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The Association of LPL Gene Variants with Type 2 Diabetes Mellitus and Obesity Susceptibility among Group of Egyptian Patients

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Abstract

Background: Lipid metabolism depends on Lipoprotein lipase enzyme whose variants were reported associated with type 2 diabetes mellitus (T2DM) and obesity. The lipoprotein lipase (LPL) gene was linked to lipoprotein metabolism, while its pathogenic genetic variants were linked to obesity, insulin resistance (IR) and so diabetes.

Aim of Study: To study the association between LPL (rs1801177, rs320) variants and diabetes regarding disease incidence and susceptibility to obesity.

Patients and Methods: This case control study included 280 subjects, T2DM (n=140) compared to healthy control subjects (n=140). Lipoprotein lipase variants (rs1801177, rs320) across the lipoprotein lipase gene were genotyped by real-time PCR using the TaqMan allele discrimination assay.

Results: The studied variant genotypes frequency was significantly different between diabetic and non diabetic subjects, p-value=0.008 & 0.034 for rs1801177, rs320, respectively. A significant association was detected between LPL gene rs1801177 & rs320 variants and BMI, waist circumference and HbA1C, FBG, TG & HDLc. There's a positive correlation between BMI and LPL rs 1801 177 variant (r=0.367, p=0.001), There's a moderate positive correlation between waist circumference and LPL rs1801177 variant (r=0.383, p=0.001), positive correlation with FBG (r=0.342, p=0.001), positive correlation with HbA1c (r=0.405, p<0.001) and a moderate positive correlation between TG level and LPL rs1801177 variant (r=0.464, p=0.025). A weak negative correlation between HDL level and LPL rs320 variant (r=–0.225, p=0.007).

Conclusions: Both variants were significantly associated with parameters related to obesity and T2DM (BMI, waist circumference, FBG, HbA1c, TG & HDLc). Due to the polygenic nature and the high prevalence of obesity & T2DM, further studies with larger study population are needed to assess our results.

Key Words: *Lipoprotein lipase – Obesity – Insulin – Resistance – Type 2 diabetes.*

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Introduction

INCREASED insulin resistance and decreased insulin secretion, the two pathogenic alterations that determine the development of type 2 diabetes mellitus (T2DM), are impacted by a number of variables, including hereditary and environmental ones. Increased adipose tissue storage as a result of dysfunctional lipid metabolism eventually leads to obesity, and consequently increased risk of T2DM development. Lipoprptein lipase (LPL) play a significant role in the transport, storage, and hydrolysis of triglycerides in the form of chylomicrons and low-density lipoprotein plasma **[1]**.

Changes in the LPL normal function could result in an increase serum free fatty acids, metabolic disorders development is limited as long as excess fats can be stored in adipose tissue. Once the adipocyte storage capacities are exceeded, fat accumulates in muscle and liver cells, which could then result in insulin resistance or a loss of insulin sensitivity in tissues, which could speed up the development of type 2 diabetes **[2]**.

The LPL gene is found on the chromosome 8 (8p22) with a 35kb length, that consists of 10 exons. Many variations are found in the coding and non-coding regions of this gene **[3]**.

Number of single-nucleotide variants (snv) in the LPL gene have been described. Some of those variants were related to disturbed lipid concentration. Several gain-of-function mutations in LPL have been associated with lower plasma triglycerides, as well, confirming its role in triglyceride metabolism **[4]**.

Interestingly, several SNVs were identified in the introns and exons of LPL gene and were reported to be associated with triglyceride levels and T2DM in Mongolian, Russian, Brazilian popula-

tions but no association was reported in Chinese population [5].

The purpose of our work is thus to study the association between LPL (rs1801177, rs320) variants and diabetes regarding disease incidence, susceptibility to obesity which will allow us to design a predictive system for the dyslipidemia treatment using gene variation, family history of diseases and anthropometric indicators. To the best of our knowledge, this is the first study in Egypt on those variants regarding diabetes and obesity patients.

Patients and Methods

Study population:

Our study was case control one conducted over 8 months from January 2021 to October 2022. The study including 280 participants; 140 patients with T2DM who were recruited from the Diabetes Outpatient Clinic, Kasr Al-Ainy Hospital and 140 normal healthy age and sex matched subjects as a control group. Patients with T2DM should have either Fasting blood glucose (FBG) levels of ≥126mg/dL and/or postprandial glucose levels of ≥200mg/dL and/or hemoglobin A1c (HbA1c) levels of ≥6.5%, patients with other endocrinological disorders as thyroid disorders were excluded. The study was approved by Ethical committee of the Kasr Al-Ainy, faculty of Medicine (MS-22-2022) and all patients and controls gave a written informed.

