RESEARCH ARTICLE

REVISED Polymorphisms of the genes *ABCG2*, *SLC22A12* and *XDH* and their relation with hyperuricemia and hypercholesterolemia in Mexican young adults [version 2; peer review: 2 approved]

Juan Manuel Vargas-Morales[1], Martha Guevara-Cruz[2], Celia Aradillas-García[3], Lilia G. Noriega[2], Armando Tovar[2], Jorge Alejandro Alegría-Torres[4]

[1]Laboratorio de Análisis Clínicos, Facultad de Química, Universidad Autónoma de San Luis Potosí, San Luis Potosí, San Luis Potosí, 78210, Mexico
[2]Departamento de Fisiología de la Nutrición, Instituto Nacional de Ciencias Médicas y Nutrición Salvador Zubirán, Ciudad de México, México, 14080, Mexico
[3]Centro de Investigación Aplicada en Ambiente y Salud, CIACYT-Facultad de Medicina, Universidad Autónoma de San Luis Potosí, San Luis Potosí, San Luis Potosí, 78210, Mexico
[4]Departamento de Farmacia, Universidad de Guanajuato, Guanajuato, Guanajuato, 36050, Mexico

v2 **First published:** 17 Mar 2021, **10**:217
https://doi.org/10.12688/f1000research.46399.1
Latest published: 24 Sep 2021, **10**:217
https://doi.org/10.12688/f1000research.46399.2

Abstract

Background: Hyperuricemia is a pathological condition associated with risk factors of cardiovascular disease. In this study, three genetic polymorphisms were genotyped as predisposing factors of hyperuricemia.
Methods: A total of 860 Mexicans (129 cases and 731 controls) between 18 and 25 years of age were genotyped for the *ABCG2* (Q191K), *SLC22A12* (517G>A), and *XDH* (518T>C) polymorphisms, as predisposing factors of hyperuricemia. Biochemical parameters were measured by spectrophotometry, while genetic polymorphisms were analyzed by real-time PCR. An analysis of the risk of hyperuricemia in relation to the variables studied was carried out using a logistic regression.
Results: Male sex, being overweight or obese, having hypercholesterolemia or having hypertriglyceridemia were factors associated with hyperuricemia ($p \leq 0.05$). The *ABCG2* polymorphism was associated with hyperuricemia (OR = 2.43, 95% CI: 1.41-4.17, p = 0.001) and hypercholesterolemia (OR = 4.89, 95% CI: 1.54-15.48, p = 0.003), employing a dominant model, but only in male participants.
Conclusions: The *ABCG2* (Q191K) polymorphism increases the risk of hyperuricemia and hypercholesterolemia in young Mexican males.

Keywords

ABCG2, SLC22A12, XDH, hyperuricemia, hypercholesterolemia

Open Peer Review

Reviewer Status ✓ ✓

	Invited Reviewers	
	1	**2**
version 2 (revision) 24 Sep 2021		✓ report
version 1 17 Mar 2021	✓ report	? report

1. **Ilham Akbar Rahman**, Hasanuddin University, Makassar, Indonesia

2. **Jing He**, Guangzhou Medical University, Guangzhou, China

Any reports and responses or comments on the article can be found at the end of the article.

Corresponding author: Jorge Alejandro Alegría-Torres (ja.alegriatorres@ugto.mx)

Author roles: Vargas-Morales JM: Conceptualization, Investigation, Methodology; **Guevara-Cruz M**: Data Curation, Formal Analysis, Investigation, Methodology; **Aradillas-García C**: Data Curation, Formal Analysis, Validation, Visualization; **G. Noriega L**: Investigation, Methodology; **Tovar A**: Investigation, Methodology, Supervision; **Alegría-Torres JA**: Conceptualization, Formal Analysis, Writing – Original Draft Preparation, Writing – Review & Editing

Competing interests: No competing interests were disclosed.

Grant information: This study was funded by The Facultad de Ciencias Químicas, project assigned to Juan Manuel Vargas Morales, and CIACYT-Medicina, project assigned to Celia Aradillas García, Universidad Autónoma de San Luis Potosí, México.
The funders had no role in study design, data collection and analysis, decision to publish, or preparation of the manuscript.

How to cite this article: Vargas-Morales JM, Guevara-Cruz M, Aradillas-García C *et al.* **Polymorphisms of the genes *ABCG2*, *SLC22A12* and *XDH* and their relation with hyperuricemia and hypercholesterolemia in Mexican young adults [version 2; peer review: 2 approved]** F1000Research 2021, **10**:217 https://doi.org/10.12688/f1000research.46399.2

First published: 17 Mar 2021, **10**:217 https://doi.org/10.12688/f1000research.46399.1

REVISED **Amendments from Version 1**

This new version shows minor changes and clarifications noted by the reviewer 2. The number of cases and controls as well as the description of sequence variants were included in the abstract. Some issues related to the statistical power and the genotype-based mRNA expression analysis were discussed in greater depth.

Any further responses from the reviewers can be found at the end of the article

Introduction

Hyperuricemia is an abnormal metabolic trait defined as serum uric acid levels above 6 and 7 mg/dL for women and men, respectively (Bardin & Richette, 2014), and is associated with other cardiometabolic risk factors such as obesity, diabetes, hypertension, and dyslipidemia (Martínez-Quintana *et al.*, 2016; Zuo *et al.*, 2016). Similarly, hyperuricemia can be a predictor of impaired kidney functions as well as kidney disease progression (Galán *et al.*, 2018; Hsu *et al.*, 2009, and Pérez-Navarro *et al.*, 2020). Serum uric acid levels depend on many factors including diet, sex, lifestyle, and alcohol consumption, as well as genetic heredity. In fact, some genes involved in the metabolism of purines or urates have versions that appear to predispose to a hyperuricemic condition. Some of these are the *ABCG2* gene that encodes a membrane transporter, which exports urates to the kidney and intestine (Woodward *et al.*, 2009); and the *SLC2A9* gene that encodes a kidney protein called GLUcose Transporter 9 (GLUT9), an important flow regulator of urates in the proximal tubules (Caulfield *et al.*, 2008). In the same way, the *XDH* gene gives rise to an enzyme denominated xanthine dehydrogenase, which breaks down purines from nucleic acids, specifically the hypoxanthine–xanthine–urate conversion pathway (Harrison, 2002).

