



Evaluation of the genetic variant -889 C>T of IL-1 α in migraine - partial analysis

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Abstract

Introduction

The pathophysiology of migraine integrates inflammatory and genetic aspects, with interleukin-1 α being a component of this picture. This pro-inflammatory cytokine, responsible for inducing pyrogenic, hematological, and metabolic phenomena, is produced by macrophages and monocytes. Genetic variants, which can be found in the regulatory region of the gene for this substance, have clinical implications in different systems.

Objective

To evaluate the frequency of the -889C>T genetic variant of IL-1 α and its association with clinical variables related to migraine.

Methods

Prospective case-control study composed of migraine patients and healthy controls aged between 18 and 60 years of age. Project approved by the Research Ethics Committee of PUCPR (No. 3,029,972). Demographic, clinical data on migraine classification and characteristics were collected using a structured form and validated questionnaires on anxiety (STAIY2), depression (BDI) and migraine-related disability (MIDAS). Genetic evaluation was performed with blood or saliva samples that were subjected to polymerase chain reaction (PCR), followed by electrophoresis in 1.5% agarose gel. Categorical data were analyzed by chi-square test or Fisher's exact test and continuous data by t-test or Mann-Whitney test.

Results

A total of 156 participants, 73 migraineurs and 83 controls, were evaluated. The -889C>T variant of IL-1 α was not associated with increased susceptibility to migraine when evaluated in allelic, codominant, dominant, or recessive models. The C allele, the lowest producer of the cytokine, was associated with a higher frequency of osmophobia in patients with migraine (65.5% vs. 48.2%; $p=0.038$).

Conclusion

No association was identified between the -889C>T variant of IL-1 α and susceptibility to migraine. Its effect on osmophobia should be further investigated. However, the present work is a partial analysis whose main limitation is the small sample size.

Keywords:
Migraine
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Introduction

The main characteristic of migraine is headache, and it belongs to the group of primary headaches because it causes physiological changes in the nervous system, which determine the pain.¹ In this context, it can be understood as an inflammatory disease resulting from the interaction of genetic, environmental, hormonal, and metabolic factors.²

This disease can present up to four phases: prodrome, aura, pain, and postdrome.^{1,2} Thus, the crises are a sum of these phenomena and can last five to six days.¹ It is rated as the third most disabling disease in the world, affecting 10-20% of the world's population, as well as 15.8% of Brazilians.^{3,4} It is noteworthy that it affects females three times more often than males, with a first peak of incidence at 18-29 years of age and a second one at 40-49, with a reduction in prevalence concomitant with menopause.^{5,6}

The pathophysiology of migraine is not yet fully understood, but it is known that cytokines play a key role in pain. Substances such as interleukin 1 (IL-1), interleukin 10 (IL-10), interleukin 4 (IL-4), interleukin 13 (IL-13), interleukin 2 (IL-2), and tumor necrosis factor- α (TNF- α) may be relevant to the condition.⁷

Therefore, as the pathophysiology of the disease involves a neurogenic inflammation, pro-inflammatory genes, such as interleukin 1 alpha, may interfere in the manifestations of migraine.⁸ This interleukin is produced by macrophages, monocytes, fibroblasts, and endothelial cells in physiological situations and in situations of cellular injury due to infection and inflammation.^{9,10} Specifically in the brain they are produced pathologically by astrocytes, oligodendrocytes, microglia and neurons.¹⁰ IL-1 induces endogenous pyrogenic phenomena and influences the hematological, metabolic, and central nervous systems.¹¹

One of the genetic variants found in the IL-1 ALPHA gene is the - 889 C > T, which consists of the exchange of a cytosine for a thymine in the regulatory region of the DNA. In the case of migraine, only one study has addressed this issue and concluded that patients homozygous for the T allele (T/T) have a greater chance of early onset of headache than patients with CC and CT genotype migraine.¹⁰ Furthermore, this same study found a higher prevalence of aura in patients homozygous for the T allele (TT) than other genotypes.¹⁰

Hence, the present study aims to analyze the association of clinical aspects of migraine and the IL-1alpha -889 C>T gene polymorphism (rs1800587) and to verify a possible

association of genetic variants and disease activity.