Sample size:

G*Power software was used for sample size calculation [6]. Primary outcome measure is the relationship between gene variant and T2DM and obesity. Using two-way ANOVA with two factors (main effects), we will get 2 possible groups (2 levels for factor A * 2 levels for factor B) and an interaction (numerator) degree of freedom of one ([2 - 1] * [2 - 1]). So, it is calculated that a sample size of 140 patients and 140 control (total 280 patients) achieves 80% power to detect a medium effect size (Cohen f) of 0.28 assuming a numerator degree of freedom of 1 and a confidence level of 95% (alpha error of 0.05).

Data collection:

Study participants were subjected to:

- Detailed history, including associated comorbidities and current treatment. Careful clinical examination with anthropometric measurement including: Height, weight and waist circumference measurement.
- Routine laboratory tests including FBG, HbA1c, HDL cholesterol and triglycerides levels.
- DNA Extraction and Genotyping: Three ml peripheral venous blood samples were collected into sterile Ethylene di amine tetra acetic acid (EDTA) vacutainer tubes. According to the manufacturer's recommendations, genomic DNA was isolated from the whole blood using a QIAamp DNA blood mini kit (Qiagen, Germany) and stored at 20°C. Genotyping of the (rs1801177) and (rs320) of LPL gene was done across all participants' sample sets using the TaqMan Allelic Discrimination Assay Kit (probe ID C___8804865_30 and C___1843003_10) respectively, Applied Biosystems, Foster City, CA, USA); and these SNPs were analyzed on StepOne Real-Time Polymerase Chain Reaction System (Applied biosystems CA94404, Foster City, USA).

Statistical methods:

The statistical package for the social sciences (SPSS) (IBM Corp., Armonk, NY, USA) used for quantitative values, standard deviation, mean, and median. Frequencies and percentages used for categorical variables. For comparisons of normally distributed quantitative variables unpaired t test or ANOVA analysis were used, for the multiple comparisons post hoc test was used. When the expected frequency is less than 5, Chi square test was used to compare categorized data [7]. Correlations between quantitative variables were calculated by Pearson correlation coefficient. To identify independent predictors of BPA, linear regression analysis was used. Results with p-values less than 0.05 were defined as Statistical significance.

Results

This study consisted of 280 participants; divided into two groups as the following: 140 diabetic patients, and 140 healthy control subjects.

There's a significant statistical difference between diabetic patients and control subjects regarding BMI, waist circumference, FBG, TG (p-value <0.001).

There's a significant difference between diabetics and control groups regarding both genes variants. LPL rs 1801177 genotypes AA, AG, GG distribution was 84.3%, 9.3%, 6.4% in diabetic patients versus 71.4%, 22.9%, 5.7 in the control group, p-value=0.008. Similarly LPL gene rs 320 AA, AT and TT distribution was 47.1 %, 43.6%

and 9.3% versus 62.1%, 32.9% and 5% in the diabetic and control group respectively, p-value= 0.034.

In diabetic patients, rs 1801177 mutant variant was significantly associated with BMI and waist circumference, HbA1c, FBG, TG, p-value <0.001. There's was also a significant association between gene rs 1801177 variant and HDLc, p-value=0.01. Furthermore, in the control subjects rs1801177 mutant variant was associated with BMI, p-value =0.031 & waist circumference, p-value=0.007 and TG, p-value=0.017.

Regarding LPL rs320 variant in diabetic patients, the mutant variant was significantly associated with BMI (p-value=0.029), waist circumference (p-value=0.037), HbA1C (p-value=0.002), FBG (p-value=0.001), TG (p-value=0.01) and HDLc (p-value=0.02). In Addition, control subjects with the mutant variant of LPL rs 320 had significantly higher FBG (p-value=0.045) and significantly lower HDLc (p-value=0.004).

