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Genetic Variant in the *CD36* Gene (rs1761667) is Associated with Higher Fat Intake and High Serum Cholesterol among the Population of West Mexico

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Abstract

High-fat diets lead to obesity and metabolic disorders. The rs1761667 *CD36* gene polymorphism may predict the preference for dietary fat.

Aim: To determine the association of the *CD36* gene polymorphism with fat intake and lipid abnormalities in subjects from West Mexico.

Methods: In a cross-sectional study, 441 subjects were divided into normal weight, overweight and obese groups. Real-time PCR determined *CD36* genotypes (AA, AG, and GG). Lipid biochemical tests and a 3-day food record were assessed.

Results: The allele of *CD36* was prevalent in 57.1% (n=252) of the total cases. The overweight A/A subjects had a significant higher intake of calories, protein, total fat, saturated fatty acids (SFA), monounsaturated fatty acids (MUFA) and polyunsaturated fatty acids (PUFA) than the other genotype carriers. Furthermore, high serum cholesterol levels were associated with the A/A genotype than to the A/G genotype carriers (OR=2.75, CI 1.33-5.69; p=0.005).

Conclusions: The allele of *CD36* was predominant in subjects from West Mexico. In addition, a high-fat diet and high serum cholesterol levels were associated with the A/A genotype.

Keywords: CD36 receptor; Food preference; High-fat foods; Obesity; Taste perception

Introduction

Over the last decade, the prevalence of obesity in westernized lifestyle countries has increased more than double [1]. Today, Mexico is one of the countries with the highest number of obese people in the world [2]. Obesity significantly increases the risk of chronic non-communicable diseases, such as diabetes, ischemic heart disease, cerebrovascular diseases, and cancer [3]. These diseases are currently the leading causes of death in our country [4].

The obesity epidemic is the result of gene-environment interactions in which the human genome is susceptible to environmental influences that favor positive energy balance and weight gain [5]. It has been reported that high-fat diets lead to excessive body fat deposition and the development of obesity [6]. Such diets promote larger meal size, less postprandial satiety per calorie, and greater daily calorie intake than a high-carbohydrate diet [7]. Moreover, high-fat diets, especially high in saturated fatty acids (SFA), increase cholesterol levels in the serum that in turn may increase the risk of heart disease [8].

On the other hand, the preference and the overconsumption of high-fat foods depend upon their high palatability and taste perception [9-12]. These biological features are modulated by the expression of the class B scavenger CD36 receptor in the gustatory papillae of humans [13]. *CD36* gene has 15 exons extending over 32 kb on chromosome 7q11.2 [14]. It plays a fundamental role in the taste perception of dietary fat [15] by capturing the long-chain fatty acids (LCFA) into the cell [16]. After the activation by LCFA, lingual CD36 triggers specific signaling mechanisms, such as an increase in free intracellular calcium concentrations, phosphorylation of protein-tyrosine kinase (PTK) and

release of serotonin and noradrenaline into synaptic clefts. Thus, it has been described that this signaling cascade is likely to be responsible for fat preference and the cephalic phase of digestion, which are physiologic responses induced by the detection of lipids in the oral cavity [17]. In animal models, combined biochemical, nutritional and behavioral studies have proposed that the lipid-mediated change in lingual CD36 expression might modulate the motivation for fat during a meal, initially high at first, then gradually decreasing after food intake [18]. Moreover, it has been observed that the inactivation of the *CD36* gene in wild-type mice entirely abolished the preference for LCFAenriched solutions and solid diet [19].

The genetic variability of the CD36 gene could explain the differences in fat perception and fat preferences across individuals [20]. Genome-wide studies have shown that a common single nucleotide polymorphism -31118G>A (rs1761667) in the promoter region of this gene reduces CD36 transcript, total and surface CD36 protein in

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different tissues [21,22]. Some studies have reported that this variant predicts oral responses and preference for dietary fat in adults of African-American ancestry [23,24]. Recently, we have reported that the regional diet of subjects with liver disease in West Mexico is high in total fat, SFA and cholesterol due to overconsumption of red meat, cold cuts, fried foods and pastries [25]. However, the relationship of this dietary pattern with *CD36* genotype among the Mexican population has not been thoroughly clarified. Thus, the aim of this study was to analyze the association of the rs1761667 *CD36* polymorphism with fat intake and lipid abnormalities in subjects from West Mexico.

