

## Relationship of ABCB1 Genetic Variants with Post-PCI Clopidogrel Response: Links to Hyperglycemia and Major Adverse Cardiovascular Events (MACE)

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### ABSTRACT

In patients undergoing PCI and treated with clopidogrel, we explored whether the combination of blood glucose status and ABCB1 C3435T genetic variation could help identify those at higher risk of developing major adverse cardiovascular events (MACE). A total of 117 patients were included in the analysis, among whom 52 experienced MACE. Genotyping of CYP2C19 and ABCB1 C3435T was performed using fluorescence-based in situ hybridization. Clinical data, including baseline characteristics, fasting glucose levels, and outcome events, were systematically collected. Logistic regression models were used to identify variables associated with MACE in patients receiving clopidogrel after PCI. When comparing patients with and without MACE, several baseline characteristics showed significant imbalance, including demographic factors (such as sex and age), metabolic and clinical history (diabetes, hypertension, alcohol use), fasting glucose levels, and genotype–glycemia combinations of ABCB1 C3435T. All of these differences reached statistical significance ( $P < 0.05$ ). In the multivariate model, four variables independently contributed to MACE risk. The ABCB1 C3435T variant showed a strong association with adverse outcomes (OR = 5.584,  $P = 0.024$ ). Increasing age was also associated with a higher risk (OR = 1.073 per unit increase,  $P = 0.014$ ), as was a history of hypertension (OR = 3.144,  $P = 0.020$ ) and diabetes mellitus (OR = 3.731,  $P = 0.030$ ). In patients younger than 75 years, the pattern of associations changed slightly: hypertension remained a significant predictor of MACE (OR = 3.151,  $P = 0.021$ ), while individuals carrying the ABCB1 CC genotype with normal glycemic status showed a significantly reduced risk, suggesting a protective effect in this subgroup (OR = 0.147,  $P = 0.023$ ). The ABCB1 C3435T polymorphism appears to independently contribute to the risk of major adverse cardiovascular events in patients receiving clopidogrel after PCI. In contrast, the combination of the CC genotype with normal glycemic status may be associated with a reduced risk of MACE, particularly in individuals younger than 75 years.

**Keywords:** Major adverse cardiac events, PCI, Genetic polymorphism, ABCB1 C3435T, Coronary artery disease

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### Introduction

Coronary atherosclerotic heart disease (CHD) is a chronic cardiovascular condition caused by progressive atherosclerotic narrowing or obstruction of the coronary arteries, which ultimately leads to myocardial ischemia, hypoxia, or infarction [1]. In recent decades, CHD has shown a continuous rise in incidence and is now recognized as one of the leading causes of global mortality [2, 3]. In China, the disease burden remains substantial. In 2020, the reported CHD mortality rates were 126.91 per 100,000 in urban populations and 135.88 per 100,000 in rural regions, with a persistent upward trend observed between 2012 and 2020, particularly in rural areas. At present, the number of patients living with CHD in China is estimated to exceed 11 million [4]. Percutaneous coronary intervention (PCI) represents a key therapeutic strategy for CHD, significantly reducing the risk of major adverse cardiovascular events (MACE) [5]. MACE is generally defined as a composite endpoint that includes outcomes

