

# Efficacy of Ezetimibe Is Not Related to *NPC1L1* Gene Polymorphisms in a Pilot Study of Chilean Hypercholesterolemic Subjects

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## Abstract

**Background and Objective** Niemann-Pick C1 Like 1 (*NPC1L1*) is a multi-transmembrane transport protein highly expressed in the small intestine. It mediates sterol transfer throughout the brush border membrane of enterocytes, becoming essential for intestinal cholesterol absorption and ensuing whole-body cholesterol homeostasis. This protein is targeted by ezetimibe, a potent cholesterol absorption inhibitor. Single nucleotide polymorphisms (SNPs) in *NPC1L1* have been associated to variation in both plasma low-density lipoprotein (LDL) cholesterol levels and lipid-lowering medication with ezetimibe. However, there are no data evaluating the impact of *NPC1L1* variants on Chilean subjects medicated with ezetimibe monotherapy. Therefore, we assessed the contribution of two unexplored *NPC1L1* variants on plasma lipids and response to ezetimibe in Chilean hypercholesterolemic individuals.

**Methods** Using PCR-restriction fragment length polymorphism (RFLP), we analyzed the SNP distribution of two common variants;  $-133A>G$  (rs17655652) and  $1679C>G$  (rs2072183), and their relation with plasma

lipids and lipid-lowering response to ezetimibe in 60 hypercholesterolemic Chilean subjects.

**Results** Genotype distribution for the rs17655652 variant was AA 57 %, 40 % AG and 3 % GG, whereas for the rs2072183 SNP was 57 % CC, 35 % CG and 8 % GG. Minor allele frequencies (MAFs) were 0.23 and 0.26, respectively. No association was observed between *NPC1L1* SNPs and baseline cholesterol. After therapy, none of the polymorphisms affected ezetimibe response in the studied cohort ( $P > 0.05$ ).

**Conclusion** Data obtained indicates that polymorphisms rs17655652 and rs2072183 were not related to cholesterol variability. Also, lipid-lowering response to ezetimibe is not impacted by the *NPC1L1* polymorphisms studied in Chilean hypercholesterolemic subjects.

## Key Points

Polymorphisms in *NPC1L1* are related to differential response to ezetimibe, but reports documented among different ethnicities are inconsistent.

Response to ezetimibe therapy in Chilean individuals evidenced wide inter-individual variability.

The variants studied are not related to plasma lipids and ezetimibe response in hypercholesterolemic subjects from Chile.

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## 1 Introduction

Although cholesterol is crucial to several functions of mammalian cells, elevated plasma cholesterol levels—or

hypercholesterolemia—is a well-established risk factor of atherosclerosis and major cardiovascular events [1]. Plasma levels of cholesterol are tightly regulated by three major metabolic processes; dietary absorption, de novo synthesis and biliary clearance and excretion [2]. About 50 % of dietary cholesterol is absorbed, where two-thirds is from the bile while the other one-third is derived from the diet [3], influencing endogenous cholesterol biosynthesis as well [4]. In contrast to the long-standing hypothesis indicating that cholesterol uptake was related to a passive diffusion process, in the early 1990s evidence showed that dietary cholesterol was absorbed through a protein-mediated mechanism [5], and discovery of inhibitors selectively blocking cholesterol absorption supported that this process is via a specific transporter [6].

Ezetimibe is a drug that blocks dietary and biliary cholesterol absorption by the small intestine [7]. It was approved by the US Food and Drug Administration (FDA) in 2002 for the treatment of primary hypercholesterolemia [8]. Contrary to the conventional rationale in drug design, it started being used as a lipid-lowering drug without a clear understanding of the molecular target and long before it was identified. Ezetimibe undergoes rapid and extensive metabolism to its phenolic glucuronide in the intestinal wall and is excreted into the bile, delivering the drug back to the intestinal lumen where it can inhibit cholesterol absorption. It has a plasma half-life of approximately 22 h, which allows for once-daily dosing [9]. Both, ezetimibe and its glucuronide are excreted mostly by feces (90 %) and urine (10 %). Ezetimibe does not influence the cytochrome P450 enzymes. Hence, no significant interactions occur with most medications [10, 11]. Ezetimibe also reduces plasma phytosterol levels, sitosterol and campesterol in patients with sitosterolemia, a condition caused by mutations in ABCG5/G8 co-transporters [12, 13]. Identification of ezetimibe, a potent cholesterol absorption inhibitor, finally confirmed that cholesterol uptake is mediated by a specific transport protein [14]. Intense efforts were made to elucidate this putative protein, hypothesizing that it should be in direct contact with the intestinal luminal content, expressed on the brush border membrane surface of enterocytes and to contain sequence motifs known to interact with sterols. Through a genomic/bioinformatics approach [15], the only candidate gene resulted in Niemann-Pick C1 Like 1 (NPC1L1), known to share diverse features related to a sterol transporter [16, 17].