Recent studies have shown that genetic polymorphisms in *ABCG2* and *SLC2A9* genes are prevalent in the Mexican population and may contribute to an abnormal condition of hyperuricemia, even at young ages (Macías-Kauffer *et al.*, 2019; Rivera-Paredez *et al.*, 2019). Interestingly, there appears to be no reports to date in the literature on *XDH* gene polymorphisms in the Mexican population. Therefore, the aim of this study was to genotype the polymorphisms of the genes *ABCG2* (Q191K), *SLC22A12* (517G>A), and *XDH* (518T>C) in 860 young Mexican volunteers aged between 18 and 25 years of age as predisposing factors of hyperuricemia associated with risk factors of cardiovascular disease.

Methods

Study design and ethical statement

A cross-sectional design and a convenience sample of 860 subjects was coducted in the City of San Luis Potosí, México. All participants were college applicants during the spring period of 2017. Data collection was carried out according to the recruitment protocols of the University of San Luis Potosí, since applicants receive a clinical evaluation as part of the admission process. This project was approved by two Bioethics Committees: the former at the National Institute of Medical Sciences and Nutrition Salvador Zubirán (Approval # FNU-669-13-15-2), and the latter at the Faculty of Chemistry of the University of San Luis Potosí (Approval # CEID2017105-S). All participants provided written informed consent.

Participants

A total of 860 applicants to the state University of San Luis Potosí, Mexico in 2017, were included in this study (448 men and 412 women). All participants were approached to take part in the study by phone and email by means of an open invitation explaining the goals of the study. Even though the invitation was open, only some accepted to participate. Participants were not paid to take part. All individuals who provided written informed consent and met the inclusion criteria were included. The inclusion criteria which were as follows: aged between 18–25 years; born in the Mexican state of San Luis Potosí; and provided written informed consent.

Clinical assessment and sample collection

Since all participants at the University of San Luis Potosí, Mexico receive a clinical evaluation as part of the admission process, we accessed the university medical records. The weight in kilograms and height in meters of each participant was obtained for anthropometry using a digital scale (UM-081 model; Tanita, Tokyo, Japan) and a stadiometer (Seca 213, 2009; Seca, Hanover, MD, USA), respectively. From this data, the Body Mass Index (BMI) was calculated (kg/m^2). Systolic and diastolic blood pressure were taken as the mean of two readings at a 5-min interval after 5 min in a seated position, employing the Omrom model HBP-1300 portable meter (Omron Healthcare, Inc., IL, USA). Also, 6 mL of blood was obtained by venipuncture after a 12-h fast; serum was obtained by centrifuging at 1,000 x g for 10 min using a laboratory centrifuge Z306 Benchmark Scientific (NY, USA), and processed inmmediately. An addition, 3 mL of blood was collected and stored in ethylenediaminetetraacetic acid (EDTA) tubes (Vacutainer®) for subsequent DNA purification. All samples were maintained at -20°C until their analysis.

Measurement of biochemical profiles

Serum was used to measure uric acid, glucose, total cholesterol, low-density lipoprotein cholesterol (LDL-C), high-density lipoprotein cholesterol (HDL-C), and triglycerides by spectrophotometry utilizing chemistry reagents (Paramedical S.r.l., Italy), specially developed to work with Mindray BS 300 Auto Chemistry Analyzer (Mindray, Shenzhen, China), with the following catalog numbers: uric acid (PDIBS200040), glucose (PDIBS200020), total cholesterol (PDIBS200030), LDL-C (PDIBS200170) HDL-C (PDIBS200160), and triglycerides (PDIBS200060).

Genotyping of polymorphisms

DNA was isolated from whole blood using the QIAamp DNA Blood Mini Kit (QIAGEN, Hilden, Germany). The quality of DNA samples was verified by spectrophotometry using NanoDrop™ 2000. Polymorphisms of the genes *ABCG2* (rs2231142), *SLC22A12* (rs476037), and *XDH* (rs1042039) were measured by allelic discrimination real-time polymerase chain reaction (PCR) with the Taqman probe (Applied Biosystems®).

All PCR reactions were carried out using an ABI Prism 7900 HT detection system in 96-well plates (Applied Biosystems®). Reactions were adjusted to a final volume of 10 µL including Master mix probes and 50 ng/µL of genomic DNA, with the following amplification protocol: denaturation 94° for 9 min; followed by 50 cycles of denaturation at 95°C for 30 s, and annealing and extension at 68°C for 11 min. Negative controls and duplicated samples were included to check the accuracy of the genotyping.

Statistical analysis

After analyzing the data distribution, comparison of medians between groups (normal uricemia vs. hyperuricemia) was carried out with the Mann–Whitney *U* test for continuous variables. Allelic and genotypic frequencies as well as the Hardy–Weinberg equilibrium were calculated for each polymorphism utilizing the chi-square test. Likewise, a logistic regression analysis was used to calculate the risk of hyperuricemia in relation to the variables studied and the influence of the different genotypes on uric acid levels in blood through a dominant model. The level of significance was set at p <0.05. Data were analyzed using SPSS version 19.0 statistical software.

Results

In total, 860 participants were included in this study: 52% men and 48% women (Alegría-Torres, 2021). Participant characteristics, as well as the allelic and genotypic frequencies of the *ABCG2* (Q191K), *SLC22A12* (517G>A) and *XDH* (518T>C) gene polymorphisms, are presented in Table 1. Medians and genotypic distribution between hyperuricemic and normouricemic participants were analyzed using the Mann-Whitney *U* test, finding differences for sex, BMI, systolic and diastolic pressure, triglycerides, total cholesterol, and LDL-C (p = <0.001 for all), as well as a marginal distribution difference for the *ABCG2* (Q191K) polymorphism corresponding to G/T alleles (p = 0.056), therefore other genetic models were tested later. All the genotypes analyzed were in Hardy–Weinberg equilibrium: *ABCG2* (Q191K) X^2 = 1.82X10^{-6}, p = 0.9; *SLC22A12* (517G>A) X^2 = 0.03, p = 0.84; and *XDH* (518T>C) X^2 = 0.08, p = 0.76. Both allelic and genotypic distributions of the three polymorphisms studied did not differ significantly between men and women (Table 2).

Considering the statistically significant differences among the variables, a multivariate logistic regression analysis was performed, including sex, BMI, hypercholesterolemia, and

Table 1. Characteristics of the study participants classified by serum uric acid levels.

