Research Article

Serum Lipid Concentrations and *FADS* Genetic Variants in Young Mexican College Students: The UP-AMIGOS Cohort Study

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Keywords

FADS genotype · Blood lipid · Young healthy Mexicans

Abstract

Background: Recent genome-wide association studies in the Mexican population have identified several genetic loci associated with blood lipid levels in adults. However, studies focusing on the fatty acid desaturase (*FADS*) gene cluster have been understudied in this population, even though it seems associated with lipid profiles in other ethnicities. The aim of this study was to test associations between single nucleotide polymorphisms (SNPs) in the *FADS* cluster (rs174546, rs1535, rs174548, rs174550, rs174450, and rs174618) and serum lipid profiles in young Mexicans. **Methods:** Anthropometrics, serum lipid profiles, and *FADS* SNPs were measured in 998 subjects in the UP-AMIGOS cohort study. Genotype-phenotype (total cholesterol [TC], triglyceride [TG], high-density lipoprotein cholesterol [HDL-C], low-density lipoprotein cholesterol [LDL-C], and very-low-density lipoprotein [VLDL]) associations were assessed using PLINK adjusted

for sex, age, and body mass index (BMI). **Results:** Among 6 *FADS* SNPs, we found that carriers of the C-allele of the *FADS1*-rs174546 showed a significant association with lower TG concentrations ($\beta = -12.6$ mg/dL, $p = 0.009$) and lower VLDL concentrations ($\beta = -2.52$ mg/dL, $p = 0.005$). We found that rs174546, rs1535, and rs174550 were in high linkage disequilibrium ($r^2 > 0.80$). There were no significant associations between rs174550, rs174548, and rs174618 and lipid profiles. **Conclusion:** A genetic variant in the *FADS1* (rs174546) gene is a major contributor of plasma TG and VLDL concentrations in healthy young Mexicans.

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Introduction

In Mexico, 65% of the adult population has low high-density lipoprotein cholesterol (HDL-C, ≤ 40 mg/dL) and 43.6% is hypercholesterolemic (total cholesterol [TC] ≥ 200

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mg/dL); in particular low HDL-C and high TC increase the risk for cardiovascular disease (CVD) [1]. Similar patterns have been found among young Mexicans aged 20–29 years, with 62% having low HDL-C (<40 mg/dL) and 22% having high levels of triglycerides (TG $\geq$ 150 mg/dL), two clinical markers of metabolic syndrome and risk factors for CVD [1]. Moreover, the prevalence of obesity has rapidly increased among the younger population during the last decade [2, 3]. In European populations, over 157 loci associated with either low HDL-C, high low-density lipoprotein cholesterol (LDL-C), high TG, or high TC have been identified in those genetically predisposed to the development of dyslipidemia [4–6]. Additional loci were identified in Mexican adults with a combined family history of hyperlipidemia and hypertriglyceridemia, further implicating the role of genetic variation in this at-risk population [7, 8].

The *FADS* gene cluster includes 3 genes: *FADS1*, *FADS2*, and *FADS3* [9]. The *FADS* gene cluster is involved in the elongation and formation of long-chain fatty acids from both dietary and endogenous precursors, and thus its role in plasma fatty acid concentration is essential [9]. Genome-wide association studies have identified single nucleotide polymorphisms (SNPs) in *FADS1* and *FADS2* to be associated with adverse lipid profiles [4–6, 10–12]. Additional studies continue to confirm these associations in both adults and children of European descent [13–17]. Over 80% of genetic association research to date has been conducted in populations of European descent, despite strong evidence that genetic associations are not identical across ethnic groups [18, 19]. A single case/control study conducted in Mexican adults identified *FADS3* as a causal gene for familial combined hyperlipidemia and elevated TG, but variants in other genes of this cluster (*FADS1*/*FADS2*) and associations with blood lipids have not been studied in healthy young Mexicans who may be at risk for the development of dyslipidemia due to genetic predisposition [20]. Therefore, the aim of this study was to establish associations between 6 variants in the *FADS* gene cluster (rs174546, rs1535, rs174548, rs174550, rs174450, and rs174618) and serum lipid profiles in young Mexicans in the UP-AMIGOS cohort study [21, 22].

