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Dopamine receptor D2 polymorphism is associated with alleviation of obesity after 8-year follow-up: a retrospective cohort study in obese Chinese children and adolescents*

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Abstract: Objective: The aim of this study was to explore the association of dopamine receptor D2 (*DRD2*) polymorphism and alleviation of obesity in children and adolescents after 8-year follow-up. Methods: This retrospective cohort study included obese children and adolescents with a follow-up period of 8 years. Baseline clinical characteristics and *DRD2* polymorphisms (including rs1076562, rs2075654, and rs4586205) were extracted from medical records. A follow-up visit was performed in May 2017 to collect related data including height, weight, diet compliance, and exercise compliance. Results: One hundred and nine obese children and adolescents were included in the current study. Among three *DRD2* single nucleotide polymorphisms, only rs2075654 had a statistically significant association with alleviation of obesity, as the alleviation rate for minor allele carriers (68.6% for TC+TT) was higher compared to the major allele homozygote (43.3% for CC). After adjusting for all related factors, the hazard ratio of rs2075654 minor allele carriers for the alleviation of obesity was 3.34 (95% confidence interval (CI): 1.30–8.58). Conclusions: The rs2075654 polymorphism of *DRD2* is related to long-term obesity alleviation in obese Chinese children and adolescents.

Key words: Obesity; Follow-up study; Dopamine receptor D2; Children; Adolescent
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1 Introduction

Obesity is a major public health problem in children and adolescents because of its high prevalence and continued increase worldwide (Ng et al., 2014). Obesity in children and adolescents is related to many health problems including psychological issues, cardiovascular diseases, and metabolic complications (Skinner et al., 2015; Sagar and Gupta, 2017). Moreover, the early development of obesity in children predicts obesity in adulthood, which subsequently leads to obesity-related health issues in adults (Ward et al., 2017).

Epidemiologic studies provide insight into the growth trajectories of children, but most studies have relatively short follow-up periods and do not follow children into adulthood (Vizcaíno et al., 2002; Julia et al., 2008; Imed et al., 2009; Nakano et al., 2010). Additionally, the role of genetic factors is not well defined for the prognosis of obesity in children and adolescents. Because genetic factors play an important role in the development of obesity, it is necessary to determine whether they are associated with

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obesity that persists from childhood and adolescence into adulthood.

The dopamine receptor D2 (*DRD2*) gene is suggested to be associated with weight gain from normal weight to overweight or obesity in adults (Kvaløy et al., 2015). A recent longitudinal study in obese children found that *DRD2* polymorphisms were associated with responses to a one-year lifestyle intervention (Roth et al., 2013). However, the long-term effect of *DRD2* gene polymorphisms on weight status has not been studied in obese children and adolescents so far. To address such concerns, we conducted a current retrospective cohort study to explore the role of *DRD2* gene polymorphisms in the alleviation of obesity in children and adolescents.

2 Materials and methods

2.1 Subjects

This retrospective cohort study included all obese children and adolescents from the ages of 7 to 16 years recruited from the outpatient department in the First Affiliated Hospital, Zhejiang University School of Medicine, China, for analysis of obesity-related single nucleotide polymorphisms (SNPs) between July 2008 and July 2010. Data from these participants were extracted from medical records, including sex, age, height, weight, *DRD2* SNP genotypes (including rs1076562, rs2075654, and rs4586205), systolic blood pressure (SBP), diastolic blood pressure (DBP), total cholesterol (TC), triglyceride (TG), high density lipoprotein cholesterol (HDL-C), low density lipoprotein cholesterol (LDL-C), non-HDL-C, fasting plasma glucose (FPG), alanine transaminase (ALT), and aspartate transaminase (AST). Additionally, the height and weight of parents were also extracted. The suggestion of comprehensive behavioral intervention was provided during the first visit by clinical pediatric experts to participants in order to alleviate obesity. A telephone interview was performed in May 2017 to collect related data, including height, weight, diet compliance, and exercise compliance.