such as cardiac death, myocardial infarction, stroke, stent thrombosis, urgent target vessel revascularization, repeat revascularization for non-emergent indications, unstable angina, atrial fibrillation, and ventricular fibrillation [6, 7]. Despite advances in interventional therapy, MACE may still occur during the months following PCI, with reported mortality rates exceeding 5% [8, 9]. Dual antiplatelet therapy (DAPT) remains the standard of care for secondary prevention after PCI and has been shown to significantly reduce the incidence of these adverse cardiovascular events [10, 11]. Clopidogrel, a key component of dual antiplatelet therapy (DAPT), is widely used after PCI; however, a considerable proportion of patients (approximately 4%–30%) exhibit reduced responsiveness or resistance to the drug [12]. The underlying causes of clopidogrel resistance remain incompletely understood. They are considered multifactorial, involving clinical characteristics such as age, smoking status, diabetes, hypertension, medication adherence, and drug–drug interactions, as well as genetic variability [13, 14]. As a prodrug, clopidogrel requires intestinal absorption followed by hepatic biotransformation to generate its active metabolite. Intestinal uptake is partly regulated by P-gp encoded by the ABCB1 gene [15], while hepatic activation depends mainly on enzymatic pathways involving CYP2C19 and, to a lesser extent, PON1 [16]. Among these, CYP2C19 is regarded as the principal determinant of antiplatelet response, and loss-of-function variants have been consistently linked to increased risk of adverse cardiovascular outcomes, including MACE [17–19]. The ABCB1 gene, a member of the ATP-binding cassette transporter family first identified in the 1970s [20], encodes P-glycoprotein, a transmembrane efflux transporter highly expressed in various tissues, including malignant cells [21]. This protein plays an important role in drug transport by facilitating the efflux of substrates from intracellular to extracellular compartments [22]. More than 50 ABCB1 variants have been described, among which C3435T, G2677T/A, and C1236T are the most extensively studied, with C3435T receiving the greatest research attention [23]. The C3435T variant is located in exon 26 and, although synonymous, has been associated with altered P-glycoprotein structure and function [24]. Evidence suggests that individuals carrying the TT genotype may exhibit increased intestinal ABCB1 mRNA expression compared with CC or CT carriers, potentially enhancing drug efflux [25]. Functionally, the T allele may reduce intestinal absorption of clopidogrel by increasing P-gp-mediated efflux, thereby decreasing systemic drug exposure and antiplatelet efficacy. Importantly, the frequency of ABCB1 polymorphisms varies across ethnic and geographic populations, which may contribute to inter-individual differences in drug response. Previous clinical studies have suggested that genetic variation in ABCB1, particularly the C3435T polymorphism, may be associated with variability in cardiovascular outcomes among patients receiving clopidogrel after acute coronary syndrome and PCI. Individuals carrying the TT genotype have been reported to experience a higher incidence of adverse cardiovascular events during antiplatelet therapy [26]. In addition, this variant has also been implicated in differences in bleeding risk following PCI, further indicating its potential influence on clopidogrel response [27]. Evidence regarding genotype-specific effects is not entirely consistent. While some studies report an increased risk of MACE in TT carriers after PCI, others have found no significant impact of the CT genotype on platelet inhibition or clinical outcomes [23, 28]. Overall, the relationship between the ABCB1 C3435T polymorphism and cardiovascular prognosis remains debated. Metabolic status may further modify P-glycoprotein function. In diabetic conditions, blood glucose levels have been shown to correlate positively with P-gp activity. However, the direction and magnitude of this effect may vary by tissue type and disease duration [29, 30]. Moreover, certain anti-diabetic medications may influence drug absorption by modulating P-gp activity, potentially affecting intestinal transport of co-administered therapies [31]. However, the current literature remains inconsistent regarding the overall impact of diabetes on ABCB1 expression and function [32]. Given these uncertainties, the present study was designed to investigate whether the combination of ABCB1 C3435T genetic variation and hyperglycemia is associated with the risk of major adverse cardiovascular events in patients treated with clopidogrel following PCI.

## Materials and Methods

### *Study participants*

Patients with coronary heart disease (CHD) who underwent percutaneous coronary intervention (PCI) at Taian Central Hospital between 1 June 2018 and 30 September 2021 were retrospectively identified and included in this study. All patients had CYP2C19 and ABCB1 C3435T genotyping performed during hospitalization. Follow-up was conducted at 1, 6, and 12 months after PCI through outpatient review and readmission records. The dataset was accessed for research analysis from 1 June 2018 to 30 September 2022. Patients were included if they were

older than 18 years, had a confirmed diagnosis of coronary artery disease according to the Diagnostic and Therapeutic Guidelines for Stable CHD, were CYP2C19 normal metabolizers, underwent first-time PCI, and received standard dual antiplatelet therapy consisting of clopidogrel (75 mg once daily) plus aspirin (100 mg once daily) for 12 months. Individuals were also required to have complete clinical data and to follow up until the occurrence of endpoint events. Exclusion criteria comprised malignant tumors, contraindications to antiplatelet therapy, bleeding disorders, severe dysfunction of major organs, and pregnancy or lactation. The study was conducted in accordance with the Declaration of Helsinki and approved by the Ethics Committee of the Affiliated Taian Central Hospital of Qingdao University (2020 Lunshen No. 60). Written informed consent was obtained from all participants or, in cases of reduced cognitive function (score  $\leq 25$ ), from their legal representatives.