Material and Methods

Study Population

The UP-AMIGOS cohort study (Universities of San Luis Potosí and Illinois: A Multidisciplinary Investigation on Genetics, Obesity, and Social Environment) is a cross-sectional study of young adult applicants from the Autonomous University of San

Luis Potosí (Universidad Autónoma de San Luis Potosí, UASLP for its acronym in Spanish). Briefly, a total of 10,000 samples and validated self-administered food frequency questionnaires (FFQ) for the Mexican population were recollected from volunteers in 2009 at the UASLP in Mexico [23]. A detailed description of the data collection and phenotypes of the subjects participating in the UP-AMIGOS cohort study has been published previously [20, 21]. As previously described [21, 22], >10,000 individuals were recruited and screened for this multidisciplinary investigation, and only 998 were found eligible on the basis of the selection criteria with completed demographics, lipid profiles, and genetic data. Dietary intakes were only available for a subset of 642 of 998 participants. According to the methodology for analysis of dietary data from the Mexican National Health and Nutrition Survey 2006 (Ensanut 2006 for its acronym in Spanish), unreliable dietary intake data are defined as reporting consumption of <500 kcal per day, or reporting a very high caloric intake, 5 standard deviations above the mean [23, 24]. Thus, a subset of 581 participants (61 participants were excluded) were found with reliable data to analyze gene-diet interactions. Written informed consent was obtained for all participants. Institutional Review Boards of both the UASLP and the University of Illinois at Urbana-Champaign approved the study protocol.

Biochemical Measurements

Serum TC, HDL-C, and TG were determined after overnight fast by standard methods at the Clinical Research Laboratory of the Chemistry School at the UASLP in Mexico. LDL-C and very-low-density lipoprotein cholesterol (VLDL-C) were calculated using the Friedewald equation [25]. Hypertriglyceridemia was defined as a TG concentration $\geq$ 150 mg/dL, hypercholesterolemia as TC $\geq$ 200 mg/dL, high LDL-C as a concentration >130 mg/dL, and low HDL-C as $\leq$ 40 mg/dL in males and $\leq$ 50 mg/dL in females [26].

DNA Extraction, SNP Selection, and Genotyping

Blood was collected in EDTA tubes, stored at -80°C at the Clinical Research Laboratory of the Chemistry School at the UASLP in Mexico, and then transported to the Terán-García Laboratory at the University of Illinois Urbana-Champaign in the USA for genotyping. DNA was extracted using Puregene reagents (Gentra Puregene Blood Kits, QIAGEN, Valencia, CA, USA) and stored at -20°C . Detailed DNA extraction and genotype determination methods had previously been described [27]. Six *FADS* SNPs (rs174546, rs1535, rs174548, rs174550, rs174450, and rs174618) were selected for analysis based on previously published evidence of their associations with serum lipid profiles [10–17].

Dietary Fatty Acid Intake

Nutritional data were available for the analysis of 581 of the 998 participants. Dietary intakes of total fat, saturated fat, monounsaturated fat, and polyunsaturated fat were extracted from the FFQ. Dietary intake of omega-3 was calculated from the sum of daily eicosapentaenoic acid (EPA; 20:5 n-3), docosapentaenoic acid (22:5 n-3), and docosahexaenoic acid (DHA; 22:6 n-3), and for omega-6 from the sum of linoleic acid (LA; 18:2 n-6), γ -linolenic acid (18:3 n-6), and arachidonic acid (AA; 20:4 n-6). Dietary intakes are reported as intakes in grams per day and as the percentage contribution to the total energy intake (%E), and were analyzed using standard methodologies published by the Ensanut 2006 [23, 24].

Table 1. Characteristics of the population

Parameters	<i>n</i>	Total (<i>n</i> = 998)	Males (<i>n</i> = 451)	Females (<i>n</i> = 547)	<i>p</i> value
Age, years	998	18.68±0.04	18.74±0.07	18.62±0.05	0.14
BMI	998	23.95±0.48	24.48±0.21	23.50±0.18	0.0004
TC, mg/dL	836	170.75±1.17	169.20±1.71	172.02±1.61	0.23
TG ^a , mg/dL	845	111.78±1.91	117.18±2.98	107.45±2.47	0.003
HDL-C, mg/dL	794	49.70±0.42	47.56±0.60	51.43±0.57	<0.0001
LDL-C, mg/dL	780	98.70±1.01	98.42±1.47	98.93±1.38	0.79
VLDL ^a , mg/dL	845	22.36±0.38	23.44±0.60	21.49±1.63	0.003

BMI, body mass index; TC, total cholesterol; TG, triglycerides; HDL-C, high-density lipoprotein cholesterol; LDL-C, low-density lipoprotein cholesterol; VLDL, very-low-density lipoprotein cholesterol. *p* values were calculated using Student *t* test to compare males vs. females. ^a log-10 transformed data.