2.2 Definitions

Body mass index (BMI, kg/m^2) was calculated as weight/(height×height), and the BMI *z*-score was calculated according to the growth reference developed by the World Health Organization (de Onis et al., 2007). Obesity was defined as above (≥) two standard deviations (SDs) of BMI-for-age. Participants were considered to have alleviation of obesity if their BMI was below (<) two SDs of BMI-for-age at the follow-up visit. Alleviation rate of obesity was calculated according to the followed formula: (number of participants with alleviation of obesity)/(total number of participants in corresponding group)×100%. The guardians of participants were asked whether the participants are willing to do exercise and control their diet. Participants were considered to be diet-compliant and exercise-compliant if they tried to control their calorie intake and partake in regular physical exercise most of the time.

2.3 Identification of *DRD2* polymorphism

Three SNPs (rs1076562, rs2075654, and rs4586205) were selected based on the genotype data from the 1000 Genomes Project. Three SNPs have minor allele frequencies (MAFs) of >30% in the southern Han Chinese population (1000 Genomes Project Consortium et al., 2015). It is well-known that SNPs with relatively high MAF are useful genetic markers. Genomic DNA was extracted from peripheral blood samples and polymorphisms were precisely genotyped using the automated MassARRAY platform (Sequenom, San Diego, CA, USA). A polymerase chain reaction for the DNA sequence with the target SNP was implemented. The products were extended by one base in the SNP sites using the SNP-specific primer. The products were applied to the MassARRAY SpectroCHIP array and crystallized with the matrix in the chip. The crystal-containing chip was moved to the mass spectrometer vacuum tube and excited using an instantaneous nanosecond laser. The molecular matrix absorbs the radiation energy, which leads to an energy accumulation causing crystal matrix sublimation, DNA molecule desorption and transformation to metastable ions. The ions arrive at the detector according to ionic quality. The flight time of an ion can reflect the quality of the analytes and can distinguish between different SNPs.

2.4 Statistical analysis

The numerical results were described as proportions for qualitative variables, means with SDs for quantitative variables with normal distribution, and

medians with interquartile ranges for quantitative variables with non-normal distribution. The Kolmogorov-Smirnov test was used to examine the distribution of quantitative variables. The test was performed to compare qualitative variables. The Student's *t*-test or analysis of variance (ANOVA) was taken to compare quantitative variables with normal distribution. For the comparison of quantitative variables with non-normal distribution, the Mann-Whitney *U* test or Kruskal-Wallis *H* test was performed. Univariate logistic regression was performed to evaluate the hazard ratio (HR) of the related risk factors for the alleviation of obesity. Finally, three multivariate logistic regression models (forward stepwise) were implemented to evaluate the adjusted HR of the rs2075654 genotypes (dominant model) for the alleviation of obesity. The data were analyzed using SPSS software (Version 22.0, SPSS Inc., Chicago, USA), and $P<0.05$ was considered statistically significant.

3 Results

The allele frequency distributions and distributions of the *DRD2* genotypes (according to rs2075654, rs1076562, and rs4586205) are described in Table 1. There was no statistically significant difference in allele or genotype frequency distributions between the participants in our study and the southern Han Chinese in the 1000 Genomes Project (1000 Genomes Project Consortium et al., 2015).

The clinical characteristics of participants per rs2075654 genotyping are summarized in Table 2. There was no association between rs2075654 genotypes and the clinical characteristics of the baseline including age, sex, BMI, BMI *z*-score, parental BMI, blood pressure (BP), FPG, serum lipid (TG, TC, LDL-C, HDL-C and non-HDL-C), and liver function tests (ALT and AST). Except for BMI (P=0.017) and SBP (P=0.042) in the rs1076562 dominant model, there was no association between rs1076562/rs4586205 genotypes and baseline clinical characteristics in the three models (additive, dominant, and recessive models).

As shown in Table 2, 67.9% and 53.2% of the participants exhibited diet and exercise compliance to reduce their weight, respectively, over an average follow-up period of (8.30±1.33) years. A reduction in obesity of 59.6% was observed in all participants at the follow-up visit. Among the three *DRD2* SNPs, only rs2075654 had a statistically significant association with the rate of obesity reduction, because the rate of reduction for minor allele carriers (69.1% for TC, 66.7% for TT, and 68.6% for TC+TT) was higher than that for the major allele homozygote (43.6% for CC).

In the univariate logistic regression analyses, 18 variables were tested for the association with the alleviation of obesity, including sex, age, BMI *z*-score at baseline, BMI of father, BMI of mother, SBP, DBP, TC, TG, HDL-C, LDL-C, non-HDL-C, FPG, ALT, AST, diet compliance, exercise compliance, and follow-up period duration. As shown in Table 3, the BMI *z*-score at baseline, TC, LDL-C, diet compliance, exercise compliance, and rs2075654 had statistically significant associations with the alleviation of obesity.