#### *Reagents and instruments*

A range of laboratory materials and instruments were used in this study, including a commercial sequencing reaction system and nucleic acid extraction reagents. Standard laboratory chemicals, such as ammonium chloride ( $\text{NH}_4\text{Cl}$ ), and sterile water for injection (500 mL) were also used. Molecular analysis was performed using a TL998A fluorescence detection system. Sample processing and centrifugation were performed using an Eppendorf 5418 high-speed centrifuge and 1.5 mL microcentrifuge tubes. Pipetting was performed using calibrated Eppendorf micropipettes (10  $\mu\text{L}$ , 200  $\mu\text{L}$ , and 1000  $\mu\text{L}$ ) together with matching sterile pipette tips. Blood samples were collected in 2 mL EDTA anticoagulation tubes.

#### *Experimental methods*

##### *Specimen collection*

A total of 1.5 mL of peripheral venous blood was drawn from each patient into EDTA anticoagulant tubes. Samples were gently inverted to ensure adequate mixing and to avoid hemolysis or clot formation, then temporarily stored at 4°C for no longer than 24 hours. For long-term storage, specimens were subsequently transferred and preserved at  $-20^\circ\text{C}$  until further analysis.

##### *ABCB1 genotyping procedure*

Genomic DNA was obtained using a stepwise processing protocol. First, 150  $\mu\text{L}$  of whole blood was added to a centrifuge tube containing 1 mL of ammonium chloride solution, and the mixture was incubated for 5 minutes. The sample was then centrifuged at 3000 rpm for 5 minutes, after which the supernatant was carefully removed. Next, 50  $\mu\text{L}$  of nucleic acid purification reagent was added to the pellet and thoroughly mixed. A 1.5  $\mu\text{L}$  aliquot of the resulting suspension was then transferred into the corresponding wells of a universal sequencing reaction kit. Pipetting was performed carefully to ensure no residual liquid remained in the tip, and the reaction tubes were securely sealed. Samples were gently inverted several times, briefly tapped to remove air bubbles, and then spun briefly in a microcentrifuge to collect any liquid from the tube walls. The prepared mixtures were then loaded into the designated system according to sample identifiers. Fluorescence-based detection was performed using a TL998A fluorescence analyzer, and the resulting fluorescence signal patterns were analyzed to determine ABCB1 genotypes.

##### *Clinical data collection*

Data collection included baseline demographic and clinical information such as age, sex, smoking and alcohol history, hypertension and diabetes status, ABCB1 genotype, fasting glucose, and homocysteine measurements obtained either at the time of event occurrence or at the 12-month assessment point. Patients were prospectively followed after discharge at 1, 6, and 12 months, using both outpatient review and hospital readmission records to ensure complete follow-up. The endpoint of interest during the follow-up period was the development of major adverse cardiovascular events (MACE).

##### *Statistical analysis*

The Hardy–Weinberg equilibrium test was performed to assess whether the genotype distribution of the study population was representative. All statistical analyses were conducted using SPSS version 25.0. Continuous variables with a normal distribution were summarized as mean  $\pm$  standard deviation and compared between groups using independent-samples t-tests. For variables that did not conform to normality, data were described as median with interquartile range [M (P25, P75)], and group comparisons were performed using the Mann–Whitney U test

(rank-sum test). Categorical variables were expressed as frequencies and percentages, and differences between groups were evaluated using the chi-square test. Univariate and multivariate logistic regression analyses were performed to identify factors associated with MACE in patients undergoing PCI. A P-value < 0.05 was considered statistically significant.

## Results and Discussion

### HWE equilibrium test

The Hardy–Weinberg equilibrium test for the ABCB1 C3435T polymorphism was conducted in 117 patients with coronary heart disease. The results showed no significant deviation from equilibrium ( $P > 0.05$ ), indicating that the genotype distribution in the study cohort was consistent with Hardy–Weinberg expectations and suggesting that the sampled population was well represented (**Table 1**).