Table 2. Genotype frequencies of *FADS* SNPs among participants of the UP-AMIGOS study

SNP	Gene	Position	MM/mm	MAF	HWE	MM	Mm	mm	SNP	LD statistics
rs174546	FADS1	61802358	T/C	0.30	0.18	392 (48)	360 (44)	65 (8)	rs1535, rs174550	>0.81
rs174550	FADS1	61804006	C/T	0.31	0.20	403 (48)	360 (44)	74 (8)	rs174550	1
rs174548	FADS1	61803876	G/C	0.30	0.09	412 (49)	359 (43)	70 (8)	rs174550	0.80
rs1535	FADS2	61830500	G/A	0.30	0.68	404 (49)	362 (44)	59 (7)	rs174546	0.89
rs174618	FADS2	61861850	A/G	0.27	0.72	461 (55)	321 (38)	60 (7)	rs174618	1
rs174450	FADS3	61874070	C/A	0.25	0.07	485 (58)	294 (35)	61 (7)	rs174450	1

Data are *n* (frequency %). MM, major; mm, minor; MAF, minor allele frequency; HWE, Hardy-Weinberg equilibrium; LD, linkage disequilibrium.

Statistical Analysis

Results are reported as means ± standard errors of the mean. All the analyses were performed using PLINK software [28]. Continuous variables were examined for normality, and non-normal variables (TG and VLDL-C) were log-10 transformed for significance testing. Linkage disequilibrium (LD) was used to analyze the correlation (*r*²) between *FADS* SNPs. General linear regression models adjusted for sex, age, and body mass index (BMI) were used to test associations between *FADS* SNPs and blood lipid concentrations (TC, TG, HDL-C, LDL-C, and VLDL) assuming an additive model, and adjusted for multiple comparisons using the Bonferroni correction. For all tests, the Bonferroni correction was set at α/n , where $\alpha = 0.05$ and $n = 3$, and therefore significant *p* was <0.016. All reported *p* values were 2-tailed, and statistical significance was defined at $\alpha = 0.05$ level. Participants with missing information on serum lipid concentrations and/or genotypes were excluded from the analyses involving a particular SNP (data can be found in Table 3). Moreover, in a subset of 581 subjects with completed FFQ data, gene-nutrient interactions were tested for *FASD1*-rs174546.

Results

Characteristics of the Study Population

Characteristics of the participants are summarized in Table 1. BMI, TG, HDL-C, and VLDL-C were significantly different between males and females (*p* < 0.01). In males, levels of TG and VLDL-C were higher, whereas HDL-C was lower compared to females (Table 1). Overall, 37% of the sample met diagnostic criteria for low HDL-C (≤ 40 mg/dL in males and ≤ 50 mg/dL in females), 16% for hypercholesterolemia (TC ≥ 200 mg/dL), 15% for hypertriglyceridemia (TG ≥ 150 mg/dL), and 9% for high LDL-C (LDL > 130 mg/dL). Finally, we found that 34% of the participants had a BMI ≥ 25 , with 23% being overweight and 11% being obese.

FADS Single Nucleotide Polymorphisms

The genotype and allele frequency of the 6 *FADS* SNPs in this analysis are shown in Table 2. We found 3 *FADS*

Fig. 1. Distributions of *FADS1*-rs174546 genotype frequency in the 1000 Genomes Browser. Data are from <https://www.ncbi.nlm.nih.gov/variation/tools/1000genomes/> [29]. Allele frequencies were ranked from low to high for the major C-allele (overall frequency was reported as C = 0.70, T = 0.30). The arrow indicates allele frequency for a population of Mexican ancestry living in Los Angeles (MXL) from the 1000 Genomes Browser. KHV, Kinh in Ho Chi Minh City, Vietnam; PEL, Peruvians from Lima, Peru; CDX, Chinese Dai in Xishuangbanna, China; MXL, Mexican ancestry from Los Angeles, USA; CHS, Southern Han Chinese; PUR, Puerto Ricans from Puerto Rico; FIN, Finnish in Finland; CLM, Colombians

from Medellin, Colombia; GBR, British in England and Scotland; CEU, Utah Residents (CEPH) with Northern and Western European Ancestry; CHB, Han Chinese in Beijing, China; JPT, Japanese in Tokyo, Japan; IBS, Iberian Population in Spain; TSI, Toscani in Italy; BEB, Bengali from Bangladesh; PJI, Punjabi from Lahore, Pakistan; STU, Sri Lankan Tamil from the UK; AWS, Americans of African Ancestry in SW USA; ITU, Indian Telugu from the UK; GIH, Gujarati Indian from Houston, Texas; ACB, African Caribbeans in Barbados; LWK, Luhya in Webuye, Kenya; YRI, Yoruba in Ibadan, Nigeria; GWD, Gambian in Western Divisions in the Gambia; MSL, Mende in Sierra Leone; ESN, Esan in Nigeria.