NPC1L1 plays a fundamental role in cholesterol homeostasis, reducing up to 70 % of cholesterol intake by the intestinal epithelium in NPC1L1 knockout mice [15]. In *Npc1l1(-/-)/ApoE(-/-)* mice, lack of NPC1L1 inhibits cholesterol absorption, reduces plasma cholesterol and inhibits the development and progression of atherosclerosis

[18], thereby establishing that NPC1L1 is critical for cholesterol uptake. A following investigation determined that NPC1L1 is the unequivocal direct molecular target of ezetimibe [19]. In humans, ezetimibe effectively lowers plasma cholesterol by 15–20 % and is well tolerated [20–22]. It also promotes a compensatory increase of cholesterol synthesis [23]. However, a significant interindividual variability has been documented in terms of intestinal cholesterol absorption and low-density lipoprotein (LDL)-C reduction at baseline and after ezetimibe treatment. LDL-C levels in response to ezetimibe therapy are reported to differ according to NPC1L1 variants. Several genetic variants of this protein were found in low cholesterol absorbers [24] and are consistent with a reduction in plasma levels of low-density lipoproteins [25]. In previous studies, a relationship between ezetimibe treatment and variations at the *NPC1L1* locus was demonstrated [26, 27]. However, to date there are still limited data in relation to NPC1L1 polymorphisms, and no evidence exists in Chilean populations. Therefore, the aim of this study was to investigate the possible effect of two common variants on the response to 10 mg/day/1 month of ezetimibe monotherapy in Chilean hypercholesterolemic subjects.

## 2 Materials and Methods

### 2.1 Subjects

Sixty unrelated male and female Chilean individuals, over 18 years old, with a diagnosis of hypercholesterolemia, according to NCEP norms [28] were enrolled. After a washout period of four weeks, these subjects underwent treatment with 10 mg/day of ezetimibe (Zient\*, Schering-Plough, Puerto Rico) for 1 month, sufficient time to achieve a significant improvement in the lipid profile as demonstrated elsewhere [21, 29, 30]. Subjects with diabetes mellitus, hypothyroidism, pregnancy, kidney and hepatic dysfunction, and those taking oral contraceptives and concomitant hypolipemiant medication, such as statins, niacin or fibrates, were discarded. Characteristics of the study group such as age, hypertension and body mass index were annotated. The study design was approved by the local ethics committee. All individuals gave their written informed consent to participate in the study.

### 2.2 Biochemical and Molecular Analysis

Two venous blood samples were obtained after a 12-h fast and a third sample obtained for biochemical determinations after ezetimibe treatment was completed. The first sample was collected using EDTA tubes (1 mg/mL) to obtain

genomic DNA from leukocytes by a protocol described elsewhere [31]. Second and last samples were obtained without the addition of anticoagulant for determination of serum glucose and lipid profile using routine enzymatic colorimetric assays [32, 33] before and after ezetimibe medication. LDL-C was determined using Friedewald's formula when triglycerides did not exceed 400 mg/dL (4.8 mmol/L). All determinations were performed in the semi-automatic biochemistry analyzer Humalyzer 3000 (Human, Germany). Accuracy of biochemical procedures was controlled using normal and pathological commercial serums (Human, Germany).

Polymorphisms rs2072183 and rs17655652 located in exon 2 and in the promoter region of *NPC1L1*, respectively, were determined by polymerase chain reaction (PCR) followed by restriction fragment length polymorphism (RFLP). Primers for the rs2072183 single nucleotide polymorphism (SNP) were as follow: 5'-TGCAATGAGTCCAAAGGTGACG-3' (forward) and 3'-ACCATCTTGCTTTGTGCCCTGGCG-5' (reverse). For the rs17655652 variant, the primers were 5'-AGGAACAGCCAAGGGCTGA A-3' (forward) and 3'-AGCAGTGTTAGGGGCTAATAG CGT-5' (reverse). Each reaction was completed using 10 mM of each dNTP, 1 U *Taq* polymerase and PCR buffer (50 mmol/L KCL, 2 mmol/L MgCl<sub>2</sub>, 20 mmol/L (NH<sub>4</sub>)<sub>2</sub>SO<sub>4</sub>, 75 mmol/L Tris-HCl, pH 9.0, in a 50 µL final reaction volume.

