The Relationship between Melanocortin 4 Receptor (MC4R) in Different Genes Polymorphisms with Obesity in Egyptian Population

Original Article

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ABSTRACT

Background: Obesity is a condition of an accumulation of excess of body fat potentially posing a threat of health and life in individual. Obesity is increasing in both developed and developing countries. It has a serious epidemic health problem, leading caused modulitity at global level.

Aim of the Work: This work aimed to study the relationship between MC4R gene polymorphism with obesity which has been identified through gene on Egyptian population.

Materials and Methods: This study investigates the interaction of MC4R on increasing obesity on adult population. In this population, rs17782313, rs12970134 and rs571312 gene polymorphism of melanocortin 4 receptor (MC4R) in obese and non-obese patients (n= 105 and 100, respectively) with age between 14 to 60 years were observed from Medicine Hospital inmates, University of Mansoura, Egypt. The lipid profile and body mass index (BMI), waist-to-hip ratio (WHR) were measured, the genotype of SNPS was obtained by restriction fragment length polymorphism (RFLP) method.

Results: A significantly higher of C/C, A/A and A/A, (p <0.0001, p <0.001, p <0.001) genotype was detected compared to controls of (rs17782313, rs12970134 and rs571312), respectively.

Conclusion: The MC4R of rs17782313 and rs12970134 and rs571312 single nucleotide polymorphism showed a strong relationship with obesity in Egyptian sample.

Key Words: Gene polymorphism, MC4R, Obesity, rs17782313, rs12970134, rs571312.

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INTRODUCTION

Obesity refers to the excessive accumulation of body fat, which can significantly endanger health and overall well-being. The increase of obesity has been rising globally, affecting industrial and the third world nations. It represents public health a major and challenged with epidemic effects worldwide[1,2].

The gene of melanocortin 4 receptor (MC4R), a G protein-coupled receptor, is involved in formation of a dipose tissue and energy homostatasis[3]. MC4R was located in 189, 21 region of chromosome 18, the rs1772313 polymorphism was detected in 190 kilo bases downstream of MC4R gene, variant nucleotide changed from (T) thymine and (C) cytosine.

The rs17782313 C allele has been investigated to be related to metabolic disorders of obesity, hyperglycemia and dyslepidemia in children and adult[4-7].

Alpha-melanocyte with MC4R gene stimulating hormone (a-MSH) was distributed in ventro medial hypothalamus and crucial modulator of energy homeostasis and food intake[8]. Association of variant obesity was replicated in Chinese of MC4R gene[9-13]. The MC4R associated with obesity in European and Asian population[5,9]. The MC4R gene and obesity were investigated in European population such as Finland and France[7,14]. The MC4R gene was recorded with obesity in both European and American children but not in African children[15]. The presence of the MC4R with obesity was investigated and result that showed rs17782313 and rs12970134 of SNPS were obesity related[13,16]. The study

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of rs17782313, rs12970134 and rs571312 polymorphisms in patient with obesity and health control to determine if the MC4R gene is a genetic risk factor for increasing of obesity in Egypt. The study further explores the correspondent between gene polymorphisms of MC4R and obesity.

METHODS AND MATERIALS

The study based on 105 obesity cases. The work began with taking their approval. Their mean age ±SD 37.17 ± 10 range of 15 to 62y compared with 100 non-obese (healthy control in cases), comparing cases to their complication with length, age, weight, cholesterols, high density lipoprotein (HDL), low density lipoprotein (LDL), (BMI), for cases and controls; the extracted DNA was later detected by PCR on rs17782313, rs12970134 and rs571312 gene polymorphisms.

ETHICAL CONSENT

Ethical approved was obtained from Damietta university with reference number (DuRaC no150), acceptance of participation of study was obtained from every patient signed an informed written. Personal privacy and confidentially was respected in all study. The work was carried out in accordance with scientific search ethics regulation issued by the supreme council of universities according to Damietta university council approval.

Measurement of anthropometric parameters

Hip circumference, body height and weight were obtained using the standard procedures of World Health Organization[17]. Body height was recorded using digital scale; waist circumference was measured as the maximal circumference over the buttock. Waist circumference was adjusted above naval midway of the lower margin and rib last and crest iliac to the nearest 0-1 cm. Waist-to-hip ratio was measured twice from the right arm of the subjection sitting position using standard sphygmomanometer mercury.