As presented in Table 4, three multivariate logistic regression models (Model 1: independent variables include rs2075654 and BMI *z*-score at baseline; Model 2: independent variables include rs2075654, BMI *z*-score at baseline, TC, LDL-C, diet compliance, and exercise compliance; Model 3: independent variables include rs2075654, BMI *z*-score at baseline, TC, LDL-C, diet compliance, exercise compliance, interaction between diet compliance and exercise

Table 1 Allele and genotype frequency distributions per *DRD2* SNP in our study and 1000 Genomes Project

SNP	Study	Major homozygote	Heterozygote	Minor homozygote	Major allele	Minor allele	P^*	$P^\dagger$
rs1076562	Current	31	61	17	123	95	0.970	0.959
	CHS	31	57	17	119	91		
rs2075654	Current	39	55	15	133	85	0.822	0.550
	CHS	41	52	12	134	76		
rs4586205	Current	34	61	14	129	89	0.313	0.277
	CHS	43	49	13	135	75		

CHS, southern Han Chinese population in 1000 Genomes Project Phase 3 (1000 Genomes Project Consortium et al., 2015). * Comparison of genotypes among three groups (major homozygote versus heterozygote versus minor homozygote). † Comparison of alleles between major allele and minor allele

Table 2 Clinical characteristics per genotype in rs2075654

Parameter	CC	TC	TT	TC+TT	CC+TC	All	*P* value		
							Additive*	Dominant†	Recessive‡
Baseline									
Number	39	55	15	70	94	109			
Male (%)	84.9	78.2	93.3	81.4	80.9	82.6	0.358	0.674	0.237
Age (year)	10.67±1.61	10.79±2.02	10.63±2.38	10.76±2.09	10.74±1.85	10.73±1.92	0.936	0.822	0.836
BMI (kg/m^2)	27.72±2.79	28.85±4.31	26.91±2.77	28.43±4.09	28.38±3.77	28.18±3.68	0.122	0.336	0.151
BMI *z*-score	3.13±0.70	3.30±1.02	3.05±0.97	3.25±1.00	3.23±0.90	3.20±0.91	0.528	0.517	0.489
BMI of father (kg/m^2)	25.63±3.19	25.73±3.86	25.75±3.46	25.74±3.75	25.69±3.58	25.70±3.55	0.988	0.879	0.950
BMI of mother (kg/m^2)	23.78±3.06	23.59±3.44	23.07±2.84	23.48±3.30	23.67±3.27	23.59±3.21	0.772	0.644	0.504
SBP (mmHg)	113.8±13.0	114.5±13.9	121.4±12.4	116.0±13.8	114.2±13.5	115.2±13.5	0.155	0.431	0.055
DBP (mmHg)	67.8±7.7	68.9±8.8	70.3±7.0	69.2±8.4	68.5±8.3	68.7±8.1	0.586	0.385	0.426
TC (mmol/L)	4.36±0.79	4.43±0.77	4.30±0.84	4.40±0.78	4.40±0.77	4.39±0.78	0.828	0.795	0.649
TG (mmol/L)	1.14 (1.12)	1.46 (0.89)	1.65 (1.63)	1.50 (0.96)	1.43 (1.02)	1.45 (1.01)	0.119	0.051	0.220
HDL-C (mmol/L)	1.24±0.30	1.23±0.28	1.22±0.18	1.23±0.26	1.24±0.29	1.23±0.28	0.944	0.775	0.794
LDL-C (mmol/L)	2.47±0.66	2.70±0.68	2.56±0.65	2.67±0.68	2.61±0.68	2.60±0.68	0.257	0.142	0.779
Non-HDL-C (mmol/L)	3.10±0.80	3.20±0.78	3.08±0.86	3.17±0.79	3.16±0.79	3.15±0.79	0.809	0.664	0.737
FPG (mmol/L)	4.90 (0.50)	5.00 (0.50)	4.90 (0.70)	4.95 (0.63)	4.90 (0.50)	4.90 (0.60)	0.152	0.099	0.142
ALT (U/L)	34.0 (41.0)	41.0 (55.0)	29.0 (80.0)	41.0 (55.5)	39.5 (45.0)	39.0 (44.5)	0.362	0.159	0.535
AST (U/L)	30.0 (23.0)	38.0 (31.0)	33.0 (21.0)	37.5 (29.5)	34.5 (26.0)	34.0 (25.5)	0.451	0.266	0.812
Follow-up									
Age (year)	18.85±1.98	19.16±2.37	19.00±2.30	19.12±2.34	19.03±2.21	19.02±2.21	0.799	0.532	0.963
Follow-up time (year)	8.17±1.31	8.36±1.35	8.37±1.35	8.37±1.34	8.29±1.33	8.30±1.33	0.774	0.474	0.823
Diet consciousness (%)	69.2	61.8	86.7	67.1	64.9	67.9	0.184	0.823	0.137
Exercise consciousness (%)	43.6	54.5	73.3	58.6	50.0	53.2	0.140	0.133	0.093
BMI (kg/m^2)	29.24±5.53	27.98±4.26	28.31±2.57	28.05±3.95	28.50±4.84	28.48±4.59	0.419	0.194	0.880
BMI *z*-score	1.81±1.22	1.64±0.89	1.74±0.57	1.66±0.83	1.71±1.04	1.72±0.99	0.713	0.448	0.934
Alleviation rate (number) of obesity	43.6% (17)	69.1% (38)	66.7% (10)	68.6% (48)	58.5% (55)	59.6% (65)	0.038	0.011	0.550

