MTRR rs326119 polymorphism is associated with plasma concentrations of homocysteine and cobalamin, but not with congenital heart disease or coronary atherosclerosis in Brazilian patients

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A B S T R A C T
Background: Differences in the distribution of the MTRR rs326119 polymorphism (c.56+781 A>C) between patients with congenital heart disease (CHD) and controls have been described in Chinese individuals. The association is thought to be due to deregulation of homocysteine-cobalamin pathways. This has not been replicated in other populations. The primary objective of this study was to assess the influence of the MTRR rs326119 polymorphism on biochemical parameters of vitamin B12 metabolism, coronary lesions, and congenital heart disease in Brazilian subjects.

Methods: We selected 722 patients with CHD, 1432 patients who underwent coronary angiography, and 156 blood donors. Genotyping for the MTRR polymorphism was evaluated by high-resolution melting analysis, and biochemical tests of vitamin B12 metabolism were measured.

Results: Subjects carrying the AC or CC genotypes had higher homocysteine concentrations (9.7 ± 0.4 μmol/L and 10.1 ± 0.6 μmol/L) and lower cobalamin concentrations (260.5 ± 13.3 pmol/L and 275.6 ± 19.9 pmol/L), compared with the subjects carrying the AA genotype (8.7 ± 0.5 μmol/L and 304.8 ± 14.7 pmol/L), respectively. A multiple linear regression model also identified a significant association between the number of C variant alleles with the concentrations of homocysteine and cobalamin. Nonetheless, the allelic and genotypic distributions for MTRR rs326119 were not associated with CHD or coronary atherosclerosis in the studied samples.

Conclusion: Our findings indicate that the MTRR rs326119 variant might be a genetic marker associated with homocysteine and cobalamin concentrations, but not a strong risk factor for CHD or coronary atherosclerosis in the Brazilian population.

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1. Introduction

Homocysteine is a molecule of the blood produced when methionine is broken down in an organism. This metabolism is dependent on vitamins B6 and B12 and folate. The main form of folate in plasma, 5-methyltetrahydrofolate (5-MTHF), participates in the re-methylation pathway and is formed from the reduction of 5,10-methylenetetrahydrofolate by the enzyme methylenetetrahydrofolate reductase (MTHFR). In this process, homocysteine receives a methyl group by the activity of the enzyme methionine-synthase (MTR). Methionine synthase reductase (MTRR) is involved in reducing cobalamin (B12r) to methylcobalamin (MeCbl), the cofactor form used in methionine synthase (MTR) [1–6].

Both MTHFR and MTRR are essential enzymes responsible for, among many other functions, keeping homocysteine at adequate levels. In fact, genetic variations in the genes that codify these enzymes have been shown to modulate homocysteine levels [7–9]. Furthermore, some studies have shown associations of hyperhomocysteinemia with the development of cardiovascular disease, and increased risks of atherosclerosis and thrombosis [9–11]. However, the relationship between genetic polymorphisms, homocysteine level, and cardiovascular phenotypes is still controversial and has been the focus of many studies [12–14].

A study, performed in a Chinese Han population, investigated polymorphisms in the MTRR gene. The study identified a significant difference in the distribution of the MTRR rs326119 polymorphism (c.56+781 A>C) between subjects with congenital heart disease (CHD) and controls. An association of the same polymorphism with
homocysteine levels was also observed [15]. Authors then hypothesized that homocysteine metabolism could be the cause of an increased risk of developmental problems in individuals with the risk allele. This, however, has not been replicated in other populations. The main aim of this study was to assess the influence of the MTRR rs326119 polymorphism on biochemical parameters of B12 vitamin metabolism, and in cardiovascular phenotypes, namely, coronary atherosclerosis and CHD in Brazilian patients.

2. Subjects and methods

In this study, patients who underwent coronary angiography (n = 1432) plus blood donors (n = 156) were used as both a control group for CHD (n = 722), and as samples for testing the association between MTRR polymorphism and coronary atherosclerosis and homocysteine levels, respectively. The University of São Paulo ethics committee approved the protocol, and all participants signed an informed consent document.

2.1. Patients who underwent coronary angiography

For this study, 1432 consecutive patients who underwent diagnostic coronary angiography for coronary artery disease were selected at the Laboratory of Hemodynamics, Heart Institute (Incor), São Paulo, Brazil. All patients had a clinical diagnosis of angina pectoris and stable angina. No patient enrolled in this study was currently experiencing an acute coronary syndrome. Patients with previous acute ischemic events, heart failure classes III–IV, hepatic dysfunction, familiar hypercholesterolemia, previous heart or kidney transplantation, and in antiviral treatment were excluded [16].