Metabolic parameters measurement

The lipid profile carried out by 5 ml of blood venous after an overnight, various lipid parameters of fast and serum was separated, by using Humatar 180 triglyceride (TG), total cholesterol (Tc) and high-density lipoprotein (HDL), chemistry analyzer (Human Weisbader, Germany). The formula used to compare low-density lipoprotein (LDL)[18].

Extraction DNA genotyping

The genomic DNA extracted from whole blood by using DNA genomic purification (Fermentase kit, USA). Genotyping of rs17782313 polymorphism of MC4R locus was obtained by polymerase chain reaction-restriction fragment length polymorphism assay (PCR-RFLP). DNA fragment rs17782313 was amplified forward primer sequences: AAGTTCTA CCTACCATG TTC TTGG and reverse primers sequence TTCCCCCT GAAG CTTTTCTTG TCA TTTTGAT. PCR was carried out using thermo cycle (L cycler 5, Bio Rad, USA). In 25 µl reaction, PCR components comprised of 50 ng of DNA primer and IUTaq DNA polymerase, thermal cycling was preformed summarized below; initial denaturation (35 cycles) for 30 S at 95°C, an healing for 30 S and 30 S at 58°C extraction at 72°C and for 5 min additional extraction accrued at 72°C. PCR produced were digested using BCII (Fermontase, Germany) enzyme digestion by (PCR product of 7µl and 0.5µl of BCII, 10 U 1µl and 2µl of 10x restruction G buffer) was incubated 56°C over night. Then electrophoresis of digested PCR product was carried out on 2% agrose gel. DNA fragment, gels were stained with green viewer. Gel DOC system (U.V p company, Cambridge, UK fragment length was shown at 30 bp and 137 bp. C allele was also restricted as 137 pb fragment polymorphisms of primers of rs12970134 G>A was carried out by using PCR of forward primer; GA CTC TTACC AAACAAAGCCTG and reverse primer TG CTAGG TTGGTCCTGGTTG) which generated the 124 bp band fragment and 20 bp and 104 bp was extracted by restricted enzyme D de I PCR for 12970134 polymorphism consists of denaturation 10 min at 94°C followed by 35S of denaturation 30S at 94°C for, annealing 45 S at 58°C for elongation 5 min at 72°C.

The polymorphism of primer rs571312 C/A (forwaved) TTTACACAAACATGGGGT and reverse TGAATGTATTGTTGTGCCACTGA, fragment for rs571312 generated at 210 pb, C>A variant. The expected fragment size was 185 pb and 25 bp for the HyI66II restruction site. The PCR profile for rs571312 C>A polymorphism consisted of an primary melting steps 95°C for 5 min; 35 cycle of 95°C for 30 S, and annealing at 57°C for 30 S and extension at 72°C for 1 min, then for 10 min final extension at 72°C.

Statistical Analysis

The variations between cases and controls were comprised using student's t-test and the quantitative variables were expressed as mean ± (SD). The observation of the allelic frequency of gene difference of genotype between obese cases groups association of rs12970134 and rs571312 and rs1778231 variant with obesity was estimated by Pearson Chi-square using codominant and dominant and recessive models. Distribution of allele and genotypes in the concerned population was applied by Hardy Weinberg equilibrium test (HWE). Obesity risk of determination related with risk allele were calculated with add ratio (OR) and sign .05 interval (CI). The genotype coded as (0, 1 and 2) in codominant, (0 and 1) in dominant model and copies numbers of risk allele were corresponding.

RESULTS

A significant statistical difference was noted between individual obese and healthy controls across all measured parameters ($p < 0.05$) except for WHR (Table 1). Also, the biochemical characteristic and clinical of obese cases compared to healthy controls obtained significantly higher values in cases against controls ($p < 0.05$) except hip-to-hip ratio and LDL level (low density lipoprotein ($p > 0.05$).

Table 1: Comparing biochemical characteristic and clinical of obese cases against healthy controls cases.

	Controls†		obese‡		*P*
	Mean	±SD	Mean	±SD	
Age	32.89	11.067	37.08	10.871	0.008**
Length	168.14	10.981	158.41	6.171	0.000***
Weight	73.20	56.990	104.47	13.140	0.000***
Cholesterol	172.98	12.477	201.73	43.770	0.000***
Triglyceride	82.74	20.981	138.42	57.890	0.000***
LDL	118.71	19.614	134.81	43.110	0.004**
HDL	40.61	5.340	44.53	12.510	0.400ns
Waist	65.14	9.240	102.58	7.951	0.000***
Hip	78.14	8.910	112.79	8.190	0.000***
BMI	24.41	1.710	42.11	5.639	0.000***
WHR	95.10	1.260	91.00	0.150	0.719ns

†n =100; ‡n=105; *=*p value* <0.05; **=*p value* < 0.01; ***=*p value* < 0.001; ns= not significant; BMI = body mass index (%); Data presented mean ±SD; WHR = waist-to-hip ratio; HDL = high density lipoprotein; LDL = low density lipoprotein.