* Additive model (analysis of variance): comparison among three groups (CC versus TC versus TT). † Dominant model (*t*-test): comparison of TC+TT with CC. ‡ Recessive model (*t*-test): comparison of TT with CC+TC. Data are expressed as mean±SD for quantitative variables with normal distribution or medians (interquartile ranges) for quantitative variables with non-normal distribution

compliance, interaction between rs2075654 and diet compliance, and interaction between rs2075654 and exercise compliance) were applied to explore the association between rs2075654 (dominant model) and alleviation of obesity. Minor allele carriers (TT+TC) showed a statistically significant association with the alleviation of obesity in every model. After adjusting for all related factors, the HR of the rs2075654 minor allele carrier for the alleviation of obesity was 3.34 (95% confidence interval (CI): 1.30–8.58).

Table 3 Hazard ratio of related variables for alleviation of obesity according to univariate logistic regression models

Variables	HR	95% CI	*P* value
Sex	1.197	0.431–3.327	0.731
Age at baseline	1.184	0.962–1.456	0.111
BMI *z*-score at baseline	0.512	0.304–0.861	0.012
BMI of father	0.972	0.870–1.085	0.611
BMI of mother	0.979	0.866–1.107	0.737
SBP	0.986	0.958–1.015	0.336
DBP	0.985	0.939–1.033	0.533
TG	1.245	0.779–1.990	0.361
TC	1.741	1.029–2.947	0.039
HDL-C	2.498	0.579–10.783	0.220
LDL-C	1.869	1.016–3.438	0.044
Non-HDL-C	1.510	0.907–2.512	0.113
FPG	0.794	0.394–1.600	0.518
ALT	0.999	0.992–1.006	0.771
AST	0.995	0.981–1.009	0.499
Follow-up period	0.849	0.634–1.139	0.275
Diet compliance	3.326	1.441–7.677	0.005
Exercise compliance	3.779	1.685–8.476	0.001
rs2075654 (dominant model)	2.824	1.257–6.344	0.012

The BMI *z*-score at baseline exhibited a negative association with the alleviation of obesity (HR: 0.39, 95% CI: 0.21–0.72). Participants who complied with their diet (HR: 2.78, 95% CI: 0.99–7.76) and were exercise-compliant (HR: 2.71, 95% CI: 1.04–7.05) had higher rates of obesity alleviation in Model 2. Moreover, if participants were both diet- and exercise-compliant at the same time, the alleviation of obesity was more significant (HR: 6.70, 95% CI: 2.50–17.94). We found no interaction between rs2075654 and diet or exercise compliance for the alleviation of obesity.

There was no association found between rs1076562/rs4586205 genotypes and the alleviation of obesity in logistic regression analyses.

