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ORIGINAL ARTICLE

Relationship between the *AGT* M235T genetic variant and the characteristics and prognosis of coronary atherosclerosis in patients with acute myocardial infarction

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Abstract

Background Along with environmental components, genetic factors play an essential role in the pathophysiology and progression of acute myocardial infarction (AMI). There is limited and conflicting data on the influence of the *AGT* M235T genetic variant on coronary atherosclerosis and death in AMI patients.

Methods We carried out a prospective cohort study among 504 Vietnamese AMI patients selected between January 2020 and May 2021. All patients underwent invasive coronary angiography, had *AGT* M235T genetic variant genotyped using the polymerase chain reaction method, and were followed up for 12-month all-cause mortality.

Results The proportions of the MM, MT, and TT genotypes were 0.4%, 20.8%, and 78.8%, respectively. There was no significant difference between the TT genotype and the MM + MT genotype groups regarding the position and number of stenosed coronary artery branches and the Gensini score. The *AGT* M235T genetic variant did not affect 12-month mortality (hazard ratio of TT vs. MM + MT: 1.185; 95% confidence interval: 0.596–2.354; $P = 0.629$). Subgroup analyses by age, sex, hypertension, diabetes mellitus, dyslipidemia, obesity, smoking, and angiotensin-converting enzyme inhibitor or angiotensin II receptor blocker therapy also did not reveal an association between the *AGT* M235T variant and all-cause mortality.

Conclusion In summary, the *AGT* M235T genetic variant was not found to be associated with coronary atherosclerosis characteristics and 12-month mortality in Vietnamese patients with AMI. Further multicenter studies with larger sample sizes and extended follow-up periods are needed to investigate this issue.

Keywords *AGT* M235T · Genetic variant · Coronary atherosclerosis · Prognosis · Acute myocardial infarction

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Abbreviations

ACEI	Angiotensin-converting enzyme inhibitor
AMI	Acute myocardial infarction
ARB	Angiotensin II receptor blocker
CAD	Coronary artery disease
CI	Confidence interval
eGFR	Estimated glomerular filtration rate
HR	Hazard ratio
IQR	Interquartile range
LVEF	Left ventricular ejection fraction
NSTEMI	Non-ST-segment elevation myocardial infarction
RAA	Renin-angiotensin-aldosterone
SD	Standard deviation
STEMI	ST-segment elevation myocardial infarction

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Introduction

Acute myocardial infarction (AMI) is one of the leading causes of mortality globally. In most cases, AMI occurs due to the rupture of a vulnerable atherosclerotic plaque or erosion of the coronary artery endothelium [1, 2]. With advances in screening and treatment, the mortality rate of AMI has been improving but still ranges from 6.0 to 12.6% [3–5]. Although cardiovascular diseases were previously thought to affect affluent nations primarily, current data shows that around 85% of cardiovascular disease cases now occur in low- and middle-income countries [6, 7]. Thus, the burden of AMI is more significant in developing regions.

As a multifactorial, complex disease, the etiology and prognosis of AMI are affected by both genetic and environmental factors [8–13]. Numerous genetic variants and different pathological pathways, including dyslipidemia, epithelium dysfunction, plaque instability, and abnormal thrombosis triggers, have been found to be associated with AMI [14–16]. In addition to these pathways, the renin-angiotensin-aldosterone (RAA) system has drawn particular focus in cardiovascular research. This neurohumoral system plays a vital role in regulating body volume, sodium balance, and vascular resistance [17]. Typically, the cleavage of angiotensinogen is implemented by renin to form angiotensin I, and then the angiotensin-converting enzyme converts inactive angiotensin I to active angiotensin II. The binding of angiotensin II to its receptors results in the formation of aldosterone, which causes the renal tubular cells to reuptake salt and water [18].

