



RESEARCH ARTICLE

ASSOCIATION OF MTHFR GENE POLYMORPHISMS C677T AND A1298C WITH  
CORONARY ARTERY DISEASE

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ABSTRACT

Gene environment interaction is an important aspect in the development of coronary artery disease (CAD). Elevated plasma Homocysteine has been identified as a risk factor for coronary atherosclerosis. Elevated Homocysteine may result from deficient Methylene tetrahydrofolate reductase (MTHFR) activity. MTHFR is involved in one carbon metabolism which is essential for DNA biosynthesis and methylation. The 5, 10-methyltetrahydrofolate reductase locus is mapped at the end of the short arm of chromosome 1(1p36.6). Though there are several single nucleotide polymorphisms (SNPs) in this gene, two SNPs are most studied in association with diseases. A case control study was designed to assess the role of the two most commonly studied SNPs of MTHFR gene C677T and A1298C in the development of CAD. A total of 300 samples were recruited in the study which includes 150 CAD cases from CARE hospitals, Visakhapatnam and 150 controls. The MTHFR genotyping was performed based on polymerase chain reaction followed by restriction fragment length polymorphism. There was no significant difference either in the distribution of MTHFR C677T genotypes (CC vs CT: OR=1.05, 95%CI=0.58-1.91, P=0.858; CC vs TT: OR=2.03, 95%CI=0.18-22.7, P=0.564) or alleles (T vs C: OR=0.893, 95%CI=0.522-1.530, P=0.681) in patients and controls. Even in case of the SNP A1298C no significant difference was observed in the distribution of alleles though significant difference was observed in genotype distribution (AA vs AC: OR=0.90, 95%CI=0.48-1.68, p=0.74; AA vs CC: OR=1.796, 95%CI=1.06-3.02, p=0.028).

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INTRODUCTION

Coronary artery disease is one of the leading factors of mortality and morbidity accounting for approximately 30% of the deaths in the world (Matam et al., 2014). It is a multifactorial disease which involves the contribution of many different genes and environmental factors. At genetic level, functional allelic variations or polymorphism in humans may play a role in an individual's susceptibility to the manifestation of the disease (Andreassi et al., 2003). A major current challenge is therefore to explain the genetic components that contribute to the pathogenesis of complex disease (Fauci et al., 2008). A high plasma level of homocysteine known to be associated with increased thrombotic tendency has been considered as a risk factor for atherosclerosis and CAD (Cattaneo et al., 1999). The homocysteine levels are affected by genetic, environmental and physiological factors.

Hyperhomocysteinemia may arise from genetic factors like mutation in MTHFR gene or due to environmental factors like vitamin B12 or folic acid deficiency (Eftychiou et al., 2012). Genetic epidemiologic studies suggest that certain genetic variants including polymorphisms in the MTHFR gene have a strong association with CAD (Matam et al., 2014). MTHFR is a key regulatory gene of the remethylation pathway and a vitamin B12 dependent enzyme. The MTHFR gene is located at 1p36.3. It is involved in folate metabolism catalysing the reduction of 5', 10' methylenetetrahydrofolate to 5'-methyltetrahydrofolate reductase, the major circulating form of folate and carbon donor for remethylation which is a multistep process that converts homocysteine to methionine (Saffari et al., 2013) which is used to make proteins and other important compounds by the body (Wang et al., 2013). Decrease in the function or amount of MTHFR leads to increased blood levels of homocysteine. Elevated homocysteine levels show an increased risk for hardening of the arteries (atherosclerosis), which may eventually result in a heart attack and venous thrombosis (Elizabeth et al., 2005).