There's a positive correlation between BMI and LPL rs 1801177 variant (r=0.367, p=0.001), There's a moderate positive correlation between waist circumference and LPL rs 1801177 variant (r=0.383, p=0.001), positive correlation with FBG (r=0.342, p=0.001), positive correlation with HbA1c (r=0.405, p<0.001) and a moderate positive correlation between TG level and LPL rs 1801177 variant (r=0.464, p=0.025). A weak negative correlation between HDL level and LPL rs320 variant (r=–0.225, p=0.007).

Table (1): Characteristics of clinical and biochemical parameters of studied diabetic and control subjects.

	Diabetic patients (No.=140)	Control (No.=140)	p-value
Sex (No., %):			
Male	63 (45%)	66 (47.1%)	0.550 **a**
Female	77 (55%)	74 (52.9%)	
Age:			
(Mean±SD)	49.17±10.96	48.35±10.98	0.535 **b**
BMI:			
(Median, IQR)	36.69, 8.15	33.57, 8.83	<0.001 **c**
Waist circumference:			
(Median, IQR)	96.75, 11	90, 12.75	<0.001 **c**
HbA1 C:			
(Median, IQR)	7.75, 2.07	4.9, 0.6	<0.001 **c**
FBG:			
(Median, IQR)	169.5, 97.75	103, 22.5	<0.001 **c**
Age of onset of T2DM:			
(Median, IQR)	43, 15	–	
TG:			
(Median, IQR)	205, 93.75	107, 21	<0.001 **c**
HDLc:			
(Median, IQR)	27, 11	27.5, 9	0.238 **c**
Oral antidiabetics (No., %)	140 (100%)		–
Combined oral +Insulin (No., %)	86 (61.4%)	–	–

BMI : Body mass index.
HbA1c : Hemoglobin A1 c.
FBG : Fasting blood glucose.
T2DM : Type 2 diabetes mellitus.
TG : Triglycerides.
HDLc : High density lipoprotein cholesterol.
a: Chi-square test.
b: Independent samples *t*-test.
c: Mann-whitney test.

Table (2): Genotype distributions of LPL rs 1801177, and LPL rs320 gene variant in the study groups expressed.

Gene/SNP	Genotype/ haplotype	Diabetic patients (No.=140)	Control non diabetic (No.=140)	p-value*
LPL rs 1801177	Wild (AA)	118 (84.3%)	100 (71.4%)	0.008
	Hetero (AG)	13 (9.3%)	32 (22.9%)	
	Mutant (GG)	9 (6.4%)	8 (5.7%)	
LPL rs320	Wild (AA)	66 (47.1%)	87 (62.1%)	0.034
	Hetero (AT)	61 (43.6%)	46 (32.9%)	
	Mutant (TT)	13 (9.3%)	7 (5%)	

*: Chi-square test.

Table (3): Relation between LPL Rs1801177 gene variants and demographic and biochemical parameters among the study groups.

Variable	Group	LPL Rs1801177			*p*-value
		Wild	Mutant	Hetero	
Sex:					
Male	G1	57 (48.3%)	4 (44.4%)	9 (69.2%)	0.786 **a**
Female		61 (51.7%)	5 (55.6%)	4 (30.8%)	
	G2	60 (54.1%)	3 (33.3%)	11 (55%)	0.478 **a**
		51 (45.9%)	6 (66.7%)	9 (45%)	
Age:	G1	49.59±11.14	47.55±12.5	46.46±8.16	0.422 **c**
(Mean±SD)	G2	48.08±10.69	53.11±14.93	47.75±10.74	0.406 **c**
BMI:	G1	36.01, 8.06	40, 6.33	39, 11.5	<0.001 **b**
(Median, IQR)	G2	33.9, 8.25	27.2, 9.46	29.39, 7.6	0.031 **b**
Waist circumference:	G1	95.5, 9.526	109, 22.5	105, 6	<0.001 **b**
(Median, IQR)	G2	91, 10	83, 12.5	89.5, 11.5	0.007 **b**
HbA1 C:	G1	7.8, 2.15	8, 1.2	7.3, 1.25	<0.001 **b**
(Median, IQR)	G2	4.9, 0.57	5.1, 0.5	4.8, 0.7	0.214 **b**
FBG:	G1	169.5, 110.25	185.5, 80.5	165, 58.5	<0.001 **b**
(Median, IQR)	G2	105, 16	100, 32.5	100, 17	0.488 **b**
Age of onset of DM: (Median, IQR)	G1	43, 15	45, 10.5	42, 10.25	0.817 **b**
TG:	G1	198, 66	380, 164.5	250, 132	<0.001 **b**
(Median, IQR)	G2	107, 21	100, 2	107, 18.75	0.017 **b**
HDL:	G1	27, 11	14, 8.5	30, 9	0.01 **b**
(Median, IQR)	G2	27, 9	30, 3.75	28, 9.5	0.054 **b**