In the RAA system, *AGT* M235T is the most-studied gene variant. This single nucleotide polymorphism is characterized by the replacement in codon 235 of methionine by threonine and has been shown to influence the level of plasma angiotensinogen [19]. Angiotensinogen concentration affects the formation of angiotensin II. Therefore, elevated angiotensinogen can increase angiotensin II concentration, promote atherosclerosis, and regulate the severity of coronary artery disease (CAD) [20–22]. In individuals with the T allele of the *AGT* M235T variant, plasma angiotensinogen concentrations are 13–20% higher than in those without [23, 24]. A meta-analysis by Rayan et al. confirmed that the TT genotype is associated with the risk of AMI [25]. Some studies have shown that the TT genotype of the *AGT* M235T variant is associated with the number of stenosed coronary artery branches and the severity of CAD [20, 26, 27], while this association was found to be negative in another study [28]. The prognostic value of *AGT* M235T in major cardiovascular events has been reported in several studies [29, 30]. However, while there were many studies on the association between the *AGT* M235T genetic variant and the risk of AMI, the data on the influence of this variant on the characteristics of coronary atherosclerosis and mortality in AMI patients is lacking and conflicting. Therefore, we conducted this study to investigate in patients diagnosed with AMI the relationship between the *AGT* M235T genetic variant and the characteristics of coronary atherosclerosis and 12-month all-cause mortality. The aim was to optimize secondary prevention strategies after AMI.

Materials and methods

Study design and participants

This prospective cohort study was conducted at the Department of Cardiology and the Department of Interventional Cardiology, Cho Ray Hospital, Ho Chi Minh City, Vietnam, from January 2020 to May 2021. Inclusion criteria were patients who were 18 years or older, were definitely diagnosed with AMI, and agreed to participate in the study. All participants provided written informed consent. Exclusion criteria included a history of AMI, percutaneous coronary intervention, coronary artery bypass graft surgery, no epicardial coronary artery stenosis on invasive coronary angiography, and loss of contact during the vital status follow-up period.

AMI and clinical types comprising ST-segment elevation myocardial infarction (STEMI) or non-ST-segment elevation myocardial infarction (NSTEMI) were determined according to the fourth universal definition of myocardial infarction [1]. Patients were evaluated for medical history and underwent a physical examination and laboratory tests at admission to confirm the diagnosis of AMI. Laboratory tests used to diagnose AMI were Troponin I, electrocardiography, transthoracic echocardiography, and invasive coronary angiography. Data collection forms were used to record information on risk factors for CAD, clinical characteristics, laboratory parameters, coronary atherosclerosis characteristics, and treatment measures. Hypertension, diabetes mellitus, and dyslipidemia were diagnosed in accordance with international guidelines [31–33]. Obesity was defined when the body mass index was ≥ 25 kg/m^2 [34]. A smoker was defined as current smoking or previous smoking within the past 12 months. Killip class was used to assess the severity of acute heart failure [35]. Left ventricular ejection fraction (LVEF) was evaluated by the Simpson method on 2D transthoracic echocardiography 1–3 days after admission [36]. Coronary atherosclerosis characteristics were collected, including the location and number of stenotic coronary arteries and the severity of coronary lesions calculated by the Gensini score [37].

Patients with AMI were followed for all-cause mortality in the hospital, then every three months up to 12 months

from the date of admission. Survival status was monitored through regular follow-up visits, hospital readmissions at Cho Ray Hospital, or telephone contact.

Genetic analyses

After patients agreed to participate in the study, two milliliters of each patient's venous blood was drawn for genotyping at the Center for Molecular Biomedicine, University of Medicine and Pharmacy at Ho Chi Minh City, Vietnam. Genomic DNA was extracted from participants' leukocytes using a GeneJet™ Whole Blood Genomic DNA Purification Mini Kit (Thermo Fisher Scientific, Waltham, MA, USA). The purity of the extracted DNA was quantified by NanoDrop™ 2000 Spectrophotometer (Thermo Fisher Scientific). The genotyping process was performed by a tetra-primer polymerase chain reaction. The protocol for the reaction was developed and described previously [38]. To ensure the accuracy of the genotyping process, fifty random samples were chosen for direct sequencing. The 400-base pair region containing M235T was sequenced using appropriately designed primers with the detailed protocols described elsewhere [39–41].