Methods

Ethical Considerations

The present study was carried out after approval by the Research Ethics Committee (CEP) of PUCPR, according to report 3.029.972, by means of Informed Consent Form (ICF) signed by the participants, after a detailed explanation of its development, being in accordance with resolution 466/2012 of the National Health Council.

Study Population

The universe of this study was made up of a convenience sample with 156 participants - 73 patients and 83 controls, and the participants were seen at the PUCPR Headache Academic Outpatient Clinic - Londrina Campus, Paraná, Brazil.

Inclusion Criteria

Patients and controls between the ages of 18 and 60 years of age, of both.

Exclusion Criteria

Individuals with severe and uncontrolled neurological, psychiatric, and inflammatory diseases were excluded.

Study design

This is a retrospective longitudinal case-control study investigating the possible association between clinical aspects of migraine, sociodemographic variables, and genetic polymorphism of IL1- α and TNF- α in individuals seen at the Academic Outpatient Clinic of PUCPR Londrina Campus, Brazil.

Instruments used

The diagnosis of migraine was made according to the 3rd International Classification of Headache, published in 2018. The interview was structured and based on the form developed electronically by the Headache Research Group of the PUCPR Londrina Campus, through the Google Forms tool®. Composed by the following topics: demographic data, diagnostic criteria, and temporality of



migraine; associated clinical characteristics; crisis triggers, medications used, lifestyle habits, performance of aerobic physical activity, sleep time, and comorbidities. The following scales were applied MIDAS (*Migraine Disability Assessment*)¹² HIT-6 (*Headache Impact Test-6*)¹³ and form Y-STAI (*State-Trait Anxiety Inventory*).¹⁴

Genotyping

To obtain DNA, extraction was performed from peripheral blood leukocytes by venipuncture in tubes containing EDTA (0.6%) and DNA extraction- kit Pure Link Genomic DNA (Invitrogen, Carlsbad, EUA) was used, following the guidelines provided by the manufacturer. The extracted DNAs were stored in a freezer at -80° C. The quality and quantity of DNA was measured by means of absorbance analysis in a spectrophotometer (NanoDrop 2000 – Thermo Scientific) at 260 nm and 280 nm. Next, DNA was diluted in ultrapure water Milli-Q® to a final concentration of 100 ng/uL. Genotyping of genetic variants of the cytokine IL-1α -889 C>T (rs1800587) was performed by PCR with allele-specific sequence primers (PCR-SSP) described by Bunce.¹⁵

Results

Table 1 presents the main characteristics of the population analyzed in this study. The mean age of patients with migraine was 31 years old. There was a prevalence of migraine in females of 82.2% of patients (p=0.036), as well as a higher prevalence in Caucasians than other ethnicities. It was found that majority of the patients did not have associated comorbidities such as diabetes and hypertension.

Table 1. General characteristics of participants with migraine and controls

| | | Migraine | | Control | | p |
|------------------------------------|---------------|----------|------|---------|------|-------|
| | | n | % | n | % | |
| Age | | 31 | | 26 | | |
| Sex | Male | 13 | 17.8 | 27 | 32.5 | 0.036 |
| | Female | 60 | 82.2 | 56 | 67.5 | |
| Ethnicity | Caucasian | 61 | 83.6 | 58 | 81.7 | 0.767 |
| | Non caucasian | 12 | 16.4 | 13 | 18.3 | |
| Hypertension | Yes | 5 | 6.8 | 7 | 8.4 | 0.711 |
| | No | 68 | 93.2 | 76 | 91.6 | |
| Diabetes | Yes | 2 | 2.7 | 5 | 6 | 0.323 |
| | No | 71 | 97.3 | 78 | 94.0 | |
| Body mass index (average in kg/m²) | | 24.6 | | 24.0 | | |

Another relevant finding is that the -889C>T variant of IL-1α was not associated with increased susceptibility

to migraine when evaluated in allelic, codominant, dominant or recessive models (Table 2). However, the C allele, a lower cytokine producer, was associated with higher frequency of osmophobia in patients with migraine (65.5% vs. 48.2%; p=0.038). This same allele is associated with higher presence of aura in patients. However, it is observed that there was no association with the classification (episodic or chronic) and other symptoms associated with migraine (Table 3).

