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TO STUDY AHSG GENE (RS4918) POLYMORPHISM IN METABOLIC SYNDROME

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Abstract:
Background: Metabolic syndrome is a major public health issue of the present century. It consists of constellation of physical conditions and metabolic abnormalities

Materials and methods: The present case control study was conducted in department of biochemistry, Maulana Azad Medical College in collaboration with department of medicine, Lok Nayak hospital, New Delhi. Total eighty (40 cases and 40 age and sex matched controls) fulfilling inclusion and exclusion criteria were included with their informed consent.

Results: The G allele of AHSG GENE Thr256Ser C>G SNP is associated with significantly increased risk of developing metabolic syndrome. (OR:5.54,95% CI: 1.03-8.17).

Conclusion: The G allele of AHSG GENE Thr256Ser C>G SNP is associated with significantly increased risk of developing metabolic syndrome

Keywords: Metabolic syndrome, AHSG GENE, High density lipoproteins

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INTRODUCTION

Metabolic syndrome is a major public health issue of the present century. It consists of constellation of physical conditions and metabolic abnormalities. Metabolic syndrome is associated with central obesity, hyperinsulinemia, low high density lipoproteins (HDL), high triglycerides, and hypertension. Metabolic syndrome is associated with the risk of developing cardiovascular disease and diabetes. The exact mechanisms of the complex pathways of Metabolic syndrome are under investigation. Insulin resistance is thought to be the primary underlying abnormality leading to Metabolic syndrome.[1-3] Recently, epidemiological studies have suggested that serum fetuin –A was associated with insulin resistance and its co-morbidities such as Metabolic syndrome and type 2 Diabetes Mellitus. So, in the present study, we investigated the association of serum fetuin –A with insulin resistance, Metabolic syndrome and Type 2 Diabetes Mellitus. There are various definition proposed for metabolic syndrome. But in this study, we used International Diabetes Federation criteria, which is more significant in clinical as well as for research purpose.

MATERIALS AND METHODS

The study was conducted in Department of Biochemistry, Maulana Azad Medical College and Department of Surgery, Lok Nayak Hospital, New Delhi.

STUDY DESIGN:

A hospital based case control study.

STUDY POPULATION:

Patients attending the medicine outpatient department in Lok Nayak Hospital with clinical diagnosis of metabolic syndrome.

SAMPLE SIZE:

Total 80 (40 cases and 40 age and sex matched controls) fulfilling the inclusion and exclusion

Criteria.

Cases:

Inclusion Criteria:

Newly diagnosed metabolic syndrome cases.

Exclusion Criteria:

- Subjects taking drugs like statins and fibrates which can alter serum lipid profile and its estimation.
- Condition affecting gross abdominal girth e.g. ascites, gross abdominal tumors, organomegaly etc.
- Subjects suffering from parathyroid disease, chronic kidney disease and metabolic bone

Disease.

Controls:

- Healthy subjects.

RESULTS:

(A).CASES: 40 patients were screened and selected as cases. The age range of case population was 11 to 60 years with the mean age of 36.4±10.04 years. Among cases there were 13 males and 27 females.

(B).CONTROLS: 40 healthy controls were recruited in the study. Their age ranged from 20 to 63 years with the mean age of 37.75±11.43 years. This group included 14 males and 26 females .The age (p=0.59) and sex (p=0.81) distribution of control group was similar to the cases in the study.

Table 1: Demographic profile of cases and controls

	CASES (n= 40).	CONTROLS (n =40)	p Value
Age in years (Mean ±SD)	36.4±10.04	37.75±11.43	0.59*
Sex (Male : Female)	13:27	14:26	0.81**

*p value calculated by unpaired t test **p value calculated by chi-square test.

Table 2: Genotypic and allelic frequencies of ahsg gene (rs 4918)

	Cases (n =40)	Controls (n =40)	p Value
Genotype, n (%) CC	26(65%)	36(90%)	
CG	12(30%)	3(7.5%)	
GG	2(5%)	1(2.5%)	0.018
Allelic frequency C	0.8	0.94	
G	0.2	0.06	

P value calculated by Fisher exact test.

Allele frequency was calculated by Hardy- Weinberg equilibrium equation.
There was a significant difference in distribution of the CG genotype between the cases and the controls. Result shows that CG genotype was more frequent in cases and the homozygous CC was more common in the controls.

Table 3: ODDS RATIO AND RELATIVE RISK OF AHSG GENE (rs 4918) FOR METABOLIC SYNDROME

Thr 256 Ser GENOTYPE	CONTROL	CASES	ODDS RATIO (95% CI)	REL. RISK	P Value
CC	36	26	REF	REF	-
CG	3	12	5.54 (1.03 to 8.17)	0.01	0.01
GG	1	2	2.77 (0.35 to 8.76)	0.57	0.57

Fisher exact test used to calculate odds ratio and p value.

The Odds ratio of subjects with CG genotype to develop metabolic syndrome was 5.54 (95% CI ;1.03-8.17) with reference to CC genotype ,which was statistically significant while odds ratio for GG genotype was 2.77 with reference to CC genotype and it is not statistically significant with p value of 0.57.

DISCUSSION:

The present case control study was designed to explore the role of the Thr256Ser C>G polymorphism of the AHSG gene, serum fetuin-A levels in the pathogenesis of MetS, involving 40 subjects with MetS and 40 healthy controls.

Table 1 shows that subjects recruited in the study had similar age and sex distribution among cases and controls. So the inferences made from this study does not have any age and gender bias. In our study the gender distribution was 45% males and 66% females which is in concordance with other studies in india where MetS prevalence in women was 1.5- 2 times higher than in men.[4]The age of the subjects ranged from 11 to 63 years. It is important to recognise the premature morbidity and mortality are higher in asian Indians in general. The first myocardial infarction(MI) attack occurs in 4.4% of asian women and 9.7% of men at age less than 40 years, which is 2-to 3.5 fold higher than in the West European population.[5]

Our data although with a small sample size show that the distribution of the risk genotype of Thr256Ser C>G SNP differ statistically between patients of MetS and healthy controls.The odds ratio is 5.54 which is statistically significant. This indicates that the presence of this SNP imparts a risk for developing metabolic syndrome. Similarly, Ma and others found the G allele confers a higher risk for ischemic stroke than the C allele[6].

In theory, the rs4918 polymorphism, which affects the exon 7 of the molecule (D3 domain region), may also result in altered function of the molecule but no functional differences for rs4918 have been reported by a study conducted by Lavebratt C.[119] In our study also the serum levels of fetuin-A were significantly increased in cases compared to controls. However, there was no significant association of the genotypes of Thr256Ser C>G polymorphism with serum fetuin- A levels.

CONCLUSION:

The G allele of AHSG GENE Thr256Ser C>G SNP is associated with significantly increased risk of developing metabolic syndrome

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