BMI : Body mass index. T2DM : Type 2 diabetes mellitus. **a**: Chi-square test. G1: Among diabetic group.
HbA1 c : Hemoglobin A1c. TG : Triglycerides. **b**: Kruskal-wallis test. G2: Among control group.
FBG : Fasting blood glucose. HDLc : High density lipoprotein cholesterol. **c**: One way ANOVA test.

Table (4): Relation between LPL Rs320 gene variants and demographic and biochemical parameters among all study groups as expressed.

Variable	Group	LPL Rs320			*p*-value
		Wild	Mutant	Hetero	
Sex:					
Male	G1	31 (47%)	5 (38.5%)	34 (55.7%)	0.366 **a**
Female		35 (53%)	8 (61.5%)	27 (44.3%)	
	G2	47 (54%)	4 (57.1%)	24 (52.2%)	0.797 **a**
		40 (46%)	3 (42.9%)	22 (47.8%)	
Age:	G1	48.5±10	50.6±13.56	49.5±11.5	0.758 **c**
(Mean±SD)	G2	48.93±10.58	43.71±10.78	47.97±11.78	0.541 **c**
BMI:	G1	36.19, 8.32	39, 4.12	35.5, 10.05	0.029 **b**
(Median, IQR)	G2	34.78, 8.6	37.46, 9.5	31.4, 8.2	0.918 **b**
Waist circumference:	G1	97.25, 12	105, 13.5	95, 8	0.037 **b**
(Median, IQR)	G2	90, 13	92, 10.75	89, 5	0.191 **b**
HbA1 C:	G1	7.75, 2.72	11, 6.15	7.4, 1.2	0.002 **b**
(Median, IQR)	G2	4.9, 0.7	4.8, 0.8	4.9, 0.525	0.231 **b**
FBG:	G1	165, 107.5	300, 166	155, 80.5	0.001 **b**
(Median, IQR)	G2	103, 24	103, 36	101, 15.25	0.045 **b**
Age of onset of DM: (Median, IQR)	G1	42, 14.25	45, 16	44, 14.5	0.894 **b**
TG:	G1	233, 111.25	241, 192.5	190, 73	0.010 **b**
(Median, IQR)	G2	107, 19	98, 23	102, 10	0.558 **b**
HDL:	G1	29, 12.25	21, 13	27, 11	0.020 **b**
(Median, IQR)	G2	33, 3	24, 9.25	27, 9	0.004 **b**

BMI : Body mass index. T2DM : Type 2 diabetes mellitus. **a**: Chi-square test. G1: Among diabetic group.
HbA1 c : Hemoglobin A1c. TG : Triglycerides. **b**: Kruskal-wallis test. G2: Among control group.
FBG : Fasting blood glucose. HDLc : High density lipoprotein cholesterol. **c**: One way ANOVA test.

Table (5): Correlation between LPL Rs1801177, and LPL Rs320 gene polymorphism and demographic and biochemical parameters among diabetic group.

Variable	Genotype	*r**	*p*-value
Age	LPL Rs1801177	–0.088	0.3
	LPL Rs320	0.05	0.558
BMI	LPL Rs1801177	0.367	0.001
	LPL Rs320	0.074	0.384
Waist circumference	LPL Rs1801177	0.383	0.0001
	LPL Rs320	0.011	0.896
FBG	LPL Rs1801177	0.342	0.001
	LPL Rs320	0.109	0.199
HbA1C	LPL Rs1801177	0.405	0.001
	LPL Rs320	0.107	0.208
TG	LPL Rs1801177	0.464	0.001
	LPL Rs320	–0.096	0.257
HDLc	LPL Rs1801177	0.007	0.936
	LPL Rs320	–0.225	0.007

BMI : Body mass index. *: Spearman correlation.
HbA1c : Hemoglobin A1 c.
FBG : Fasting blood glucose.
T2DM : Type 2 diabetes mellitus.
TG : Triglycerides.
HDLc : High density lipoprotein cholesterol.