**Table 1.** Hardy–Weinberg equilibrium analysis of ABCB1 C3435T genotypes.

| ABCB1 C3435T | Frequency         |                      | $\chi^2$ | P-value |
|--------------|-------------------|----------------------|----------|---------|
|              | Measured<br>N (%) | Theoretical<br>N (%) |          |         |
| CC           | 29 (24.8%)        | 23 (19.7%)           | 2.169    | 0.338   |
| CT           | 47 (40.2%)        | 58 (49.6%)           |          |         |
| TT           | 41 (35.0%)        | 36 (30.8%)           |          |         |

Notes: CC = wild-type homozygous genotype; CT = heterozygous genotype; TT = mutant homozygous genotype.

### Patients' baseline characteristics

Among the 117 enrolled patients, 52 experienced MACE, corresponding to an incidence of 44.4%. Baseline comparison between the MACE and non-MACE groups showed no significant differences in hypertension history, smoking status, homocysteine levels, ABCB1 CC genotype with hyperglycemia, or ABCB1 CT/TT genotype with normoglycemia ( $P > 0.05$ ). In contrast, significant differences were observed for sex, age, diabetes history, alcohol consumption, fasting blood glucose, ABCB1 CC combined with normoglycemia, and ABCB1 CT/TT combined with hyperglycemia ( $P < 0.05$ ). The detailed baseline characteristics are presented in **Table 2**.

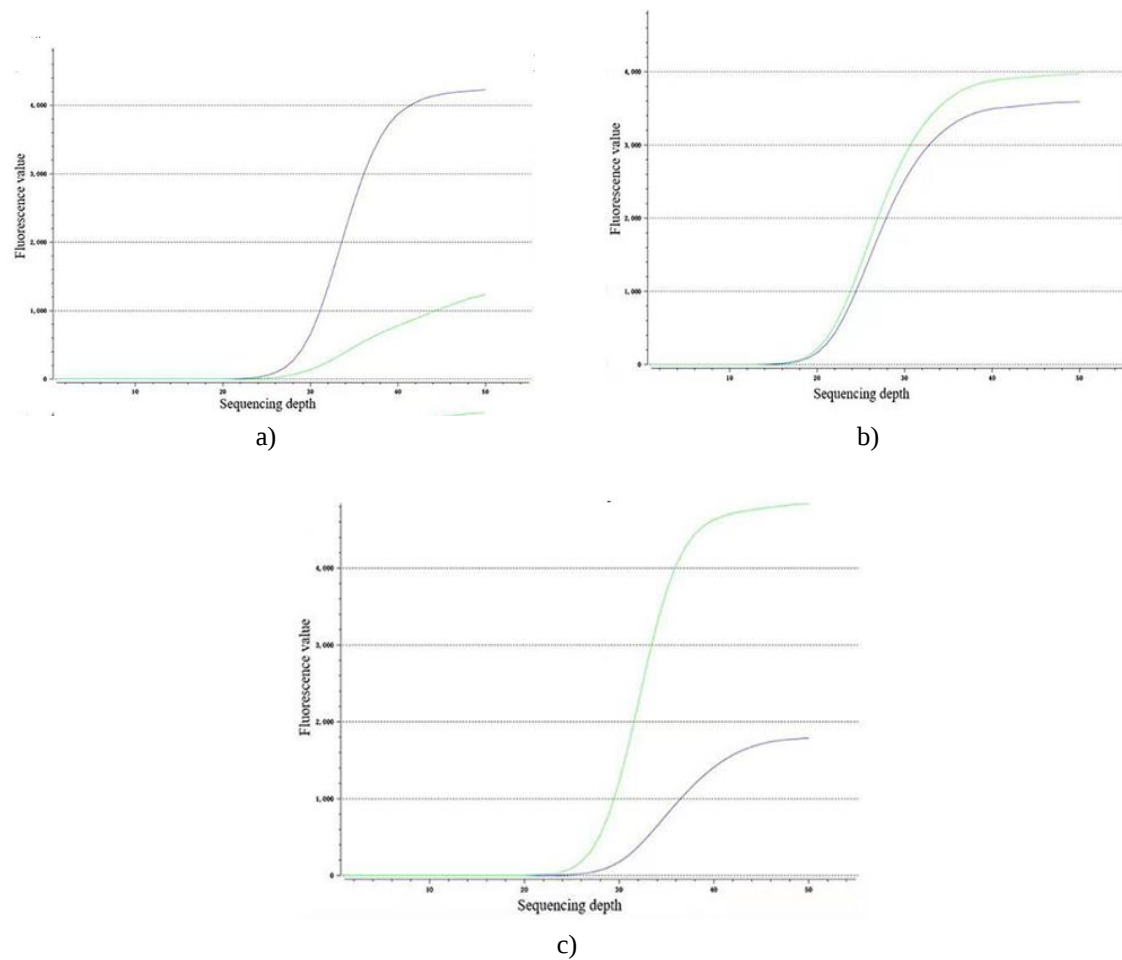
**Table 2.** Baseline characteristics.