The frequency of MC4R rs17782313 polymorphism in cases of obese and controls is shown (Table 2). The relationship and frequency of MC4R gene variants with obesity risks was also shown using several genetic models. A significantly of CC genotype of CC genotype of obese cases compared to controls in codomination model has been detected (21.6% versus 5% $p < 0.0001$). The obtained recessive model ($p = 0.0001$) and over dominant model show T allele of wild type higher in the control group than in cases obese (66.6% versus 60%).

There was also a significant association of polymorphism recessive genetic model (21.8 vs 5% $p < 0.001$). (Table 2) listed the frequency of MC4R of rs12970134 polymorphism of total obese cases against the controls. Moreover, observed of significantly higher GG genotype frequency in comparison with controls (21.9% versus 3%, $p = 0.001$) in codominant model. There is also a significant relationship of polymorphism rs12970134 with risk of obesity in both recessive and over dominant genetic model. (95% CI OR, 0.56 [1.29 – 0.29], $p = 0.011$); (OR 95% CI, 5.56 [1.59-18.34], $p = 0.0036$). Also, the frequency of MC4R rs571312 polymorphism in total obese cases against the non-obese cases (controls) adjusted for age is shown in (Table 2).

Table 2: Frequency of MC4R rs17782313, rs12970134 and rs571312 polymorphic forms in obese cases against controls that adjusted by age and obesity.

	Genotype	Controls (n = 100)	Obese (n = 105)	OR (95°C/CI)	*p-value*
Model MC4R rs17782313:					
Codominant	T/T	36 (36%)	45 (42.9%)	1.00	0.0001***
	T/C	59 (59%)	38 (35.4%)	0.59 (0.32-1.07)	
	C/C	5 (5%)	21 (21.6%)	4.98 (1.53-16.16)	
Dominant	T/T	36 (36%)	45 (42.9%)	1.00	0.64ns
	C/T – C/C	64 (64%)	60 (57.1%)	0.39 (0.49-1.57)	
Recessive	T/T – C/T	95 (95%)	83 (78.2%)	1.00	0.0001***
	C/C	5 (5%)	21 (21.8%)	6.81 (2.23-20.91)	
Over dominant	T/T – C/C	39 (39%)	68 (64.8%)	1.00	0.0025**
	C/T	61 (61%)	37 (35.2%)	0.41 (0.23-0.74)	
Alleles	T	133 (66.6%)	127 (60%)	1.28 (0.80-1.90)	
	C	67 (33.4%)	83 (40%)	1.00	0.28ns
Model MC4R rs12970134:					
Codominant	G/G	35 (35%)	45 (42.9%)	1.00	0.001***
	A/G	62 (62%)	37 (35.2%)	0.78 (0.36-1.62)	
	A/A	3 (3%)	23 (21.9%)	4.65 (1.37-17.01)	
Dominant	G/G	37 (37%)	44 (42.8%)	1.00	0.93ns
	A/G – A/A	63 (63%)	61 (57.2%)	1.12 (0.52-2.08)	
Recessive	G/G – G/A	95 (95%)	81 (78.1%)	1.00	0.0036**
	A/A	5 (5%)	24 (22.9%)	5.56 (1.59-18.30)	
Over dominant	G/G – A/A	40 (40%)	68 (64.8%)	1.00	0.011*
	A/G	60 (60%)	37 (35.2%)	0.56 (0.29-1.80)	
Alleles	G	131 (66.4%)	127 (60%)	1.28 (0.80-1.90)	
	A	69 (34.6%)	83 (40%)	1.00	0.28ns
Model MC4R rs571312:					
Codominant	CC	69 (69%)	35 (33.3%)	1.00	0.0001***
	CA	26 (26%)	40 (37.1%)	2.59 (1.46-4.89)	
	AA	4 (3%)	30 (29.4%)	21.11 (1.36-4.79)	
Dominant	C/C	67 (67%)	35 (33.3%)	1.00	0.0001***
	A/C – A/A	33 (33%)	70 (66.7%)	4.23 (2.23-7.63)	
Recessive	C/C – A/C	97 (97%)	74 (29.5%)	1.00	0.0001***
	A/A	3 (3%)	31 (29.5%)	14.16 (4.08-48.90)	
Over dominant	C/C – A/A	72 (72%)	65 (62.8%)	1.00	0.26ns
	A/C	28 (28%)	40 (37.2%)	1.42 (0.77-2.67)	
Alleles	C	166 (82%)	117 (51%)	1.00	0.0001***
	A	34 (18%)	102 (49%)	4.36 (2.90-6.70)	