Variable	All participants median (p25-p75) *n* (%)	With hyperuricemia median (p25-p75) *n*(%)	With normal uricemia median (p25-p75) *n*(%)	*P* value
Total Men Women	860 (100) 448 (52) 412 (48)	129 (15) 88 (19.6) 41 (10)	731 (85) 360 (80.4) 371 (90)	<0.001[a]
Age (years)	19.0 (18.0-20.0)	19.0 (18.0-20.0)	19.0 (18.0-20.0)	0.138[b]
BMI (Kg/m^2)	23.03 (20.56-26.58)	25.7 (23.0-29.7)	22.6 (20.2-26.1)	<0.001[b]
Systolic pressure (mmHg)	110 (100-110)	110 (100-120)	110 (100-110)	<0.001[b]
Diastolic pressure (mmHg)	70 (60-70)	70(70-80)	70 (60-70)	<0.001[b]
Glucose (mg/dL)	79.0 (74.5-84.0)	81.0 (75.0-86.0)	79.0 (74.0-84.0)	0.087[b]
Uric acid (mg/dL)	5.3 (4.2-6.2)	7.6 (6.9-8.2)	4.9 (4.1-5.7)	<0.001[b]
Triglycerides (mg/dL)	96.0 (71.0-133.0)	126.0 (96.0-178.0)	90.0 (68.0-126.5)	<0.001[b]
Total Cholesterol (mg/dL)	150.0 (131.0-170.0)	164.0 (144.0-188.5)	146.0 (128.0-166.0)	<0.001[b]
LDL Cholesterol (mg/dL)	58.5 (40.8-70.05)	69.1 (49.7-94.3)	57.1 (40.2-73.0)	<0.001[b]
HDL Cholesterol (mg/dL)	67.9 (58.8-76.9)	64.8 (56.1-74.9)	68.3 (59.3-76.9)	0.083[b]
ABCG2 (Q191K)				
Alleles G	1298 (75)	183 (71)	1115 (76)	
T	422 (25)	75 (29)	347 (24)	0.056[a]
Genotypes GG	490 (57)	64 (49.6)	426 (58)	
GT	318 (37)	55 (42.5)	263 (36)	
TT	52 (6)	10 (7.9)	42 (6)	0.17[a]

Variable		All participants median (p25-p75) *n* (%)	With hyperuricemia median (p25-p75) *n*(%)	With normal uricemia median (p25-p75) *n*(%)	*P* value
SLC22A12 (517G>A)					
Alleles	G	558 (32)	84 (33)	474 (32)	
	A	1162 (68)	174 (67)	988 (68)	0.9[a]
Genotypes	GG	94 (11)	15 (11.8)	79 (11)	
	GA	370 (43)	54 (41.7)	316 (43)	
	AA	396 (46)	60 (46.5)	336 (46)	0.94[a]
XDH (518T>C)					
Alleles	T	1083 (63)	167 (65)	916 (63)	
	C	637 (37)	91 (35)	546 (37)	0.52[a]
Genotypes	TT	335 (39)	53 (41)	282 (39)	
	TC	413 (48)	61 (47.2)	352 (48)	0.8[a]
	CC	112 (13)	15 (11.8)	97 (13)	

Abbreviations: BMI, body mass index; *ABCG2,* gene that encodes an ATP-binding cassette transporter subfamily G member 2; *SLC22A12,* gene that encodes an urate transporter 1 gene; *XDH,* gene that encodes a xanthine dehydrogenase.

[a]Chi-square test.

[b]Mann–Whitney *U* test.

[c]Serum uric acid >6 and 7 mg/dL was considered as hyperuricemia for women and men, respectively.

Data are shown as median and 25th and 75th percentile range (p25–p75).

The level of significance was set at p <0.05.

Table 2. Allele and genotype frequencies between male and female participants.

		Men *n*(%)	Women *n* (%)	*P* value[a]
ABCG2 (Q191K)				
Alleles	G	683 (76)	615 (75)	
	T	213 (24)	209 (25)	0.44
Genotypes	GG	255 (57)	233 (57)	
	GT	173 (39)	149 (36)	
	TT	20 (4)	30 (7)	0.19
SLC22A12 (517G>A)				
Alleles	G	286 (32)	272 (33)	
	A	610 (68)	552 (67)	0.63
Genotypes	GG	47 (10)	49 (12)	
	GA	192 (43)	174 (42)	
	AA	209 (47)	189 (46)	0.80
XDH (518T>C)				
Alleles	T	567 (63)	516 (63)	
	C	329 (37)	308 (37)	0.77
Genotypes	TT	181 (40)	156 (38)	
	TC	205 (46)	204 (50)	
	CC	62 (14)	52 (12)	0.54

Abbreviations: *ABCG2*, gene that encodes an ATP-binding cassette transporter subfamily G member 2; *SLC22A12,* gene that encodes an urate transporter 1 gene; *XDH*, gene that encodes a xanthine dehydrogenase.

[a]Chi-square test.

The level of significance was set at p <0.05.

hypertriglyceridemia as predictors of hyperuricemia (Figure 1). A predisposition to abnormal serum uric acid levels was found in some conditions as follows: male sex (odds ratio (OR): 2.14, 95% confidence interval (CI): 1.41-3.24, p = < 0.001); overweight or obese (OR: 2.6, 95% CI: 1.71-3.88, p = <0.001); having hypercholesterolemia (OR: 2.8, 95% CI: 1.47-5.46, p = 0.002); or having hypertriglyceridemia (OR: 1.7, 95% CI: 1.04-2.69, p = 0.033).

In Table 3, an analysis by genotype is shown for the *ABCG2* (Q191K), *SLC22A12* (r517G >A), and *XDH* (518T>C) polymorphisms, employing a dominant model for all three. With respect to the *ABCG2* (Q191K) polymorphism, statistically significant differences were found between the GT+TT genotypes vs. GG for serum uric acid (p = 0.003) total cholesterol (p = 0.005) and HDL-C levels (p = 0.003). GA+AA genotypes vs. GG of the *SLC22A12* (517G>A) polymorphism only showed to influence LDL-C levels (p = 0.043). Finally, no statistically significant differences were found by genotype for the *XDH* (518T>C) polymorphism (p > 0.05).

When the OR and the association between genotypes for the *BCG2* (Q191K) and *SLC22A12* (517G>A) polymorphisms and cardiovascular risks were calculated by sex, some significant results were found utilizing a dominant model. Table 4 reports that GT+TT genotypes for the *ABCG2* (Q191K) polymorphism significantly statistically increases the risk of hyperuricemia (OR = 2.43, 95% CI: 1.41-4.17, p = 0.001) and hypercholesterolemia (OR = 4.89, 95% CI: 1.54-15.48, p = 0.003), but only in male participants. On the other hand, no significant results were found for the genotypes of the *SLC22A12* (517G>A) and *XDH* (518T>C) and *XDH* (rs1042039) polymorphisms.