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There are two common polymorphisms - C677T and A1298C in the gene that codes for MTHFR enzyme. The C677T polymorphism (rs1801133), in exon 4 of the gene, lies within the NH<sub>2</sub>-terminal catalytic domain, whereas the A1298C polymorphism is in the COOH-terminal regulatory region in exon 7 (Pandey *et al.*, 2011). The C677T genetic variant consists of a C to T transition in exon 4 at base 677 of the gene which encodes alanine in place of valine at amino acid 222 (Frosst *et al.*, 1995). The most striking characteristic of this mutant is its in vitro thermolability at 46°C, which gives a clear distinction between this mutant and the normal enzyme found in the majority of the individuals (Kang *et al.*, 1988a, 1988b). The second prevalent polymorphism A1298C (rs1801131) is associated with decreased enzyme activity in vitro (Vanderput *et al.*, 1998; Weisberg *et al.*, 1998; Naomi *et al.*, 2001). This genetic variant consists of an A to C transversion at nucleotide 1298, in exon 7 which encodes glutamate in place of alanine at amino acid 429 (Jakubowski *et al.*, 2000; 2004). The prevalence of these two polymorphisms varies greatly in different ethnic groups. While several studies have been carried out to find out the association between C677T and CAD only few studies were carried out with respect to A1298C. Due to the lack of information in the Andhra Pradesh population, the present study has been attempted for the first time to find out the association between these two SNPs in MTHFR gene and their relation to CAD.

## MATERIALS AND METHODS

This study was carried out on 150 angiographically documented CAD patients with at least 50% coronary artery stenosis or a history of coronary angioplasty or surgical revascularization in CARE Hospitals, Visakhapatnam during the period from December 2011-June 2012. The control group consists of 150 randomly chosen volunteers without a history of CAD. Informed consent was obtained from all the participants and the study was approved by Institutional Ethical Committee of Andhra University, Visakhapatnam. Five mL of blood sample was obtained from both the cases and the controls. Genomic DNA was extracted using standard salting out method described by Miller *et al.*, (1988). The MTHFR polymorphisms C677T and A1298C were analyzed using polymerase chain reaction– restriction fragment length polymorphism (PCR-RFLP).

For the detection of C677T polymorphism, amplification was carried out using the following primer set

F-5' TGA AGG AGA AGG TGT CTG CGG GA-3'  
R-5' AGG ACG GTG CGG TGA GAG TG -3'

and the 198-bp product obtained was digested with HinfI restriction enzyme. Mutation creates a HinfI restriction site causing cleavage of the 198 bp fragment into 175 bp and 23 bp.

A1298C polymorphism was detected using the following primer set

F-5' CAA GGA GGA GCT GCT GCT GAA GA 3'  
R-5' CCA CTC CAG CAT CAT CAC TCA CT 3'

and the resulted 128 -bp PCR product was digested with MboII restriction enzyme. After resolving in 3% agarose wild type allele shows two fragments of size 72 bp and 28 bp whereas the mutant allele shows 100 bp and 28 bp fragments.

## Statistical analysis

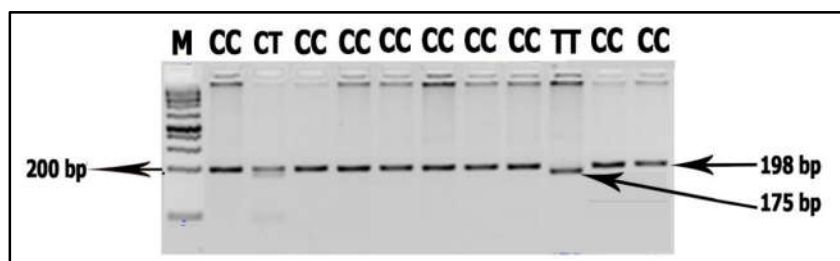
Chi-square test was performed to determine if the samples were in Hardy-Weinberg equilibrium. Binary logistic regression was used to calculate odds ratios (OR) and 95% confidence intervals (CI) for allele and genotype frequencies. Statistical analysis was carried out using SPSS Version 20.0 for windows software (SPSS, Inc., Chicago, IL, USA). A p-value of less than 0.05 was considered statistically significant.

