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Original Article

Association between gene polymorphisms of PYY and obesity in a central Chinese population

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Abstract: Objective: This study is to investigate the relationship between gene polymorphisms of peptide tyrosine tyrosine (PYY) and obesity in a central Chinese population. Methods: A total of 410 obese patients and an equal number of non-obese volunteers matched by age and sex were enrolled in this study. Blood biochemical indicator detection and physical examination were performed. Genotype analysis and haplotype analysis were undertaken. Restriction fragment length polymorphism-polymerase chain reaction (RFLP-PCR) was used for the determination of alleles of PYY in the cohort. Results: The genotype frequencies of AA, AC, CC in rs2880212 and GG, GC, CC in rs2880216 were consistent with the distribution predicted by Hardy-Weinberg equilibrium in the controls ($P > 0.5$). Addictive model, dominant mode, and recessive model showed significantly different distribution of rs2880412 genotypes AA, AC, CC and rs2880416 genotypes GG, GC, CC in the patients than that of the controls ($P < 0.5$). Haplotype analysis presented that haplotypes CA and CC could bring risk of obesity (OR, 2.64; 95% CI, 2.00-3.49 and OR, 1.64; 95% CI, 1.01-2.66). There were significant differences in Waist-to-hip ratio (WHtR), systolic blood pressure (SBP), and blood pressure (DBP) in different genotype distribution in site rs2880412 ($P < 0.5$). And there were significant differences in waist circumference (WC), body mass index (BMI), WHtR, SBP, DBP, triglyceride (TG), and high density lipoprotein cholesterol (HDL-C) in different genotype distribution of rs2880416 ($P < 0.5$). Conclusion: PYY might contribute to obesity risk in this central Chinese population.

Keywords: Obesity, polymorphism, genotype, peptide YY

Introduction

Obesity has become a popular global public health problem worldwide along with the development of the economics and people's lifestyle changes. It is a risk factor for serious health problems like diabetes, hypertension, cardiovascular diseases etc., and these problems not only lead to a high morbidity and mortality, but also bring about serious economic burden both to the suffers and the whole society [1]. For the past few years, the incidence of overweight and obesity rose rapidly in China [2].

Epidemiological studies suggest that high-energy diet, decline in physical activity, and social psychological obstacle are the main environmental risk factors for obesity [3], however, the genetic etiology of obesity remains unclear. It is well documented that there is a strong bias of familial aggregation of obesity [4], indicating that an individual's genetic susceptibility may play an important role in obesity. Recently, it is demonstrated that gene mutation of peptide tyrosine-tyrosine (PYY) could induce recruitment obstacle of PYY and Y2, thereby lead to unbridled synthesis of NPY, which in turn result in increased appetite and weight gain. PYY is secreted by ileum, colon, and rectum after a meal in the form of PYY1-36 which breaks up into PYY3-36 during blood circulation, and PYY3-36 integrates with Y2 of neuropeptide Y (NPY). NPY could induce inactivation of hypothalamus and thereby lead to anorexia [5].

Notwithstanding appetite-regulating hormone PYY is closely associated with obesity, and related studies have confirmed that there is sig-

nificant association between gene polymorphism of PYY and obesity in Indians [6], little is known about people in Asia especially in China. To address this issue, single nucleotide polymorphism (SNP) information of a central Chinese population was acquired by tag SNPS method in the current study.

Materials and methods

Study population

A total of 410 obese patients and 410 healthy controls were enrolled in this study. All subjects were Han Ethnicity in central China. Patients with BMI ≥ 28 kg/m^2 and healthy controls that with 18.5 kg/m^2 < BMI < 28 kg/m^2 were recruited from Xin'an Country of Henan Province. The controls were matched to the suffers on age and gender and they had no obesity history or other related clinical signs.