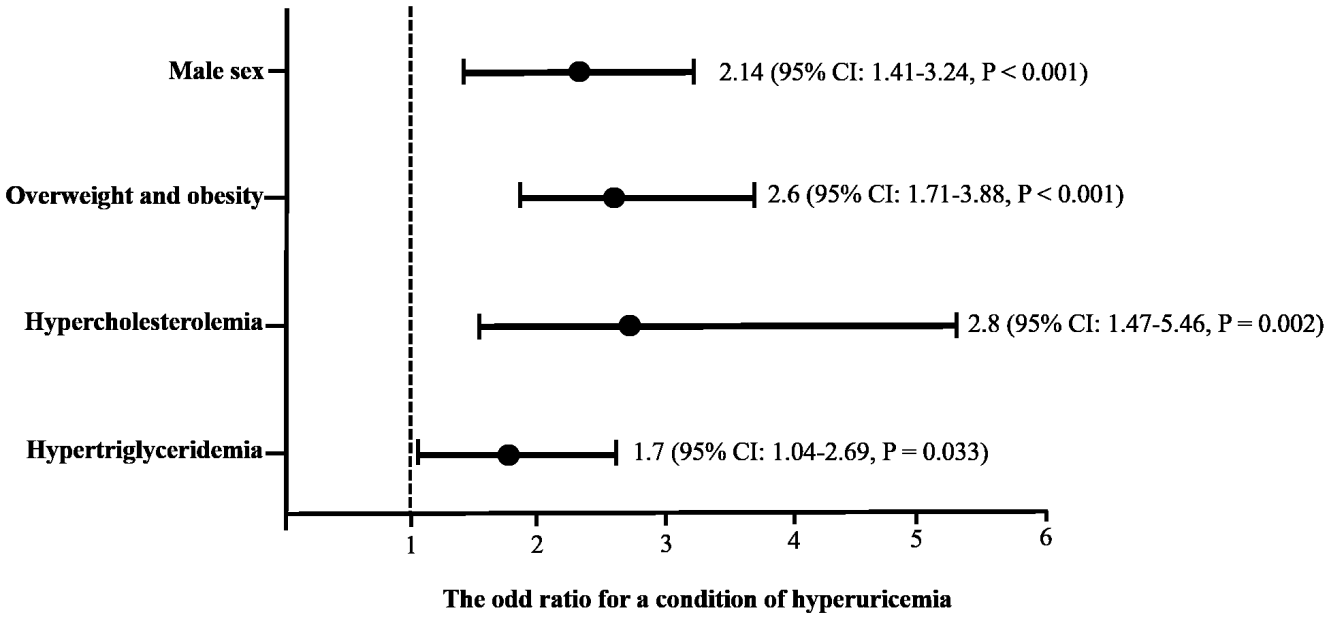

Figure 1. Association of sex, body mass index and dyslipidemias as predictive factors of hiperuricemia using a multivariate logistic regression analysis. The cutoff criteria were based on the World Health Organization and the National Cholesterol Education Program Adult (ATP III). Overweight: body mass index ≥ 25, Obesity: body mass index >30; hypercholesterolemia: fasting serum cholesterol levels > 200 mg/dL; hypertriglyceridemia: fasting serum triglycerides levels > 150 mg/dL.

Table 3. Analysis of variables by genotype for the *ABCG2* (Q191K), *SLC22A12* (517G>A), and *XDH* (518T>C) genetic polymorphisms.

Variable	*ABCG2* (Q191K) Dominant model		*P*-Value[a]
	GT+TT median (25th-75th percentile range)	GG median (25th-75th percentile range)	
BMI (Kg/m^2)	23.1 (20.4 – 27.0)	22.7 (20.2 – 26.3)	0.393
Systolic pressure (mmHg)	110 (100.0 – 110.0)	110 (100.0 – 110.0)	0.632
Diastolic pressure (mmHg)	70.0 (60.0 – 70.0)	70.0 (60.0 – 70.0)	0.220
Glucose (mg/dL)	80.0 (76.0 – 85.0)	80.0 (75.0 – 84.0)	0.129
Uric Acid (mg/dL)	5.00 (4.2 – 6.2)	4.7 (3.9 – 5.4)	**0.003**
Triglycerides (mg/dL)	94.0 (69.5 – 134.0)	92.0 (68.0 – 127.0)	0.634
Total Cholesterol (mg/dL)	151 (132.0 – 173.0)	145 (125.0 – 164.0)	**0.005**
LDL Cholesterol (mg/dL)	59.2 (42.5 – 74.8)	53.8 (38.8 – 72.7)	0.070
HDL Cholesterol (mg/dL)	70.9 (62.3 – 78.5)	67.3 (57.8 – 76.8)	**0.003**
	SLC22A12 (517G>A) Dominant model		
	GA+AA median (p25-p75)	GG median (p25-p75)	
BMI (Kg/m^2)	22.6 (20.1–26.2)	23.2 (20.4–26.6)	0.136
Systolic pressure (mmHg)	110.0 (100.0 – 110.0)	110.0 (100.0 – 110.0)	0.662
Diastolic pressure (mmHg)	70.0 (60.0 – 70.0)	70.0 (60.0 – 70.0)	0.600

	***SLC22A12* (517G>A) Dominant model**		
	GA+AA median (p25-p75)	**GG median (p25-p75)**	
Glucose (mg/dL)	80.0 (76.0 – 85.0)	80.0 (75.0 – 84.5)	0.302
Uric Acid (mg/dL)	4.8 (4.0 – 5.5)	4.90 (4.1 – 5.6)	0.537
Triglycerides (mg/dL)	91.0 (68.0 – 135.0)	94.5 (70.0 – 125.5)	0.763
Total Cholesterol (mg/dL)	144.0 (126.0 – 167.0)	149.5 (131.5 – 169.0)	0.127
LDL Cholesterol (mg/dL)	54.3 (36.1 – 70.5)	58.4 (40.6 – 75.2)	**0.043**
HDL Cholesterol (mg/dL)	69.3 (59.1 – 77.6)	68.1 (59.8 – 77.1)	0.659
	***XDH* (518T>C) Dominant model**		
	TC+CC median (p25-p75)	**TT median (p25-p75)**	
BMI (Kg/m^2)	22.8 (20.2–26.4)	23.0 (20.4–26.6)	0.618
Systolic pressure (mmHg)	110.0 (100.0 – 110.0)	110.0 (100.0 – 110.0)	0.460
Diastolic pressure (mmHg)	70.0 (60.0 – 70.0)	70.0 (60.0 – 70.0)	0.949
Glucose (mg/dL)	80.0 (75.0 – 85.0)	79.5 (76.0 – 84.0)	0.521
Uric Acid (mg/dL)	4.80 (4.0 – 5.5)	4.90 (4.0 – 5.5)	0.840
Triglycerides (mg/dL)	94 (69.0 – 128.5)	91.0 (68.0 – 132.0)	0.944
Total Cholesterol (mg/dL)	147.0 (128.0 – 168.0)	145.5 (129.0 – 167.0)	0.564
LDL Cholesterol (mg/dL)	56.6 (39.5 – 73.3)	56.1 (39.1 – 72.9)	0.640
HDL Cholesterol (mg/dL)	69.1 (60.1 – 77.6)	67.4 (58.9 – 76.9)	0.370