Materials and Methods

Study subjects

In a cross-sectional study, a total of 441 mestizo unrelated subjects were enrolled. The study was conducted in the Department of Molecular Biology in Medicine of the Civil Hospital of Guadalajara «Fray Antonio Alcalde» in Guadalajara, Jalisco, Mexico. The participants were grouped according to the World Health Organization's (WHO) BMI Classification: Normal Weight (BMI 18.5-24.9 kg/m²); Overweight (BMI 25-29.9 kg/m²) and Obesity (BMI ≥30 kg/m²). BMI was determined by electrical bioimpedance (INBODY 3.0, Analyzer Body Composition, and Bio space, Korea). Women who were pregnant or breastfeeding, smokers, subjects with sinusitis, subjects taking prescribed medication that might affect taste perception or who reported consuming a diet that restricted fat or calories were excluded.

CD36 Genotyping

DNA was extracted from leucocytes by a modified salting-out method [26]. The rs1761667 *CD36* gene polymorphism was detected by a Real-Time PCR System (TaqMan, Applied Biosystems, Assay number C_8314999_10; Foster City, CA, USA) on a 96-well format and read by a Step One Plus thermocycler (Applied Biosystems, Foster City, CA, USA). DNA was used at a final concentration of 70 ng. Conditions of the polymerase chain reaction were 95°C for 10 min and 40 cycles of denaturation at 92°C for 15 s and annealing/extension at 60°C, for 1 min. Genotyping was verified by using positive controls of the DNA samples corresponding to the three possible genotypes in each 96well plate as well as rerunning 10% of the samples, which were 100% concordant.

Dietary assessment

A 3-day food record was used to assess habitual intake of nutrients. Each subject was instructed on how to complete the questionnaire, including two weekdays and one weekend day. The food records were coded by a trained registered dietitian using the Nutrikcal computer program (Nutrikcal VO[®], México) which is based on the Mexican Food System and Equivalents [27]. Nutrient intakes were averaged over the 3-day food records.

Biochemical tests

Ten mL blood samples were drawn by venipuncture after a 12-hour fast and separated into two aliquots; one for DNA isolation and another for determination of lipid profile that included total cholesterol (TC), triglycerides (TG) and high-density lipoprotein cholesterol (HDL-c). Low-density lipoprotein cholesterol (LDL-c) was calculated using the Friedewald formula [28], and very low-density lipoprotein cholesterol (VLDL-c) concentration was calculated as Total Cholesterol - (LDL-c + HDL-c). Dry chemistry determined all biochemical tests on a Vitros 250 Analyzer (Ortho Clinical Diagnostics, Johnson & Johnson Co, Rochester, NY). For quality control purposes, we used a pooled human serum and a commercial control serum (Ortho Clinical Diagnostics, Johnson & Johnson Co) to account for imprecision and the inaccuracy of the biochemical measurements. The intra-assay variability (CV%) of biochemical assays was relative to ten repeated determinations of the control serum in the same analytical session. Inter-assay CV% for each variable was calculated from the mean values of control serum measured in five analytical sessions. When necessary, the serum was diluted with bovine serum albumin according to the manufacturers' instructions.

