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Single nucleotide polymorphism analysis of LPL gene and its impact in fibrate therapy in hypertriglyceridemic patients

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Abstract: Identifying new genetic variants linked to plasma lipoprotein-lipid concentrations is of significant public health importance, as it can aid in developing genetic markers for CVD risk assessment, diagnosis, and prognosis. Our work aimed to investigate the relationship between lipoprotein lipase (LPL) genetic polymorphisms and hyperlipidemia in Pakistani population. To achieve this goal, 400 blood samples were obtained. DNA was extracted for the measurement of biochemical variables and genetic profiling. A lipid lowering agent, fibrate (200mg/day) is administered to the patients for two months. The online genetic epidemiology tool (http/www.oege.org) was used to determine the allelic and genomic frequencies. Odds ratio (OR) and 95% CI were calculated by chi-square. Single nucleotide polymorphism (SNP) in LPL gene, rs258 (T > C) and rs268 (A>G) were genotyped in 300 hypertriglyceridemia patients and 100 healthy/control individuals. The LPL gene showed a significant association with a high risk of hyperlipidemia diseases when differentiate the genotype evaluations between treated and untreated patients. Lipid levels were significantly ($p<0.05$) reduced after treatment. LPL SNP rs258 and rs268 were observed to be associated to hypertriglyceridemia in the Pakistani patients. Fibrate therapy showed a positive effect on the serum lipid levels after treating the patients with 200mg/day for two months.

Keywords: Single nucleotide polymorphism, hypertriglyceridemia, cardiovascular disease, lipoprotein lipase, fibrate.

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INTRODUCTION

Hypertriglyceridemia (HTG) is a complex disorder related to metabolism of lipids, which is caused by the environmental and genetic factors. According to the studies approximately the 30% of world population is affected by disease Hypertriglyceridemia (HTG): i.e. tested value of triglyceride (TG) more than 150 mg/ dL. About 37 % of men likely to be affected than the woman (30) % (Ain *et al.,* 2024). Electronic health record from all over the Pakistan revealed that more than half (53.7%) of the study population had HTG while 0.3% and 0.1% of the study individuals were severe and very severe HTG respectively (Ain *et al.,* 2025). A modest rise in the serum levels of TG is enough to enhance the threats of CVD (Kayani *et al.,* 2024).

About 60-80% of fatalities worldwide are attributable to CVD, which accounts for 30% of all deaths worldwide. In contrast, 29% of casualties of CVD occur among people under the age of 50 years. (Nishtar, 2002). The statistics about the prevalence of CVD in Pakistan are limited, while research estimates that CVD accounts for 30-40% of all fatalities in Pakistan (Aziz *et al.,* 2008). There is no doubt that hereditary factors contribute, and several genes that regulate triglyceride levels have been linked to the condition (Khovidhunkit *et al.,* 2016). It is thought that genetics controls over 50 % of the variance in lipid levels (Heller *et al.,* 1993; Boekholdt *et al.,* 2006). HTG susceptibility is influenced by the both common and rare genetic variations (Johansen and Hegele, 2011).

LPL is a crucial rate limiting enzyme that produces free fatty acids and glycerol from the hydrolysis of triglyceride (TG) rich particles. It is also responsible to convert very low density lipoprotein (VLDL) to low density lipoprotein (LDL). It is well known that variations in TG and high density lipoprotein cholesterol (HDL-C) level are associated with LPL mass and activity. Numerous investigations have been found that a functional variations and a number of common polymorphism in the LPL gene are linked to lipid profile and the risk of CVD (Pirim *et al.,* 2017). Over 100 variations have been found in the highly polymorphic LPL gene (Shahid *et al.,* 2017). Many single nucleotide polymorphism (SNPs) in or around LPL have been linked to plasma levels of TG and HDL-C, according to the number of genome wide association studies (GWAS) in recent years (Mo *et al.,* 2013). Reduced HDL-C and elevated TG levels are linked to the reduced LPL activity (Shahid *et al.,* 2017).