Table 1 General characteristics of the study population

Variables	Study population ($n=504$)
Demographic characteristics and CAD risk factors	
Age (years), mean ± SD	63.9 ± 11.7
Male, n (%)	358 (71.0)
Dyslipidemia, n (%)	449 (89.1)
Hypertension, n (%)	409 (81.2)
Smoking, n (%)	216 (42.9)
Diabetes mellitus, n (%)	125 (24.8)
Obesity, n (%)	104 (20.6)
Clinical diagnosis	
STEMI, n (%)	321 (63.7)
NSTEMI, n (%)	183 (36.3)
Killip Class	
Class I, n (%)	385 (76.4)
Class II, n (%)	41 (8.1)
Class III, n (%)	32 (6.3)
Class IV, n (%)	46 (9.2)
Blood investigations at admission	
Hemoglobin (g/dL), mean ± SD	13.1 ± 1.7
Glucose (mg/dL), median (IQR)	115.0 (97.0–149.0)
Creatinine (mg/dL), median (IQR)	0.90 (0.76–1.09)
Troponin I (pg/mL), median (IQR)	14.6 (2.6–50.0)
2D Echocardiography	
LVEF (%), median (IQR)	46.5 (39.0–53.0)
***AGT*M235T genotypes**	
MM, n (%)	2 (0.4)
MT, n (%)	105 (20.8)
TT, n (%)	397 (78.8)
Therapy	
Coronary revascularization, n (%)	476 (94.4)
Aspirin, n (%)	503 (99.8)
P2Y12 inhibitor, n (%)	504 (100.0)
Statin, n (%)	497 (98.6)
ACEI/ARB, n (%)	457 (90.7)
Beta-blocker, n (%)	395 (78.4)

CAD: coronary artery disease, SD: standard deviation, STEMI: ST-segment elevation myocardial infarction, NSTEMI: non-ST-segment elevation myocardial infarction, IQR: interquartile range, LVEF: left ventricular ejection fraction, ACEI: angiotensin-converting enzyme inhibitor, ARB: angiotensin II receptor blocker. Reference values for parameters provided by the laboratory at Cho Ray Hospital: hemoglobin (12.0–17.0 g/dL), glucose (70–110 mg/dL), creatinine (0.7–1.5 mg/dL) and troponin I (< 0.2 ng/mL)

Statistical analysis

The data were processed using SPSS Statistics for Windows version 22.0 (IBM Corp., Armonk, NY, USA). The normal distribution of continuous variables was assessed by the Kolmogorov-Smirnov test. Continuous variables were presented as mean ± standard deviation (SD) if normally distributed and median (interquartile range [IQR]) if not normally distributed. Categorical variables are presented as frequencies and percentages. The characteristics of coronary atherosclerosis between the *AGT* M235T genotype groups and the factors between the survival/deceased groups were compared using the Chi-squared tests for categorical variables, Student's t-tests, or Mann-Whitney U tests for continuous variables based on the data distribution. The cumulative survival probability of the *AGT* M235T genotype groups was determined using the Kaplan-Meier estimator and compared using a log-rank test. The impact of the *AGT* M235T genetic variant on 12-month all-cause mortality was evaluated using Cox regression analysis in eight predefined subgroups: age, gender, hypertension, diabetes mellitus, dyslipidemia, obesity, smoking, and ACEI/ARB therapy. Factors associated with mortality in univariate analysis were further analyzed in a multivariable Cox regression model to identify independent prognostic factors for mortality. A p-value of < 0.05 was considered statistically significant.

Results

General characteristics of subjects

There were 504 eligible AMI patients enrolled in this study. The general characteristics of the study population are shown in Table 1. The mean age was 64 years. Men were more prevalent, accounting for approximately 71%. High rates of traditional cardiovascular risk factors were observed, including dyslipidemia (89.1%), hypertension

(81.2%), smoking (42.9%), diabetes mellitus (24.8%), and obesity (20.6%). Most of the patients were diagnosed with ST-elevation AMI and were assessed as Killip class I. The distribution of genotypes of the *AGT* M235T variant in Vietnamese patients with AMI conformed to the Hardy-Weinberg equilibrium ($P=0.186$), with the TT genotype being predominant (78.8%) and the MM genotype being rare (0.4%). Most patients underwent coronary revascularization, and a high proportion of medications in guideline-directed medical therapy were found, with nearly all patients receiving aspirin, P2Y12 inhibitors, statins, and angiotensin-converting enzyme inhibitor (ACEI)/angiotensin II receptor blocker (ARB).

Relationship between the *AGT* M235T genetic variant and coronary atherosclerosis

Table 2 presents the relationship between the *AGT* M235T genetic variant and coronary atherosclerosis, with variables examined, namely the location of stenosed coronary arteries, the number of stenosed coronary arteries, and the Gensini score. There were no significant differences between the MM + MT and TT genotypes regarding which coronary arteries were affected. The proportions of single-vessel, double-vessel, and triple-vessel disease were similar in the two genotype groups ($P=0.858$). There was also no significant association between the *AGT* M235T genetic variant and the Gensini score ($P=0.931$).