4 Discussion

The most important finding of this retrospective cohort study is that the minor allele carriers at the *DRD2* rs2075654 locus are associated with increased alleviation of obesity in children and adolescents after an 8-year follow-up. Additionally, we also found that a higher BMI *z*-score in childhood and adolescence is associated with a lower rate of obesity alleviation in early adulthood. Finally, children and adolescents who are diet- and exercise-compliant at the same time have a more significant reduction in obesity compared to those who are compliant with either diet or exercise.

DRD2 is suggested to play a metabolic role by regulating food intake behavior (Garcia-Tornadú et al., 2010). A recent study showed that obese women had

Table 4 Hazard ratio of related variables for alleviation of obesity in multivariate logistic regression models

Model	Variables	HR	95% CI	*P* value
1	TT+TC	3.297	1.406–7.729	0.006
	BMI *z*-score at baseline	0.475	0.277–0.815	0.007
2	TT+TC	3.627	1.406–9.358	0.008
	BMI *z*-score at baseline	0.417	0.227–0.764	0.005
	Diet compliance	2.778	0.994–7.763	0.051
	Exercise compliance	2.711	1.042–7.053	0.041
3	TT+TC	3.339	1.299–8.581	0.012
	BMI *z*-score at baseline	0.386	0.208–0.716	0.003
	Diet compliance×exercise compliance	6.701	2.503–17.941	<0.001

Model 1: independent variables include rs2075654 (dominant model) and the BMI *z*-score at baseline. Model 2: independent variables include rs2075654 (dominant model), the BMI *z*-score at baseline, TC, LDL-C, diet compliance, and exercise compliance. Model 3: independent variables include rs2075654 (dominant model), the BMI *z*-score at baseline, TC, LDL-C, diet compliance, exercise compliance, interaction between diet compliance and exercise compliance, interaction between rs2075654 and diet compliance, and interaction between rs2075654 and exercise compliance

lower striatal *DRD2/3* availability as compared with normal-weight women (van de Giessen et al., 2014). However, no direct association between striatal *DRD2/3* availability and BMI, food craving, insulin resistance, or leptin signaling was found. Similar to this study, our research did not find any associations between *DRD2* gene polymorphisms and metabolic indicators in the baseline or diet compliance. However, Asian American college students with the *DRD2* A1 allele have shown greater carbohydrate and fast food cravings in recent research according to Yeh et al. (2016). Additionally, a study of Chilean children suggested that the *DRD2* TaqI A1 polymorphism (rs1800497) may be a risk factor for eating behavior traits that may predispose them to higher energy intake and obesity (Obregón et al., 2017). Similar results were reported in adults with clinically severe obesity (Carpenter et al., 2013). In the current study, participants with TT genotypes showed greater diet compliance (13/15=86.7%) as compared with CC (27/39=69.2%) and TC (34/55=61.8%), although no statistical significance was found. This may be caused by the relatively small sample size in the current study. The reason that a lack of association between *DRD2* genotypes and BMI *z*-score at baseline was found may be due to the specific obese population we chose. Henceforth, further studies with larger sample sizes and more extensive populations should be performed to address these issues.

The relationship between *DRD2* genotypes and obesity is controversial. A study conducted by Hardman et al. (2014) failed to provide evidence of association between *DRD2* Taq1A polymorphism and obesity in children aged 7 to 11 years. However, the research by Roth et al. (2013) showed overweight/obesity in children with two rs1800497 T-alleles had the weakest BMI-standard deviation score (SDS) reduction as compared with the C allele carriers after one year of lifestyle intervention. Up to now, there has been no related research published focusing on the relationship between the rs2075654 polymorphism and long-term weight status. Research by Gosso et al. (2008) identified rs2075654 as a tag-SNP for *DRD2*, and reported a linkage disequilibrium between rs2075654 and rs1800497 in the Centre d'Etude du Polymorphisme Humain (CEPH) population (r^2=0.65). The linkage disequilibrium is more significant in the southern Han Chinese population with r^2=0.94 and D'=1.00 according to the 1000 Genomes Project (http://www.ensembl.org/index.html; 1000 Genomes Project Consortium et al., 2015). Thus, the rs2075654 polymorphism can be used to predict *DRD2* function. As shown by our study, carriers of rs2075654 minor alleles showed significant alleviation of obesity (HR: 3.34, 95% CI: 1.30–8.58) in children and adolescents after an 8-year follow-up. These results are different from the aforementioned studies, and the reason may be the much longer follow-up period and ethnic differences.

