

**INFLUENCE OF THE HMG-CoA REDUCTASE (TTA)_n REPEAT GENE
POLYMORPHISM ON THE EFFECTS OF ATORVASTATIN IN CORONARY
ARTERY DISEASE PATIENTS**

Viviana Noriega MSc^{a,b}, Christian Pennanen MSc^{a,b}, Maria Pilar Sánchez MSc^b,
Mario Chiong MSc^{a,b}, Marcelo Llancaqueo MD^d, Sergio Lavandero PhD^{a,b,c} and
Juan Carlos Prieto MD^{c,d*}

^aFONDAP Center for Molecular Studies of the Cell, ^bFaculty of Chemical and
Pharmaceutical Sciences, ^{b,c}Institute of Biomedical Sciences, Faculty of Medicine and ^e
^dCardiovascular Center, Clinical Hospital, University of Chile, Santiago, Chile.

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Short title: Polymorphism HMGCR in coronary artery disease patient.

Running title: polymorphism HMG-CoA and cholesterol levels

*Corresponding authors: Juan Carlos Prieto MD, Cardiovascular Center, Clinical
Hospital, Universidad de Chile, Santos Dumont 999, Santiago 8380492, Chile. Tel:
+562-978-6044; E-mail: jprieto@med.uchile.cl or Sergio Lavandero PhD, FONDAP
Center for Molecular Studies of the Cell, Faculty of Chemical and Pharmaceutical
Sciences, Olivos 1007, Santiago 8380492, Chile. Tel: +562-978-2903; E-mail:
slavander@uchile.cl

Background Inhibitors of 3-hydroxy-3-methylglutaryl-coenzyme A (HMG-CoA) reductase have been clinically used for lowering total and low-density lipoprotein cholesterol (LDL-C). Interindividual pharmacological differences observed with this treatment have been attributed to genetic differences. The aim of the present study was to examine the association between LDL-C reduction by atorvastatin and (TTA)_n repeat polymorphism in the HMG-CoA reductase gene (HMGCR) in patients with coronary artery disease (CAD). Also, changes in levels of total cholesterol, high sensitivity C-reactive protein (hsCRP) and free F₂-isoprostanes induced by atorvastatin and their association with the (TTA)_n polymorphism were also assessed.

Methods Sixty-four patients with documented CAD completed the trial receiving 40 mg of atorvastatin daily for 8 weeks. Lipid levels as, total cholesterol, high-density lipoprotein cholesterol (HDL-C) and serum triglyceride levels were determined using enzymatic methods. LDL-C was calculated using the Friedewald's formula. The hsCRP levels were determined by latex method assay and free F₂-isoprostanes were performed using enzyme immunoassay (EIA). Genotyping was done by the polymerase chain reaction.

Results The genotype distribution of the HMGCR (TTA)_n polymorphism was: >10/>10 in 22 of 64 patients (34%), >10/10 in 14 of 64 patients (22%) and 10/10 in 28 of 64 patients (44%). Atorvastatin significantly reduced LDL-C levels in all patients ($p < 0.0001$), regardless the type of HMGCR (TTA)_n polymorphism. Reduction on hsCRP was observed in atorvastatin-treated patients with HMGCR (TTA)_n alleles >10/>10 and 10/10 ($p < 0.05$). Free F₂-isoprostanes and total cholesterol were also reduced significantly after treatment for all alleles ($p < 0.001$).

Conclusions In a sample of patients with chronic stable CAD, no associations were found in the atorvastatin-induced reduction of LDL-C, total cholesterol, hsCRP and free F₂-isoprostanes with the HMGCR (TTA)_n polymorphism.

Therapy with 3-hydroxy-3-methylglutaryl-coenzyme A (HMG-CoA) reductase inhibitors (statins), is widely used in the treatment of hypercholesterolemia, lowering the total and low-density lipoprotein cholesterol (LDL-C). Statins therapy also lowers C-reactive protein (CRP) levels in a LDL cholesterol-independent manner (1-7). Statins also have antioxidant properties (8), and is prescribed for both, primary (9-11) and secondary (12-16) prevention of coronary artery disease (CAD). However, considerable interindividual variation exists in response to statin therapy (17). Studies about genetic variations in HMG-CoA reductase gene (HMGCR), the direct target of statin therapy, and the relation with the changes in lipid levels with statin therapy are limited (18,19). Previous studies have indicated that variable number of tandem repeats (VNTR) polymorphism (TTA)_n of the HMGCR gene was associated with pathologies such as CAD and hypercholesterolemia (20,21). Moreover, it has been reported an almost significant difference between the (TTA)_n repeat polymorphism in the HMGCR gene and cholesterol absorption in response to plant stanol consumption (22).