2.2. Blood donors

Also included in the study were 156 subjects from the Blood Donor Center/University of São Paulo Medical School [17]. Inclusion and exclusion criteria for enrollment were the same as for those who donated blood.

2.3. Patients with CHD

Prospectively recruited to the study were 722 patients with CHD from the Pediatric Cardiology Outpatient Clinic – Heart Institute (Incor), São Paulo, Brazil. Patients were evaluated by history, review of the medical records, and physical examination and were classified according to their anatomical defect as previously described [18]. No patient enrolled in this study had clinical features of syndromic disease. An informed consent was obtained from progenitors or participants in accordance with protocols approved by the local IRB.

2.4. Demographic and laboratory tests

A trained interviewer collected demographic and clinical information from all participants. Twelve-hour fasting blood samples were used for biochemical testing conducted according to standard techniques. Serum folate, serum cobalamin, and total homocysteine were determined by the ion capture method, enzyme immunoassay, and fluorescence polarization immunoassay, respectively.

2.5. Coronary artery disease scores

From the individuals who underwent coronary angiography, 20 coronary segments were scored: each vessel was divided into 3 segments (proximal, medial, and distal), except for the secondary branches of the right coronary artery (posterior ventricular and posterior descending), which were divided into proximal and distal segments. Stenosis greater than 50% in any coronary segment was granted 1 point, and the sum of points for all 20 segments constituted what is here referred to as an Extension Score. Lesion severity was calculated as follows: none and irregularities, 0 points; <50%, 0.3 points; 50–70%, 0.6 points; >70–90%, 0.8 points; and >90–100%, 0.95 points. The Severity Score was calculated through the sum of points for all 20 coronary segments [19].

2.6. Genotyping

Genomic DNA was extracted from peripheral blood following a standard salting-out procedure. MTHFR polymorphisms (c.677C>T, c.1317T>C, and c.1298A>C) were detected by polymerase chain reaction (PCR) followed by digestion by restriction enzyme. Genotyping for the MTRR rs326119 was detected by PCR followed by high-resolution melting (HRM) analysis with the Rotor Gene 6000 instrument (Qiagen, Courtaboeuf, France). The QiAgility (Qiagen, Courtaboeuf, France), an automated instrument, was used according to manufacturer’s instructions to optimize the sample preparation step [20]. Amplification of the fragment for the MTRR rs326119 (c.56 + 781 A>C, intron 1) polymorphism was performed using the primer sense 5’-CGGTTCATTCACGAAGC-3′ and antisense 5’-AATTGGGCGCTGTCATT-3′ (79 pairs base). A 40-cycle PCR was carried out with the following conditions: denaturation of the template DNA for first cycle at 94 °C for 120 s, denaturation at 94 °C for 20 s, annealing at 50.5 °C for 20 s, and extension at 72 °C for 22 s. PCR was performed with the addition of fluorescence DNA-intercalating SYTO9 (1.5 μM; Invitrogen, Carlsbad, USA). In the HRM phase, the Rotor Gene 6000 was used to measure the fluorescence in each 0.1 °C temperature increase in the range of 70–85 °C. Melting curves were generated by the decrease in fluorescence with the increase in the temperature; and for genotype calling, nucleotide changes resulted in different curve patterns. Samples of the observed curves were analyzed using bidirectional sequencing as a validation procedure (ABI Terminator Sequencing Kit and ABI 3500XL Sequencer - Applied Biosystems, Foster City, CA, USA) [21–23].

2.7. Statistical analysis

Categorical variables are presented as percentages, while continuous variables are presented as mean ± standard deviation. The chi-square test was performed for comparative analysis of general characteristics, frequencies of the MTRR genotype or variant allele, and for Hardy–Weinberg equilibrium. ANOVA test was performed for comparing the biochemical parameters of B12 vitamin metabolism, and angiographic data means according to MTRR polymorphism. When p value was significant in the ANOVA test, Tukey’s post hoc test was performed to identify the different group. Biochemical data and angiographic data were adjusted for age, sex, and race. Biochemical parameters of the B12 vitamin metabolism were also adjusted for MTHFR polymorphisms (c.677C>T, c.1317T>C, and c.1298A>C). The following variables were included, as independent variables, in the multiple linear regressions for the biochemical parameters of the B12 vitamin metabolism: number of variant alleles for the MTRR rs326119 (0, 1 or 2 for AA, AC, or CC, respectively), age, sex, race, and MTHFR polymorphisms (c.677C>T, c.1317T>C, and c.1298A>C). Multivariate logistic regression analysis was performed to evaluate the odds ratio (OR) for coronary lesions. In this model, coronary lesion frequency was compared between normal coronary arteries versus 1-vessel, 2-vessel, and 3-vessel disease. Statistical analyses were carried out using SPSS software (version 16.0, IBM, New York, NY), with the level of significance set at p ≤ 0.05.