SNPs in high LD with each other. *FADS1*-rs174546 and *FADS2*-rs1535 were in strong LD ($r^2 = 0.89$) and belong to the same block. *FADS1*-rs174546 was in high LD with rs174550 ($r^2 = 0.80$), and *FADS1*-rs174550 was in high LD with rs174548 ($r^2 = 0.81$). Hence, we included 3 *FADS* SNPs (rs174546, rs174618, and rs174450) for further analysis.

Frequency Distribution of *FADS1*-rs174546 among Populations

Striking differences were observed in the allele frequencies across several populations (Fig. 1). In the UP-AMIGOS cohort study, the T-allele was the major allele

which replicates the allele frequencies reported by the 1000 Genomes Browser for the Mexican population [29]. Thus, only 5 (Vietnam, Peru, and China) out of 26 populations included in the 1000 Genomes Browser project had the C-allele as the minor allele, including Mexicans (the overall minor allele frequency [MAF] was 30% TT genotypes) (Fig. 1).

Associations between *FADS* SNPs, Dietary Intakes and Blood Lipid Concentrations

Means of blood lipid concentrations according to *FADS* genotype are presented in Table 3. Homozygous carriers of the minor C-allele of *FADS1*-rs174546 were

Table 3. Blood lipid concentrations by *FADS* genotypes in the UP-AMIGOS study

SNPs	<i>n</i>	MM	Mm	mm	β	<i>p</i> value
TC						
rs174546	816	153.4±60.5	151.1±67.9	127.6±74.0	−8.03	0.03
rs174548	836	144.3±69.4	149.4±64.5	121.7±80.4	−3.50	0.34
rs174618	841	144.1±69.8	145.8±66.7	141.3±71.1	0.74	0.84
TG						
rs174546	817	107.3±70.9	95.8±62.7	78.3±50.5	−12.6	0.009*
rs174548	837	100.5±71.9	97.8±65.4	72.1±50.2	−7.96	0.27
rs174618	842	96.6±66.2	100.2±72.5	82.6±52.8	−1.17	0.95
HDL-C						
rs174546	817	44.0±19.0	42.7±21.1	39.7±21.3	−1.92	0.08
rs174548	837	41.3±23.0	41.3±21.5	35.0±24.3	−2.20	0.12
rs174618	842	40.0±22.5	41.1±21.8	44.7±26.1	1.74	0.15
LDL-C						
rs174546	817	86.2±40.9	86.6±46.1	74.5±47.5	−2.88	0.23
rs174548	841	78.7±46.0	82.4±46.3	69.1±53.3	−0.45	0.86
rs174618	842	76.7±47.8	80.5±46.7	80.2±46.5	1.82	0.47
VLDL						
rs174546	817	21.5±14.2	19.2±12.5	15.7±10.1	−2.52	0.005*
rs174548	837	20.1±14.4	19.6±13.1	14.4±10.0	−2.24	0.18
rs174618	842	19.3±13.2	20.0±14.5	16.5±10.6	−0.32	0.87

Data are expressed as means ± standard deviation (in mg/dL). *p* values were adjusted by age, sex, and body mass index. TC, total cholesterol; TG, triglycerides; HDL-C, high-density lipoprotein cholesterol; LDL-C, low-density lipoprotein cholesterol; VLDL, very-low-density lipoprotein cholesterol. * Significant *p* value of log-10 transformed data adjusted after Bonferroni correction.