OR (95% CI) = odd ratio; *=*p value* <0.05; **=*p value* < 0.01; ***=*p value* < 0.001, ns= not significant

TT-GG-CC = normal homozygous; TC-GA-CA = heterozygous; CC-AA = Homozygous mutation; T-C-A-G = allele

In different generate models of rs571312 polymorphism showed AA genotype with significantly higher frequency in obese cases against controls (29.4% versus 4%) in the codominant model ($p <= 0.0001$). Moreover, both dominant and recessive model showed significant relationship of polymorphism with obesity risk, (OR 95% CI; 423 [2.23-763]; $p < 0.0001$); (OR 95% CI; 14.18 [4.08-48.90]; $p < 0.001$). A significantly higher frequency of A allele of cases have been observed (49% versus 17%, $p < 0.0001$).

The distribution of the MC4R rs571312 polymorphism allele in obese cases and health cases in different genetic models showed significant relationship with obesity risks. On the other hand, each individual group and health cases reading showed significantly departing from the equilibrium departing from the equilibrium. This is may be attributed to the high value of AA and CA in cases to lipid profile parameter in all obese cases regarding their MC4R rs17782313, rs12970134 and rs571312 gene polymorphisms in (Table 3). No significant differences have been shown of the cases for all lipid profile values (cholesterols, HDL and LDL) except triglyceride was significantly associated with the wild CC genotype of rs571312 polymorphism ($p = 0.042$) in obese patients. There was no significant association of BMI and WHR with the rs571312 gene polymorphism. There was a significant association of risk of obesity with MC4R of rs12970134 polymorphism with obesity compared to controls of allel A compared with wild GG genotype ($p = 0.001$). Moreover, there was no significant association of WHR related to their polymorphism of rs12970134 and rs17782313 in (Table 3). Moreover, there was a significant relationship between the MC4R of rs17782313 and rs1290134 gene polymorphisms with BMI ($p = 0.098$, $p = 0.001$), respectively.

Table 3: Parameter lipid profile in obese case regarding their MC4R rs17782313, rs12970134 and rs571312 gene polymorphism.

Parameter	MC4R rs17782313			MC4R rs12970134			MC4R rs571312		
	Genotype	±SD	*p-value*	Genotype	±SD	*p-value*	Genotype	±SD	*p-value*
Age	TT	38.2 2±86.9	0.112	GG	39.28 ±9.04	0.961	CC	39.12 ±8.71	0.161
	TC/CC	39.91 91±10.1		GA/AA	39.12 ±9.81		CA/AA	40.10 ±10.12	
BMI	TT	27.66 ±8.73	0.098	GG	27.52 ±5.16	0.001	CC	28.24 ±5.30	0.88
	TC/CC	27.94 ±5.32		GA/AA	29.67 ±5.18		CA/AA	28.41 ±5.20	
Cholesterols	TT	248.86 ±15.9	0.712	GG	246.86 ±15.41	0.38	CC	257.00 ±15.90	0.821
	TC/CC	249.31 ±14.10		GA/AA	247.65 ±14.51		CA/AA	258.00 ±14.10	
HDL	TT	44.99 ±10.8	0.34	GG	46.21 ±12.21	0.35	CC	45.10 ±11.71	0.361
	TC/CC	45.54 ±17.46		GA/AA	44.91 ±11.10		CA/AA	45.91 ±11.70	
LDL	TT	203.64 ±18.1	0.39	GG	203.18 ±12.4	0.26	CC	207.65 ±19.50	0.421
	TC/CC	204.61 ±19.3		GA/AA	206.13 ±17.10		CA/AA	209.65 ±19.50	
Triglyceride	TT	395.64 ±86.42	0.91	GG	391.61 ±81.00	0.33	CC	390.65 ±88.54	0.04
	TC/CC	385.62 ±86.43		GA/AA	381.65 ±29.10		CA/AA	366.91 ±84.65	
WHR	TT	91.1 ±0.03	178	GG	91.12 ±0.025	231	CC	91.20 ±0.005	243
	TC/CC	91.4 ±0.072		GA/AA	91.14 ±0.008		CA/AA	91.40 ±0.008	