## RESULTS

The genotype and the allele distribution of MTHFR C677T and A1298C variants are summarized in the Tables 1 and 2 respectively. Both the cases and the controls were in Hardy-Weinberg equilibrium. With reference to rs1801133 polymorphism, no significant difference was observed either in the genotype distribution or in the allele distribution between the patients and the controls. The wild genotype homozygous MTHFR 677CC was prevalent in both the groups (80.6% in cases and 81.3% in controls). The polymorphic allele MTHFR 677T presented a frequency of 5.1% in the CAD group and 4.6% in the control group. There was a statistically significant difference between the cases and the controls ( $p = 0.028$ ) in the distribution of genotypes with regards to rs1801131 polymorphism. Though the CC genotype frequency is relatively higher in controls the heterozygous genotype MTHFR 1298AC frequency was higher in cases (52% in cases and 36.7% in controls). However no significant difference was observed between the cases and the controls in the distribution of alleles. The polymorphic allele MTHFR 1298C presented equal frequency of 28% in the CAD group and the control group.

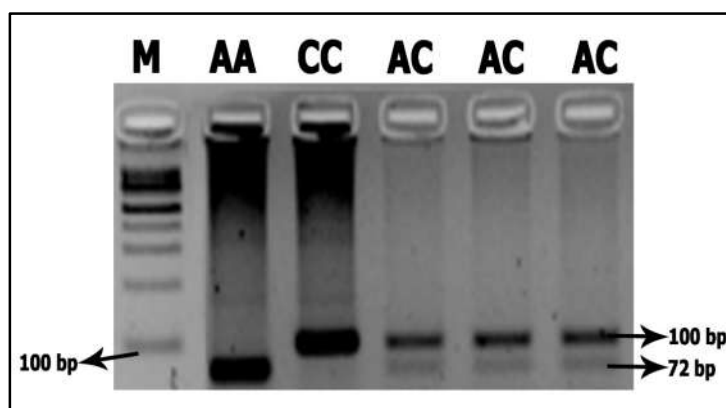
## DISCUSSION

Genetic differences between individuals are caused by natural variations known as SNPs. For fine mapping of alleles, association studies at the population level are helpful (Pandey *et al.*, 2011). Polymorphisms in MTHFR gene is one of the several enzyme deficiencies and defects that can lead to elevated plasma homocysteine (Verhoef *et al.*, 1997). MTHFR C677T mutation was found to cause mild to moderate homocysteinemia due to the loss of FAD- binding capacity of the enzyme and dissociation of active dimer into monomers which leads to hypomethylation (Yamanda *et al.*, 2001). Several meta-analyses have shown a correlation between hyperhomocysteinemia and vascular disease (Boushey *et al.*, 1995, Wald *et al.*, 2002, 2012). As MTHFR is one of the candidate gene responsible for increasing homocysteine in serum, the present study was conducted to appraise the distribution of MTHFR polymorphisms C677T and A1298C in CAD cases and controls and to explore whether they confer susceptibility to CAD.



M = 100 bp DNA molecular ladder

Figure 1. Agarose gel picture with the three genotypes of MTHFR C677T polymorphism



M = 100 bp DNA molecular ladder

Figure 2. Agarose gel picture with the three genotypes of MTHFR A1298C polymorphism

Table 1. Distribution of genotype and allele frequencies of MTHFR C677T polymorphism in cases and controls

Genotype/allele	Cases (n=150)	Controls (n=150)	( $\chi^2$ )	Odds ratio	95% CI	p value
CC	121(80.6%)	122(81.3%)		1.05	0.583-1.9	0.858
CT	27(18.0%)	27(18.0%)		2.03	0.182-22.7	0.564
TT	2(1.4%)	1(0.7%)	0.369			
C	0.90	0.91		0.893	0.522-1.530	0.681
T	0.10	0.09	0.169			

Table 2. Distribution of genotype and allele frequencies of MTHFR A1298C polymorphism in cases and controls