Statistical analyses

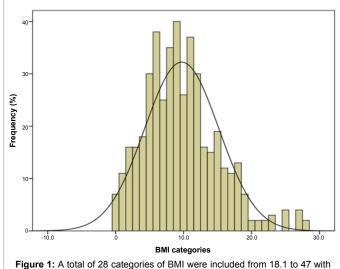
Quantitative values are expressed as mean \pm standard deviation (SD). A Kolmogorov-Smirnov test was used to show that the samples were not skewed towards a certain range of BMI. BMI frequencies were plotted on a histogram. Statistical differences between experimental groups were analyzed by one-way ANOVA test. Subsequently, post hoc tests were run to define intergroup differences according to the homogeneity of variances. Bonferroni's test assuming equal variances and Dunnett's T3 test assuming unequal variances were used. Qualitative variables and Hardy-Weinberg equilibrium (HWE) was analyzed by chi-square test. The association between *CD36* genotypes and lipid abnormalities was analyzed by odds ratio (OR), logistic and lineal regression tests. A p-value <0.05 was considered significant. Statistical analyzes were performed by using Epi-info TM7 (CDC, Atlanta, GA) and SPSS (version 20.0) software.

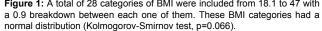
Ethical guidelines

The study protocol complied with the ethical guideline for the 2013 Declaration of Helsinki and was approved by the local Hospital Ethical Committee. All participants filled out a written informed consent.

Results

Figure 1 depicts the distribution of the BMI categories, which had a normal distribution (Kolmogorov-Smirnov test, p=0.066). Overall, the frequencies of the *CD36* genotype were A/A (33.6%), A/G (47.4%) and G/G (19%), while the allelic frequencies were A allele (57.1%) and G allele (42.9%). The distribution of genotypes was concordant





with the Hardy-Weinberg Equilibrium (p=0.50). Demographic and biochemical characteristics of subjects with different BMI categories are shown in Table 1. The groups were matched for age and gender. The overweight and obese subjects had higher levels of TC, TG, and VLDL-c (Table 1).

No differences in nutrient intake among the study groups were found regardless of *CD36* genotypes (Table 2). However, within the overweight group, subjects homozygous for the Aallele had a higher intake of calories, protein, total fat, SFA, mono unsaturated fatty acids (MUFA) and poly-unsaturated fatty acids (PUFA) than the other genotypes (Table 3). In this same group, subjects with high serum cholesterol showed a higher frequency of A/A genotype than those who did not have this lipid abnormality (46.6% versus 26.7%, p=0.003) (Table 4). Furthermore, high serum cholesterol was associated with the A/A genotype carriers than to A/G genotype carriers (OR=2.75, 95% CI 1.33-5.69, p=0.005). This result was later confirmed with a logistic regression test (OR=2.96, CI 95% 1.40-6.23, p=0.004). Finally, by using a linear regression test with the raw cholesterol values, an increase

of 19.97 mg/dL of cholesterol was attributed to the A/A genotype (B=19.91, CI 95% 2.18-37.76, p=0.028). No association with CD36 genotypes for other lipid abnormalities was found (data not shown).

Discussion

In this study, we have shown that homozygous subjects for the A allele had a higher intake of calories, protein, and fat in the diet than those who are non-A carriers. This result was supported by the fact that no differences in nutrient intake regardless CD36 polymorphism were observed. Although it has been reported that A/A genotype individuals have more preference for added fats than those who are not [23], this is the first study that demonstrates its association with fat intake. These findings may be explained since the A allele reduces the expression of the CD36 receptor and increases the taste perception thresholds, which ultimately leads to the consumption of a greater amount of fat [21,22]. However, the genetic effect of CD36 on food intake had its peak in the overweight group, but once obesity was reached, this effect was lost. Obesity has been associated with multiple metabolic alterations related to the up regulation of CD36 expression [29-33], which could have a

Variable	Normal weight	Overweight	Obesity	p-value
Study participants (n)	132	163	146	
Age (years)	40.2 ± 15.1	43.2 ± 13.9	42.5 ± 12.4	0.15
Gender (F/M, n)	(64/68)	(85/78) (90/56)		0.07
BMI(kg/m ²)	22.4 ± 1.9	22.4 ± 1.9 27.5 ± 1.4 34.5 ± 4		<0.001*
TC (mg/dL)	171.7.4 ± 40.5	4 ± 40.5 186.3 ± 51.3 191.3 ± 5		<0.001**
TG (mg/dL)	124.2 ± 66.6	124.2 ± 66.6 171 ± 132.5 193.5 ± 183.1		<0.001**
HDL-c (mg/dL)	44.4 ± 15.3 40.5 ± 11.5 39.8.2 ± 16.3		39.8.2 ± 16.3	0.05
LDL-c (mg/dL)	ng/dL) 105.3 ± 31.6 115.8 ± 45.9 117.7 ± 42.1		117.7 ± 42.1	0.07
VLDL-c (mg/dL)	24.8 ± 13.3	35.1 ± 28.2	38.9 ± 36.7	<0.001**