Investigators who were unified trained collected data from the cohort by a special questionnaire. Each object was personally interviewed to gather demographic data including age, gender, education, occupation, average monthly individual income, marital status, and physical exercise intensity. Physical exercise intensity scale was graded as the follows: severe (such as mountaineering, rapid moving, weight training), moderate (such as jogging, Yangko dancing, swimming, playing tennis), mild (e.g strolling, doing qigong, stretching exercises), and no (watching TV, reading a book, eating, etc.).

Physical examination and blood tests

Physical examination consisting of body weight, height, waist circumference (WC), systolic blood pressure (SBP), diastolic blood pressure (DBP), and hip circumference was performed. Body mass index (BMI) and Waist-to-hip Ratio (WHTR) were thereby calculated.

From each participant, 5 mL venous blood was collected in EDTA tube and stored at -80°C for genomic DNA extraction and blood biochemical index detection. Blood biochemical indices including fasting blood-glucose (FPG), total cholesterol (TC), triglyceride (TG), high density lipoprotein cholesterol (HDL-C), and low density lipoprotein cholesterol (LDL-C) were tested.

Genomic DNA extraction

Genomic DNA was extracted using DNA extraction kit (Lifefeng, Shanghai, China) strictly according to the manufacture's instruction. Briefly, 200 μL of blood sample in 1.5 mL EP tube was mixed with 20 μL Proteinase K and 200 μL Buffer GL and was incubated at 65°C for 5 min. Then 350 μL preheated (56°C) Buffer GL was added, the EP tube was gently emulsified by inversion (3-5 times) and centrifuged at 10,000 rpm for 2 min. The supernatant was transferred to DNA adsorption column and incubated for 2 min, and then the column was centrifuged at 7,000 rpm for 1 min and DNA adsorption column was transferred to another collecting tube. Added with 500 μL preheated (56°C) Buffer WAG, centrifuged at 7,000 rpm for 1 min, and the column was transferred to another collecting tube. The column was then washed with WB1 for twice and finally eluted with 40 μL deionized water.

Polymerase chain reaction-restriction fragment length polymorphism (PCR-RFLP)

Rs2880412 and rs2880416 were genotyped using PCR-RFLP assay. The primers were designed by primer 5.0 and the sequences for rs2880412 were 5'-ATTCAATGACGTAAACCAGAA-3' and 5'-AGAGAGCCAACATAGAAAAAC-3'. The upstream primer for rs2880416 was 5'-GAGGAGAAGGAGCAGAAGGA-3' and the downstream primer was 5'-CGTTTTACTTTGAATGACTACTTGC-3'. PCR-RFLP was performed in a 15 μL reaction mixture for each tube, containing 1.0 μL genome DNA, 7.5 μL 2 × Taq PCR PlusMasterMix (Bio-Rad Laboratories, Hercules, USA), 0.8 μM each corresponding primer, and 6 μL distilled water. The PCR amplification program was as follows: 94°C for 5 min, followed by 35 cycles of denaturation at 94°C for 30 s, annealing for 40 s at 60°C, and extension at 72°C for 30 s, and finial extension step at 72°C for 8 min. The products were digested with restriction enzymes Eco81I (Fermentas, CA, USA) for 2-10 h at 37°C. The digestion patterns were separated by 4% agarose gel electrophoresis with ethidium bromide (Biovision, San Francisco, USA).

Statistical analysis

SAS 9.1 software was used for analysis of differences between obesity cases and non-obe-

Table 1. Distributions of selected characteristics in obesity cases and non-obesity controls

Characteristics	Case (N = 410)	Control (N = 410)	t/x^2	P
Age	55.87 ± 12.49	54.61 ± 13.17	1.41	1.16
Sex			1.25	0.26
Males	197	213		
Females	213	197		
BMI/(kg.m^2)	30.97 ± 2.20	22.58 ± 2.08	56.04	0.00
WHTR	0.62 ± 0.05	0.49 ± 0.05	39.20	0.00
WC/cm	99.38 ± 7.04	78.53 ± 7.52	39.99	0.00
Education			1.16	0.28
Less than high school	354	343		
High school or higher	56	67		
Occupation			1.45	0.48
Professional	24	32		
Laborer	368	363		
Other	18	15		
Marital status			0.06	0.80
Not married	35	33		
Married	375	377		
Average monthly individual income (Chinese Yuan)			0.14	0.71
< 1000	376	373		
≥ 1000	34	37		
Physical exercise intensity scale			-	0.00*
Severe	0	6		
Moderate	14	35		
Mild	143	153		
No	253	216		