Genotype/allele	Cases (n=150)	Controls (n=150)	( $\chi^2$ )	Odds ratio	95% CI	p value
AA	27(18%)	38(25.3%)		0.900	0.480-1.689	0.743
AC	78(52%)	55(36.7%)	7.251	1.796	1.066-3.026	0.028
CC	45(30%)	57(38%)				
A	0.44	0.44		1.014	0.734-1.399	0.934
C	0.56	0.56	0.007			

The present study failed to show any association between C677T polymorphism and CAD. This is consistent with other earlier findings (Biselli *et al.*, 2009, Botto *et al.*, 2003, Chambers *et al.*, 2000, Eftychiou *et al.*, 2012, Folsom *et al.*, 1998, Girelli *et al.*, 1998, Gonzalez-perez *et al.*, 2002, Goracy *et al.*, 1999, Gueant Rodriguez *et al.*, 2005, Gupta *et al.*, 2010, Hanson *et al.*, 2001, Hsu *et al.*, 2001, Ibraheim *et al.*, 2009, Iqbal *et al.*, 2005, Kolling *et al.*, 2004, Lin PT *et al.*, 2008, Liu *et al.*, 2014, Meisel *et al.* (2001), Pandey *et al.*, 2011, Pezzini *et al.*, 2002, Rahimi *et al.*, 2009, Reinhardt *et al.*, 1998, Saffari *et al.*, 2013, Soriente *et al.*, 1998, Van Bockxmeer *et al.*, 1997, Vasisht *et al.*, 2002, Zee *et al.*, 2007, Zheng *et al.*, 2000). On the other hand some studies reported positive association between MTHFR C677T polymorphism and CAD (Alam *et al.*, 2008, Aleyasin *et al.*, 2006, Bennour *et al.*, 2007,

Christensen *et al.*, 1997, Dhar *et al.*, 2010, Frosst *et al.*, 1995, Gardemann *et al.*, 1999, Gulec *et al.*, 2000, Kang *et al.*, 1988a, 1991, Kluijtmans *et al.*, 1996, Lakshmi *et al.*, 2010, Matam *et al.*, 2014, Morita *et al.*, 1997, Nasiri *et al.*, 2014, Rassoul F *et al.*, 2000, Tripathi *et al.*, 2010). There are only a few studies with regards to MTHFR A1298C polymorphism and the presence of CAD. While a lack of association was reported by several studies (Biselli *et al.*, 2009, Botto *et al.*, 2003, Chango *et al.*, 2000, Eftychiou *et al.*, 2012, Ghaedi *et al.*, 2007, Gueant Rodriguez *et al.*, 2005, Hanson *et al.*, 2001, Jenks *et al.*, 1987, Meisel *et al.* (2001), Nasiri *et al.*, 2014) a single study (Szczeplik *et al.*, 2001) reported significant difference in the allele frequency. Though the present study reveals a significant difference in the genotype distribution with high frequency of heterozygotes in the cases and CC

homozygotes in the controls it is contradicting the study of Szczeklik *et al.* (2001) by demonstrating no difference in the distribution of allele frequency. While no meta-analysis studies were available for MTHFR A1298C polymorphism, meta-analyses observations for MTHFR C677T SNP reflected the inconsistency in the findings reported by several individual studies. Meta-analyses by Kluijtmans and Whitehead (2001) and Klerk *et al.*, (2002) reported an increased risk of CAD in patients with TT genotype. A recent meta-analysis by Clarke *et al.* (2012) observed an increase risk of CAD in TT homozygotes when compared to CC homozygotes in both published and unpublished data with 15% in the former data and 2% in the latter. Interestingly another meta-analysis had given an estimate of 14% greater risk of CAD associated with MTHFR CC genotype (Lewis *et al.*, 2005). While in a meta-analysis carried out by Cronin *et al.* (2005) found no strong evidence to support the association of this polymorphism with CAD in Europe, North America or Australia but in Asia. Small size of the population is one of the limitations of the present study. Hence large and heterogeneous study populations are necessary to quantify the small effects of common mutations and their association. Further polymorphisms in MTHFR gene need to be evaluated together with other genetic markers involved in the homocysteine pathway for predisposition of the disease.

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