Average values are expressed as mean ± SD. n: number; BMI: Body Mass Index; TC: Total Cholesterol, TG: Triglycerides; HDL-c: High Density Lipoprotein cholesterol; LDL-c: Low Density Lipoprotein cholesterol; VLDL-c: Very Low Lipoprotein cholesterol; *Compared among all groups; **Normal weight *vs*. overweight and obesity

Table 1: Demographic and biochemical characteristics of the 441 subjects with different BMI categories.

Nutrient	Normal weight	Overweight	Obesity	<i>p-value</i>	
Study participants (n)	132	163	146		
Calories	2022.5 ± 557.8	2045.6 ± 582.9	2111.8 ± 671	0.45	
Carbohydrates (g)	264.9 ± 103.7	269.2 ± 101.4	285.3 ± 99.8	0.21	
Protein (g)	81.8 ± 25.1	83.3 ± 27.4	86.5 ± 29.7	0.35	
Fat (g)	74.0 ± 26.6	74.4 ± 30.3	71.9 ± 34.8	0.76	
SFA (g)	20 ± 9.4	20 ± 9.4 20 ± 10 18.3 ± 10.5		0.24	
MUFA (g)	MUFA (g) 24.9 ± 12.1		22.4 ± 13.4	0.15	
PUFA (g)	10.8 ± 5.7	11.4 ± 7.4	11.2 ± 6.9	0.75	

Average values are expressed as mean ± SD. n: number; SFA: Saturated Fatty Acids; MUFA: Monounsaturated Fatty Acids; PUFAs:Polyunsaturated Fatty Acids

 Table 2: Nutrient intake of the 441 subjects with different BMI categories.

Nutrient	Normal weight n=132			Overweight n=163			Obesity n=146					
Nument	A/A n=43	A/G n=58	G/G n=31	p-value	A/A n=53	A/G n=82	G/G n=28	p-value	A/A n=52	A/G n=69	G/G n=25	p-value
Calories	1916 ± 30.5	2109 ± 598	2016.6 ± 509	0.16	2236 ± 713	1902.5 ± 451	2115 ± 570	<0.001*	2188 ± 673	2104 ± 699	1961.6 ± 572	0.51
CH (g)	248.4 ± 98.4	285.4 ± 109	251.8 ± 98.3	0.10	286.6 ± 118	250.9 ± 80	290.5 ± 116	0.07	298.8 ± 87.7	286.5 ± 107	251.6 ± 97.6	0.18
Protein (g)	78.9 ± 24	84.9 ± 24.9	80.2 ± 27.3	0.47	90.4 ± 32.5	77.4 ± 23.1	87.6 ± 25.9	0.02*	88.9 ± 28.4	84.6 ± 32	86.8 ± 26	0.79
Fat (g)	70.4 ± 26.4	73.9 ± 27	79.2 ± 26	0.38	85.7 ± 38.4	68.5 ± 24.3	71.3 ± 25	<0.001*	73.3 ± 39	70.7 ± 35	72.3 ± 24	0.98
SFA (g)	18.8 ± 10	20.7 ± 9.9	20.3 ± 7.6	0.60	24.3 ± 11.4	18.2 ± 9.2	17.9 ± 7.5	<0.001**	17.8 ± 10	18.6 ± 11	18.4 ± 9	0.68
MUFA (g)	22.5 ± 11.2	25.8 ± 13	26.5 ± 11.5	0.19	30 ± 15.7	22.6 ± 11.7	23.7 ± 9.2	<0.001*	21.2 ± 13	22.9 ± 15	23.7 ± 12	0.45
PUFA (g)	9.7 ± 5.1	11.2 ± 5.7	11.4 ± 6.3	0.20	14 ± 9.7	9.6 ± 5.2	11.5 ± 6.7	<0.001*	11.3 ± 7	11.1 ± 7.5	11.2 ± 6	0.99

Average values are expressed as mean ± SD. CH: carbohydrates; BMI: Body Mass Index; SFA: Saturated Fatty Acids; MUFA: Monounsaturated Fatty Acids; PUFAs:Polyunsaturated Fatty Acids. *A/A vs. A/G genotype; ** A/A vs. A/G and G/G genotypes, respectively.