*: Fisher's exact test.

sity controls. Numerical variable was evaluated using *t*-test, whereas categorical variable was analyzed by χ^2-test. Hardy-Weinberg equilibrium was tested by a pearson's goodness-of-fit χ^2-test. Logistic regression analysis was used to detect the relationship between rs2880412 and rs2880416 gene polymorphism with obesity. Linkage disequilibrium (LD) test were undertaken to evaluate pairwise linkage disequilibrium using Haploview4.0 software and haplotype analysis was inferred by SHEsis software. One-way analysis of variance (ANOVA) was performed for analyzing correlation between genotypes and correlated clinical indexes. $P < 0.05$ was considered as statistically significant.

Ethics

Prior written and informed consent were obtained from each participant and the study was approved by the ethics review board of Zhengzhou University (No. 20140818).

Results

The basic characteristics of the study population

In order to ensure that there were no significant differences in the general condition of the two groups of subjects included in this study, comparative analysis was understand pre examination. Adequate frequency matched by age and gender ($P = 0.16$ and $P = 0.26$) are shown in the **Table 1**. There were no significant differences in the distributions of education, occupation, average monthly individual income, marital status ($P = 0.48$, $P = 0.80$, $P = 0.71$, and $P = 0.80$). The mean values for BMI, WHTR, WC, and physical exercise intensity scale were significantly higher in the obesity group than that in the non-obesity group ($P < 0.05$). In summary, the results showed that there were no significant differences in the general condition of the two groups enrolled in this study and the participants met the requirements of the study.

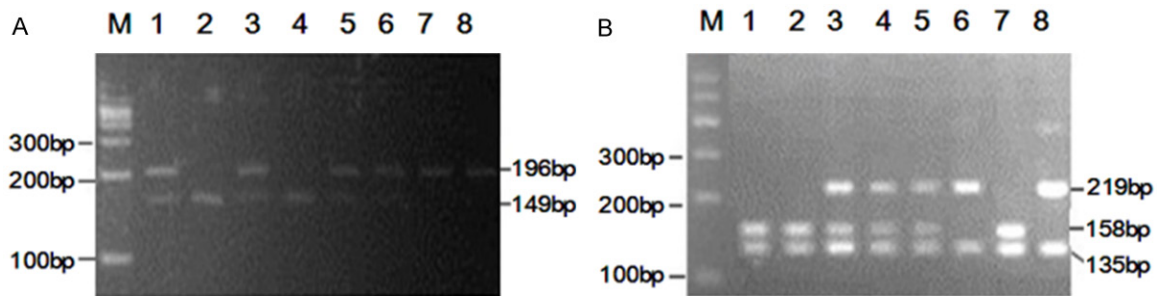

Figure 1. PCR results for genotyping. A: Agarose gel electrophoresis of rs2880412 genotype. M: marker; AA genotype: lane 6, 7, and 8; AC genotype: lane 1, 3 and 5; CC genotype: lane 2 and 4. B: Agarose gel electrophoresis of rs2880416 genotype. M: marker; GG genotype: lane 6 and 8; GC genotype: lane 3, 4, and 5; CC genotype: lane 1, 2, and 7.