| Characteristics                             | P-value | MACE group (52)   | Normal group (65) |
|---------------------------------------------|---------|-------------------|-------------------|
| Male (n, %)                                 | 0.025   | 29 (55.8)         | 49 (75.4)         |
| Age (years) (Mean $\pm$ SD)                 | 0.001   | 64.44 $\pm$ 8.974 | 58.82 $\pm$ 8.761 |
| Prior history of hypertension (n, %)        | 0.08    | 34 (65.4)         | 32 (49.2)         |
| Medical history of diabetes mellitus (n, %) | < 0.001 | 27 (51.9)         | 11 (16.9)         |
| History of smoking (n, %)                   | 0.518   | 17 (32.7)         | 25 (38.5)         |
| Alcohol use history (n, %)                  | 0.035   | 8 (15.4)          | 21 (32.3)         |
| Fasting blood glucose M level (P25, P75)    | 0.038   | 6.52 (5.40,8.09)  | 5.79 (5.33,6.09)  |
| Homocysteine M level (P25, P75)             | 0.683   | 13.3 (10.6,17.6)  | 13.4 (11.2,15.8)  |
| TT+ Hyperglycemia level (n, %)              | 0.482   | 6 (11.5)          | 4 (6.2)           |
| TT+ Normoglycaemia level (n, %)             | 0.025   | 4 (7.7)           | 15 (23.1)         |
| CT/CC+ Hyperglycemia level (n, %)           | 0.002   | 22 (42.3)         | 11 (16.9)         |
| CT/CC+ Normoglycaemia level (n, %)          | 0.098   | 20 (38.5)         | 35 (53.8)         |

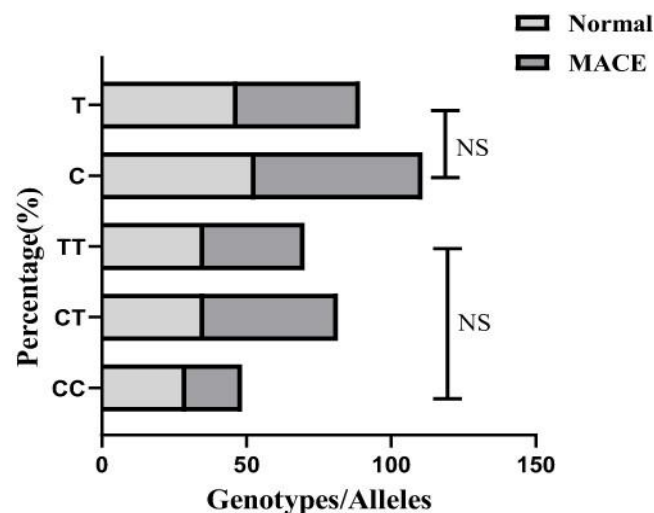
### Genotype distribution

The ABCB1 C3435T polymorphism was identified using fluorescence-based detection, as illustrated in **Figure 1**. The frequency of the T allele was 53.1% in one group and 57.7% in the other group.

Comparison of genotype distribution and allele frequencies between the two groups revealed no statistically significant differences ( $P > 0.05$ ), as shown in **Figure 2**.