In general, fibrates are useful in reducing high cholesterol and plasma triglyceride (Tikkanen, 1192). Fibrates are a cost effective option for the hypercholesterolemia or mixed dyslipidemia in individuals with statin contraindication or intolerance, and they are continue to be the most widely used class of non-statin lipid lowering medications worldwide (Blais *et al.,* 2021). Based on the

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existing research work, we examined the association between the LPL polymorphism SNP and lipid-related hypertriglyceridemia. In current study we investigated two different SNPs of LPL gene i.e. rs258 (T/C) and rs268 (A/G) for their association with hypertriglyceridemia. The effects of a lipid lowering agent fibrate were also tested on the hypertriglyceridemia patients.

MATERIALS AND METHODS

Patients/Samples

A total of 400 subjects were investigated in this study, in which 100 were normal or healthy and 300 were the patients of hypertriglyceridemia and hypercholesterolemia. In three hundred hypertriglyceridemia patients two hundred were treated with 200mg/day of fibrates for two months and remaining one hundred were not treated with any medicine. Sampling was done from Faisalabad Institute of Cardiology. For this study written informed agreement was acquired from all subjects/patients.

Inclusion/ Exclusion criteria

Both male and female subjects aged 20 years or above that do not have any chronic infection, metabolic, neurological diseases or cancers, was included randomly. Subject under 20 years or those that fulfills inclusion criteria but not giving written consent was not included in this study. Pregnant woman and heart patients with type 1 diabetes were excluded.

Blood Sampling and Genotyping

Almost 5 ml of blood was taken from each participant in sterilized EDTA tubes. For further processing, this whole blood was shifted to -20C^{o} immediately after collecting the samples. A standard protocol of Phenol-chloroform is used to extract the genomic DNA from the whole blood. The plasma levels of total cholesterol, HDL-C, LDL-C and triglycerides (TG) were measured through enzymatic procedures with kits available commercially on a Hitachi 7180 Autoanalyzer (Hitachi Ltd, Tokyo, Japan). PCR amplification was accomplished in a 96-well plate in the CFX 96 touch real-time PCR System (Bio-Rad, CA, USA). For rs258 (LPL): oligonucleotide primers sequences were: forward; 5`GGCCACATGTTGTCAT AC`3 and reverse 5`CCAGCTTGGGCAATAGAA`3 and similarly for SNP rs268 of LPL gene was forward; 5`CCTACAGGTGCAGTTCCAAG`3 and reverse was 5`ACAACATGCTCCAGCCTACC`3 (table 1).

PCR conditions for rs258 were first the denaturation at 94C^{o} for 3 minutes, after that amplification for 40 cycles by denaturing at 94C^{o} for 30sec, then annealing for 30sec at 58 C^{o}, in the end the extension at 72 C^{o} for 45 sec. For rs268 the annealing temperature is 59.5 C^{o}. A total of 20 µL of PCR reaction was made having 0.5 µL of each primer, 2 µL of (50ng) of genomic DNA, 10 µL of master mix and 7 µL of nuclease free water. High-resolution melting (HRM) analysis was performed by consistently increasing the temperature from 65 to 95 C^{o} near to a rate of 0.01◦C/s. Precision Melting curve analysis software v1.2 (Bio-Rad, USA) was used to analyze the data coming from HRM.

Ethical approval

Manuscripts containing data has been approved by Institutional Review Board of Government College University Faisalabad Pakistan.
(Ref. No. GCUF/ERC/4204).

STATISTICAL ANALYSIS

Statistical Package for the Social Sciences, Version 22.0, Armonk, New York, USA (SPSS) was used to perform the statistical analysis. The online genetic epidemiology tool (http/www.oege.org) was used to determine the allelic and genomic frequencies, co-dominant, dominant and recessive models were established to express the association of hypertriglyceridemia and genotypes. Odds ratio (OR) and 95% CI were calculated by chi-square.

RESULTS

In this study, SNP analysis of two SNPs in different individuals (n=400) were performed. Among these four hundred individuals, three hundred were the patients of hypertriglyceridemia and one hundred were healthy controls. In three hundred hypertriglyceridemia patients two hundred were treated with 200mg/day of fibrates for two months and remaining one hundred were not treated with any medicine. According to the significant differences between the base-line and post-treatment levels of Triglycerides, the population under study was split into two groups as, responders and non-responders. One hundred and fifty patients in which the blood levels of TG were significantly decreased (>100mg/dL) and fifty patients in which the levels of TG were not declined significantly were named as responders and non-responders respectively.