Discussion

Obesity is a highly prevalent health issue with great impact on the society, health facilities, it's associated with increased risk of other comorbidities including insulin resistance and T2DM **[8]**.

Various variants of LPL gene have been linked to changes in TG and HDL-C levels in obese individuals. Previous studies have also demonstrated that people with different BMIs had variable LPL activity in addition to variable insulin level and activity. Collectively, these studies could explain an interaction between LPL genotype and obesity, insulin resistance & T2DM **[9,10]**.

Our study was aiming to investigate whether or not LPL gene (rs 320) and (rs 1801177) variants were associated with association T2DM and obesity susceptibility.

We detected a statistically significant difference between diabetic and non diabetic subjects in LPL rs 1801177 genotypes AA, AG, GG distribution, as the frequency was 84.3%, 9.3%, 6.4% in diabetic patients versus 71.4%, 22.9%, 5.7 in the control group, p=0.008. Similarly LPL gene rs 320 AA, AT and TT distribution was 47.1%, 43.6% and 9.3% versus 62.1%, 32.9% and 5% in the diabetic and control group respectively, p=0.034.

In our study, LPL (rs 1807711) was associated with dyslipidemia with triglyceride-rich lipoprotein metabolism and lipoprotein remodeling including HD, as patients with the mutant variant had statistically significant higher levels of TG, lower levels of HDL than other variants. Interestingly, this difference was also evident in the TG levels in non dyslipidimic control subjects. Similar to our study significant association was found in the study done by Marateb et al. **[11]**.

While in the study of Izar et al. **[12]**, the lipid parameters in diabetic patients were not affected by LPL (rs 1801177) variant.

We found significant association between LPL (rs 1801177) variant with high fasting blood sugar and HbA1C in diabetic patients having the mutant variant (p<0.001).

Lotta et al., **[13]** findings were similar to ours where LPL(rs1801 177) minor allele (MAF=1.9%) in the patients was associated with lower insulin sensitivity, higher fasting glucose, higher levels of liver markers and higher risk of type 2 diabetes (p=0.0086).

Regarding LPL (rs320) variant our study revealed a significant association between the mutant variant and BMI of the patients (p=0.029). As well as waist circumference (p=0.037), high HbA1C level (p=0.002) and high FBG (p<0.001). The mutant variant was also associated with higher TG, Lower HDL in diabetic patients (p=0.01, p= 0.02) respectively. Further more control subjects with the mutant variant had lower HDL levels (p=0.003).

These data are consistent with the results obtained by others such as Bushueva et al., **[14]** in the Russian population, Javorsky´ et al. **[15]** in the Slovak population, and Vardarl et al. **[16]** in the Turkish population. They showed that the mutant genotype of the rs320 locus of the LPL gene is a marker for the development of T2DM and dyslipidemia without possible relationship with gender was identified.

Similar results were also detected by Hubacek et al., and Kahn et al., who reported that LPL (rs320) variant was associated with hypertriglyceridemia and T2DM among Russian and Mexican population **[17,18]**.

On the other hand, Kochetova et al., **[10]** studied LPL (rs320) variant in 930 Russian individuals and they didn't detect an associations with anthropometric parameters. However, similar to our

results the mutant variant is a risk factor for the development of T2DM in individuals with normal body weight.

In contradiction, Durgawale et al., showed no association between LPL (rs320) variant and the occurrence T2DM **[1]**.

Opposite to our findings were He T et al., who suggested that the risk allele for LPL (rs320) variant was the T allele **[19]** and that the G/A (minor alleles) allele exerts a protective role in the populations of Asia, but not Europe, since Europeans have a reverse relationship with the G allele. As we have found.

Similar studies in Saudi and Chinese Han patients failed to report any association with development of T2DM **[20,21]**. Another interesting study among Polish and Russian athletes showed that rs320 SVP has variable phenotypic effects of T2DM depending on the type and intensity of physical activity **[22]**.

Conclusion:

In our study, LPL (rs1801177) and LPL (rs320) variant distribution were significantly different between diabetic and non diabetic subjects. Both variants were significantly associated with parameters related to obesity and T2DM (BMI, waist circumference, FBG, HbA1c, TG & HDLc). Even in the non diabetic subjects, the studied variants were associated with some of these parameters. Due to the polygenic nature and the high prevalence of obesity & T2DM, further studies with larger study population are needed to assess our results.

