

ABSTRACT

Title of the study:

A study of genetic polymorphism in ATP binding cassette protein gene (ABCA1) among type 2 diabetes mellitus(DM) patients

Introduction:

Type 2 DM is a complex polygenic disorder with high glucose levels characterized by impaired insulin resistance and secretion along with dysregulation of lipid and protein metabolism. Eventhough the number of studies describing the epidemiology of diabetes over the last 20 years has been extraordinary, DM still remains an enigma due to its multifactorial etiology. Development of dyslipidemia with hypertriglyceridemia, elevated low density lipoprotein(LDL) and low levels of high density lipoprotein(HDL-cholesterol) concentration may be a harbinger of future diabetes.

ATP- binding cassette transporter A1 (ABCA1) is a subfamily of proteins , involved in transportation of phospholipids and cholesterol from the intracellular compartments to lipid-poor apolipoproteins. ABCA1 gene is located on the chromosome 9 region q31.1. ABCA-1 is also known as cholesterol efflux regulator protein and mediates the efflux of cholesterol and phospholipids to lipid-poor apolipoproteins (apo-A1 and apoE), which then form nascent high-density lipoproteins. Down regulation of

ABCA1, disrupts the cell's ability to remove cholesterol from its cytoplasm, leading to pathologic atherogenesis. Although dyslipidemia in type 2 DM is being treated meticulously, there is augmented increase in the onset of cardiovascular complications. The qualitative and quantitative derangement of HDL cholesterol in type 2 DM may reflect an impaired ABCA-1 pathway.

This study is done to find the association between ABCA-1 gene polymorphism and type 2 DM, which might serve as a revelation of the ambiguity involved in treatment of dyslipidemia in type 2 DM.

Objectives:

1. To study the genotype and allele frequencies of ABCA1 gene polymorphism (R219K & C69T) in Type 2 Diabetes mellitus patients and non-diabetic individuals
2. To find out the association between ABCA1 gene polymorphism and Type 2 Diabetes mellitus

Methodology:

The study design was a case control study and each group consisted of 50 subjects. Analysis of genotype was performed by PCR-RFLP method and the biochemical parameters like FPG, HbA1c, lipid profile were analyzed by autoanalyzer.

Conclusion:

The findings of our study showed that there was noteworthy difference in the genotype distribution of both C69T and R219K among cases when compared with the controls. However, the difference was not statistically evident, the reason for which might be due to the small sample size. Our study results showed that the presence of dominant allele alone (A allele in R219K and T allele in C69T) is a risk factor for the development of pathological changes in HDL-c metabolism in type 2 DM. This reflects that there is an association between ABCA1 gene polymorphism and type 2 DM which can be reinforced by conducting the study with a larger sample size.