3. Results

3.1. Allele and genotype distribution of the MTRR rs326119 polymorphism

For the CHD sample (n = 722), the frequency of the rs326119 C variant allele was 46.3% and the distribution of the genotypes was 19.3% for variant homozygous, 54.4% for heterozygous, and 26.3% for wild-type.
3.2. Biochemical parameters of vitamin B12 metabolism according to MTRR rs326119 polymorphism

Table 1 shows significant differences in the biochemical parameters of vitamin B12 metabolism among MTRR rs326119 genotypes. Subjects carrying AC or CC genotypes had higher homocysteine concentrations and lower cobalamin concentrations compared to individuals carrying the AA genotype, adjusted for age, sex, race, and MTHFR polymorphisms. We did not observe any difference in the folate concentration among studied genotypes (Table 1).

Table 2 shows a multiple linear regression model. We identified a significant association between the number of C variant alleles and the concentrations of homocysteine and cobalamin. Also, with the presence of 3 MTHFR polymorphisms, the MTHFR c.677C>T polymorphism was associated with concentrations of homocysteine, cobalamin, and folate (Table 2).

3.3. Angiographic data according to MTRR rs326119 polymorphism in patients who underwent coronary angiography

Table 3 shows no significant association between coronary atherosclerosis extension and MTRR genotypes (AA versus AC or CC) in a multivariate model (OR = 1.08, 95% CI = 0.85–1.37, p = 0.50). Also, no significant association was observed for 1 variant allele (OR = 1.01, 95% CI = 0.69–1.47, p = 0.96) or for 2 variant alleles (OR = 1.18, 95% CI = 0.84–1.66, p = 0.33). Regarding the derived scores of coronary atherosclerosis burden, no significant difference was found among MTRR genotypes AA, AC, and CC (Extension Score: 2.2 ± 1.7, 2.2 ± 1.6, and 2.3 ± 1.7; Severity Score: 1.6 ± 1.3, 1.6 ± 1.2, and 1.7 ± 1.3) (p = 0.58 and p = 0.45, respectively).

3.4. Comparison of frequencies of the MTRR genotypes or C variant allele among CHD patients and controls

Table 4 shows the distribution of the MTRR genotypes among sample groups. We did not observe an association between the MTRR polymorphism and CHD or ventricular septal defects (VSD), as previously reported in a Chinese population, in our samples. Genotypic and allelic frequencies for the MTRR polymorphism in patients with CHD and those with CHD and VSD were compared with frequencies of blood donors and of patients who underwent coronary angiography (we considered these 2 last sample groups as controls).

| Variable | β coefficient (standard error) | p value |
|----------|-------------------------------|---------|
| Homocysteine, μmol/L | | |
| Number of variant alleles for the MTRR rs326119 | 1.1 (0.6) | 0.02 |
| Age | −0.01 (0.03) | 0.98 |
| Sex (male) | 2.1 (0.6) | <0.001 |
| Race (non-White) | −0.1 (0.4) | 0.85 |
| MTHFR c.677C>T | 2.4 (0.5) | 0.001 |
| MTHFR c.1317T>C | 0.5 (0.7) | 0.40 |
| MTHFR c.1298A>C | −0.4 (0.5) | 0.42 |
| Cobalamin, pmol/L | | |
| Number of variant alleles for the MTRR rs326119 | −33.0 (19.5) | 0.03 |
| Age | −0.4 (0.9) | 0.69 |
| Sex (male) | 0.7 (18.6) | 0.97 |
| Race (non-White) | 11.0 (14.4) | 0.45 |
| MTHFR c.677C>T | −36.8 (15.4) | 0.02 |
| MTHFR c.1317T>C | 0.7 (22.1) | 0.98 |
| MTHFR c.1298A>C | −3.4 (16.8) | 0.84 |
| Folate, nmol/L | | |
| Number of variant alleles for the MTRR rs326119 | 0.4 (0.7) | 0.60 |
| Age | 0.04 (0.03) | 0.30 |
| Sex (male) | −1.8 (0.7) | 0.02 |
| Race (non-White) | −0.4 (0.6) | 0.49 |
| MTHFR c.677C>T | −1.6 (0.6) | 0.01 |
| MTHFR c.1317T>C | 0.7 (0.9) | 0.43 |
| MTHFR c.1298A>C | −0.4 (0.7) | 0.51 |

Number of variant alleles for MTRR rs326119: 0, 1 or 2 for AA, AC, or CC, respectively.