Table 4. Dietary intakes stratified by *FADS1*-rs174546 genotypes in the UP-AMIGOS study

Dietary intake	<i>n</i>	TT (MM)	CT (Mm)	CC (mm)	<i>p</i> value
Energy, kcal	581	2,287±1,131	2,307±1,065	2,619±1,581	0.23
TFA, g/day	581	90.7±52.1	92.5±46.1	108.4±69.4	0.20
SFA, g/day	581	28.9±17.8	28.6±14.3	36.5±25.2	0.08
MUFA, g/day	581	35.2±21.8	35.2±18.4	41.8±26.3	0.31
PUFA, g/day	581	17.5±12.8	18.1±11.9	20.6±16.3	0.41
Omega-3, g/day	581	1.3±0.9	1.3±1.2	1.3±1.1	0.33
Omega-6, g/day	581	9.5±7.0	9.7±6.3	10.4±6.8	0.89
TFA, %E	581	35.2±7.7	36.4±7.6	37.3±6.7	0.14
SFA, %E	581	11.2±2.9	11.3±2.8	12.3±2.6	0.26
MUFA, %E	581	13.5±3.6	13.8±3.5	14.5±2.9	0.06
PUFA, %E	581	6.9±3.2	7.0±3.0	7.0±2.7	0.81
Omega-3, %E	581	0.5±0.3	0.5±0.3	0.5±0.2	0.78
Omega-6, %E	581	6.7±1.5	3.8±1.8	3.7±1.4	0.16

Data are expressed as means ± standard deviation in grams per day or percentage of energy (%E) from calories. *p* values were adjusted by age, sex, and body mass index for gene-nutrient interaction. Dietary intake of omega-3 was calculated from the sum of daily eicosapentaenoic acid (20:5 n-3), docosapentaenoic acid (22:5 n-3), and docosahexaenoic acid (22:6 n-3), and for omega-6 from the sum of linoleic acid (18:2 n-6), γ -linolenic acid (18:3 n-6), and arachidonic acid (20:4 n-6). TFA, total fat; SFA, saturated fat; MUFA, monounsaturated fat; PUFA, polyunsaturated fat; MM, major; mm, minor.

strongly associated with lower TG ($\beta = -12.6$ mg/dL, $p = 0.009$) and lower VLDL ($\beta = -2.52$ mg/dL, $p = 0.005$) concentrations compared to carriers of the T-allele. Table 4 shows total dietary intakes stratified by *FADS1*-rs174546. There were no significant differences in dietary intakes across *FADS1*-rs174546 genotypes. Moreover, no significant interaction effects were observed between dietary intakes and *FADS1*-rs174546 genotypes on blood cholesterol concentrations (data not shown).

Discussion

In this cross-sectional analysis, we found that the minor C-allele of *FADS1*-rs174546 was associated with lower plasma TG and VLDL concentrations in this cohort of young Mexican adults. To our knowledge, this is the first study to assess plasma lipid profiles and *FADS* genotype in healthy young Mexican adults. A study conducted in older Mexican adults diagnosed with familial hypercholesterolemia found *FADS3*-rs174547 to be strongly associated with high TG levels [20]. Evidence indicated that *FADS1*-rs174546 and *FADS3*-rs174547 are in strong LD [29].

MAF varies by population, and even though the C-allele of *FADS1*-rs174546 is minor in the Mexican population, it is not in other populations [29]. Two independent studies in diverse populations have confirmed these dramatic differences in the allele frequencies of variants in the *FADS* gene cluster across populations [19, 30].

Numerous studies have reported a significant association between *FADS* variants and lower TC, LDL-C, HDL-C, and higher TG concentrations in the European population [13–17]. Despite the population MAF found in our study, the T-allele of *FADS1*-rs174546 was associated with increased TG concentrations, and replicates previous associations in diverse populations, such as the association of higher TG concentrations among carriers of the minor T-allele of *FADS1*-rs174546 (CT + TT genotype) in French Canadians [31]. On the other hand, our results did not replicate previous associations between the minor T-allele in the *FADS1*-rs174546 and lower TC, non-HDL-C, and HDL-C concentrations [14–16]. Nevertheless, our study confirms the marked differences between populations regarding MAF in the *FADS* gene cluster, and replicates the effect of *FADS1*-rs174546 on TG concentrations previously reported by others [7, 8, 31]. In East Asian subpopulations, the C-allele of *FADS1*-rs174547 (in LD with rs174546) has been associated with lipid dysregulation, but these associations are not identical be-

tween ethnic subgroups [32]. This study found that in the Japanese population, the C-allele of *FADS1*-rs174547 was associated with increased TG and lower HDL-C concentrations, but in the Mongolian population it was associated with lower LDL-C concentrations [32]. Similar associations were reported in the Northern and Southern Chinese populations; the C-allele of rs174550 was associated with high TC levels in Beijing participants, but this allele was associated with lower HDL-C in Shanghai residents [33]. A possible explanation for the variability in lipid-gene associations could be due to differences in dietary fat intake between these two populations [19, 32, 33]. Moreover, the different LD patterns across populations may explain the different associations found in lipid traits [19, 30].