The mean age of controls, untreated, treated, responders and non-responders were 54.19±4.01, 49.31±2.32, 50.33±1.87, 50.97±2.19 and 48.42±3.63 years respectively. In control group, 75(75%) were males and 25(25%) were females, in untreated 69(69%) were males and 31(31%) were females, and in case of treated group, 121(60.42%) were males and 79(39.58%) were females. Amongst the responders, 92(61.11%) were males and 58(38.89%) were females. Similarly, in non-responders 29(58.33%) were males and 21(41.67%) were females (table 2).

Table 3 showed the mean differences of all the lipid variables before and after the treatment with 200mg/day

of fibrate and it is noticed that all the variable serum values were significantly ($p<0.001$) declined.

Table 4 describes the mean difference of cholesterol, HDL, cholesterol to HDL ratio, LDL and triglyceride (TG) between the untreated and treated group. When characteristics were compared between two groups, after two month treatment with 200mg per day of fibrate, a significant decrease ($p<0.05$*) in the levels was found.

After treating the hypertriglyceridemia patients with fibrate therapy for two months, the serum lipid levels for cholesterol, HDL, cholesterol to HDL ratio, LDL and triglycerides were measured between the fibrate responders and non-responders groups. It showed that only the levels of triglycerides were significantly differs p=0.02 (table 5).

Genotyping results of LPL rs258 and rs268

Fig. 1(a) describes the overall frequency distribution of rs258 and rs268 genotypes in study population. It showed that, the wild type genotype TT has the highest frequency distribution (45.0%) as compared to mutant type CC (32.5%) and heterozygous type CT genotype is (22.5%) in case of rs258. The overall frequency distribution of rs268 genotypes in study population showed that, the heterozygous type genotype AG has the highest frequency distribution (40.0%) as compared to wild type AA (32.5%) and mutant type GG genotype is (27.5%). When it comes to healthy control group and patients, the mutant genotype CC of rs258 is present in high percentage (34.40%) in hyperlipidemia patients as compared to the healthy controls (25.00%): while wild type TT is present in 69.00% of healthy controls and 39.06% in the patients, while heterozygous genotype CT is present less 06.00% in controls in the patients26.56%. While the genotype distribution of rs268 of LPL gene in the healthy control group and patients, the mutant genotype GG is present in high percentage (56.0%) in patients as compared to the healthy controls (19.0%): while heterozygous type AG is present in 56.0% of healthy controls and 31.0% in the patients, the wild type genotype AA is present more 25.0% in controls then in the patients 13.0% (fig. 1b). Amongst the patients, the mutant genotype CC of rs258 is present in 62.0% of the patients who were not treated with any medicine while it reduced to 25.0% when the patients of the hyperlipidemia were treated with 200mg/day of fibrates for two months. The distribution of the other genotypes e.g. wild type TT in untreated and treated groups is 12.6% and 47.9% and heterozygous CT is 25.0% and 27.1% in untreated and treated groups respectively. The percentage distribution of rs268 amongst the patients, the mutant genotype GG is present in 56.0% of the patients who were not treated with any medicine while it declined to 20.8% when the patients of the hyperlipidemia were treated with 200mg/day of fibrates for two months. The distribution of the other genotypes e.g. wild type AA in untreated and treated groups is 13.0% and 41.7% and heterozygous AG is 31.0% and 37.5% in untreated and treated groups respectively (fig. 1c). Fig. 1(d) shows the genetic distribution of rs258 and rs268 across the responders and non-responders. It indicates that the mutant genotype CC of rs258 is equally distributed 25% in responders and non-responders. The percentage distribution heterozygous CT and wild type TT in responders and non-responders is 30.6%, 16.7% and 44.4%, 58.3% respectively. On the other hand the genetic distribution of rs268 across the responders and non-responders, it indicates that the mutant genotype GG is highly distributed 25% in non-responders then in responders 19.4%. The percentage distribution heterozygous AG and wild type AA in responders and non-responders is 36.2%, 41.7% and 44.4%, 33.3% respectively.