The aim of the present study was to evaluate the role of HMG-CoA reductase gene (HMGCR) (TTA)_n repeat polymorphism in relation to the LDL-C lowering efficacy of atorvastatin in Chilean patients with CAD. A secondary objective was to determine the change in levels of total cholesterol, high-sensitivity CRP (hsCRP) and free F₂-isoprostanes after atorvastatin treatment and its relation with the presence of HMGCR (TTA)_n polymorphism in patients with CAD.

Methods

Study design and patient selection

This study was composed of 69 patients who were obtained from the database of Cardiovascular Center, Clinical Hospital, University of Chile, these patients had history of coronary heart disease treated with coronary artery bypass grafting (CABG) or angioplasty. This study was an open study where one daily dosing of 40 mg atorvastatin (Saval S.A. Chile) was administered for 8 weeks. Medical history and current medications were recorded at the first visit. Physical examination was performed and a dietary approach was given. At the follow-up, potential adverse effects were registered at each visit. This study was approved by the Ethics Committee of the Clinical Hospital of the University of Chile (Santiago, Chile) and all patients gave their informed consent.

Subjects

Male and female patients, >18 years-old with angiographically documented CAD, baseline levels of LDL-C 100 to 220 mg/dL, triglyceride levels <400 mg/dL, with no use of statins during 2 months previous to the enrollment, and without contraindications to statin therapy. Subjects were excluded if they had been hospitalized within 90 days with an acute coronary syndrome, undergone coronary revascularization procedure within 90 days, or had a known acute or long-term inflammatory process. Additionally, patients with active liver disease or dysfunction determined by hepatic transaminase \geq 2 fold normal upper limit, serum creatine kinase level > 3 fold normal upper limit and serum creatinine > 2.0 mg/dL, were excluded. Test for pregnancy was not performed because all patients were in post-menopause.

Laboratory testing

As part of the protocol, venous blood was obtained at baseline and after 8 weeks for lipids levels, hsCRP and free F₂-isoprostanes. The hsCRP levels were determined by an assay from Dade-Behring (Deerfield, IL) (23) and free F₂-isoprostanes were determined as described by Pradelles *et al.* (24). Lipid levels were determined using enzymatic methods. Low-density lipoprotein cholesterol was calculated using the Friedewald formula (25).

Genotyping

Genomic DNA was extracted from a whole blood sample using standard extraction procedures. Genotyping for the (TTA)_n repeat polymorphism within the intron 2 of the HMGCR gene was performed by a polymerase chain reaction (PCR) according to Lalovic *et al* (26). Seven different products ranging from 175-193 bp were amplified using the primers 5'CAGAGTGACACTCTGTCTCC-3' and 5'CATGTTCCATCCATGTCTGC-3', corresponding to 10 to 16 repeats of the triplet TTA. Therefore, patients were divided into 3 categories. The first group had two alleles with more than 10 TTA repeats (>10/>10), the second group one allele >10 and the other allele with 10 TTA repeats (<10/10), and the third group had two alleles with 10 TTA repeats (10/10).

Statistical analysis

Hardy-Weinberg equilibrium was assessed using the χ^2 test. The genotype frequency were in Hardy-Weinberg equilibrium.

The primary comparison of this study was the reduction magnitude in LDL-C at 8 weeks versus the presence the different (TTA)_n polymorphisms in the HMGCR post-treatment with atorvastatin.

Categorical data were analyzed using chi-square test or Fisher's exact test as indicated. Differences in continuous variables were evaluated by Student's test, one-way analysis of variance or the Kruskal Wallis rank test. Nonparametric testing (Kruskal Wallis rank test) was used to assess differences in changes in the baseline. Data were reported as mean and SD. For PCR also were reported the medians. The statistical significance was set at $p < 0.05$.

Enrollment of 64 patients was designed to provide 80% power significance (α) level of 0.05 to detect a 20% difference in LDL-C levels in $>10/>10$ (TTA)_n polymorphism compared with 10/10 repeat.

Results

Characteristics of study population

Ninety-four patients were screened, and 69 met LDL-C and other inclusion criteria. Two patients were withdrawal, one for angioedema and other for being diagnosed gastric cancer, two weeks after he entered the study and three patients were lost at the follow-up. Sixty-four patients completed the 8 week statin treatment period. Baseline characteristics of the 64 evaluated subjects are presented in Table I.