4. Discussion

Elevated levels of homocysteine have been associated with many diseases, such as neurodegenerative disorders, recurrent pregnancy loss, neural tube defects, ischemic heart disease and stroke, atherosclerosis, and congenital defects[24–34]. Our study shows that the MTRR rs326119 polymorphism is associated with levels of plasma homocysteine. This finding was the first replication of Zhao et al.’s and Cheng et al.’s studies, in a non-Chinese population[15,34]. However, our study did not identify an association of the MTRR polymorphism with CHD or coronary artery disease.

Subjects carrying AC or CC genotypes of MTRR rs326119 polymorphism had higher homocysteine and lower cobalamin concentrations, compared with subjects carrying the AA genotype. Our finding suggests that the MTRR rs326119 polymorphism might be a genetic marker for homocysteine and cobalamin concentrations. Some studies showed a negative correlation between homocysteine and B12 vitamin levels[15,35]. Regarding vitamin B12 metabolism, increased levels of homocysteine may reflect folate and B12 vitamin deficiency. These
Table 4

| Genotype comparison | Patients with CHD (n = 722) | Patients with VSD (n = 213) | Blood donors (n = 156) | Patients who underwent coronary angiography (n = 1432) |
|---------------------|-----------------------------|----------------------------|------------------------|------------------------------------------------------|
| AA                  | 190                         | 52                         | 56                     | 397                                                  |
| AC                  | 393                         | 116                        | 72                     | 755                                                  |
| CC                  | 139                         | 45                         | 28                     | 280                                                  |
| p value<sup>a</sup> |                             | 0.77                       | 0.08                   | 0.62                                                 |

| Variant allele comparison | C variant allele | C variant allele | C variant allele | C variant allele |
|---------------------------|-----------------|-----------------|-----------------|-----------------|
| p value<sup>a</sup>       | 46.5%           | 48.3%           | 41.0%           | 45.9%           |

<sup>a</sup> Comparison of frequencies of the MTRR genotypes or C variant allele of the congenital heart disease (CHD) group with other groups.

<sup>b</sup> Comparison of frequencies of the MTRR genotypes or C variant allele of the CHD patients with ventricular septal defects (VSD) with other groups.

associations may also be due to the effects of changed vitamin B12 metabolism on homocysteine remethylation and synthesis of DNA methyltransferase, resulting in elevated plasma concentrations of homocysteine [34, 36,37]. The functional variant of MTRR rs326119 is likely to stimulate hyperhomocysteinemia and can further induce DNA hypomethylation. This variant can also result in low levels of methionine and hyperhomocysteinemia by dysfunction of MTR-catalyzed homocysteine recycling to methionine [34].

Zhai et al.’s interesting study found a genetic association by using biochemical data, but they also describe an association with CHD in patient samples from a Han Chinese population [15]. Zhao et al. demonstrated the decay of MTRR transcription activity using a functional assay. They examined 28 in vivo cardiovascular tissue samples and observed decreased MTRR RNASm levels. In vitro luciferase assays confirmed the influence of the functional c.56+781 A→C variant [15]. Concerning cardiovascular diseases, a possible pathway is that increased levels of homocysteine inhibit a nitric oxide (NO)-dependent mechanism regulating cardiac O2 consumption and NO-dependent vasodilatation [38].

Our main hypothesis for the lack of a genetic association with CHD is that the different ethnicity of our patient samples might be involved. This could lead to different associations by linkage disequilibrium with other functional variants. It can also lead to a completely different genetic environment scenario and justify a different threshold for association with CHD. It can also lead to a completely different genetic scenario and justify a different threshold for association with CHD.

In conclusion, our findings indicate that the MTRR rs326119 variant might be a genetic marker associated with concentrations of homocysteine and cobalamin, but not with CHD and coronary atherosclerosis in the Brazilian population.

Competing interests

The authors declare that they have no competing interests.
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