Treatment based data for rs258 and rs268

In the total 300 numbers of patients, 200 were treated with medicine fibrate, including 150 treatment responders and 50 non-responders, 100 were those who were not taking any medicine and 100 were healthy controls. The allele and genotype frequency of rs258 T/C and rs268 A/G polymorphism was determined in untreated and patients treated with fibrates (table 6). There were noteworthy differences ($p<0.05$) in genotype frequencies with reference to the LPL rs258 T/C and rs268 A/G polymorphism between untreated and treated patients.

Genetic models were arranged to associate the frequency differences between fibrate users and untreated patients, as shown in table 10. The data analysis of two groups indicate a significant difference ($p<0.05$) against the polymorphism of the LPL gene.

Amongst the models, in the co-dominant model between the patients of both the groups, the significant allele frequency differences of LPL rs258 T/C were OR = 1.39; 95% CI = 1.03-1.80; p = 0.002 in the co-dominant, OR = 0.15; 95% CI = 0.03-0.76; p = 0.01 in dominant and OR = 0.20; 95% CI = 0.06-0.67; p = 0.01 in the recessive model respectively. It was significantly different in allelic model as well with OR = 0.21; 95% CI = 0.08-0.51; p = .0003. Similarly, in case of LPL rs268 a significant differences were noticed in all different genetic models i.e. in co-dominant, OR = 1.39; 95% CI = 1.04-1.92; p = 0.031, in dominant model, OR = 0.20; 95% CI = 0.04-0.98; p = 0.03, OR = 0.20; 95% CI = 1.06-0.68; p = 0.01 and OR = 0.26; 95% CI = 0.15-0.44; p = <0.0001 in recessive and allelic model respectively.

Response Based for rs258 and rs268

There were no notable dissimilarities between fibrate responder patients and fibrate non-responder patients for genotype frequencies with regard to the LPL rs258 T/C polymorphism as shown by the co-dominant model (table 7).

Table 1: Basic information of single nucleotide polymorphism LPL genotypes

SNP	Primer	Sequence	Genotype	Tm ◦C	Size bp
rs258	Forward	5`GGCCACATGTTGTCATAC`3	T/C	58◦C	18 bp
	Reverse	5`CCAGCTTGGGCAATAGAA`3			18 bp
rs258	Forward	5`CCTACAGGTGCAGTTCCAAG`3	A/G	59.5◦C	20bp
	Reverse	5`ACAACATGCTCCAGCCTACC`3.			20bp

Tables 2: Age, groups and gender distribution of study population

Number of patients	Controls 100(25%)	Untreated 100(25%)	Treated 200(50%)	Responders 150(75%)	Non-responders 050(25%)
Age (year)	54.19±4.01	49.31±2.32	50.33±1.87	50.97±2.19	48.42±3.63
			Gender		
Male	75(75%)	69(69%)	121(60.42%)	92(61.11%)	29(58.33%)
Female	25(25%)	31(31%)	79(39.58%)	58(38.89%)	21(41.67%)

Table 3: Differences in lipid parameters before and after the treatment

Paired Samples Test

	Parameters	Paired Differences					t	df	Sig. (2-tailed)
		Mean	Std. Deviation	Std. Error Mean	95% Confidence Interval of the Difference				
					Lower	Upper			
Pair 1	Pre-Cholesterol - Post-Cholesterol	38.43	72.26	8.07972	22.36	54.52	4.76	79	<0.001
Pair 2	Pre-HDL – Post-HDL	-8.45	10.60	1.18521	-10.81	-6.09	-7.13	79	<0.001
Pair 3	Pre-LDL – Post-LDL	21.80	38.62	4.32	13.20	30.39	5.05	79	<0.001
Pair 4	Pre-Ratio – Post-Ratio	1.66	2.64	0.29	1.08	2.25	5.63	79	<0.001
Pair 5	Pre-TG – Post-TG	83.39	108.61	12.14	59.22	107.55	6.87	79	<0.001