The genotype distribution of the HMGCR (TTA)_n polymorphism was as follows: 22 of 64 patients (34%) were $>10/>10$ allele, 14 of 64 patients (22%) were $>10/10$ allele and 28 of 64 patients (44%) were 10/10 allele (Table II). The 3 groups had homogeneous baseline characteristics (Table I).

Changes in LDL-C and total serum cholesterol

The primary end point was the change in the LDL-C by atorvastatin, in relation to baseline (Table III). At the end of 8 weeks, LDL-C levels were significantly lower with a percent change of -46.1, -45.6 and -44.5 for the groups patients $>10/>10$, $>10/10$ and 10/10, respectively ($p < 0.0001$; Figure 1). Also, total serum cholesterol levels were significantly lower in relation to basal values with a percent change of -35.1, -32.3 and -33.7 for the groups patients $>10/>10$, $>10/10$ and 10/10, respectively ($p < 0.0001$; Figure 2). Overall statistical testing showed that these responses were not different between groups of patients with different (TTA)_n polymorphism, with p value 0.743 for LDL-C and p value 0.117 for total cholesterol.

Changes in hsCRP and free F₂-isoprostanes:

Changes in hsCRP and free F₂-isoprostanes by atorvastatin are presented in Table III. At the end of 8 weeks, hsCRP levels were significantly lower with a mean change of -1.22 and -0.94 mg/L for the groups patients >10/>10 and 10/10 respectively (p<0.05). Also, free F₂-isoprostane levels were significantly lower in relation to basal values with a percent change of -41.9, -38.2 and -44.9 for the groups patients >10/>10, >10/10 and 10/10 respectively (p value <0.001). Overall statistical testing showed that these responses were not different between the patients groups with different (TTA)_n polymorphism with p value 0.406 for hsCRP and p value 0.542 for free F₂-isoprostanes.

Discussion

In the present study, we examined the association between LDL-C reduction by atorvastatin and (TTA)_n repeat polymorphism in the HMGCR gene in patients with CAD. We also assessed atorvastatin-induced change of levels of total cholesterol, hsCRP, free F₂-isoprostane and their association with the (TTA)_n polymorphism.

Our main observations were 1) the allele frequencies were different to the observed in another population, Plat et al report that the genotype distribution of the HMGCR (TTA)_n polymorphism was 21.4% for >10/>10 allele, 47.3% for >10/10 allele and 31.3% for 10/10 allele, in our population the genotype distribution was 34% for >10/>10 allele, 22% for >10/10 allele and 44% for 10/10 allele. 2) the magnitudes of reduction of both LDL-C and total cholesterol were not different between the allelic variants 3) atorvastatin treatment induced hsCRP and free F₂-isoprostane reduction.

Previous studies have indicated that variable number of tandem repeats (VNTR) polymorphism (TTA)_n of the HMGCR gene was associated with pathologies such as CAD and hypercholesterolemia (20,21). Moreover, it has been reported an almost significant difference between the (TTA)_n repeat polymorphism in the HMGCR gene and cholesterol absorption in response to plant stanol consumption (22).

Although atorvastatin is widely prescribed for the treatment of hypercholesterolemia, it displays marked interindividual variability in lipid-lowering efficacy (17). Genetics variation in HMGCR, the direct target of statin therapy, is surprisingly understudied. The PRINCE (the Pravastatin Inflammation/CRP Evaluation) that reported two non-coding HMGCR variants in tight linkage disequilibrium (SNPs12 and 29) associated with the magnitude of total cholesterol and LDL-C response. Carriers of the haplotype constituted by these SNPs displayed smaller reductions in LDL-C than non-carriers (18). Even so, association between these HMGCR SNPs and LDL-C response failed to replicate in the ACCESS cohort (19). Aside from the PRINCE

and ACCESS, there are but no pharmacogenetics studies that have studied the HMGCR and the response to statins. Our findings showed no relationship between the reduction of LDL-C levels and the (TTA)_n repeat polymorphism. In fact, very small differences in percent change of the LDL-C were observed among the three groups of patients with the (TTA)_n polymorphism. In particular neither SNP or the (TTA)_n polymorphism alter the function or expression of HMGCR. The other important consideration is that, PRINCE and ACCESS pharmacogenetics studies included patients of other ethnic group different from ours.

In the current analysis, we found that statins decreased hsCRP levels, reflecting its anti-inflammatory effects beside the lipid-lowering action (27). To evaluate oxidative stress, the levels of free F₂-isoprostanes were measured. A reduction of the plasma levels of this biomarker was observed independently of patients' haplotype.