**Figure 1.** Sequencing chromatograms illustrating ABCB1 C3435T genotypes. (a) CC homozygous wild-type, (b) CT heterozygous, and (c) TT homozygous mutant.



**Figure 2.** Comparison of ABCB1 C3435T genotype distribution between the non-MACE (normal) group and the MACE group.

*A multivariable logistic regression approach was applied to identify determinants of MACE following clopidogrel therapy in patients undergoing PCI*

MACE was defined as the dependent outcome variable. At the same time, demographic characteristics, clinical history, laboratory indicators, and genetic factors—including sex, age, ABCB1 C3435T genotype, hypertension, diabetes mellitus, smoking, alcohol consumption, fasting blood glucose, homocysteine, and genotype–glycemia

interaction—were entered as explanatory variables. After adjustment for covariates, four factors remained statistically significant. The ABCB1 C3435T polymorphism showed a strong association with MACE risk (OR = 5.584,  $P = 0.024$ ), followed by age (OR = 1.073,  $P = 0.014$ ), hypertension history (OR = 3.144,  $P = 0.020$ ), and diabetes mellitus (OR = 3.731,  $P = 0.030$ ). These findings are summarized in **Table 3**.

**Table 3.** Multivariate logistic regression analysis of MACE in PCI patients.

|                                             | Item S | EXP (B) 95.0% CI | Exp (B) | P-value | Wald  | SE    | B      |
|---------------------------------------------|--------|------------------|---------|---------|-------|-------|--------|
| <b>Gender</b>                               | 0*     |                  |         |         |       |       |        |
|                                             | 1      | 0.774–9.656      | 2.734   | 0.118   | 2.440 | 0.644 | 1.006  |
| <b>Age (years)</b>                          |        | 1.014–1.135      | 1.073   | 0.014   | 6.011 | 0.029 | 0.071  |
| <b>ABCB1 (C3435T)</b>                       | 0*     |                  |         |         |       |       |        |
|                                             | 1      | 1.258–24.780     | 5.584   | 0.024   | 5.117 | 0.760 | 1.720  |
| <b>Prior history of hypertension</b>        | 0*     |                  |         |         |       |       |        |
|                                             | 1      | 1.200–8.238      | 3.144   | 0.020   | 5.434 | 0.491 | 1.146  |
| <b>Medical history of diabetes mellitus</b> | 0*     |                  |         |         |       |       |        |
|                                             | 1      | 1.135–12.270     | 3.731   | 0.030   | 4.700 | 0.607 | 1.317  |
| <b>History of smoking</b>                   | 0*     |                  |         |         |       |       |        |
|                                             | 1      | 0.968–11.808     | 3.382   | 0.056   | 3.647 | 0.638 | 1.218  |
| <b>Alcohol use history</b>                  | 0*     |                  |         |         |       |       |        |
|                                             | 1      | 0.106–1.086      | 0.339   | 0.069   | 3.317 | 0.595 | –1.083 |
| <b>Fasting blood glucose level</b>          |        | 0.699–1.747      | 1.105   | 0.668   | 0.184 | 0.233 | 0.100  |
| <b>Homocysteine level</b>                   |        | 0.909–1.043      | 0.973   | 0.442   | 0.592 | 0.035 | –0.027 |
| <b>CC+ Hyperglycemia level</b>              | 0*     |                  |         |         |       |       |        |
|                                             | 1      | 0.711–99.255     | 8.401   | 0.091   | 2.854 | 1.260 | 2.128  |
| <b>CT/TT+ Hyperglycemia level</b>           | 0*     |                  |         |         |       |       |        |
|                                             | 1      | 0.230–5.510      | 1.125   | 0.884   | 0.021 | 0.810 | 0.118  |

Notes: Gender coded as 0 = male and 1 = female. \*Reference (control) category. For clinical history variables, 0 indicates absence, and 1 indicates presence.