Table 2 Association between the *AGT* M235T genetic variant and coronary atherosclerosis

Variables	Total ($n=504$)	Genotype MM + MT ($n=107$)	Genotype TT ($n=397$)	*P* value
Location of stenosed coronary artery				
Left main coronary artery, n (%)	51 (10.1)	10 (9.3)	41 (10.3)	0.858
Left anterior descending artery, n (%)	447 (88.7)	93 (86.9)	354 (89.2)	0.495
Left circumflex artery, n (%)	281 (55.8)	64 (59.8)	217 (54.7)	0.381
Right coronary artery, n (%)	358 (71.0)	75 (70.1)	283 (71.3)	0.811
Number of stenosed coronary arteries				
Single vessel disease, n (%)	125 (24.8)	27 (25.2)	98 (24.7)	0.858
Double vessel disease, n (%)	176 (34.9)	35 (32.7)	141 (35.5)	
Triple vessel disease, n (%)	203 (40.3)	45 (42.1)	158 (39.8)	
Gensini score, median (IQR)	34.0 (17.0–58.0)	32.0 (16.0–56.0)	34.0 (17.0–59.5)	0.931

IQR: interquartile range

Relationship between the *AGT* M235T genetic variant and prognosis

During the 12 months of follow-up, 54 participants died, accounting for 10.7%. The characteristics of the survivors and deceased participants are compared in Table 3. A total of 44 out of 397 TT genotype-carrying patients died, as did 10 out of 107 of those carrying the MM + MT genotype. The 12-month mortality hazard ratio in Cox regression analysis of the TT genotype compared to MM + MT was 1.185 (95% confidence interval [CI]: 0.596–2.354; $P=0.629$). Kaplan Meier survival curve analysis also showed no statistically significant difference in 12-month mortality between patients with the TT genotype and those with the MM + MT genotype in the entire study population (Log-rank $P=0.627$) (Fig. 1). The effect of *AGT* M235T genotypes (TT vs. MM + MT) on the risk of overall 12-month mortality was not significantly different across the subgroups defined by age, gender, hypertension, diabetes mellitus, dyslipidemia, obesity, smoking, and ACEI/ARB therapy status (Fig. 2).

In univariate analysis, age, Killip class ≥ II, creatinine, troponin I concentration at admission, LVEF, and ACEI/ARB therapy were associated with 12-month mortality (Table 3). After adjusting for confounding factors in the multivariable Cox regression analysis, Killip class ≥ II and admission creatinine concentration were independent predictors for 12-month mortality in AMI patients (Table 4).

Discussion

In our study, the *AGT* M235T variant genotypes in AMI patients were distributed according to Hardy-Weinberg equilibrium. The TT genotype accounted for the highest proportion, and the MM genotype was rare. The lowest frequency of the MM genotype is similar to previous studies of Asian and African patients with AMI [26, 42, 43]. In contrast, the TT genotype in Western countries is the least common [44, 45]. The difference in genotype frequency of *AGT* M235T may be due to the genetic characteristics of different races and continents. There have been many studies on the association between the *AGT* M235T genetic variant and the risk of AMI in the context of primary prevention of atherosclerotic cardiovascular disease. However, few studies have explored the relationship between this genetic variant and coronary atherosclerosis and mortality prognosis in AMI patients in the secondary prevention settings of our study.

We found no relationship between the genotype of the *AGT* M235T variant and the characteristics of coronary atherosclerosis in AMI patients regarding the location of stenosed coronary arteries, number of stenosed coronary arteries, and Gensini score. In the CORGENE study,