$p < 0.05$ is considered as significant

Table 4: Mean differences in lipid levels between untreated and treated patients

Parameters	Groups	Mean	Mean Difference	Std Deviation	Range	95% CI for mean	p-value	95% Confidence Interval of the Difference	
								Lower	Upper
Post-Cholesterol	Untreated	269.91	229.67	121.08	336.00-478	226.25-313.56	.000	200.05985	259.27349
	Treated	176.83		24.63	130.00-243.00	166.43-187.24			
Post-HDL	Untreated	38.00	-12.00000	7.15	29.00-52.00	32.02-43.98	.012	-21.16877	-2.83123
	Treated	50.00		11.92	37.00-83.00	44.96-55.03			
Cholestrol to HDL	Untreated	11.01	7.35417	2.70	8.20-16.20	8.75-13.27	.000	6.13575	8.57258
	Treated	3.66		0.75	2.10-5.20	3.34-3.98			
Post-LDL	Untreated	139.38	40.66667	35.50	86.00-193.00	109.70-169.05	.001	18.31395	63.01938
	Treated	98.71		23.54	65.00-158.00	88.77-108-65			
Post-Triglyceride	Untreated	583.25	414.29167	80.77	486.00-686.00	515.72-650.78	.000	372.26558	456.31775
	Treated	168.96		36.45	119.00-249	153.57-184.35			

$p < 0.05$ is considered as significant

Table 5: Mean differences in lipid parameters between responders and non-responders

Factors	Groups	Mean Difference	Std. Error Difference	95% Confidence Interval of the Difference		*p-value*
				Lower Bound	Upper Bound	
Post-Cholesterol	R -NR	18.75000	11.68733	-4.77537	42.27537	0.11
Post-HDL	R -NR	1.75000	3.56318	-5.42231	8.92231	0.62
Post Cholesterol to HDL	R -NR	.17611	.29956	-.42686	.77909	0.56
Post-LDL	R -NR	-9.80556	8.77647	-27.47168	7.86057	0.27
Post-Triglyceride	R-NR	-68.25000	39.63522	-148.0315	11.53155	0.02

$p < 0.05$ is considered as significant

Table 6: Comparison of genotype and allele frequencies for rs258 and rs268 in untreated and treated hypertriglyceridemia patients

Genotype	Untreated	Treated	OR(95%CI)	*p* Value
LPL rs258				
Allelic model				
T	25(25%)	122(61%)	-	.0003
C	75(75%)	78(39%)	0.21(0.08-0.51)	
Co-dominant model				
T/T	13(12.6%)	96(47.9%)		
C/T	25(25.0%)	54(27.1%)	1.39(1.03-1.80)	0.002
C/C	62(62.4%)	50(25.0%)		
Dominant model				
T/T	13(13.0%)	96(47.9%)	-	0.01
C/T-C/C	87(87.0%)	104(52.1%)	0.15(0.03-0.76)	
Recessive model				
T/T-C/T	38(37.8%)	150(75.0%)	-	0.01
C/C	62(62.2%)	50(25.0%)	0.20(0.06-0.67)	
		LPL rs268		
Allelic model				
A	28(28%)	120(60%)	-	<.0001
G	72(72%)	80(40%)	0.26(0.15-0.44)	
Co-dominant model				
A/A	13(12.5%)	83(41.7%)		
A/G	31(31.2%)	75(37.5%)	1.39(1.04-1.92)	0.031
G/G	56(56.2%)	42(20.8%)		
Dominant model				
A/A	13(13.0%)	83(41.7%)	-	0.03
A/G-G/G	87(87.0%)	117(58.3%)	0.20(0.04-0.98)	
Recessive model				
A/A-A/G	44(43.8%)	158(79.2%)	-	0.01
G/G	56(56.2%)	42(20.8%)	0.20(0.06-0.68)	

$p < 0.05$ is considered as significant, 1 degree of freedom was used for odds calculation.

In the co-dominant model between responders and non-responders, the allele frequency differences of LPL rs258 T/C was also insignificant i.e. OR = 1.42; 95% CI = 0.72-2.79; p = 0.31. Meanwhile in recessive model, the described allele frequency differences were OR = 0.93; 95% CI = 0.45-1.94; p = 0.84. The noticed allele frequency differences for rs258 between responders and non-responders were OR = 1.71; 95% CI = 0.89-3.23; p = 0.14 in the dominant model (table 7).

No noteworthy difference was found between genotypes 'of rs268 with fibrate responders and non-responders (P<0.67). Moreover 'A' and 'G' alleles are presenting no link between responders and non-responders (P = 0.47). The occurrence of ancestral allele 'A' was observed to be (62%) in responders and (54%) in non-responders. Whereas the frequency of risk allele 'G' was (38%) in responders and (46%) in non-responders. Both dominant (p=0.57) and recessive model (p=0.67) was found to be insignificant with response to the fibrate therapy. SNP analysis shows that of rs268 polymorphism is linked with treatment consequences in patients. Individuals with a high percentage of heterozygous genotypes and risk alleles are at high-risk of treatment failure (table 7).