Table 2. Genotype and allele frequencies distributions in obesity cases and non-obesity controls

Variants	Case (%) N = 410	Control (%) N = 410	X^2	P	OR (95% CI)
rs2880412			10.08	0.01	
Genotype AA	105 (25.6%)	140 (34.1%)	Reference		1.00
AC	212 (51.7%)	205 (50.0%)	3.94	0.04	1.38 (1.01-1.89)
CC	93 (22.7%)	65 (15.9%)	9.84	0.00	1.91 (1.27-2.86)
Allele A	422 (51.5%)	485 (59.1%)	Reference		1.00
C	398 (48.5%)	335 (40.9%)	9.79	0.00	1.37 (1.12-1.66)
rs2880416			56.84	0.00	
Genotype GG	172 (42.0%)	279 (68.0%)	Reference		1.00
CC	43 (10.5%)	20 (4.9%)	20.61	0.00	3.49 (1.99-6.13)
CG	159 (47.5%)	110 (27.1%)	29.83	0.00	2.35 (1.72-3.19)
Allele G	539 (65.7%)	669 (81.6%)	Reference		1.00
C	281 (34.3%)	151 (18.4%)	53..81	0.00	2.31 (1.84-2.90)

PCR-RFLP assay results

To unravel the genetic causes of obesity, rs2880412 and rs2880416 were genotyped using PCR-RFLP assay. As demonstrated in **Figure 1A**, the wild-type genotypes of rs2880412 AA produced a single 196 bp fragment, the AC genotype produced 196 bp, 149 bp, and 47 bp fragments, and the CC genotype produced 149 bp and 47 bp fragments. The wild-type genotypes of rs2880416 GG produced both 135 bp and 219 bp fragments, the GC genotype produced 135 bp, 219 bp, and 158 bp fragments, and the CC genotype produced 135 bp and 158 bp fragments (**Figure 1B**). Together, PCR-RFLP assay results argued that the specific fragments produced could be used as a genetic marker for further analyzing the relationship between rs2880416 and rs2880412 gene mutations and obesity.

Hardy-Weinberg equilibrium test and genotype frequencies distributions of rs2880412 and rs2880416

In order to characterize genotype and allele frequency distributions of rs2880412 and rs2880416 in patients and the controls, Hardy-Weinberg equilibrium test was performed. As illustrated in **Table 2**, the genotype frequencies in the controls were in full accordance with the expected ones from the Hardy-Weinberg equilibrium prediction (rs2880412: χ^2 = 0.50, P = 0.48; rs2880416: χ^2 = 3.50, P = 0.06). There was significant difference in the overall genotype frequency distributions between the patients and the controls (rs2880412: χ^2 = 10.08, P = 0.01; rs2880416: χ^2 = 56.84, P = 0.00). As for rs2880412, compared with the wild AA genotype, variants AC, CC had creased risk to obesity (OR, 1.38; 95% CI, 1.01-1.89 and OR, 1.91; 95% CI, 1.27-2.86); additionally, there was significant association between allele C and the risk of obesity while compared with allele A (OR, 1.37; 95% CI, 1.12-1.66). With GG as a reference, genotypes CC and GC of rs2880416 had induced risk of obesity (OR, 3.49; 95% CI, 1.99-6.13 and OR, 2.35; 95% CI, 1.72-3.19). And allele C showed significant risk of obesity (OR, 2.31; 95% CI, 1.84-2.90) while compared with allele G. In total, the results demonstrated that the genotype distri-

Table 3. Correlation analysis between genotypes of rs2880412 and rs2880416 loci and obesity