Table 3 Comparative characteristics between survived and deceased participants

Variables	Survivors ($n=450$; 89.3%)	Deceased ($n=54$; 10.7%)	*P* value
Demographic characteristics and CAD risk factors			
Age (years), mean ± SD	63.4 ± 11.8	67.6 ± 10.1	*0.014*
Male gender, n (%)	325 (72.2)	33 (61.1)	0.111
Dyslipidemia, n (%)	401 (89.1)	48 (88.9)	1.000
Hypertension, n (%)	365 (81.1)	44 (81.5)	1.000
Diabetes mellitus, n (%)	104 (23.1)	21 (38.9)	*0.018*
Smoking, n (%)	196 (43.6)	20 (37.0)	0.386
Obesity, n (%)	94 (20.9)	10 (18.5)	0.859
Clinical diagnosis			
STEMI, n (%)	286 (63.6)	35 (64.8)	0.856
NSTEMI, n (%)	164 (36.4)	19 (35.2)	
Killip Class ≥ II, n (%)	93 (20.7)	27 (50.0)	*< 0.001*
Blood investigations at admission			
Hemoglobin (g/dL), median (IQR)	13.2 ± 1.7	12.7 ± 1.8	0.052
Glucose (mg/dL), median (IQR)	115.0 (97.0–146.5)	117.0 (101.0–185.0)	0.236
Creatinine (mg/dL), median (IQR)	0.89 (0.76–1.06)	1.10 (0.82–1.55)	*0.001*
Troponin I (pg/mL), median (IQR)	12.9 (2.5–50.0)	37.5 (3.2–50.0)	*0.020*
2D Echocardiography			
LVEF (%), median (IQR)	47.0 (40.0–53.0)	41.5 (31.5–50.0)	*0.005*
Location of stenosed coronary artery			
Left main coronary artery, n (%)	44 (9.8)	7 (13.0)	0.463
Left anterior descending artery, n (%)	398 (88.4)	49 (90.7)	0.615
Left circumflex artery, n (%)	249 (55.3)	32 (59.3)	0.583
Right coronary artery, n (%)	319 (70.9)	39 (72.2)	0.838
Number of stenosed coronary arteries			
Single vessel disease, n (%)	114 (25.3)	11 (20.4)	0.727
Double vessel disease, n (%)	156 (34.7)	20 (37.0)	
Triple vessel disease, n (%)	180 (40.0)	23 (42.6)	
Gensini score, median (IQR)	34.0 (16.0–57.0)	45.5 (17.8–77.8)	0.173
***AGT*M235T genotypes**			
MM + MT, n (%)	97 (21.6)	10 (18.5)	0.606
TT, n (%)	353 (78.4)	44 (81.5)	
Therapy			
Coronary revascularization, n (%)	427 (94.9)	49 (90.7)	0.207
Aspirin, n (%)	450 (100.0)	53 (98.1)	0.107
P2Y12 inhibitor, n (%)	450 (100.0)	54 (100.0)	-
Statin, n (%)	444 (98.7)	53 (98.1)	0.550
ACEI/ARB, n (%)	414 (92.0)	43 (79.6)	*0.003*
Beta-blocker, n (%)	354 (78.7)	41 (75.9)	0.644

Italic values are statistically significant ($P < 0.05$)

CAD: coronary artery disease, SD: standard deviation, STEMI: ST-segment elevation myocardial infarction, NSTEMI: non-ST-segment elevation myocardial infarction, IQR: interquartile range, LVEF: left ventricular ejection fraction, ACEI: angiotensin-converting enzyme inhibitor, ARB: angiotensin II receptor blocker

Jeunemaitre et al. carried out a cross-sectional study of 463 Caucasians undergoing coronary angiography for known or suspected coronary artery disease and did not find a significant association between the *AGT* M235T genetic variant and coronary atherosclerosis [28]. However, several other studies have reported an association between this genetic variant and coronary atherosclerosis in patients with AMI [20, 26, 27]. Research by Lanz et al. [20] showed that the TT genotype increases the risk of multivessel CAD by 1.86 times, independent of other cardiovascular risk factors, and the T allele is also associated with a higher Gensini score in multivariable analysis. Gardemann et al. [27] concluded from a study of 2,250 Caucasian males that the frequencies of the M and T alleles of the *AGT* M235T variant are not statistically different between patients with single, double, and triple vessel disease. Nevertheless, in patients under 62 years of age, Gensini scores were higher in T allele carriers than in those with MM homozygotes. Data on the association between the *AGT* M235T genetic variant and coronary atherosclerosis in AMI patients are lacking, especially in Asian populations.

In terms of prognosis, our AMI patients with the TT genotype had a mortality rate that was not significantly different from those carrying the MM and MT genotypes in the general population as well as in various subgroups. In contrast, Goldenberg et al. [29] showed after a median 28-month follow-up period, that the TT genotype increased the risk of coronary events, including coronary-related mortality, non-fatal AMI, and unstable angina (HR = 2.37; $P = 0.04$) in post-AMI Black patients but not in White patients. Additionally, in 190 patients in Croatia five years after coronary stent placement, the *AGT* M235T gene variant was found to be associated with major cardiovascular events (death, target revascularization, and myocardial infarction) [30]. Our study did not detect an association between the *AGT* M235T gene variant and mortality in patients with AMI, possibly due to the high proportion of patients prescribed ACEI/ARB (90.1%). In addition, participants in the present study received coronary revascularization (94.5%) and standard treatment with medications that improve the survival status, such as dual antiplatelets, statins, and beta blockers, which can reduce the risk of death and obscure the mortality prognostic value of *AGT* M235T in AMI patients. This effect has been observed in our previous study [46], while trying to stratify the mortality risk based on the *ACE* I/D genetic variant, we found that the survival rate of DD genotype group was significant lower compared with the II/ID genotype group in patients without ACEI/ARB treatment. On the contrary, the survival rate of DD genotype group was not statistically different from the II/ID genotype group in patients with ACEI/ARB treatment. Another reason may be