A significant limitation of our study is that only a single statin was tested, besides the study tested only one dose. However, the dose of atorvastatin used is high, compared to dose routinely given for this agent. Moreover, this study was relatively small, and requires to be replicate in larges prospective cohorts of patient

In conclusion LDL-C and total cholesterol concentrations, as well as their changes after treatment with atorvastatin, were not related to presence in the HMGCR polymorphism (TTA)_n. Futures studies may determine whether this small difference in the cholesterol reduction that there is between the genotypes, could be explained by dose adjustment. Data from pharmacogenetics studies are expected to have great impact in the clinical area in the future and will allow the identification of people likely to get the greatest and least benefit from a given intervention.

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Table I. Baseline characteristics of recruited patients with CAD distributed according to the HMGCT (TTA)n repeat polymorphism (n=64)

	(TTA) >10/>10 (n=22)	(TTA) >10/10 (n=14)	(TTA) 10/10 (n=28)	P value
Age (years)	64 ± 8	65 ± 9	66 ± 8	0.796¥
Men	16 (73%)	12 (86%)	23 (82%)	0.668§
Body mass index (Kg/mt ²)	29 ± 5	26 ± 4	28 ± 3	0.227¥
<i>Cardiovascular risk factors</i>				
Hypertension	21 (95%)	13 (93%)	27 (96%)	0.875§
Diabetes mellitus	5 (23%)	3 (21%)	9 (32%)	0.762§
Dyslipidemia	22(100%)	14(100%)	28(100%)	
Smoking	3 (14%)	4 (29%)	1 (4%)	0.070§
Family history of CAD	8 (36%)	4 (29%)	17 (61%)	0.114§
<i>Etiology</i>				
Previous myocardial infarction	11 (50%)	9 (64%)	14 (50%)	0.691§
Previous coronary bypass surgery	17 (77%)	8 (57%)	23 (82%)	0.242§
Previous PTCA	9 (41%)	9 (64%)	10 (36%)	0.228§
Previous cerebrovascular accident	2 (9%)	2 (14%)	3 (11%)	0.886§
Vascular disease	3 (14%)	6 (43%)	2 (7%)	0.102§
Stable angina	6 (27%)	4 (29%)	9 (32%)	0.939§
Unstable angina	7 (32%)	7 (50%)	12 (43%)	0.529#
<i>Chronic therapy</i>				
ACE inhibitors	13 (59%)	9 (64%)	14 (50%)	0.649§
Angiotensin receptor antagonists	1 (5%)	1 (7%)	5 (18%)	0.353§
β-blockers	15 (68%)	7 (50%)	17 (61%)	0.552#
Diuretics	5 (23%)	2 (14%)	11 (39%)	0.216§
Calcium antagonists	5 (23%)	2 (14%)	2 (7%)	0.335§
Aspirin	11 (50%)	13 (93%)	26 (93%)	0.235§
<i>Laboratory</i>				
Total cholesterol (mg/dL)	207 ±29	229 ± 39	213 ± 37	0.173¥
LDL cholesterol (mg/dL)	134 ± 23	141 ± 30	137 ± 34	0.793*
HDL cholesterol (mg/dL)	41 ± 9	49 ± 17	41 ± 10	0.342*
Triglycerides (mg/dL)	158 ± 63	183 ± 69	175 ± 86	0.645*
hsCRP (mg/L), (range)	2.6 (0.4 - 20.3)	1.2 (0.1 - 6.9)	2.1 (0.1 - 14.1)	0.267*
F2-isoprostane (pg/mL)	44.2 ± 20	53.1 ± 19	48.9 ± 23	0.317*

Values are means ± SD, numbers of patients (percentages), or medians (ranges).

CAD: coronary artery disease.

hsCRP: high-sensitivity C-reactive protein

PTCA: Previous percutaneous coronary angioplasty

¥ ANOVA (Analysis of Variance) * Kruskal-Wallis rank test. § Fisher's exact test. #Chi-square test

TABLE II. Genotype distribution and allele frequency the (TTA)_n polymorphism in the HMGCR gene from CAD patients.

	(TTA) >10/>10	(TTA) >10/10	(TTA) 10/10
	n (%)	n (%)	n (%)
Total CAD patients	22 (34)	14 (22)	28 (44)

CAD: coronary artery disease.

TABLE III. Effect of 8 week treatment with atorvastatin and HMGCR (TTA)n polymorphism on cholesterol, triglycerides, hsCRP and F-2 isoprostane in patients with CAD.