Model	Case (%) N = 410	Control (%) N = 410	X^2*	P*	OR (95% CI)*
Rs2880412					
Addictive model					
AA	105 (25.6%)	140 (34.1%)	12.46	0.00	2.38 (1.86-2.98)
AC	212 (51.7%)	205 (50.0%)			
CC	93 (22.7%)	65 (15.9%)			
Dominant model					
AA	105 (25.6%)	140 (34.1%)	13.04	0.00	2.80 (1.45-5.39)
AC/CC	305 (74.4%)	270 (65.9%)			
Recessive model					
AA/AC	317 (77.3)	345 (84.1)	7.16	0.01	1.65 (1.10-2.24)
CC	93 (22.7%)	65 (15.9)			
Rs2880416					
Addictive model					
GG	172 (41.9%)	279 (27.1%)	57.58	0.00	2.34 (1.85-2.96)
GC	195 (47.6%)	111 (41.9%)			
CC	43 (10.5%)	20 (4.9%)			
Dominant model					
GG	172 (41.9%)	279 (68.0%)	57.11	0.00	3.01 (2.56-4.02)
GC/CC	238 (58.1%)	131 (32.0%)			
Recessive model					
GG/GC	367 (89.5%)	390 (95.1%)	9.29	0.00	2.33 (1.34-4.05)
CC	43 (10.5%)	20 (4.9%)			

*: Adjusted for physical exercise intensity (severe, moderate, mild and no).

Table 4. Haplotype analysis for PYY and obesity risk

PYY Haplotype	Case (%) N = 410	Control (%) N = 410	X^2	OR (95% CI)	P	P*
GA	235 (28.7)	305 (37.2)	Reference	1.00		0.00
CA	238 (29.0)	117 (14.3)	47.56	2.64 (2.00-3.49)	0.00	0.00
CC	43 (5.3)	34 (4.1)	4.14	1.64 (1.01-2.66)	0.04	0.28
GC	304 (37.0)	364 (44.4)	0.48	1.08 (0.87-1.36)	0.49	0.00

*: Haplotype distribution test in case and control groups.

bution of these two sites was in a balanced state in the cohort, hence had certain population representative.

Correlation between genotypes and obesity

To elucidate the relationship between genotype and obesity, rs2880412 and rs2880416 genotype frequency distributions were analyzed. As shown in **Table 3**, logistic regression model was performed with physical exercise intensity scale as an adjustment factor, obesity as the dependent variable (0 = non-obesity, 1 = obesity), and low frequency allele C as mutational gene. Correlation between genotypes and obesity of addictive model (Rs2880412: OR, 2.38; 95% CI, 1.86-2.98, rs2880416: OR, 2.34; 95% CI, 1.85-2.96), dominant model (Rs2880412: OR, 2.80; 95% CI, 1.45-5.39, rs2880416: OR, 3.01; 95% CI, 2.56-4.02), and recessive model (Rs2880412: OR, 1.65; 95% CI, 1.10-2.24, rs2880416: OR, 2.33; 95% CI, 1.34-4.05) were analyzed. From the data in **Table 3**, it is possible to assume that the corresponding C mutations of these two alleles were significantly associated with obesity.

Haplotype analysis3

Haplotype analysis is more efficient than analysis of each of the points. In order to investigate the association between haplotype frequency and obesity, the combined effect of the two polymorphisms on the risk of obesity were evaluated by Haplotype analysis (**Table 4**). Linkage disequilibrium test showed that the LD of rs2880412 and rs2880416 loci was 0.7. A total of four haplotypes were derived from genotypes thereafter. Compared with haplotype GA, haplotypes CA and CC had creased risk of obesity (OR, 2.64; 95% CI, 2.00-3.49 and OR, 1.64; 95% CI, 1.01-2.66), whereas haplotype GC had no danger to obesity (OR, 1.08; 95% CI, 0.87-1.36). The distributions of haplotypes GA, CA and GC were significantly different (P = 0.00). In conclusion, the results indicated that haplotypes CA and CC were correlated with the occurrence of obesity and the occurrence of obesity significantly increased in individuals with haplotypes CA and CC.