Table 7: Analysis of association of LPL rs258 and rs268 polymorphism in fibrate responders and non-responders

Genotype	Non-Responders	Responders	OR(95%CI)	*p* Value
LPL rs258				
Allelic model				
T	34(67%)	90(60%)	-	0.31
C	16(33%)	60(40%)	1.42(0.72-2.79	
Co-dominant model				
T/T	29(58.3%)	67(44.4%)	-	
C/T	08(16.7%)	46(30.6%)	2.31(0.40-13.39)	0.62
C/C	13(25.0%)	37(25.0%)	1.24(0.25-6.15)	
Dominant model				
T/T	29(58.3%)	67(44.4%)	-	0.14
C/T-C/C	21(41.7%)	83(55.6%)	1.71(0.89-3.23)	
Recessive model				
T/T-C/T	37(75.0%)	113(75.0%)	-	0.84
C/C	13(25.0%)	37(25.0%)	0.93(0.45-1.94)	
LPL rs268				
Allelic model				
A	27(54%)	93(62%)	-	0.47
G	23(46%)	57(38%)	0.71(0.28-1.80)	
Co-dominant model				
A/A	17(33.3%)	67(44.4%)	-	
A/G	21(41.7%)	54(36.1%)	0.53(0.10-2.66)	0.67
G/G	12(25.0%)	29(19.4%)	0.51(0.08-3.13)	
Dominant model				
A/A	17(33.3%)	67(44.4%)	-	0.57
A/G-G/G	33(66.7%)	83(55.6%)	0.62(0.16-2.45)	
Recessive model				
A/A-A/G	38(75.0%)	121(80.6%)	-	0.67
G/G	12(25.0%)	29(19.4%)	0.72(0.15-3.40)	

$p < 0.05$ is considered as significant, 1 degree of freedom was used for odds ratio calculation.

