALS AND METHODS

DNA from 203 donors (105 migraineurs and 98 controls) was obtained from saliva samples and genotyped for the SNPs rs12134493 (*TSPAN2*), rs10166942 (*TRPM8*), rs10456100 (*KCNK5*), rs4910165 (*MRVI1*), rs11031122 (*MPPED2*) and rs6081613 (*SLC24A3*) through allele-specific PCR amplification. Resolution of bands was performed through 2% agarose gel electrophoresis. The data were analyzed using the programs Arlequin, Genalex, Infostat, and SNPStats for calculating allele and genotype frequencies, Hardy-Weinberg equilibrium (HWE), genetic differentiation (FST and AMOVA), and association analysis. This study was previously approved by the Ethics Committee of IMBICE, and all donors gave written consent for participation in it.

RESULTS

The cases fitted the HWE ($p>0.05$) for all the SNPs and in the control group they fitted with the exception of rs12134493 and rs4910165. Concerning differentiation between groups, non-significant differences were found between cases and controls (Figures 1 and 2). A model of logistic regression was performed using all genotypes of the analyzed markers. For rs10456100, association was significant ($X2=4.15$; $p=0.0416$) in TT genotype taking as reference CC, giving an odds ratio (OR) of 0.11 (confidence interval 0.01-0.92) while the other SNPs did not show significant association (Table 1).

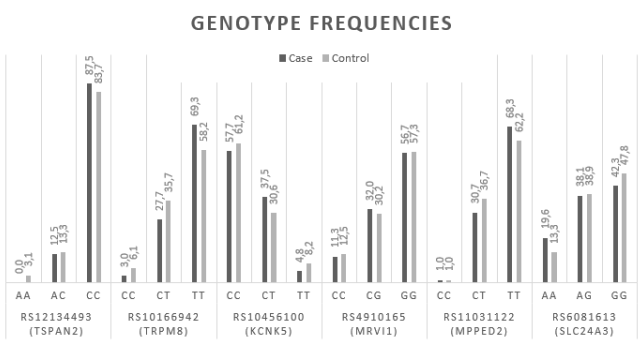

Figure 1. Genotype frequencies (percentages) of cases and controls.

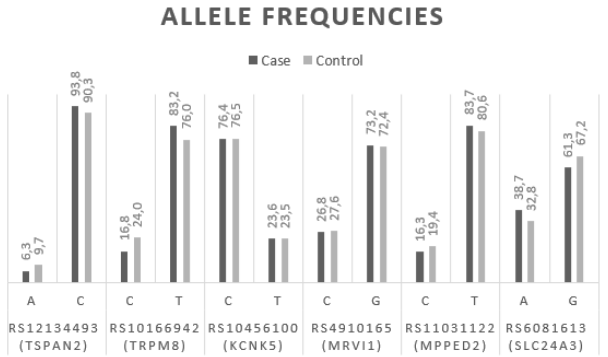

Figure 2. Allele frequencies (percentages) of cases and controls.

Genotipo	X^2	p	OR	CI
CT	0,51	0,4772	1,29	0,64-2,57
TT	4,15	0,0416	0,11	0,01-0,92

Table 1. X^2 and odds ratio (OR) estimations for rs10456100 (taking CC genotype as reference).

CONCLUSIONS

We found that the T allele of rs10456100, which has been reported as a risk allele in other populations of the world, is probably acting as protective when it is present in homozygous genotype in our population. These preliminary results need confirmation in a larger sample size, nevertheless they suggest a particular genetic basis of migraine with aura in the studied population. Moreover, as additional genetic markers will be included in this study, the information might be of help for defining a better treatment of local migraine patients.

FUNDING: Proyecto I+D Bienal 2019 - N895, Universidad Nacional de La Plata; PICT-2020-SERIEA-01075 Agencia Nacional de Promoción Científica y Técnica; PIP 2020-2111, Consejo Nacional de Investigaciones Científicas y Técnicas.