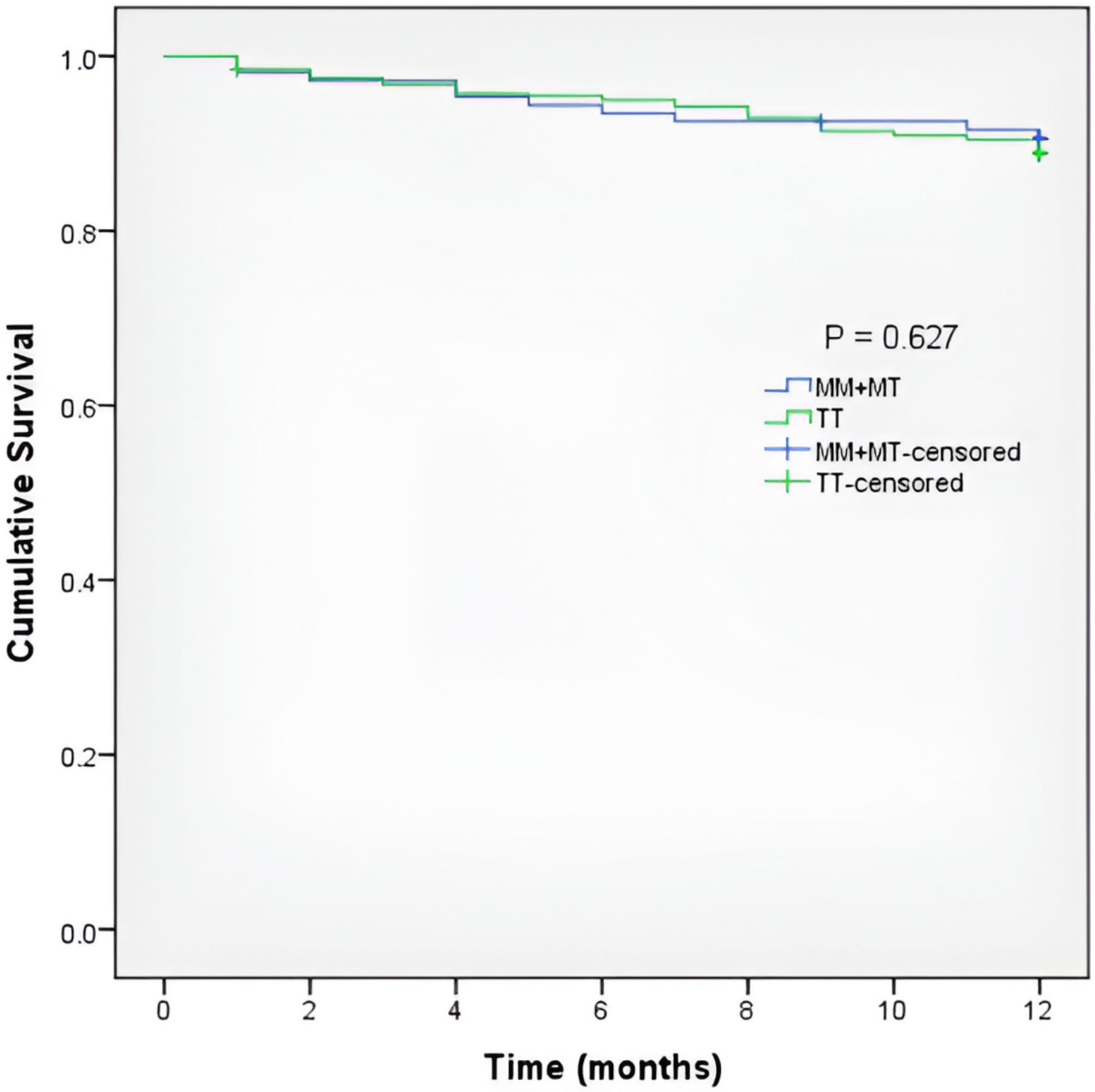

Fig. 1 Kaplan-Meier estimates of the survival probability according to *AGT* M235T genotypes

that the patient mortality in our study was not followed up long enough.