DISCUSSION

Study showed the relationship between obesity and MC4R gene polymorphism on Egyptian population adjusted by age. The AA genotype of rs12970134, and CC genotype of rs17782313 and AA genotype of rs571312 were corresponded to obesity in Egyptian population. In the first section of this work, the researcher studied MC4R gene rs17782313 and MC4R rs12970134 gene polymorphism from total obese cases compared to non obese cases (healthy control) with age adjust. This work obtained significantly of (CC and AA) genotype against to control ($p = 0.0001$, $p = 0.00$), respectively. Also, the study showed no significant association of lipid profile, cholesterol, (HDL) and low density lipoprotein, triglyceride in all obese cases in MC4R rs17782313 and rs12970134 gene polymorphisms and also no significant association of waist hip ratio (WHR) with obesity in this study of both MC4R rs17782313 and rs12970134 gene polymorphism with obesity. On the other hand, there was an association of MC4R of rs17782313 and rs12970134 gene polymorphism with BMI that increases risk of obesity ($p = 0.98$, $p = 0.001$). This was more related to high increase in (CC and AA) genotype than wild (TT and GG) genotype, respectively.

The relationship between obesity and MC4R gene was early noticed in European population and subsequently in France and Finland[14,19], Japan and Denmark[9,15]. MC4R gene polymorphism was related with obesity in American European children but not in African children[12,16]. The data showed an agreement with ***Yang et al.***[20] in northwest China, they reported that there was a strong relationship of MC4R rs17782313 and rs12970134 with obesity and highly significant on obesity in children and adolescents[21]. On the other hand, the data showed no agreement with in Chinese population which reported that polymorphism of MC4R rs17782313 was corresponding to overweight and obesity and CC genotype is an independent risk factor for obesity. My data also in agreement with Indian population of ***Khan et al.***[22] which recorded no significant obesity related with risk A allele of MC4R of rs177821313 and rs12970134 toward lipid profile[23,24]. My data also in agreement in Kuwait population that reported BMI rising in population with MC4R gene polymorphism of rs17782313 with risk of allele was significantly association with obesity. Also, my data in agreement with Saudi Arabia population of ***Batarfi et al.***[25] that reported signification association of A and C allels in rs12970134 and rs17782313 with high BMI in obese women[25,26]. But, my study showed that there is no agreement with Indian population which reported no significant relationship of rs12970134 MC4R and rs17782313 gene polymorphism with obesity[27] that reported C allele of the MC4R rs17782313 polymorphism conforms of risk of obesity and by porglycemia. My study was find relationship between MC4R gene polymorphism and obesity on Egyptian Population of MC4R of rs571312 gene polymorphism adjusted by age of AA genotype and also A allele related in obesity in Egyptian people. The study observed significantly and higher frequency of AA genotype against wild GG genotype (p = 0.00). Also, the study was showed did not appeared any to influence of lipid profile (LDL, HDL, cholesterols) except in triglyceride which was showed significantly higher frequency of MC4R of rs571312 of its genotype AA compared to wild GG type (p – 0.042) in all obese cases. Also, in all cases was showed higher of A allele (p = <0.0001) of MC4R of rs571312 of gene polymorphism from total case compared to controls. Moreover, my data found there no significant association of MC4R of rs571312 with BMI and WHR related to gene polymorphism. Sharma and Badaruddoza, ***Hong et al.***[26,28] were reported where in Northwest Indian Population that a halo type of MC4R gene rs571312 A and rs12970134 A halo type had positive association with obesity in my population. ***Huang et al.***[29] was reported on Chinese Population a nearly threefold risk linked to rs12970134 with obesity. ***Yilmaz and Khodarahmi et al.***[30,31] recorded that there was a strong relationship of rs17782313 gene polymorphism of MC4R with over eating and also that with BMI was associated with C allel of rs17782313. In Korean women and men population; ***Sull et al.***[6] also reported that MC4R of rs17782313 was corresponded with obesity and diabetic in cardiovascular patients.