Table 2. Assessment of genetic susceptibility to migraine of the -889 C>T variant

| | | Control | | Migraine | | p |
|------------------|---------|---------|------|----------|------|-------|
| | | n | % | n | % | |
| Allelic Model | C | 97 | 58.4 | 90 | 61.6 | 0.564 |
| | T | 69 | 41.6 | 56 | 38.4 | |
| Codominant Model | CC | 22 | 26.5 | 24 | 32.9 | 0.674 |
| | CT | 53 | 63.9 | 42 | 57.5 | |
| | TT | 8 | 9.6 | 7 | 9.6 | |
| Dominant Model | CC | 22 | 26.5 | 24 | 32.9 | 0.384 |
| | CC + CT | 61 | 73.5 | 49 | 67.1 | |
| Recessive Model | CC + CT | 75 | 90.4 | 66 | 90.4 | 0.992 |
| | TT | 8 | 9.6 | 7 | 9.6 | |

Table 3. Evaluation of comparative clinical characteristics in T and C alleles

| | | C | | T | |
|--------------------|-------------------------------|-------|-------|-------|-------|
| | | Count | % | Count | % |
| Type of migraine | Episodic | 46 | 52.3 | 34 | 60.7 |
| | Chronic | 42 | 47.7 | 22 | 39.3 |
| Migraine with aura | Yes | 38 | 42.20 | 20 | 35.70 |
| | No | 52 | 57.80 | 36 | 64.30 |
| Phonophobia | Yes | 78 | 86.70 | 46 | 82.10 |
| | No | 12 | 13.30 | 10 | 17.90 |
| Photophobia | Yes | 82 | 91.10 | 50 | 89.30 |
| | No | 8 | 8.90 | 6 | 10.70 |
| Osmophobia | Yes | 59 | 65.60 | 27 | 48.20 |
| | No | 31 | 34.40 | 29 | 51.80 |
| Allodynia | Yes | 43 | 47.80 | 19 | 33.90 |
| | No | 47 | 52.20 | 37 | 66.10 |
| Prodrome | Yes | 69 | 76.70 | 41 | 73.20 |
| | No | 21 | 23.30 | 15 | 26.80 |
| Postdrome | Yes | 75 | 87.20 | 43 | 76.80 |
| | No | 11 | 12.80 | 13 | 23.20 |
| MIDAS_dico | Mild or no disability | 28 | 33.30 | 18 | 33.30 |
| | Moderate to severe disability | 56 | 66.70 | 36 | 66.70 |
| HIT6_dico | Moderate to no impact | 13 | 15.30 | 13 | 23.60 |
| | Substantial to severe impact | 72 | 84.70 | 42 | 76.40 |



Discussion

In agreement with the epidemiological data presented in the literature, the results found in the present study indicate that patients in the migraine group are mostly female and Caucasian.⁶ In addition, individuals aged 15-49 years are the most affected, as evidenced by the average age of the patients analyzed, i.e. 31 years.¹⁰

Studies show that women with migraine are 15% more likely than women without migraine to develop hypertension. However, the correlation of comorbidities with migraine in the present analysis was divergent from the evidence in the literature.¹⁶

The scarcity of studies in the literature that definitively correlate the genotype of such polymorphisms and migraine incidence is equivalent to this study, since there was no relevant change in susceptibility in any genetic model. However, the association of the C allele with osmophobia and aura reinforces the need for further research.

Finally, it is believed that, since this is a partial analysis, with a reduced sample size, there are losses. Thus, it is necessary to continue the analysis.

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