Table 5. Analysis between correlated clinical indexes and genotypes of rs2880412

Variants	Genotype of rs2880412 (mean ± s)			F	P
	AA N = 245	AC N = 417	CC N = 158		
WC/cm	87.33 ± 13.16	88.83 ± 13.10	90.31 ± 11.20	2.59	0.07
BMI/(kg.m^2)	26.19 ± 4.77	26.75 ± 4.70	27.21 ± 4.67	2.24	0.11
WHTR	0.57 ± 0.08	0.56 ± 0.08	0.54 ± 0.09	3.85	0.02
SBP (mmHg)	123.94 ± 18.29	128.68 ± 20.03	130.16 ± 23.06	4.54	0.01
DBP (mmHg)	78.93 ± 10.72	81.20 ± 11.77	82.16 ± 13.08	3.52	0.03
FPG (mmol L-1)	5.84 ± 1.87	5.68 ± 1.33	6.01 ± 1.96	2.99	0.05
TC (mmol L-1)	4.61 ± 0.89	4.62 ± 0.99	4.65 ± 1.04	0.06	0.94
TG (mmol L-1)	1.79 ± 1.23	1.96 ± 1.23	2.05 ± 1.42	1.77	0.17
HDL-C (mmol L-1)	1.15 ± 0.27	1.15 ± 0.29	1.16 ± 0.26	0.05	0.95
LDL-C (mmol L-1)	2.52 ± 0.79	2.58 ± 0.82	2.68 ± 0.80	1.68	0.19

BMI: body mass index, WHTR: Waist-to-hip Ratio, WC: waist circumference, SB: Systolic blood pressure, DBP: Diastolic blood pressure, FPG: fasting plasma glucose, TC: total cholesterol, TG: triglyceride, HDL-C: HDL cholesterol, LDL-C: LDL cholesterol.

Table 6. Analysis between correlated clinical indexes and genotypes of rs2880416

Variants	Genotypes of rs2880416 (mean ± s)			F	P
	GG N = 451	GC N = 306	CC N = 63		
WC/cm	86.28 ± 12.66	91.99 ± 12.68	93.44 ± 10.04	23.46	0.00
BMI/(kg m^2)	25.72 ± 4.50	28.01 ± 4.82	28.31 ± 3.77	26.60	0.00
WHTR	0.54 ± 0.08	0.56 ± 0.08	0.58 ± 0.07	21.39	0.00
SBP (mmHg)	125.96 ± 20.85	130.31 ± 20.04	133.81 ± 21.12	6.64	0.01
DBP (mmHg)	79.29 ± 11.63	82.49 ± 11.62	86.42 ± 13.99	13.75	0.00
FPG (mmol L-1)	5.82 ± 1.65	5.80 ± 1.74	5.69 ± 0.94	0.17	0.84
TC (mmol L-1)	4.65 ± 1.01	4.58 ± 0.91	4.63 ± 0.99	0.49	0.62
TG (mmol L-1)	1.85 ± 1.23	2.03 ± 1.44	2.31 ± 1.49	4.06	0.02
HDL-C (mmol L-1)	1.11 ± 0.23	1.13 ± 0.27	1.18 ± 0.28	7.70	0.00
LDL-C (mmol L-1)	2.62 ± 0.81	2.56 ± 0.82	2.47 ± 0.77	1.20	0.30

BMI: body mass index, WHTR: Waist-to-hip Ratio, WC: waist circumference, SBP: Systolic blood pressure, DBP: Diastolic blood pressure, FPG: fasting plasma glucose, TC: total cholesterol, TG: triglyceride, HDL-C: HDL cholesterol, LDL-C: LDL cholesterol.

Correlation between clinical indexes and genotypes

To explore the correlations between clinical indexes and different genotypes, ANOVA was performed. As displayed in **Tables 5** and **6**, homogeneity test of variances in each group showed no significant difference ($P > 0.05$). Tested by ANOVA, WHTR, SBP and DBP showed significant differences ($F = 3.85$, $P = 0.02$; $F = 4.54$, $P = 0.01$ and $F = 3.52$, $P = 0.03$) in rs2880412, whereas no significant differences were found in other indexes ($P > 0.05$). As for rs2880416, there were no statistically significant differences in FPG, TC and LDL-C while significant differences ($P < 0.05$) were found in the other indexes. Altogether, the results illustrated that the changes of rs2880412 and rs2880416 genotypes all were able to influence the transform of corresponding elevated clinical indexes.