The role of dietary fat intake, specifically long-chain polyunsaturated fatty acids (LCPUFA), on lipid profiles modified by genetic variation has been well studied [17, 34, 35]. Briefly, the *FADS1*/*FADS2* gene encodes two enzymes (delta-5 [D5D] and delta-6 [D6D]) responsible for the double bond formation of LCPUFA through desaturation and elongation of essential fatty acids (EFA) such as α -linolenic acid (ALA) and LA [9]. The amount of substrates (ALA and LA) derived from the diet is equivalent to the fatty acid composition in the body [36]. The activities of D5D and D6D, encoded by *FADS1* and *FADS2*, respectively, can be modulated by diet [9, 36, 37]. Variants in the *FADS* gene cluster that result in a decreased transcription of key enzymes in these pathways may result in decreased efficiency of these enzymes to convert EFA to LCPUFA [9, 16, 37, 38]. A large family-based study of the genetics of coronary artery disease in Mexican Americans (San Antonio Family Heart Study) found that *FADS1*/*FADS2* SNPs have a significant influence on the variation in estimated plasma and erythrocyte D5D activities. D5D is a rate-limiting enzyme involved in the conversion of EFA to AA (20:4 ω -6) and EPA (20:5 ω -3) [39]. This study also found that D5D and D6D activities were highly heritable, with a strong linkage (LD) to chromosome 11 for estimated erythrocyte D5D activity [39]. Thus, minor alleles of *FADS1* and *FADS2* SNPs were associated with higher D5D activity, which results in an increased plasma and erythrocyte AA, and reduced EPA levels [39]. Hence, individuals with these variants may then possibly benefit from dietary increases in LCPUFA. In contrast, in the European population, minor alleles in *FADS1* and *FADS2* genes were associated with higher ALA and LA levels, and lower AA and EPA levels [19, 36, 37]. In this manner, higher D5D activity has also been associated with lower LDL-C and TG, and higher HDL-C

concentrations, which play an important role in the prevention of atherosclerosis and CVD [17, 40]. These differences in desaturase activities may be related to differences in the genetic background and dietary patterns across populations [31–36]. These associations have been demonstrated in cross-sectional analyses and feeding interventions, but not in Mexican populations [15, 16, 31–38]. Currently, dietary intakes of EFA (ALA, LA), the *FADS* enzyme substrates, and LCPUFA are low in the Mexican population [41], and thus carriers of the T-allele of *FADS1*-rs174546 may be at an even greater disadvantage if they do not meet dietary recommendations. Furthermore, a meta-analysis for dyslipidemias found that a high intake of unsaturated fat relative to saturated fat reduces TC levels by 10.68 mg/dL, as LCPUFAs serve as key transcription regulators in genes related to de novo lipogenesis [42, 43]. A high intake of unsaturated fat, especially LA, is associated with a decreased risk of CVD and coronary heart events, despite the role of these compounds in pro-inflammatory signaling pathways [44].

Several limitations of our study should be addressed. First, no data were available regarding lifestyle factors, such as medication use, smoking habits, alcohol consumption, or physical activity for our population. Second, this study is a convenience sample from Mexican college students in an urban city from Mexico, and thus results may not be generalizable to other populations. Third, the UP-AMIGOS survey is a self-administrated questionnaire with multidisciplinary outcomes; therefore, a high percentage of individuals either decided not to respond to the FFQ or reported unrealistic total calorie intake (<500 kcal, >8,672 kcal). Strengths of our study include the sample size, as this is the largest cohort study to our knowledge in healthy young Mexican adults examining these genetic associations. In addition, we were able to replicate the distribution of the MAF for *FADS1*-rs174546 reported by the 1000 Genomes Browser for the Mexican population.

In conclusion, the overall results showed that *FADS1*-rs174546 is a major contributor to plasma TG and VLDL concentrations in young healthy Mexican college students from the UP-AMIGOS cohort study. Longitudinal studies are needed to elucidate the genetic mechanism which underlies lipoprotein profiles and their future consequences for this population. It is worthwhile to mention that this population requires dietary interventions designed to improve their lipid profiles. The results of this investigation emphasize the importance of identifying genetically at-risk individuals, and the development of personalized nutritional recommendations to maintain health and quality of life beginning at a young age, as well as to prevent CVD later in life.

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Disclosure Statement

The authors declare no conflicts of interest.

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