Table 3: Nutrient intake by genotype of the rs1761667 CD36 gene polymorphism in 441 subjects with different BMI categories.

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Group	High serum ch	olesterol n (%)	OR (CI 95%) A/A vs. A/G	p-value	OR (CI 95%)	p-value	
	No	Yes			A/A vs. G/G		
Normal weight			· · ·				
A/A	32 (30.5)	12 (44.4)	1.80				
A/G	48 (45.7)	10 (37)		1.80 (0.69-4.65)	0.99	0.22	1.87 (0.58-6.02)
G/G	25 (23.8)	5 (18.5)	(0.03-4.00)		(0.00-0.02)		
Over weight			· ·				
A/A	28 (26.7)	27 (46.6)	2.75 (1.33-5.69) 0.005				
A/G	60 (57.1)	21 (36.2)		0.005	1.63 (0.63-4.21)	0.30	
G/G	17 (16.2)	10 (17.2)	(1.55-5.69)		(0.00-4.21)		
Obesity	-						
A/A	32 (37.2)	19 (31.7)	0.92 (0.43-1.94) 0.83				
A/G	42 (48.8)	27 (45)		0.83	0.50 (0.19-1.32)	0.16	
G/G	12 (14)	14 (23.3)			(0.101.02)		

The cutoff point for considering high serum cholesterol was TC \ge 200 mg/dL.

Table 4: Association of the rs1761667 CD36 gene polymorphism with high serum cholesterol in 441 subjects with different BMI categories.

greater effect than *CD36* genetic variation. Furthermore, additional environmental factors may modulate CD36 expression. Among these, alcohol and fatty acids are known to modify the epigenome which include DNA methylation, histones acetylation, and recruitment of transcription-related enzymes to specific genetic loci [34-36]. Nonetheless, further studies are needed to confirm this hypothesis.

Another important finding is that in the group of overweight subjects, increased serum cholesterol levels were associated with the A/A genotype carriers but not with the other genotypes. This finding is consistent with another study previously reported in Mexicans; however, unlike our results, this association was found in lean subjects [37]. Together, these findings suggest that the Aallele of the *CD36* gene polymorphism is associated with altered blood lipid levels that may contribute to an atherogenic profile.

Due to its capacity of being a high-affinity receptor for native HDL, LDL, and VLDL lipoproteins, CD36 contributes directly to their regulation [38]. Nonetheless, low expression of CD36 due to the rs1761667 polymorphism effect could result in lower cholesterol uptake by lipoproteins increasing serum cholesterol levels, therefore. Another key point in this study is that homozygous subjects for the A allele had a high intake of SFA, which have been associated with high serum cholesterol levels and LDL-c [39]. Furthermore, although the A/A genotype carriers had a higher intake of MUFA and PUFA, which have proven hypolipidemic effects [40-43]; their intake was lower than what has been recommended for the Mexican population [44].

Nowadays, Mexico's obesity prevalence is one of the world's highest [45]. However, despite the negative impact of obesity on public health, no interventions have been effective in reducing obesity rates in our population [46]. With the current knowledge that many genes influence food intake and eating behaviors [47], the success of these strategies may largely depend on the individual's genetic characteristics [48]. Based on our results, *CD36* could be a useful genetic marker for designing patient-specific prescriptions for diet and lifestyle. In conclusion, the A allele of *CD36* was predominant in subjects from West Mexico. In addition, a high-fat diet and high serum cholesterol levels were associated with the A/A genotype.

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