Discussion

To date, China has become the world's second largest economy, accordingly, the prevalence of obesity increased rapidly in the past few years. Unhealthy lifestyles and bad eating habits are generally documented as risk factors [7], at the same time, genetic factors are concerned these days. In this study, the comparative results of basic characteristics argued that there were no significant differences in the distribution of age, gender, education, occupation, average, monthly individual, and income and marital status. However, BMI, WC, and WHTR of obesity group were significantly higher than that of the controls, which confirmed the distribution of disease state.

The participants of the present study resided in the area of Henan province where they were born and live. The observed genotype frequencies accorded with that expected from the Hardy-Weinberg equilibrium in the controls, suggesting that the objects were representative. The genotype and allele frequency distributions of rs2880412 and rs2880416 in the patients and controls showed that genotypes {rs2880412: AC (OR, 1.38; 95% CI, 1.01-1.89), CC (OR, 1.91; 95% CI, 1.27-2.86), rs2880416: CC (OR, 3.49; 95% CI, 1.99-6.13), GC (OR, 2.35; 95% CI, 1.72-3.19)} and alleles {rs2880412: C (OR, 1.37; 95% CI, 1.12-1.66, rs2880416: OR, 2.31; 95% CI, 1.84-2.90)} could increase the risk of obesity. This was in accordance with the situation of people from Pima Indian [6, 8], however, as China has a vast territory, and there are a large number of ethnic groups, whether genotype and allele frequencies distribution exists similar difference in different geographical range remains to be explored [9].

We further confirmed the result by three kinds of models, the dominant model suggested that AC/CC (OR, 2.80; 95% CI, 1.45-5.39) of rs2880412 had the highest effect, and so did GC/CC (OR, 3.01; 95% CI, 2.56-4.02) of rs2880416. Haplotype analysis also presented that haplotypes CA and CC had creased risk of obesity (OR, 2.64; 95% CI, 2.00-3.49 and OR, 1.64; 95% CI, 1.01-2.66).

Obesity is a complex disease, which might be caused by the way of life and the diet custom [10-12], drug-induced [13, 14], material metabolism and endocrine function changing [15], etc. This study analyzed the association between rs2880412 and rs2880416 loci and obesity genetically on the adjustment basis of physical exercise intensity using addictive mode, dominant model, and recessive model [16]. Our results demonstrated that the corresponding allele C of rs2880412 and rs2880416 as well as C mutations were positively correlated to obesity.

Moreover, the correlation between genotypes and correlated clinical indexes was analyzed. There were significant differences in the distribution of WHTR, SBP, and DBP in rs2880412, whereas other indexes showed no significantly differences. The result showed that the transformation of genotypes had influenced the level of WHTR, SBP and DBP, WC ($P > 0.05$), suggesting that changes of the rs2880412 genotype affected the change of SBP, DBP, and WHTR in this central Chinese population. And as for rs2880416, the changes of genotype affected the level of blood pressure (SBP, DBP), WC, BMI, WHTR, TG, and HDL-C (GG > GC > CC). Most of the indicators were in normal level and no significant difference were found in genotype distribution, suggesting that the occurrence of obesity might be caused by combined actions of multiple genes [17, 18].

Collectively, we provided statistical evidence that confirmed the association between PYY and the risk of obesity, suggesting that genetic variations in PYY gene might play an important role in the development of obesity. This study, however, exists some shortcomings. Firstly, only Chinese Han Ethnicity and people from central region of China were enrolled, hence, verification with large sample, different populations, and different geographical range is needed. Secondly, related study has shown that melanocortin which maintains the body's metabolic balance also plays an important role in obesity [19]. Additionally, environmental factors play a significant role in obesity development. In light of this, the underlying mechanism between the occurrence of obesity and many factors should be analyzed so as to further extend the observations.

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Disclosure of conflict of interest

None.

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