Abbreviations: BMI, body mass index; *ABCG2,* gene that encodes an ATP-binding cassette transporter subfamily G member 2; *SLC22A12,* gene that encodes an urate transporter 1 gene; *XDH,* gene that encodes a xanthine dehydrogenase.

[a]Mann–Whitney *U* test. The level of significance was set at $p < 0.05$.

Table 4. Analyses for the *ABCG2* (Q191K), *SLC22A12* (517G>A), and *XDH* (518T>C) polymorphisms and risk associated by sex.

Condition[a]	**Dominant model for the *ABCG2* (Q191K) polymorphism GT+TT vs. GG**					
	All participants		**Men**		**Women**	
	OR (95% CI)	***P* value**	**OR (95% CI)**	***P* value**	**OR (95% CI)**	***P* value**
Overweight and obesity	1.10 (0.78-1.56)	0.559	1.57 (0.93-2.67)	0.089	0.84 (0.53-1.34)	0.481
SP >130 mmHg	1.15 (0.38-3.47)	0.799	2.81 (0.68-11.52)	0.135	0.32 (0.03-2.97)	0.298
DP >85 mmHg	0.33 (0.03-2.99)	0.303	1.35 (0.08-21.94)	0.829	0.44 (0.04-4.28)	0.468
Fasting glucose >100 mg/dL	4.1 (0.82-20.49)	0.063	2.74 (0.24-30.63)	0.394	5.4 (0.60-49.39)	0.091
Hyperuricemia	**1.49 (1.00-2.21)**	**0.047**	**2.43 (1.41-4.17)**	**0.001**	0.77 (0.39-1.53)	0.465
Hypertriglyceridemia	0.84 (0.54-1.31)	0.463	1.32 (0.76-2.30)	0.315	0.87 (0.50-1.51)	0.635
Hypercholesterolemia	**3.27 (1.62-6.59)**	**0.001**	**4.89 (1.54-15.48)**	**0.003**	2.09 (0.83-5.26)	0.110
LDL-C ≥130 mg/dL	3.1 (0.81-12.47)	0.078	5.59 (0.61-50.80)	0.086	2.0 (0.33-12.26)	0.435
Low HDL-C	0.37 (0.07-1.83)	0.210	0.72 (0.319-1.644)	0.440	0.44 (0.045-4.2)	0.468

Condition[a]	Dominant model for the *SLC22A12* (517G>A)polymorphism GA+AA vs. GG					
	All participants		Men		Women	
	OR (95% CI)	*P* value	OR (95% CI)	*P* value	OR (95% CI)	*P* value
Overweight and obesity	0.81 (0.57-1.14)	0.232	0.72 (0.42-1.22)	0.227	0.88 (0.56-1.39)	0.599
SP >130 mmHg	1.01 (0.33-3.04)	0.986	1.09 (0.28-4.19)	0.892	0.85 (0.11-6.15)	0.878
DP >85 mmHg	1.30 (0.21-7.84)	0.773	1.76 (0.15-19.69)	0.641	0.42 (0.03-4.74)	0.475
Fasting glucose >100 mg/dL	2.6 (0.52-13.13)	0.222	0.43 (0.03-4.84)	0.485	4.3 (0.50-37.99)	0.143
Hyperuricemia	0.99 (0.67-1.48)	0.988	1.23 (0.66-1.90)	0.667	0.84 (0.43-1.62)	0.607
Hypertriglyceridemia	1.15 (0.74-1.78)	0.515	1.32 (0.76-2.29)	0.322	1.25 (0.72-2.15)	0.417
Hypercholesterolemia	1.26 (0.65-2.44)	0.486	1.66 (0.59-4.64)	0.330	0.85 (0.34-2.10)	0.725
LDL-C ≥130 mg/dL	1.30 (0.36-4.67)	0.682	3.58 (0.39-35.51)	0.227	0.56 (0.09-3.44)	0.533
Low HDL-C	0.68 (0.18-2.56)	0.579	1.011 (0.045-2.22)	0.979	0.42 (0.03-4.74)	0.475
Condition[a]	**Dominant model for the *XDH* (518T>C) polymorphism TC+CC vs. TT**					
	All participants		**Men**		**Women**	
	OR (95% CI)	***P* value**	**OR (95% CI)**	***P* value**	**OR (95% CI)**	***P* value**
Overweight and obesity	0.97 (0.68-1.38)	0.886	1.17 (0.68-1.99)	0.559	0.85 (0.53-1.36)	0.503
SP >130 mmHg	0.74 (0.24-2.23)	0.594	0.85 (0.22-3.27)	0.882	0.60 (0.08-4.23)	0.609
DP >85 mmHg	0.95 (0.15-5.78)	0.964	0.68 (0.04-11.13)	0.791	1.2 (0.10-13.50)	0.876
Fasting glucose >100 mg/dL	4.5 (0.55-37.23)	0.122	1.38 (0.12-15.49)	0.790	3.0 (0.35-26.63)	0.284
Hyperuricemia	0.90 (0.63-1.34)	0.613	0.77 (0.45-1.31)	0.342	1.29 (0.64-2.61)	0.470
Hypertriglyceridemia	0.84 (0.54-1.30)	0.444	0.68 (0.39-1.18)	0.174	1.41 (0.80-2.51)	0.230
Hypercholesterolemia	1.30 (0.65-2.59)	0.451	1.28 (0.46-3.60)	0.630	1.44 (0.53-3.85)	0.464
LDL-C ≥130 mg/dL	1.50 (0.38-5.87)	0.555	1.03 (0.17-6.31)	0.969	2.4 (0.27-22.15)	0.411
Low HDL-C	1.28 (0.31-5.18)	0.725	0.722 (0.350-1.70)	0.522	1.8 (0.18-17.75)	0.598

Abbreviations: BMI, body mass index; SP, systolic pressure; DP, diastolic pressure. LDL-C, LDL cholesterol; HDL-C, HDL cholesterol; *ABCG2,* gene that encodes an ATP-binding cassette transporter subfamily G member 2; *SLC22A12,* gene that encodes an urate transporter 1 gene; *XDH,* gene that encodes a xanthine dehydrogenase.