Once the PCR reaction was concluded, products were incubated with *TaqI* (rs2072183) or *BspI* (rs17655652) for enzymatic digestion, during 60 min, at 37° C in a final volume of 30 µL. The resulting fragments were separated on 2 % agarose gel for 45 min at 100 V, stained with ethidium bromide and visualized on a digital photo-documentation system E-Box 1000 (VilberLourmat, France). Twenty percent of the samples were selected randomly and reanalyzed as quality control criteria. Gels were re-read blindly by two more persons without any change in the genotypes.

### 2.3 Statistical Analysis

Data analysis was completed using the Sigma Stat software v. 3.5 (SPSS Inc., Chicago IL, USA). Allelic frequencies and genotype distribution were estimated by gene counting and tested for Hardy-Weinberg equilibrium. Lipid values before and after ezetimibe treatment were evaluated by paired *t* test. Gaussian distribution of variables was assessed by Shapiro-Wilk normality test ( $\alpha = 0.05$ ). Coefficient of variation (CV) was also obtained. Since the after-treatment values of triglycerides were the only borderline data ( $P = 0.04$ ), along with similar CVs between therapies, these values were considered and analyzed in the same manner as before-treatment, using the standard deviation as

a scatter measure. Due to the low frequency of the recessive genotypes, further association analyses were concluded by clustering genotypes into a dominant inheritance model. Differences in non-continuous variables, genotype and allelic distributions were compared by Chi-square test. Statistical significance was considered at  $P < 0.05$ .

## 3 Results

### 3.1 Clinical Data

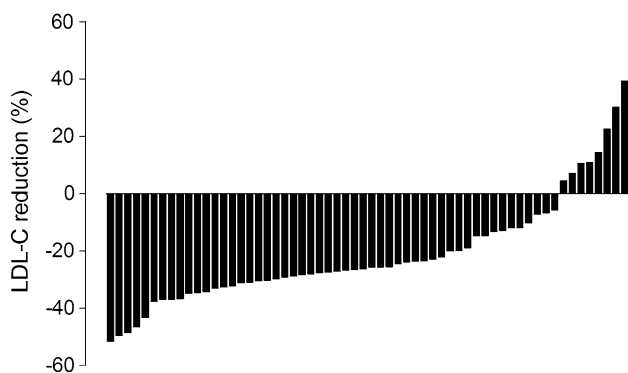
Clinical characteristics, along with changes in lipid profile before and after completion of lipid-lowering treatment in the Chilean cohort are summarized in Table 1. As expected, ezetimibe was effective in reducing plasma lipids after 4 weeks, observing an 18 % reduction in TC and a 23 % of LDL-C reduction ( $P < 0.0001$ ). No significant differences were found regarding HDL-C nor triglycerides response after the treatment was completed ( $P = NS$ ). Despite a mean 23 % reduction in LDL-C levels following lipid-lowering therapy, we observed large interindividual

**Table 1** Clinical and laboratory determinations

Variables	HC ( $n = 60$ )	<i>P</i> value
Age, years	51.3 ± 9.4	–
Gender (Female), %	72	–
Ethnicity (Amerindian), %	90	–
Menopause, %	28	–
Cigarette smoking, %	20	–
Systolic pressure, mmHg	132.4 ± 22.6	–
Diastolic pressure, mmHg	79.1 ± 12.0	–
Body mass index, kg/m <sup>2</sup>	28.7 ± 4.3	–
WHR	0.918 ± 0.08	–
Total cholesterol, mg/dL		
Basal	271.9 ± 29.1	<0.0001
Treatment	222.4 ± 33.6	
LDL cholesterol, mg/dL		
Basal	180.7 ± 28.5	<0.0001
Treatment	139.7 ± 28.3	
HDL cholesterol, mg/dL		
Basal	44.0 ± 14.2	0.275
Treatment	42.8 ± 12.9	
Triglycerides, mg/dL		
Basal	165.7 ± 56.9	0.053
Treatment	155.9 ± 57.3	

Continuous variables presented as mean ± SD. Ezetimibe treatment results were evaluated by paired *t* test