CONCLUSION

Finally, the present work reported for the first time a significant association of MC4R of rs17782313 and rs12970134 and rs571312 with their genotype C/C and A/A and A/A with obesity in Egyptian people. The work also detected a high relationship between MC4R of rs12970134 and rs17782313 variant genotype with elevated BMI. Moreover, the study observed a high association between MC4R rs571312 genotype variants with elevated triglyceride level which correlated with A allel in all cases. Finally, the present work showed a strong association between MC4R rs17782313, rs12970134 and rs571312 gene variant with obesity among Egyptian population.

COMPETING INTERESTS

The authors have no relevant financial or nonfinancial interests to disclose.

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AUTHORS CONTRIBUTION

Abeer Saad El Zekred: Carried out all laboratory work, wrote full paper, result and discussion.

Mohamed Osama Megahed: Build all reference, collation data building tables,revise the paper.

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عنوان البحث: ارتباط تعدد النمط الجيني لمستقبلات الميلاكورتين٤ بالسمنة في المجتمع المصري

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المقدمة: يُعد السمنة هي تراكم غير طبيعي للدهون بنسبة قد تزيد عن ٢٠٪ من الوزن المثالي للفرد. وإذا زادت نسبة نسبة كتلة الجسم عن ٣٠ كجم/م٢ يعد الشخص مريض بالسمنة.

الهدف: تهدف هذه الدراسة الى تقييم مدى ارتباط مستقبلات الميلاكورتين٤ بالأنماط الجينية المختلفة لمرض السمنة في المجتمع المصري.

مادة وطرق البحث: اشتملت الدراسة على ١٠٥ حالة مصابة بالسمنة مقارنة ب١٠٠ حالة من الأصحاء كمجموعة ضابطة سلبية، وتم اختيار تلك الحالات من المنطقة الوسطى من دلتا النيل بمصر من قسم السمنة بمستشفى الباطنة التخصصي، جامعة المنصورة، حيث تم قياس مؤشر كتلة الجسم، كذلك نسبة الخصر إلى الورك لجميع الحالات، كما تم قياس نسبة الكوليسترول، الدهون الثلاثية، الكوليسترول منخفض الكثافة، وعالي الكثافة وتم ايضاً استخلاص الحامض النووي.

النتائج: أظهرت الدراسة وجود فروق معنوية عالية لكل من الأنماط الجينية ١٧٧٨٢٣١٣، ١٢٩٧٠١٣٤ و٥٧١٣٢١ لحالات السمنة مقارنة بالأصحاء نتيجة لزيادة وتيرة الطراز الجيني A/A, A/A, C/C على الترتيب كعامل من عوامل الخطر الجيني للسمنة بين المصريين وظهور الأليل A للنمط الجيني ٥٧١٣٢١ مؤشر لخطر السمنة بين المصريين. كما أظهرت الدراسة أيضاً وجود فروق معنوية عالية لكل من النمطين الجينيين ١٧٧٨٢٣١٣ و١٢٩٧٠١٣٤ ومؤشر كتلة الجسم BMI في حالات السمنة نتيجة لزيادة وتيرة الطراز الجيني A/A, C/C بالترتيب كعامل من عوامل الخطر الجيني للسمنة. ومن ناحية أخرى تبين عدم وجود فروق معنوية للنمط الجيني ٥٧١٣٢١ مع مؤشر كتلة الجسم BMI ومع معدل الخصر للورك WHR في حالات السمنة. ولكن يوجد فروق معنوية للنمط الجيني ٥٧١٣١٢ المرتبط بالدهون الثلاثية نتيجة لزيادة وتيرة A/A في حالات السمنة. كما تبين أنه لا يوجد فروق معنوية لكل من النمطين الجينيين ١٧٧٨٢٣١٣ و١٢٩٧٠١٣٤ مقارنة بالكوليسترول والكوليسترول مرتفع ومنخفض الكثافة والدهون الثلاثية ومعدل الخصر إلى الورك WHR في حالات السمنة.

الاستنتاج: أظهرت الدراسة وجود ارتباط بين الأنماط الجينية لمستقبلات الميلاكورتين٤ مع السمنة، لذا يوصى بعمل مسح للأفراد الذين لهم تاريخ عائلي مع مرض السمنة، كذلك إجراء تحاليل PCR للجين MC٤R المسبب للسمنة ١٧٧٨٢٣١٣، ١٢٩٧٠١٣٤ و٥٧١٣١٢ للحد من خطر الإصابة بمرض السمنة.