References

1- DURGAWALE PP, DATKHILE KD, PATIL VC, DEVKAR V V., DABANE SA, WADER VS, et al.: Association of genetic polymorphism in apolipoprotein A5 and lipoprotein lipase genes with type II diabetes mellitus patients in rural South-Western Maharashtra. Biomed Pharmacol. J., 14 (3): 1695-706, 2021.

2- KOJTA I, CHACIN´SKA M. and BŁACHNIO-ZABIELSKA A.: Obesity, bioactive lipids, and adipose tissue inflammation in insulin resistance. Nutrients, 12 (5), 2020.

3- LIU M., SARIYA S., KHASIYEV F., TOSTO G., DUEKER N.D., CHEUNG Y.K., et al.: Genetic determinants of intracranial large artery stenosis in the northern Manhattan study. J. Neurol. Sci., 436 (December 2021): 120218, 2022.

4- LAKBAKBI F., CHAROUTE H., BAKHCHANE A., AJJEMAMI M., BENRAHMA H., ERROUAGUI A., et al.: Science Direct Association analysis of APOA5 rs662799 and rs3135506 polymorphisms with obesity in Moroccan patients site APOA5 avec l ' obe. Pathol Biol., 63 (6): 243-7, 2015.

5- SHESTAKOVA M., MAYOROV A., GALSTYAN G., KOLBIN A., AREPEVA M., PROSKURIN M., et al.: Diabetes / Endocrine / Metabolic Disorders - Health Policy & Regulatory, (November): 585-6, 2019.

6- ERDFELDER E., FAUL F., BUCHNER A. and LANG A.G.: Statistical power analyses using G*Power 3. 1: Tests for correlation and regression analyses. Behav. Res. Methods, 41 (4): 1149-60, 2009.

7- CHAN Y.H.: Biostatistics 102: Quantitative Data - Parametric., 44 (8): 391-6, 2003.

8- ALQUBALI F., ALBALAWI K.A. and ALSWAT A.E.: Prevalence of Type 2 Diabetes Mellitus and Hypertension in Overweight and Obese People in Riyadh City, KSA 2017.The Egyptain Journal of Hospital Medicine, 69 (October): 2614-7, 2017.

9- ASKARI G., HEIDARI-BENI M., MANSOURIAN M. and ESMAEIL-MOTLAGH M.K.R.: Interaction of lipoprotein lipase polymorphisms with body mass index and birth weight to modulate lipid profiles in children and adolescents_: the CASPIAN-III Study Interação de polimorfismos da lipoproteína lipase com índice de massa corporal e peso ao n. Sao Paulo Med. J., 134 (2): 121-9, 2016.

10- KOCHETOVA O.V., AVZALETDINOVA D.S., SHARIPOVA L.F., KORYTINA G.F., AKHMADISHINA L.Z., MORUGOVA T.V., et al.: An Analysis of the Associations of Polymorphic Variants Genes with the Risk of Developing Type 2 Diabetes Mellitus. Russian Journal of Genetics, 55 (4): 495-503, 2019.

11- MARATEB H.R., MOHEBIAN M.R., JAVANMARD S.H., TAVALLAEI A.A., TAJADINI M.H., HEIDARI-BENI M., et al.: Prediction of dyslipidemia using gene mutations, family history of diseases and anthropometric indicators in children and adolescents: The CASPIAN-III study. Comput Struct Biotechnol. J., 16 (1): 121-30, 2018.

12- IZAR M.C., HELFENSTEIN T., IHARA S.S., RELVAS W.G., SANTOS A.O., FISCHER S.C., et al.: Association of lipoprotein lipase D9N polymorphism with myocardial infarction in type 2 diabetes. The genetics, outcomes, and lipids in type 2 diabetes (GOLD) study. Atherosclerosis., 204 (1): 165-70, 2009.

13- LOTTA L.A., GULATI P., DAY F.R., PAYNE F., ONGEN H., VAN DE BUNT M., et al.: Integrative genomic analysis implicates limited peripheral adipose storage capacity in the pathogenesis of human insulin resistance. Nat. Genet., 49 (1): 17-26, 2017.

14- BUSHUEVA O.Y., STETSKAYA T.A., KOROGODINA T V, IVANOV V.P. and POLONIKOV A.V.: Investigation of the relationship between Hind III polymorphisms of the LPL gene and Taq1b polymorphisms of the CETP gene with the risk of atherothrombotic stroke in residents of Central Russia. Ther. Arkh., 87 (8): 86-91, 2015.