[a]The cut-off criteria were according to The World Health Organization and the National Cholesterol Education Program Adult (ATP III). Overweight was defined as BMI ≥25, while Obesity was BMI >30; Hyperuricemia was defined as serum uric acid >6 and 7 mg/dL for women and men, respectively; hypertriglyceridemia as fasting serum triglycerides >150 mg/dL, hypercholesterolemia as fasting serum cholesterol >200 mg/dL, and low HDL-C as a serum concentration of <50 mg/dL and 40 mg/dL for women and men, respectively.

Multivariate logistic regression analysis: data are shown as odd ratio (95% Confidence Interval). The level of significance was set at p <0.05.

Discussion

A total of 860 college applicants between the ages of 18 and 25 years of both sexes were included in this study, an important age range to identify early disorders. Indeed, we found a 15% prevalence of hyperuricemia, being higher among males (19.6%) than females (10%), as previously observed in another study with comparable age groups in Mexico (Alegría-Díaz *et al.*, 2018). Regarding uric acid levels, similar blood concentrations have also been reported in Mexican young persons (Pérez-Navarro *et al.*, 2020). The subgroup with hyperuricemia was prone to higher levels of BMI, blood pressure, triglycerides, total cholesterol, and LDL cholesterol (Table 1). In fact, the association

between serum uric acid levels and the traits of metabolic syndrome has been previously analyzed (Lin *et al.*, 2006; Zhang *et al.*, 2020a), although some authors found no causal evidence of uric acid levels being associated with metabolic syndrome and its components (Wang *et al.*, 2020). According to our results, being a man, being overweight or obese, or having dyslipidemia are related to high uric acid levels (Figure 1). Men have a lower capacity to eliminate urate via the kidney compared with females due to a deficiency of estrogen and progesterone (Hak *et al.*, 2010). Likewise, the involvement of uric acid in lipid metabolism can lead to hyperuricemia, a condition considered as predictor factor of dyslipidemia (Kuwabara *et al.*, 2020; Lima *et al.*, 2015; Son *et al.*, 2016) and can subsequently alter blood pressure (Teng *et al.*, 2011; Zhang *et al.*, 2020a). In this way, our results summarized in Figure 1 show that being male, being obese and having dyslipidemia increases the risk of hyperuricemia (Liu *et al.*, 2020a).

The study of the genetic influence on blood uric acid levels has included the search for single nucleotide polymorphisms (SNP) in genes involved in purine metabolism and urate removal. Here, we analyzed three polymorphisms in three different genes, including *ABCG2* (Q191K), *SLC22A12* (517G>A), and *XDH* (518T>C). The first corresponds to the exchange of a glutamine for a lysine at position 141 of an adenosine triphosphate (ATP)-binding cassette transporter subfamily G member 2 (*ABCG2*). This exchange predisposes individuals to hyperuricemia (Nakashima *et al.*, 2020; Wrigley *et al.*, 2020). A frequency of 0.25 for the risk for T allele was found, a slightly lower prevalence than that reported in Asian and New Zealand populations (Kim *et al.*, 2015; Liu *et al.*, 2020b; Toyoda *et al.*, 2019). The distribution of the T allele was marginal between hyperuricemic and normouricemic groups, being more frequent in the hyperuricemic group ($p = 0.056$). When a dominant model was carried out, the risk for the T allele was associated with hyperuricemia and hypercholesterolemia (total and HDL cholesterol). This association was confirmed only in men, showing that the *ABCG2* (Q191K) polymorphism increases the risk for hyperuricemia 2.43 times (95% CI: 1.41-4.17, $p = 0.001$) and hypercholesterolemia 4.89 times (95% CI: 1.54-15.48, $p = 0.003$) in a dominant model. Other studies have also found a greater influence of this polymorphism in men (Narang *et al.*, 2019) although, under some conditions, the *ABCG2* (Q191K) polymorphism could contribute to increased uric acid in women (Guo *et al.*, 2020; Roman *et al.*, 2020). Although initially our work focused on hyperuricemia in young people, the increase in serum cholesterol in men associated with the *ABCG2* (Q191K) polymorphism was observed. There are still few studies linking the *ABCG2* gene and cholesterolemia. A relevant fact is that mRNA expression levels of *ABCG2* appear to be higher in individuals with hypercholesterolemia (Rodrigues *et al.*, 2009); likewise, the activity of ABCG2 has been associated with cholesterol levels both *in vitro* and *in vivo (*To *et al.*, 2014). Therefore, perform genotype-based mRNA expression analysis to further explore the role of the *ABCG2* (Q191K) polymorphism in hyperuricemia and hypercholesterolemia should be contemplated.

The *SLC22A12* (517G>A) polymorphism comprises the transition from guanine to adenine in the 3´-UTR region in the urate transporter 1 gene; this transition appears to modify uric acid levels (Flynn *et al.*, 2013; Köttgen *et al.*, 2013). In this study, the frequency of the minor allele was 0.32; however, there was no statistically different distribution of this between hyperuricemic and normouricemic groups. Although no differences in uric acid levels were associated with this polymorphism, lower LDL cholesterol levels were observed in the group of carriers of the A allele when data were analyzed in a dominant model ($p = 0.043$), suggesting a protective effect of this allele (Simon *et al.*, 2014). Since the *SLC22A12* (517G>A) polymorphism is located at a potential miRNA binding site (Flynn *et al.*, 2013), the epigenetic mechanism involved in the regulation of uric acid levels needs to be studied.

With respect to the *XDH* (518T>C) polymorphism, we studied the xanthine dehydrogenase polymorphism located in the 3´-UnTRanslated (UTR) region of the *XDH* gene. The replacement of T by C is considered a risk factor related to hypertension (Wu *et al.*, 2015). We found that the minor allele frequency was 0.37 for the C allele, contrary to what was reported in a Chinese population, where the C allele had a higher frequency, in addition to its being associated with hypertension (Wu *et al.*, 2015). However, the link between the *XDH* (518T>C) polymorphism and hypertension was not demostrated in Taiwanese women (Lee *et al.*, 2019). In the present study, we did not find a statistically significant different distribution of the C allele between the hyperuricemic and normouricemic groups, and the risk allele was also not associated with any component of the metabolic syndrome.