#### *Multivariable logistic regression analysis of determinants of MACE in PCI Patients younger than 75 years receiving clopidogrel therapy*

Patients aged 75 years or older were excluded from this subgroup analysis. A total of 108 participants were included for evaluation. Initially, univariate logistic regression was performed, and variables with  $P < 0.1$  were subsequently entered into a multivariable model for further analysis. The results indicated that a history of hypertension was independently associated with an increased risk of MACE following clopidogrel therapy after PCI (OR = 3.151, 95% CI: 1.189–8.350;  $P = 0.021$ ). In contrast, the combination of the ABCB1 CC genotype with normal glycemic status was identified as a protective factor against MACE (OR = 0.147, 95% CI: 0.028–0.767;  $P = 0.023$ ). These findings are summarized in **Table 4**.

**Table 4.** Logistic regression analysis of MACE risk in PCI patients aged < 75 years.

|                                             | Item S | EXP (B) 95.0% CI | Exp (B) | P value | Wald  | SE    | B      |
|---------------------------------------------|--------|------------------|---------|---------|-------|-------|--------|
| <b>Gender</b>                               | 0*     |                  |         |         |       |       |        |
|                                             | 1      | 0.550–5.568      | 1.750   | 0.344   | 0.897 | 0.591 | 0.559  |
| <b>Age</b>                                  |        | 0.998–1.127      | 1.061   | 0.056   | 3.644 | 0.031 | 0.059  |
| <b>Prior history of hypertension</b>        | 0*     |                  |         |         |       |       |        |
|                                             | 1      | 1.189–8.350      | 3.151   | 0.021   | 5.326 | 0.497 | 1.148  |
| <b>Medical history of diabetes mellitus</b> | 0*     |                  |         |         |       |       |        |
|                                             | 1      | 0.918–9.598      | 2.969   | 0.069   | 3.304 | 0.599 | 1.088  |
| <b>Alcohol use history</b>                  | 0*     |                  |         |         |       |       |        |
|                                             | 1      | 0.143–1.340      | 0.438   | 0.148   | 2.092 | 0.570 | –0.825 |

|                                    |    |             |       |       |       |       |        |
|------------------------------------|----|-------------|-------|-------|-------|-------|--------|
| <b>Fasting blood glucose level</b> |    | 0.741–1.639 | 1.102 | 0.631 | 0.230 | 0.203 | 0.097  |
| <b>CC+ Normoglycaemia level</b>    | 0* |             |       |       |       |       |        |
|                                    | 1  | 0.028–0.767 | 0.147 | 0.023 | 5.178 | 0.842 | –1.915 |
| <b>CT/TT+ Hyperglycemia level</b>  | 0* |             |       |       |       |       |        |
|                                    | 1  | 0.304–4.088 | 1.115 | 0.869 | 0.027 | 0.663 | 0.109  |

Notes: Gender was coded as 0 = male and 1 = female. \*Reference category (control group). For binary variables, 0 indicates absence, and 1 indicates the presence of the condition.

This work examined the combined impact of the ABCB1 C3435T genetic polymorphism and elevated blood glucose on MACE occurrence following clopidogrel treatment in patients who underwent PCI. Our analysis revealed a T allele prevalence of 55.1% for the ABCB1 C3435T variant, a figure that corresponds generally with previously published T allele frequencies of 34–63% among Asian cohorts [33]. Age, ABCB1 carrier status, a clinical background of hypertension, and a diabetes diagnosis were identified as independent contributors to MACE after clopidogrel administration in PCI-treated individuals exhibiting a normal CYP2C19 metabolic profile. Among those below 75 years, a hypertensive history independently predicted MACE post-clopidogrel therapy following PCI. Moreover, possessing the ABCB1 (CC) genotype in the setting of normal blood glucose was protective against MACE in this therapeutic scenario.