*HC* hypercholesterolemic, *BMI* body mass index, *WHR* waist-hip ratio, *LDL* low-density lipoprotein, *HDL* high-density lipoprotein, *WHR* waist-hip ratio



**Fig. 1** Individual response to ezetimibe treatment using a 10 mg/day dose during 4 weeks in the studied population. Evaluation was performed using LDL-C as the variable of efficacy

**Table 2** Allelic and genotype frequencies for *NPC1L1* polymorphisms in hypercholesterolemic subjects

SNP	Genotype			HWE ( <i>P</i> )	Alleles	
-133A>G (rs17655652)	AA	AG	GG	0.360	A	G
	57 % (34)	40 % (24)	3 % (2)		77 %	23 %
1679C>G (rs2072183)	CC	CG	GG	0.502	C	G
	57 % (34)	35 % (21)	8 % (5)		74 %	26 %

Number of individual in parentheses

HWE Hardy–Weinberg equilibrium

variability when individual response to medication was examined (Fig. 1).

### 3.2 *NPC1L1* Single Nucleotide Polymorphisms

Unbiased selection of patients was confirmed accordance to Hardy-Weinberg equilibrium when the genotype frequencies of the *NPC1L1* variants were evaluated. Genotype distribution and minor allele frequency (MAF) for the rs17655652 and rs2072183 polymorphisms are shown in Table 2. In addition, MAFs registered in this study and from different cohorts previously reported were listed in Table 3.

### 3.3 Single Nucleotide Polymorphisms in *NPC1L1* and Lipid-Lowering Response to Ezetimibe

Lipid levels according to genotypes are shown in Table 4. As observed, the rs2072183 variant did not influence the lipid profile. Also, SNP rs17655652 was not related to lipid levels in hypercholesterolemic subjects. Furthermore, when using the dominant inheritance model, no significant association was observed between ezetimibe treatment and the two polymorphisms investigated ( $P > 0.05$ ).

## 4 Discussion

In this study, we have evaluated two single nucleotide polymorphisms in the *NPC1L1* locus, and their relation with plasma lipids and lipid-lowering response to ezetimibe in a cohort of Chilean hypercholesterolemic subjects.

Absorption of cholesterol and plasma levels of the low-density lipoprotein fraction are complicated traits strongly influenced by environmental and but genetic factors. It has been estimated that up to 50 % of the inter-individual plasma LDL-C variation is due to genetic factors [34]. Furthermore, there are multiple genes involved in LDL regulation contributing to the dyslipidemic phenotype [24]. After its discovery, *NPC1L1* has acquired great relevance as the pharmacological target of ezetimibe, a potent and selective cholesterol absorption inhibitor [35]. However, blocking intestinal cholesterol uptake results in an increased rate of endogenous cholesterol synthesis [36]. This outcome is taken as the norm for the use of combined therapy between ezetimibe and 3-hydroxy-3-methyl-glutaryl-CoA reductase (HMGCR) inhibitors known as statins, inducing an additional and substantial decrease of plasma LDL-C [37–41]. Our data support the extensive evidence documenting the potent hypolipemiant action of ezetimibe [39, 40, 42]. As shown in Table 1, four weeks of therapy was sufficient time to achieve a considerable decrease in total and LDL-cholesterol. Although it has been confirmed that four weeks of treatment are adequate to observe significant lipid diminutions [30], two independent reports demonstrated an even earlier and equally effective reduction, starting from the 2nd week of ezetimibe therapy [21, 29]. In spite of studies showing that ezetimibe also improves non-LDL cholesterol fractions, raising high-density lipoprotein cholesterol and reducing triglycerides levels [20–22], we did not observe these effects in the cohort evaluated. Additionally, response to this drug showed high inter-individual variability, resulting in not all patients achieving an adequate clinical response [43]. Since *NPC1L1* is considered to be an important factor affecting plasma cholesterol levels and clinical response to ezetimibe, exploring genetic variations in this gene are mandatory to value more precisely this response disparity. Such studies ultimately will lead to improved understanding of the response-related dynamics of the drug. Determination of the frequency of SNPs in a particular population is also practical for translating the variants into clinical use. Factors such as ethnicity and gender, affecting the allelic association with disease, are unlikely to be determined without population based allele frequencies [44].