Apart from the *AGT* M235T genetic variant, traditional cardiovascular risk factors were also not associated with 12-month mortality. Diabetes was associated with a higher risk of death in univariate analysis but did not affect mortality in AMI patients after adjusting for confounders. The independent prognostic factors of mortality in the participants were Killip class ≥ II and creatinine concentration at admission. Ye et al. [3] noted in a survey of 296 Chinese patients that pump failure ($P = 0.006$) and reduced left ventricular ejection fraction ($P < 0.001$) had predictive value for mortality one year after AMI. Additionally, a study of 13,707 acute coronary syndrome patients from the GRACE (Global Registry of Acute Coronary Events) registry found that heart failure at admission (Killip class II or III) increased mortality in-hospital (12.0% vs. 2.9%; $P < 0.0001$) and at six months (8.5% vs. 2.8%; $P < 0.0001$)

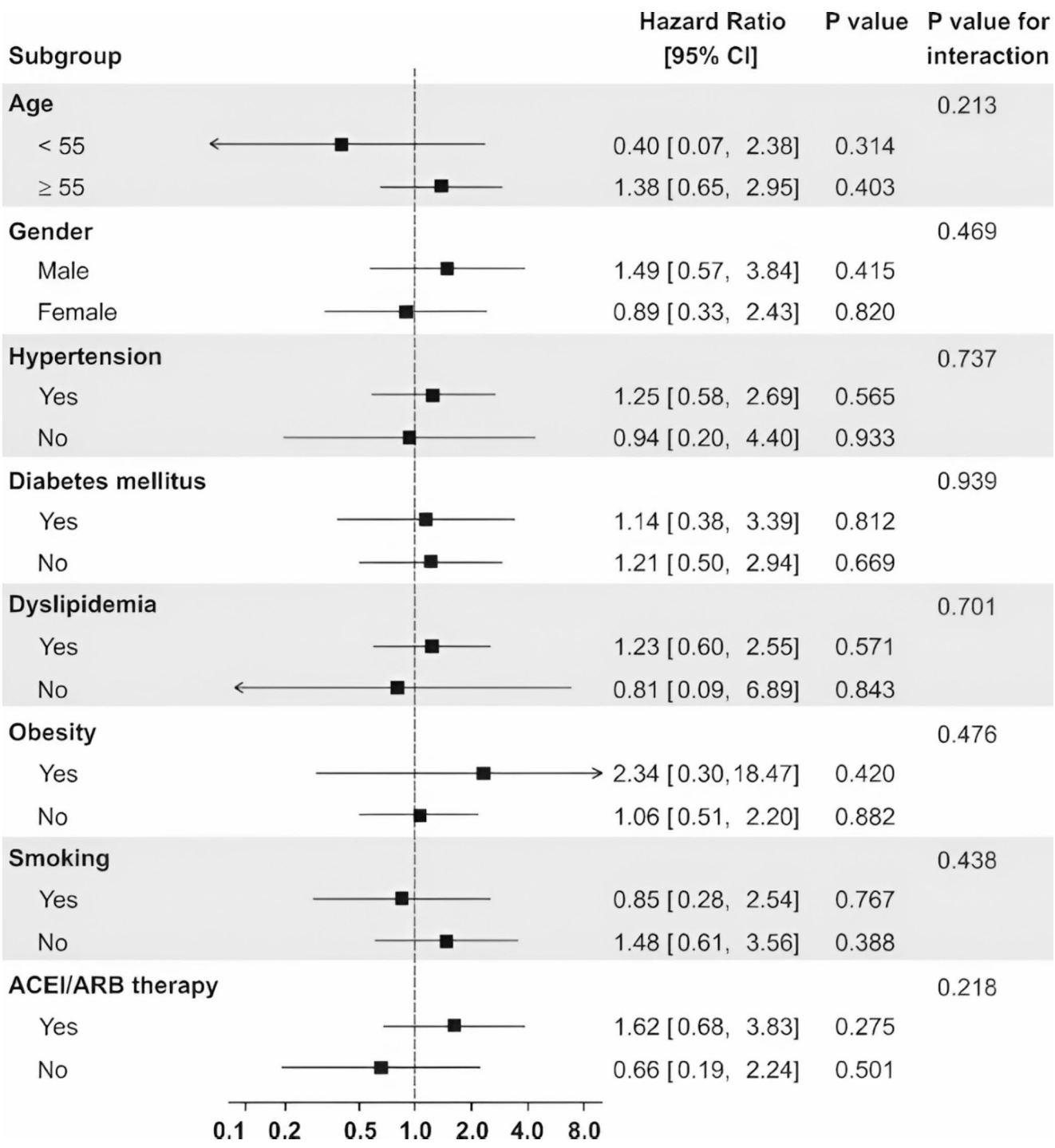

Fig. 2 Cox regression analysis for overall 12-month mortality risk in different subgroups according to *AGT* M235T genotypes