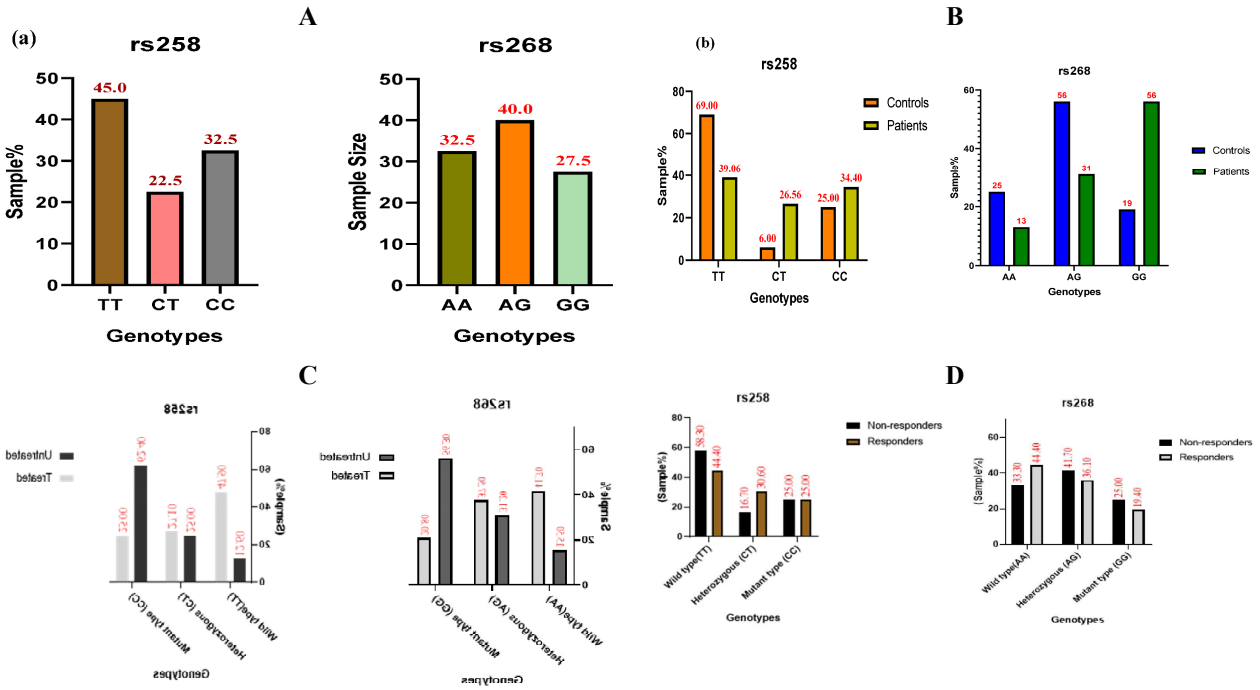
DISCUSSION

Hypertriglyceridemia (HTG) is known as high levels of circulating triglycerides (TGs) in the blood plasma. It is a type of hyperlipidemia. Elevated levels of triglycerides are linked with cardiovascular (CV) and many other related diseases (e.g. acute pancreatitis) (Corbo *et al.,* 2025; Lin *et al.,* 2018; Ariza *et al.,* 2025). In some of the previous studies, hypertriglyceridemia is known as major independent risk factor for CVD (Toth *et al.,* 2018; Arca *et al.,* 2020). Changes in the TG metabolism are responsible for many situations like food intake irregularities and many other genetic conditions that may harm the complex biochemical processes which control the synthesis, processing and degradation of TGs (Abou Rjaili *et al.,* 2010).

LPL hydrolyses the triglycerides in to chylomicrons and very low density lipoprotein (VLDL) and is responsible for cleaning the TG rich lipoproteins from blood circulations. LPL is also responsible for the exchange of lipids between VLDL to HDL. So, LPL has a predominant role in the metabolism of lipids (Kong *et al.,* 2024). More than 100 genetic variants consisting of single nucleotide polymorphisms (SNPs) have been found in LPL gene, out of which many of them are linked with lipid level variations but the effects of many are still unknown (Al-Bustan *et al.,* 2019).

LPL play a major role in the uptake of VLDL followed by its hydrolysis. The relationship between rs258 and its decreasing effect on VLDL levels may also be through affecting the protein binding and/or controlling the LPL expression levels like other intronic variants (Salazar-Tortosa *et al.,* 2020). In another study LPL polymorphisms rs1534649, rs258, rs268 and rs328, were significantly associated with CVD risk factors in European adolescents (Salazar-Tortosa *et al.,* 2020).

Fibric acids or fibrates are the special type of antagonists that belongs to a family of transcriptional factors named as PPAR-α. When these PPARs are stimulated with fibric acids they have the ability to affect the wide range of metabolic processes. LPL mediated lipolysis is increased via decreased production of LPL inhibitors Apo-CIII, and the direct activation of LPL promoter that has a peroxisome proliferator response element. As a result, whenever the treatment is done with fibrates they influence triglycerides (TGs) metabolism by reducing the hepatic synthesis and secretion of VLDL and enhance its clearance from the circulations (Franssen *et al*., 2008).



(a) overall frequency distribution of rs258 and rs268 genotypes (b) Genotype distribution of rs258 and rs268 between healthy controls and HTG patients (c) Comparison of genotype distribution of LPL between untreated and treated patients(d) Comparison of genotype distribution of LPL between non-responders and responders.

Fig. 1: Comparison of genotype distribution of LPL rs258 and rs268 among different groups

In the present study, an association between LPL polymorphism rs258 (T/C) and rs268 (A/G) was observed in the hyperlipidemia patients. The effects of fibrate therapy on these patients were also significant ($p<0.05$). Even though these findings indicate that these genotypes may have an influence in disease, additional research is needed to support its clinical significance. The present study should be expanded to include more subjects to minimize the possibility of population bias or differences in ethnic patterns.

CONCLUSION

The LPL SNPs, rs258 and rs268, investigated in this study, was observed to be linked with hypertriglyceridemia in the Pakistani population. Fibrate therapy showed a positive effect on the serum lipid levels. In summary, LPL gene polymorphism may be a possible risk factor for HTG and associated diseases. In order to ensure the relationship between LPL and the risk of HTG and related diseases, additional investigations involving more samples and ethnic groups are needed.

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Conflicts of interest

The authors declare no conflicts of interest.

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