Finally, hyperuricemia is an undesirable condition that has been seen as a minor trait of metabolic syndrome, cardiovascular risk, as well as other types of disorders such as psoriasis and alopecia, which have been associated with high levels of blood uric acid (Guo *et al.*, 2020; Ma *et al.*, 2020; Talebi *et al.*, 2020; Zhang *et al.*, 2020a). Even though our criterion for hyperuricemia were defined as blood uric acid >6 mg/dL for women and 7 mg/dL for men, cut-off points could be reconsidered according to the considerations made by Alegría-Díaz *et al.* (2018). In this regard, a recent study considers uric acid levels below 5 mg/dL for men and below 2-4 mg/dL for women to be optimal for a lesser risk of cardiometabolic diseases in a Japanese population (Kuwabara *et al.*, 2020). Although there are modifiable factors related to lifestyle, genetic inheritance plays a decisive role in the control of uricemia.

This study has three main limitations: i) only one polymorphism was genotyped for every gene, analysis of multiple SNPs by haplotypes could be more appropriate; ii) the analysis of the *ABCG2* (Q191K) polymorphism is limited by the small sample size and the compromised statistical power; and, iii) new cut-off values for hyperuricemia have been suggested (Alegría-Díaz *et al.*, 2018); however the conservative criteria of >6 mg/dL for women and 7 mg/dL for men were considered in this study.

Conclusions

In this study, we found that the *ABCG2* (Q191K) polymorphism increases the risk of hyperuricemia as well as of hypercholesterolemia in young Mexican males. Since the *ABCG2* (Q191K) polymorphism can modify the efficacy of statins in reducing cholesterol (Zhang *et al.*, 2020b), carriers of the risk

allele represent a vulnerable group of interest for future pharmacogenetic research. Some considerations for future studies are including lifestyle and diet factors, the monitoring of the study population, and exploring more polymorphisms in the *ABCG2*, *SLC22A12*, and *XDH* genes, as well as studying haplotypes.

Data availability

Underlying data

Data mendeley: Polymorphisms of the genes ABCG2, SLC22A12 and XDH and their relation with hyperuricemia and hypercholesterolemia in Mexican young adults. http://dx.doi.org/10.17632/243ft29b7m.1 (Alegría-Torres, 2021).

This project contains the following underlying data:

- DATABASE ART ARCHIVES OF PHYSIOL AND BIOCHEM.sav (spreadsheet of participant data)

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Current Peer Review Status: ✔ ✔

Version 2

Reviewer Report 24 September 2021

https://doi.org/10.5256/f1000research.77844.r95320

✔ **Jing He**
Department of Pediatric Surgery, Guangzhou Institute of Pediatrics, Guangdong Provincial Key Laboratory of Research in Structural Birth Defect Disease, Guangzhou Women and Children's Medical Center, Guangzhou Medical University, Guangzhou, China

Acceptable.

Competing Interests: No competing interests were disclosed.

Reviewer Expertise: Molecular Epidemiology.

I confirm that I have read this submission and believe that I have an appropriate level of expertise to confirm that it is of an acceptable scientific standard.

Version 1

Reviewer Report 24 August 2021

https://doi.org/10.5256/f1000research.49473.r91797

? **Jing He**
Department of Pediatric Surgery, Guangzhou Institute of Pediatrics, Guangdong Provincial Key Laboratory of Research in Structural Birth Defect Disease, Guangzhou Women and Children's Medical Center, Guangzhou Medical University, Guangzhou, China

In the current study, the authors investigate the association between three polymorphisms in the *ABCG2*, *SLC22A12*, and *XDH* genes and hyperuricemia risk by including 860 subjects. They found the *ABCG2* rs2231142 polymorphism increases the risk of hyperuricemia and hypercholesterolemia in young Mexican males.

I have some comments that should be addressed by the authors:

1. In the Abstract, it's better provide the number of cases and controls, as well as the nucleotide alterations for the polymorphisms they chose.

2. The authors only chose one polymorphism for each gene, that was not rationalised. It's better chose at least two potentially functional SNPs for each gene.

3. In the Materials and Methods, there was no need to provide the sequences of the probes. The authors should provide the function of the selected polymorphisms.

4. False-positive report probability and statistical power should be calculated as the positive findings for the samples included were so small (see the following articles, in which I have been involved with: He *et al.* Mol Carcinog. 2013; 52 Suppl 1: E70-9[1] and He *et al.* Mol Ther Nucleic Acids. 2018; 11: 1-8[2]).

5. The authors found the *ABCG2* (rs2231142) polymorphism increases the risk of hyperuricemia and hypercholesterolemia in young Mexican males. It is lacking functional validation for the function of *ABCG2* (rs2231142) polymorphism. It's better to perform genotype-based mRNA expression analysis to further explore the potential role of the significant polymorphism (He *et al.* Mol Ther Oncolytics, 2021; 20: 199-208[3]; Zhuo *et al.* Mol Ther Nucleic Acids, 2020; 22:17-26[4]). From these two references, which I have been involved with, the authors can perform genotype based mRNA expression analysis to further explore the potential role of the *ABCG2* (rs2231142) polymorphism.

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Is the work clearly and accurately presented and does it cite the current literature?

Partly

Is the study design appropriate and is the work technically sound?

Yes

Are sufficient details of methods and analysis provided to allow replication by others?
Yes

If applicable, is the statistical analysis and its interpretation appropriate?
Partly

Are all the source data underlying the results available to ensure full reproducibility?
Yes

Are the conclusions drawn adequately supported by the results?
Yes

Competing Interests: No competing interests were disclosed.

Reviewer Expertise: Molecular Epidemiology.

I confirm that I have read this submission and believe that I have an appropriate level of expertise to confirm that it is of an acceptable scientific standard, however I have significant reservations, as outlined above.