compared with patients without heart failure [47]. In the VALIANT (Valsartan in Acute Myocardial Infarction Trial), each 10-unit decrease in glomerular filtration rate below 81 mL/min/1.73 m^2 was found to be associated with a 10% increased risk of death after AMI [48]. Additionally, creatinine concentration at admission has been associated with mortality in AMI patients in previous studies [49, 50]. Walsh et al. reported from a study of 483 patients with AMI that the hazard ratio for 12-month mortality after AMI was higher in patients with increased creatinine levels compared with those with normal creatinine levels (HR = 2.40; 95% CI 1.55–3.72), after adjustment for baseline characteristics and treatment [48].

Table 4 Predictors of overall 12-month mortality in AMI patients in multivariable Cox regression analysis

Variables	HR	95% CI	*P*-value
Age (years)	1.024	0.999–1.049	0.058
Diabetes mellitus	1.548	0.878–2.728	0.131
Killip class ≥ II	2.493	1.405–4.424	*0.002*
Creatinine at admission (mg/dL)	1.444	1.086–1.921	*0.012*
Troponin I at admission (pg/mL)	1.000	0.999–1.002	0.695
LVEF (%)	0.978	0.954–1.004	0.096
ACEI/ARB therapy	0.546	0.273–1.091	0.086

Italic values are statistically significant ($P < 0.05$)

LVEF: left ventricular ejection fraction, ACEI: angiotensin-converting enzyme inhibitor, ARB: angiotensin II receptor blocker

Despite great effort, our study encountered some limitations. AMI has a complex pathogenesis with interactions between many factors and various genes. Thus, the genotypes of the *AGT* M235T variant might not fully explain the relationship between this variant and coronary atherosclerosis and 12-month all-cause mortality in patients with AMI. Due to the limited availability of biochemical testing techniques, we did not test angiotensinogen levels and evaluate the association of this biomarker with the genotypes of the *AGT* M235T variant and characteristics of AMI patients. Finally, more than a 12-month follow-up period might be required to detect the effect of the *AGT* M235T genetic variant on mortality in patients with AMI.

Conclusion

In summary, our study did not detect a statistically significant relationship between the *AGT* M235T genetic variant and coronary atherosclerosis in patients diagnosed with AMI. In addition, this genetic variant also did not affect 12-month overall mortality after AMI. Multicenter studies with larger sample sizes and longer follow-up periods might be required to evaluate precisely and comprehensively the association of the *AGT* M235T genetic variant with features of coronary lesions and mortality in Vietnamese post-AMI patients.

Supplementary Information The online version contains supplementary material available at https://doi.org/10.1007/s11033-024-09986-5.

Author contributions Author contributionsConceptualization: Duy Cong Tran, Binh Quang Truong. Data curation: Duy Cong Tran, Truc Thanh Thai. Formal analysis: Duy Cong Tran, Linh Hoang Gia Le, Truc Thanh Thai, Sy Van Hoang, Minh Duc Do, Binh Quang Truong. Investigation: Duy Cong Tran, Linh Hoang Gia Le, Minh Duc Do. Methodology: Duy Cong Tran, Truc Thanh Thai. Writing – original draft: Duy Cong Tran, Minh Duc Do. Writing – review & editing: Duy Cong Tran, Linh Hoang Gia Le, Truc Thanh Thai, Sy Van Hoang, Minh Duc Do, Binh Quang Truong. Project administration: Duy Cong Tran, Binh Quang Truong.

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Data availability No datasets were generated or analysed during the current study.

Declarations

Competing interests The authors declare no competing interests.

Disclosure The authors report no conflicts of interest in this work.

Ethical statement The study was conducted in accordance with the Declaration of Helsinki (as revised in 2013). The study was approved by the Ethics Committee of the University of Medicine and Pharmacy at Ho Chi Minh City, Vietnam (FWA registered number: FWA00023448). Approval number: 550/UMP-BOARD and informed consent was taken from all individual participants.

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