



The Journal of **Macro**Trends in Health and Medicine

ASSOCIATION OF THE FTO GENE SNP RS17817449 WITH OBESITY IN ASTANA.

**A.Kossumov^{*}, A.Supiyev^{*}, A.Kassenova^{*}, T.Nurgozhin^{*}, S.Kozhakhmetov^{*},
A.Kushugulova^{*}, Zh.Zhumadilov^{*} and M.Bobak^{**}**

^{*}Center for Life Sciences, Nazarbayev University, Kazakhstan

^{**}Department of Epidemiology and Public Health, University College London, UK

Abstract

This study replicated the genetic association of SNP of FTO (rs17817449) with obesity in Kazakhstan population and, which is the first such association study in a Central Asia region. We establish association FTO (rs17817449) with obesity measure (waist and WTH ratio).

Keywords: *the genetic association of SNP of FTO (rs17817449), obesity, Kazakhstan*

1. Introduction

Obesity is one of the major worldwide health problem. The prevalence of obesity increased dramatically over the last decades, the worldwide prevalence of obesity has nearly doubled between 1980 and 2008. Currently, More than two-thirds of adults are considered to be overweight or obese.

The FTO gene variants are very important genetic determinant of body weight and obesity.

The first knowledge on the association between FTO gene and obesity were obtained from a genomewide association study showing that FTO variants are associated with type 2 diabetes in a European population. However this association between FTO and diabetes disappeared after adjusting for body-mass index, suggesting that the association were-mediated by an association with BMI and type 2 diabetes. (Frayling 2007)

In replication studies, a significant association of FTO variant (rs17817449) and obesity was observed in different European populations (Hubacek et al. 2008; Price et al. 2008), in Korean

population (Cha et al. 2008) etc., no associations were found among African Americans (Wing et al. 2009).

Due to lack of data in Central Asian region, we designed the Astana study to investigate the association of the FTO rs17817449 variant gene polymorphism with obesity and other cardiometabolic risk factors in Kazakhstani individuals.

2. Material and Methods

We studied the association of FTO gene (fat mass and obesity associated) variation (rs17817449) with BMI and the risk of being overweight and obese in Astana city population.

We conducted a cross-sectional study of random samples of men and women aged 50-75 years old residents in Astana and registered in 8 policlinics in Astana.

Between November 2012 and August 2013, 888 subjects were invited to participate and 497 participated (response rate 56%).

DNA was extracted using a salting out method. FTO SNP was genotyped using PCR-RT method.

ANOVA was used for the analysis of the potential effect of FTO variant on individual cardiometabolic risk factors. Values are given as means and standard deviations.

3. Results

Associations between FTO genotype and variables of interest are summarized in Table 1.

Table 1 Association between FTO genotypes and individual characteristics				
Variable	TT	TG	GG	P-value
N = 482	193	235	54	
Age	61.17 (7.61)	61.79 (7.69)	60.64 (6.90)	0.960
Total cholesterol	5.97 (1.48)	5.88 (1.61)	5.73 (1.14)	0.297
HDL	1.31 (0.36)	1.31 (0.37)	1.26 (0.38)	0.456
LDL	3.73 (1.00)	3.70 (1.00)	3.68 (0.91)	0.717
Triglycerides	1.57 (0.95)	1.73 (1.21)	1.63 (0.90)	0.314
BMI	29.40 (4.96)	29.95 (4.88)	30.29 (4.63)	0.157
Waist	96.66 (12.04)	98.40 (11.31)	100.53 (12.11)	0.022
DM prevalence (%)	18.95% (36/190)	20.00% (47/235)	16.67% (9/54)	0.849
HT prevalence (%)	72.25	70.21	66.67	0.715

As in other studies FTO SNP rs17817449 was associated with waist circumference , the mean waist values were as follows: 100.5 ±12.1 sm in GG homozygotes, 98.4 ±11.3 in GT heterozygotes and 96.7 ±12.0 sm in TT homozygotes (p<0.02). Other analyzed cardiometabolic

risk factors (total cholesterol, HDL, LDL, triglycerides, diabetes and arterial hypertension) were not associated with FTO genotypes.

Distribution of FTO gene in different populations are presented the Table 2.

	Astana, Kazakhstan	Czech Republic	Japan, Tokyo	Toscana, Italy	Indians, USA	Chinese, USA	African, Kenya
TT	40.0%	32.7%	67.4%	33%	56.3%	71.8%	32.2%
TG	48.8%	51.4%	29.1%	42%	35.6%	25.9%	48.9%
GG	11.2%	15.9%	3.5%	25%	8%	2.4%	18.9%

In Astana study we received proportion of 11.2% who have GG homozygotes and compared to other studies of different ethnic groups worldwide. (See table 3)

	Kazakh	Russian	Other	Total
TT	111 (40.36%)	48 (38.40%)	34 (41.46%)	193 (40.04 %)
TG	134 (48.73%)	64 (51.20%)	37 (45.12%)	235 (48.76%)
GG	30 (10.91%)	13 (10.40%)	11 (13.41%)	54 (11.20%)
Total	275 (100%)	125 (100%)	82 (100%)	482 (100%)

4. Conclusion

This study replicated the genetic association of SNP of FTO (rs17817449) with obesity in Kazakhstan population and, which is the first such association study in a Central Asia region.

We establish association FTO (rs17817449) with obesity measure (waist and WTH ratio).

A study with large sample size is needed to further evaluate the associations between the FTO polymorphism and obesity risk in Kazakhstan national study.

References

1. Frayling TM, Timpson NJ, Weedon MN, Zeggini E, Freathy RM, Lindgren CM, et al. A common variant in the FTO gene is associated with body mass index and predisposes to childhood and adult obesity. *Science*. May 11 2007;316(5826):889-94
2. Cha W, Choi M, Kim S, Park L, Kim R, Kim Y, Shin D. 2008. Replication of genetic effects of FTO polymorphisms on BMI in a Korean population. *Obesity (Silver Spring)* 16:2187–2189
3. Hubacek A, Bohuslavova R, Kuthanova L, Kubinova R, Peasey A, Pikhart H, Marmot G, Bobak M. 2008. The FTO gene and obesity in a large Eastern European population sample: the HAPIEE study. *Obesity (Silver Spring)* 16:2764–2766.
4. Price A, Li D, Zhao H. 2008. FTO gene SNPs associated with extreme obesity in cases, controls and extremely discordant sister pairs. *BMC Med Genet* 9:4.
5. Wing R, Ziegler J, Langefeld D, Ng C, Haffner M, Norris M, Goodarz O, Bowden W. 2009. Analysis of FTO gene variants with measures of obesity and glucose homeostasis in the IRAS Family Study. *Hum Genet* 125:615–626.