Author Response 21 Sep 2021

Jorge Alegría, Universidad de Guanajuato, Guanajuato, Mexico

Regarding the five points discussed, we respond to each of them:

1. The number of the cases
and controls as well as the description of sequence variants were included in the abstract.

2.
According to the introduction section, we selected three genes involved in the metabolism of purines or urat
gene that encodes a membrane transporter, which exports urates to the kidney and
intestine (Woodward *et al*. 2009); and the SLC2A9
gene that encodes a kidney protein called GLUcose Transporter 9
(GLUT9), an important flow regulator of urates in the proximal tubules (Caulfield *et al.* 2008).
In the same way, the XDH
gene gives rise to an enzyme denominated xanthine dehydrogenase, which breaks down purines from nucle
2002). We chose polymorphisms in different genes for the following two reasons:

1. Previous reports have shown the combined effect of genetic variants (specifically SLC2A9
and ABCG2) are able to explain 3-
4% of hyperuricemia, modulated by gender and body mass index (Brandstätter *et al.*,
2010; Köttgen *et al.,* 2013; Huffman *et al.*, 2015 and Merriman *et al.*,
2015;). Further, the ABCG2 (Q191K) and SLC22A12
(517G>A) polymorophisms have been studied in Mexican population showing a high prevalence (Mací
Kauffer et al., 2019 and Rivera-Paredez *et al.* 2019). Besides, since the XDH
(518T>C) polymorphism it has been poorly studied in Mexicans, we wanted to explore if it plays a

role in hyperuricemia.

2. We only analyzed polymorphisms with a minor allele frequency >5%, being: ABCG2 (Q191K) 25%, SLC22A12 (517G>A) 32%, and XDH (518T>C) 37%; as well as that the polymorphisms were in Hardy-Weinberg equilibrium.

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3. The sequences of the probes was deleted from the Materials and Methods section. The function of the sel
position 141 of an adenosine triphosphate (ATP)-
binding cassette transporter subfamily G member 2
(ABCG2). This exchange predisposes individuals to hyperuricemia (Nakashima *et al.* 2020, Wrigley *et al.*
2020). The SLC22A12 (517G>A) polymorphism comprises the transition from guanin
to adenine in the 3´-UTR region in the urate transporter 1
gene; this transition appears to modify uric acid levels (Flynn et al. 2013, Köttgen *et al.*
2013). With respect to the XDH
(518T>C) polymorphism, the replacement of T by C is considered a risk factor related to hypertension (Wu *et al.* 2015).

4.
In fact, our results are impacted by the small sample size and the compromised statistical power. This point a limitation of this study.

5. This point is argued in the discussion section: There are still few studies linking the ABCG2 gene and cholesterolemia.

A relevant fact is that mRNA expression levels of ABCG2 appear to be higher in individuals with hypercholest
et al. 2009); likewise, the activity of ABCG2
has been associated with cholesterol levels both in vitro and in vivo (To *et al.*
2014). Therefore, perform genotype-
based mRNA expression analysis to further explore the role of the ABCG2
(Q191K) polymorphism in hyperuricemia and hypercholesterolemia should be contemplated.

Competing Interests: No competing interests were disclosed.

Reviewer Report 25 March 2021

https://doi.org/10.5256/f1000research.49473.r81558

Ilham Akbar Rahman
Lecturer staff in Bachelor of Medicine Programme, Hasanuddin University, Makassar, Indonesia

The study assessed the relationship of ABCG2, SLC22A12, and XDH genes polymorphism on their relationship with hyperuricemia and risk factors of cardiovascular disease. It seems that the authors have provided a significantly huge amount of effort and cost in conducting this study. This polymorphism study could provide potential implications in the future on the prevention, diagnosis, and treatment of hyperuricemia associated with cardiovascular risk factors. The authors display the knowledge on good writing skills including grammar and word choice, sentence structure, and paragraph development. However, several points need to be addressed:

1. The study has provided a significant relationship on ABCG2 polymorphism gene in the risk of hyperuricemia on specific age of 18-25 years old. Detailed explanation has been provided for the reasons of relationship between ABCG2 polymorphism on hyperuricemia. However, are there any specific relations on the ABCG2 on specific young adults of age? Why perform the study in specific young adult age groups? Is it better to examine the relationship in a more general group?

2. Is there any consideration of excluding preexisting disease such as cardiovascular, liver, kidney, and secondary hyperuricemia (leukemia, myeloma, drugs induced, hypothyroidism, etc) in this study?

3. Is there any specific reason to choose the rs2231142 SNPs from all polymorphisms? The study should also describe the reasons to choose this rs2231142 SNP.

4. It has been revealed in the study that gender, obesity/overweight, hypercholesterolemia, and hypertriglyceridemia are associated with the risk of developing hyperuricemia. Therefore, in the analysis of the relationship of ABCG2 gene polymorphism and hyperuricemia, it is better to perform the analysis of other subgroups other than gender (such as BMI, cholesterol levels, and triglyceride)

5. The author should earlier define the diagnostic criteria used for hyperuricemia and its cut off value in the methods section.

Is the work clearly and accurately presented and does it cite the current literature?
Yes

Is the study design appropriate and is the work technically sound?
Yes

Are sufficient details of methods and analysis provided to allow replication by others?
Yes

If applicable, is the statistical analysis and its interpretation appropriate?
Yes

Are all the source data underlying the results available to ensure full reproducibility?
Yes

Are the conclusions drawn adequately supported by the results?
Yes

Competing Interests: No competing interests were disclosed.

Reviewer Expertise: Metabolic syndrome, hyperuricemia, insulin resistance, endocrinology, internal medicine, urology

I confirm that I have read this submission and believe that I have an appropriate level of expertise to confirm that it is of an acceptable scientific standard.

Author Response 02 Apr 2021

Jorge Alegría, Universidad de Guanajuato, Guanajuato, Mexico

Regarding the five points discussed, we respond to each of them:

1. Although examining the relationship in a more general group could provide more information, this study included college applicants due to the facilities to be recruited. In addition, we directed the study to recognize risk factors in young population, an age group less likely to have metabolic diseases.

2. In fact, participants with pre-existing diseases were not excluded. As mentioned in the methods section: “All participants were approached to take part in the study by phone and email by means of an open invitation explaining the goals of the study”.

3. The ABCG2 (rs2231142) polymorphism is one of the most studied and it seems to have the greatest influence on uric acid levels in both men and women (Guo *et al*., 2020; Narang *et al*., 2019; Roman *et al*., 2020). Likewise, this polymorphism could be influencing both the mRNA expression levels and activity of ABCG2 modulated by cholesterol levels (Rodrigues *et al*., 2009; To *et al.,* 2014), as this was mentioned in the discussion. In relation to the first point, most studies of polymorphisms focus on older patients or hemodialysis patients; however, we studied young people.

4. In order to summarize and present the most relevant results, the data were shown taking into account the genotype as a grouping criterion (Table 3). When the data was grouped and analyzed by another criterion (data not shown), there were no relevant findings.

5. Serum uric acid >6 and 7 mg/dL was considered as hyperuricemia for women and men, respectively (Table 1). We considered it more appropriate to include this information where the study group data are shown.

Competing Interests: No competing interests were disclosed.