The ABCB1 C3435T mutation can drive enhanced P-glycoprotein activity, thereby limiting systemic exposure to clopidogrel and its active metabolite and ultimately blunting clinical antiplatelet efficacy. As a consequence, carriers of the ABCB1 C3435T variant are theoretically at diminished risk for ischemic events but may instead be predisposed to a greater bleeding hazard. Among clopidogrel recipients, the ABCB1 C3435T genotype showed a strong relationship with the composite endpoint of cardiovascular mortality, myocardial infarction, or stroke ( $P = 0.0064$ ). When compared with CT/CC individuals, TT homozygotes demonstrated a 72% increase in MACE risk (HR 1.72, 95% CI 1.22–2.44,  $P = 0.002$ ) [26]. Evidence from the PLATO dataset indicated that those carrying the ABCB1 C3435T wild-type allele actually suffered more ischemic events than mutation carriers, hinting that allelic variants might facilitate greater clopidogrel bioavailability and more favorable clinical trajectories [27]. Complementing this, another report noted that AMI patients with TT and CT genotypes had a higher one-year ischemic event rate than CC wild-type subjects (15.5% vs 10.7%; adjusted HR 1.72; 95% CI 1.20–2.47) [34]. Conversely, some investigations failed to uncover any meaningful impact of the ABCB1 C3435T variant on clopidogrel-induced platelet inhibition or MACE rates, with no discernible divergence in MACE incidence across genotype strata (HR 0.8; 95% CI 0.3–1.9;  $P = 0.603$ ) [28, 35]. Hence, the ABCB1 C3435T genotype, taken alone, is insufficient to guide personalized clopidogrel prescribing for improved management of high-risk populations [36]. These contradictory findings likely reflect the modulating influence of factors such as CYP2C19 genetic background, age, and glycemic status. It has been established that the rate of MACE among patients with comorbid T2DM approximates 117.46% at 30 days and 29.68% at 3 years following PCI [37]. Circulating glucose concentrations are known to affect the functional activity of the ABCB1-encoded P-glycoprotein [32]. To reduce confounding from these sources, we restricted our cohort to individuals with normal CYP2C19 metabolism and accounted for concomitant hyperglycemia and ABCB1 genotype. Our data demonstrated that the proportion of patients with the ABCB1 (CC) genotype and normoglycemia was appreciably higher in the event-free group than in the MACE group.

In contrast, the proportion with ABCB1 (CT/TT) and hyperglycemia was substantially lower in the event-free group. Multivariable logistic regression established the ABCB1 C3435T genotype as an independent risk determinant for MACE following clopidogrel therapy in PCI patients (OR = 5.584; 95% CI 1.258–24.780;  $P = 0.024$ ). That said, the combination of ABCB1 C3435T genotype and hyperglycemia did not exhibit a significant association with MACE. Our analysis also brought to light a markedly higher CHD burden in the over-75 age bracket [38]. To reduce the confounding effect of advanced age, we excluded subjects aged 75 or older and conducted a subgroup analysis. The results from this refined dataset showed that the combination of ABCB1 (CC) and normoglycemia was a protective factor against MACE after clopidogrel treatment in PCI patients ( $P = 0.023$ ; OR = 0.147; 95% CI 0.028–0.767). The ABCB1 C3435T mutation can upregulate P-glycoprotein expression, leading to decreased intestinal absorption of clopidogrel. Hyperglycemia, through PKC-mediated enhancement of P-gp phosphorylation, further depresses drug bioavailability—an interaction that appears particularly consequential in individuals younger than 75 years. This investigation provides the first demonstration, within a

cohort with unimpaired CYP2C19 metabolism, that the concurrent presence of the ABCB1 (CC) genotype and euglycemia reduces MACE risk by 85%.

Several limitations warrant acknowledgment, including the modest patient numbers from a single center, which limit statistical robustness and hinder a comprehensive appraisal of genetic contributions. Future efforts should therefore encompass larger sample sizes and multicenter designs to mitigate statistical bias. Additionally, the distribution of ABCB1 polymorphisms differs across ethnicities and geographic regions, suggesting that confirmatory studies in other populations will be necessary to extend the generalizability of these results.

## Conclusion

This study suggests that the ABCB1 C3435T polymorphism is independently associated with the risk of MACE in PCI patients receiving clopidogrel, especially in those with concomitant hypertension or diabetes. In patients younger than 75 years, the combination of the ABCB1 CC genotype and normal glycemic status appears to be associated with a reduced risk of MACE following PCI with clopidogrel.

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**Conflict of Interest:** None

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**Ethics Statement:** This study was reviewed and approved by the Ethics Committee of the Affiliated Taian Central Hospital of Qingdao University (Approval No. 2021-06-50; approval date: 11 May 2021). Written informed consent was obtained from all participants or, where applicable, from their legal family representatives before inclusion in the study.

All authors have read and approved the final manuscript and consent to its publication in this journal.

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