15- JAVORSKEY´ M, GAS PERÍKOVÁ D., UKROPEC J., SEDLÁKOVÁ B., RIEC I, KRIZ ANOVÁ O., et al.: Lipoprotein lipase Hin dIII polymorphism influences HDL-cholesterol levels in statin-treated patients with coronary artery disease. Wiener klinische Wochenschrift, 476-82, 2007.

16- VARDARLI A.T., HARMAN E., ÇETINTAS V.B., KAYIKÇIOG LU M., VARDARLI E., ZENGI A., et al.:

Polymorphisms of lipid metabolism enzyme-coding genes in patients with diabetic dyslipidemia. Anatol. J. Cardiol., 17 (4): 313-21, 2017.

17- HUBACEK J.A.: Apolipoprotein A5 and triglyceridemia. Focus on the effects of the common variants 1 Description and function of the apolipoprotein. Clinical Chemistry and Laboratory Medicine (CCLM), 43 (9): 897-902, 2005.

18- KAHN S.E., HULL R.L. and UTZSCHNEIDER K.M.: Mechanisms linking obesity to insulin resistance and type 2 diabetes. Nature, 444 (7121): pp.840-846, 2006.

19- HE T., WANG J. and DENG W.: Association between Lipoprotein Lipase Polymorphism and the Risk of Stroke: A Meta-analysis PhD ,* PhD *. J. Stroke Cerebrovasc Dis., 26 (11): 2570-8, 2017.

20- UKKOLA O., TM M.J.S., SALMELA P.I. and KESFIN-IEMI Y.A.: DNA polymorphisms at the lipoprotein lipase gene are associated with macroangiopathy in type 2 (non-insulin-dependent) diabetes mellitus. Atherosclerosis, 115 (1): 99-105, 1995.

21- SONG K.H., YU S., CHA S. and KIM J.Y.: Association of the Apolipoprotein A5 Gene - 1131 T > C Polymorphism with Serum Lipids in Korean Subjects: Impact of Sasang Constitution. Evidence-Based Complement Altern Med., 2012.

22- BANTING L.K., PUSHKAREV V.P., CIESZCZYK P., ZAREBSKA A., MACIEJEWSKA-KARLOWSKA A., SAWCZUK M., et al.: Elite athletes ' genetic predisposition for altered risk of complex metabolic traits. BMC Genomics., 1-10, 2015.

ارتباط المتغيرات الجينية لانزيم ليباز البروتين الدهنى مع داء السكرى من النوع الثانى والقابلية لحدوث السمنة بين مجموعة من المرضى المصريين

يعتمد التمثيل الغذائى للدهون على إنزيم ليباز البروتين الدهنى الذى تم الإعلان عن ارتباط متغيراته بداء السكرى من النوع الثانى وقابلية الأفراد للسمنة. تم ربط جين ليباز البروتين الدهنى بعملية التمثيل الغذائى للبروتين الدهنى، فى حين تم ربط المتغيرات الجينية المسببة للأمراض بالسمنة ومقاومة الأنسولين ومرض السكرى.

قمنا بعمل بحث لدراسة الارتباط بين متغيرات إنزيم ليباز البروتين الدهنى (rs 1801177 وrs 320) ومرض السكرى فيما يتعلق بالإصابة بالمرض وقابلية المرضى للإصابة بالسمنة.

فى دراستنا، كان توزيع المتغير إنزيم ليباز البروتين الدهنى (rs 1801177 وrs 320) مختلفاً باخلاف ذو دلالة إحصائية فى وتوزيعه بين الأشخاص المصابين بداء السكرى من النوع الثانى وغير المصابين لداء السكرى.

ارتبط كلا المتغيرين بشكل كبير بالمعايير المتعلقة بالسمنة ومؤشر كتلة الجسم ومحيط الخصر.

حتى فى الأشخاص غير المصابين بالسكرى، ارتبطت المتغيرات المدروسة ببعض هذه المعايير. ولكن نظراً للطبيعة المتعددة للجينات والانتشار الواسع للسمنة وداء السكرى من النوع الثانى، هناك الحاجة إلى مزيد من الدراسات تشمل عدد أكبر من المرضى لتقييم نتائجنا.