	(TTA) >10/>10 (n=22)	(TTA) >10/10 (n=14)	(TTA) 10/10 (n=28)	P value*
Total cholesterol (mg/dL), (%)	-74 ± 29 (-35.1)	-74 ± 28 (-32.3)	-73 ± 28 (-33.7)	0.117
LDL cholesterol (mg/dL), (%)	-63 ± 22 (-46.1)	-65 ± 25 (-45.6)	-61 ± 24 (-44.5)	0.743
HDL cholesterol (mg/dL), (%)	-0.7 ± 7 (-1.4)	-3 ± 8 (-5.0)	0.7 ± 6 (2.0)	0.292
Triglycerides (mg/dL), (%)	-53 ± 55 (-27.0)	-37 ± 60 (-20.3)	-60 ± 71 (-28.7)	0.667
hsCRP (mg/L), median (range)	-1.2 ± 6.4 0.8 (-18.2 to 19.0)	-0.3 ± 2.4 0.2 (-2.3 to 6.6)	-0.9 ± 3.9 0.5 (-11.5 to 12.5)	0.406
F-2 isoprostane (pg/mL), (%)	-21 ± 18 (-41.9)	-23 ± 21 (-38.2)	-25 ± 25 (-44.9)	0.542

Values are mean of change ± SD. For hsCRP is also displayed median (range)

hsCRP: high-sensitivity C-reactive protein

* Kruskal-Wallis test.

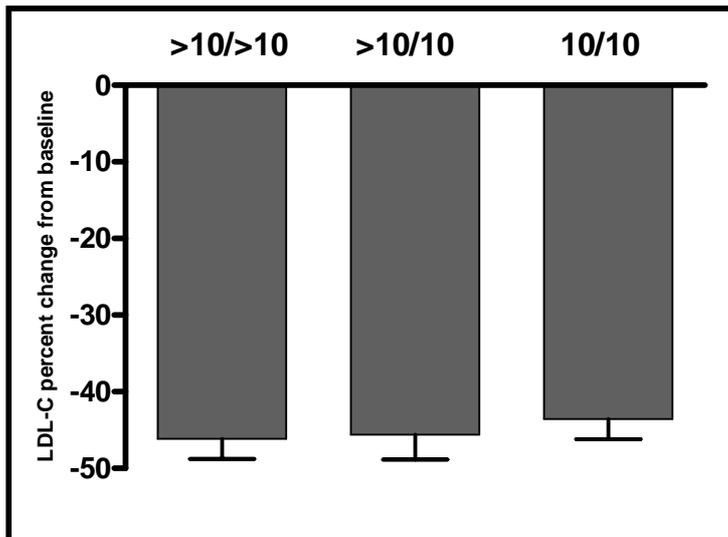


Figure 1. Percent change from baseline in LDL cholesterol for different (TTA)_n polymorphism at 8 weeks treatment with atorvastatin; $p=0.743$. >10/>10 polymorphism had two alleles with more than 10 TTA repeats, >10/10 one allele and 10/10 had two alleles with 10 TTA repeats.

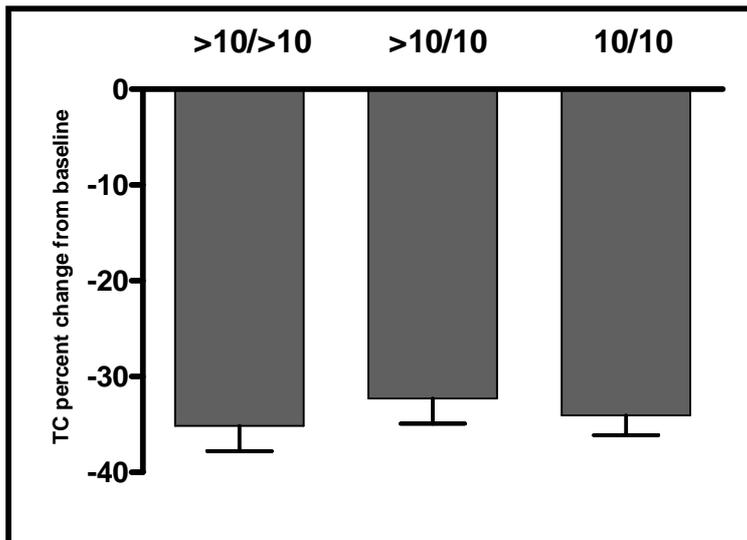


Figure 2. Percent change from baseline in total cholesterol (TC) for different (TTA)_n polymorphism at 8 weeks treatment with atorvastatin; $p = 0.117$. >10/>10 polymorphism had two alleles with more than 10 TTA repeats, >10/10 one allele and 10/10 had two alleles with 10 TTA repeats.