The allele and genotype frequencies of *DRD2* SNPs in our study were similar to those of the southern Han Chinese in the 1000 Genomes Project. Yet, according to the 1000 Genomes Project, the frequency of the rs2075654 T allele is 0.414 in East Asian, 0.256 in American, and 0.146 in European populations. Therefore, this may partly account for the differences in obesity prevalence and responses to lifestyle interventions among various ethnic groups (Collaboration, 2017).

One of the unexplained issues in the management of obesity is the marked variability in response to the treatment of obesity. Genetic factors play a key role in the individual variability (Su et al., 2017; Bray et al., 2018). The relationship between rs2075654 polymorphism and alleviation of obesity found in the current study suggests that rs2075654 polymorphism could be used to predict prognosis of obesity in children and may contribute to individualized treatment in the future. In other words, more attention should be paid to obese children with CC genotypes.

The second finding of our study is that a higher BMI *z*-score in children and adolescents lowers (HR: 0.39, 95% CI: 0.21–0.72) the alleviation of obesity in early adulthood. Most of the participants (78%) in the current study had reached 18 years old at their follow-up visit. This is different from previous studies because the weight status was tracked from childhood and adolescence into early adulthood in our study, although the results are similar (Vizcaíno et al., 2002; Julia et al., 2008; Imed et al., 2009; Nakano et al., 2010). It is well known that lifestyle interventions that include a realistic diet plan and exercise regimen will promote a reduction in obesity (Trivedi et al., 2014; Wang et al., 2016). However, few studies have evaluated the interaction between diet and exercise interventions. As shown in our results, participants who

were both diet- and exercise-compliant had a greater improvement in obesity. Hence, it is very important for pediatric clinicians to screen for obesity in children and adolescents and to refer them for lifestyle interventions to promote improvement in weight status (US Preventive Services Task Force et al., 2017).

The major strength of our study is the relatively long follow-up period, which allowed us to explore the genetic effect of *DRD2* on the weight status change from childhood and adolescence into early adulthood. However, two potential limitations in our study should be noted. First of all, although the current study shows no statistically significant difference in baseline characteristics per rs2075654 genotype, it is still a retrospective study and is not specifically designed for the current study's purpose. A randomized controlled trial is therefore essential to confirm the association between rs2075654 polymorphisms and weight status change in the future. Second, the evaluation of diet and exercise compliance is relatively imprecise, although the major findings of our study were not affected since the associations remain statistically significant both before and after adjusting for diet and exercise compliance. However, the interaction between diet and exercise compliance should be evaluated more precisely in future studies.

5 Conclusions

In conclusion, the rs2075654 SNP of *DRD2* is related to long-term weight status in obese Chinese children and adolescents. This association could be used to predict future improvement in obesity in early adulthood. Additionally, targeted therapy for the treatment of obesity could be developed in future studies.

Compliance with ethics guidelines

Jian-fang ZHU, Lian-hui CHEN, Ke YUAN, Li LIANG, and Chun-lin WANG declare that they have no conflict of interest.

All procedures followed were in accordance with the ethical standards of the responsible committee on human experimentation (institutional and national) and with the Helsinki Declaration of 1975, as revised in 2008 (5). Informed consent was obtained from all patients and their parents to be included in the study. Additional informed consent was obtained from all patients for whom identifying information is included in this article.

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中文概要

题　目：中国肥胖儿童青少年多巴胺受体 D2 基因多态性与随访 8 年后体重变化的相关性研究

目　的：在经过 8 年随访的中国肥胖儿童青少年中，评价多巴胺受体 D2（*DRD2*）基因多态性和肥胖缓解的相关性。

创新点：探索肥胖儿童青少年的基因多态性与长期体重变化的相关性，期望能够指导肥胖儿童青少年的临床诊疗。

方　法：该研究纳入了我院随访 8 年的 108 名肥胖儿童及青少年。基线的临床资料和 *DRD2* 基因多态性（包括 rs1076562、rs2075654 和 rs4586205）相关数据从原始病历及检验结果中提取。于 2017 年 5 月份进行电话随访，采集相关数据，包括身高、体重、饮食和运动干预依从性。

结　论：*DRD2* 基因 rs2075654 位点多态性与肥胖儿童青少年的长期体重变化有相关性。

关键词：肥胖；随访研究；多巴胺受体D2；儿童；青少年