The minor allele frequencies (MAFs) determined in this study were similar to those previously described in a Spanish population [45]. A second larger study, including Spanish subjects, also showed MAF similarities [46],

**Table 3** MAF for *NPC1L1* polymorphisms from ethnically diverse individuals

SNP	Chilean	[45]	[46]			[55]	[58]	
		Hispanic	Caucasian	Hispanic	African American	Taiwanese	Mulao	Han
−133A>G (rs17655652)	23.0	25.0	29.9	18.6	9.2	–	–	–
1679C>G (rs2072183)	26.0	24.0	21.9	28.3	17.9	36.0	29.7	37.2

MAF minor allele frequency

**Table 4** Influence of *NPC1L1* polymorphisms on serum lipid profile in HC patients treated with ezetimibe

Variables, mg/dL	−133A>G (rs17655652)			1679C>G (rs2072183)		
	AA (34)	AG+GG (26)	<i>P</i> value	CC (34)	CG+GG (26)	<i>P</i> value
<b>Total cholesterol</b>						
Basal	267.1 ± 23.2	280.0 ± 34.7	0.095	271.6 ± 31.0	272.1 ± 27.5	0.945
Treatment	221.4 ± 31.5	224.5 ± 37.8	0.736	228.3 ± 35.1	218.5 ± 32.6	0.301
% Change	−16.8 ± 11.9	−19.2 ± 13.5	0.463	−15.4 ± 13.1	−19.4 ± 11.2	0.240
<b>LDL cholesterol</b>						
Basal	180.2 ± 25.1	182.6 ± 33.8	0.768	175.4 ± 29.6	186.1 ± 26.8	0.193
Treatment	138.8 ± 28.7	140.0 ± 28.8	0.877	143.0 ± 31.6	136.7 ± 26.7	0.454
% Change	−24.4 ± 23.7	−21.5 ± 19.9	0.637	−20.5 ± 25.4	−25.5 ± 18.9	0.452
<b>HDL cholesterol</b>						
Basal	47.2 ± 16.9	41.1 ± 8.2	0.103	43.0 ± 15.7	47.1 ± 13.0	0.322
Treatment	45.2 ± 14.6	41.0 ± 9.6	0.218	42.7 ± 14.2	45.7 ± 11.4	0.421
% Change	−1.0 ± 23.3	−0.5 ± 19.3	0.785	−1.9 ± 23.1	−0.5 ± 21.1	0.687
<b>Triglycerides</b>						
Basal	161.1 ± 57.1	168.7 ± 57.0	0.695	175.4 ± 60.5	141.1 ± 42.5	0.061
Treatment	150.4 ± 56.1	161.9 ± 60.8	0.515	166.0 ± 55.9	143.0 ± 56.8	0.199
% Change	−8.4 ± 32.9	−7.7 ± 38.0	0.951	−5.3 ± 33.1	−8.0 ± 35.5	0.813

Number of subjects in parentheses. Values are expressed as mean ± SD and compared by *t* test

LDL low-density lipoprotein, HDL high-density lipoprotein

indicative of the common ethnic background as the southern Chilean population had a strong influx of Spanish genes during the colonization of the country [47]. In contrast, MAFs from Caucasians, African American and Asian populations were dissimilar from ours, showing interethnic differences in allele frequencies and highlighting the importance of MAF determination across diverse populations.

The polymorphisms studied in this investigation were not related to baseline low-density lipoprotein levels. This result is likely to be due to the hypercholesterolemic nature of the cohort studied, reducing the power to detect baseline associations. Concerning the lipid-lowering response, our results point out that the two polymorphisms in *NPC1L1* are unrelated to lipid-lowering response using 10 mg/day for 1 month of ezetimibe monotherapy in Chilean hypercholesterolemic individuals.

In relation to the SNP located in the promoter region of *NPC1L1*, results are controversial. This variant was shown to have a significant effect on the gene promoter activity,

linking this variation to autosomal dominant hypercholesterolemia (ADH) [45]. In the PROSPER trial [48] the −133A>G polymorphism—or rs17655652—and not other variants, was associated with 6-month LDL-C lowering. However, subjects evaluated in the PROSPER cohort were mostly elderly with a mean age of 75 years, while individuals enrolled in our study had a mean age more than 20 years younger, a covariate that can define lipid response [49]. Also, the MAFs found in the PROSPER trial were more related to a Caucasian phenotype, contrasting with the Amerindian background reported for Chilean subjects [50]. Ethnicity has been reported to be a decisive factor contributing to control of dyslipidemia [51]. Finally, another difference between the studies was that, response in PROSPER was evaluated using pravastatin instead of ezetimibe. Hence, reduction of LDL-C levels was not achieved only by a cholesterol absorption inhibition mechanism. On the contrary, a recently published study supported our results demonstrating that the −133A>G SNP did not influence lipid parameters after 3, 6 or



12 months of ezetimibe monotherapy medication in hyperlipidemic subjects [52]. This publication did find elevation in Apo-A1 levels associated with a particular allele of *NPC1L1*.

In 2010, a large meta-analysis strongly correlated the rs2072183 variant with total and LDL-C levels [53]. The PROSPER study also reported an association between the rs2072183 SNP with slightly higher baseline LDL-C levels, indicating that *NPC1L1* variants do associate with LDL-C. Maeda et al. [54] demonstrated this variant to be correlated with significantly higher levels of campesterol, a marker of cholesterol absorption, thus enhancing this process in Japanese subjects. In a prior report, this variant was absent in responders to ezetimibe and normal subjects, and was associated with non-responsiveness to this drug [27], probably due to the higher cholesterol absorption by these individuals. There was no relation reported between this allele and basal cholesterol levels in control subjects from different ethnic backgrounds [46]. Similarly, it was not associated with cholesterol levels in subjects from Taiwan [55], similar to results obtained elsewhere [56]. Nevertheless, this variant was associated with higher total cholesterol levels in 127 Japanese subjects with Crohn's disease [57] and was documented to cause different plasma lipid profiles between the Mulao and Han populations in China [58]. Recently, the rs2072183 genotype distribution was found to be significantly different in dyslipidemic vs. healthy Japanese individuals [59]. Furthermore, a significant association was shown between this SNP and LDL-C response using an extreme responder analysis, defined as the upper and lower 10th percentiles of LDL-C responders [46]. However, the influence of this polymorphism was evaluated in a large Caucasian cohort using a combined ezetimibe-statin therapy, which provides greater reductions in LDL-C as combined therapy achieves inhibition in both cholesterol synthesis and absorption [60], thus allowing a marked extreme response to lipid-lowering medication. Moreover, association between the SNP and LDL-C was further supported through haplotype analyses, which was not explored in this study.

According to the common disease-common variant hypothesis, we explored two frequent polymorphisms in a Chilean cohort. Although we did not find an association between the polymorphisms and lipid variability, we cannot exclude that those SNPs with MAF <5 % in *NPC1L1* may be affecting the lipid profile, since it was demonstrated that rare variants account for a significant effect on lipid levels [25]. Additionally, a unique Amerindian component has been demonstrated in our population, which besides affecting the allelic distribution in our cohort, as discussed above, may influence control of plasma lipid levels. Moreover, cholesterol response to lipid-lowering therapies is variable. Many reasons for this

variability can be conjectured. Absorption, activation, modification, binding, interactions, transport, degradation and elimination are just a few processes that can influence a particular drug, modifying its action. The two polymorphisms studied only account for a small percentage of the more than 25 previously described variants in *NPC1L1* gene [61]. Also, is important to remember that cholesterol absorption is not exclusively regulated by *NPC1L1*, although explaining about 70 % of the reduction in absorption of dietary cholesterol, other proteins, such as SR-B1 and CD36, are also involved in this process [62, 63]. Lastly, efficiency of cholesterol absorption is also critical, which ranges from 29 to 80 % among healthy individuals [64] and also contributes to differences in plasma levels of LDL-C.

A major limitation in this study is the small sample size, which could contribute some bias of the final results. However, when sample sizes are restricted, statistical power can be overcome by evaluating single nucleotide polymorphisms with MAFs superior than 5 % [65]. Additional studies including a bigger cohort and analyzing simultaneously multiple genes critical to cholesterol homeostasis are necessary. To our knowledge, this is the first study reporting the influence of the *NPC1L1* rs2072183 and rs17655652 single nucleotide polymorphisms on ezetimibe therapy in Chilean subjects. In summary, the results obtained indicate that the two variants studied were not related to cholesterol variability. Additionally, none of the polymorphisms influenced lipid-lowering therapy with ezetimibe.

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**Author contributions** Conceived and designed the experiment: LAS TZ FL; Performed the experiments: TZ NS JC; Analyzed the data: TZ NS LAS; Contributed reagents/materials/analysis tools: JC FL LAS; Wrote the paper: TZ LAS.

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