CI 1.88～52.3,p=0.007) were independent predictors of informed consent delay. However, self-rated severe symptoms (OR 0.033,95% CI 0.13～0.85,p=0.021),ST segment elevation in first ECG (OR 0.33,95% CI 0.13～0.83, p=0.019) and discussion of strategies of risks (OR 0.19,95% CI 0.05～0.67,p=0.010)were associated with timely informed consent.

CONCLUSIONS The decision making process of primary PCI was not standardized. Informed consent of primary PCI was affected by multiple clinical features and decision making process. Informed decision making should be conducted according to the characteristics of different types of patients.

GW28-e0930

Abnormal Expression of PRMT5 in Peripheral Blood May Serve as a Genetic Marker for Assessment on the Risk of Progression from Stable Coronary Artery Disease to Acute Myocardial Infarction

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OBJECTIVES The purpose of this research is to make an assessment on whether expression quantity of PRMT5 gene in peripheral blood can be used as a biomarker for predicting the risk of progression from Stable Coronary Artery Disease (SCAD) to Acute Myocardial Infarction (AMI) and to discuss the possible mechanism of PRMT5 gene involved in the pathogenesis of acute AMI.

METHODS In this research, peripheral blood of 91 patients with acute myocardial infarction and 87 patients with stable coronary artery disease were collected. Real-time fluorescent quantitative PCR test was used to measure expression quantity of PRMT5 gene at the mRNA level and western blot method was used to measure the expression quantity of PRMT5 gene at the protein level.

RESULTS The result indicates that whether at the RNA level or at the protein level, expression quantity of PRMT5 gene in peripheral blood of patients with acute myocardial infarction is obviously lower than that in peripheral blood of patients with stable coronary artery disease. Binary Logistic regression analysis indicates that: Low expression of PRMT5 gene serves as the only independent risk factor for progression from stable coronary artery disease to acute myocardial infarction. Low expression of PRMT5 gene is irrelevant to level of serum blood lipid, relevant to Gensini score of coronary artery, irrelevant to quantity of cardiac troponin and irrelevant to time interval of occurrence. Result of creation of ROC curve by using expression quantity of PRMT5 gene at the mRNA level indicates that: When relevant expression quantity of PRMT5 gene at the mRNA level in peripheral blood is used as the criterion for diagnosis of acute myocardial infarction, its sensitivity, specificity, positive predictive value and negative predictive value are 0.713, 0.681, 71.26% and 68.13% respectively.

CONCLUSIONS PRMT5 gene has a low expression in peripheral blood of patients with acute myocardial infarction, and low expression of PRMT5 gene serves as an independent risk factor for occurrence of acute myocardial infarction among patients with stable coronary artery disease. Low expression of PRMT5 gene in peripheral blood increases the risk of acute myocardial infarction by 5.472 times. Expression quantity of PRMT5 gene can be used as a genetic marker indicating the risk of occurrence of acute myocardial infarction among patients with stable coronary artery disease. It can be speculated that it may further promote occurrence of acute myocardial infarction through exerting an influence on inflammatory response.

GW28-e0931

Abnormal Expression of CPNE3 in Peripheral Blood of Acute Myocardial Infarction and Stable Coronary Artery Disease: Potential Prediction Marker

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OBJECTIVES This research aims to make an assessment on whether expression quantity of CPNE3 gene can be used as a biomarker for predicting the risk of progression from stable coronary artery disease (SCAD) to acute myocardial infarction (AMI) and to discuss the possible mechanism of CPNE3 gene involved in the pathogenesis of AMI.

METHODS In this research, we collected peripheral blood of 87 SCAD patients and 91 AMI patients. The western blot method was adopted to measure expression quantity of CPNE3 gene at the protein level and real-time quantitative PCR test was adopted to measure expression quantity of CPNE3 gene at the mRNA level.

RESULTS The result indicates that: The expression quantity of CPNE3 gene in peripheral blood of AMI patients is significantly lower than that in peripheral blood of SCAD patients, whether at the protein level or the mRNA level. Binary Logistic regression analysis indicates that: Low expression quantity of CPNE3 gene serves as an independent risk factor for progression from stable coronary artery disease to acute myocardial infarction. Low expression quantity of CPNE3 gene is unrelated to level of fasting blood glucose and serum blood lipid of patients, correlated to Gensini score for coronary artery and unrelated to quantity of cardiac troponin and time of onset. The result of creation of ROC curve by using expression quantity of CPNE3 gene at the mRNA level indicates that: When relevant expression quantity of CPNE3 gene at the mRNA level in peripheral blood is used as the criterion for diagnosis of acute myocardial infarction, its sensitivity, specificity, positive predictive value and negative predictive value are 0.690, 0.648, 68.6% and 65.2% respectively.

CONCLUSIONS CPNE3 gene has a low expression in peripheral blood of AMI patients, which serves as an independent risk factor for occurrence of acute myocardial infarction among patients with stable coronary artery disease. Low expression of CPNE3 gene in peripheral blood causes the risk of acute myocardial infarction to increase by 3.845 times. Expression quantity of CPNE3 gene can be used as a genetic marker for assessment on the risk of occurrence of acute myocardial infarction among patients with stable coronary artery disease.

GW28-e0934

GTPBP4 is overexpressed in Peripheral Blood: Potential as a Genetic Marker for Assessment on the Progression from Stable Coronary Artery Disease to Acute Myocardial Infarction

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OBJECTIVES We aim to discover the role of progression from stable coronary artery disease (SCAD) to acute myocardial infarction (AMI). To explore whether the high expression of GTPBP4 in peripheral blood can be the molecular marker in the genetic evaluation of acute myocardial infarction or not and to discuss the possible mechanism of GTPBP4 gene involved in the pathogenesis of AMI.

METHODS In this research, peripheral blood of 70 patients with acute myocardial infarction and 63 patients with stable coronary artery disease were collected. We measure expression quantity of GTPBP4 gene at the mRNA level by real-time quantitative PCR test.

RESULTS It indicates that: The expression quantity of GTPBP4 gene in peripheral blood of AMI patients is significantly higher than that in peripheral blood of SCAD patients at the mRNA level. Binary Logistic regression analysis indicates that: high expression quantity of GTPBP4 gene serves as an independent risk factor for progression from stable coronary artery disease to acute myocardial infarction. High expression quantity of GTPBP4 gene is unrelated to level of Gensini score for coronary artery and quantity of cardiac troponin. The result of creation of ROC curve by using expression quantity of GTPBP4 gene at the mRNA level indicates that: When relevant expression quantity of GTPBP4 gene at the mRNA level in peripheral blood is used as the criterion for diagnosis of acute myocardial infarction, its sensitivity, specificity, positive predictive value and negative predictive value are 0.800, 0.492, 61.5% and 66.7% respectively.

CONCLUSIONS GTPBP4 gene has a high expression in peripheral blood of patients with acute myocardial infarction, and high expression of GTPBP gene serves as an independent risk factor for occurrence of acute myocardial infarction among patients with stable coronary artery disease. High expression of GTPBP4 gene in peripheral blood increases the risk of acute myocardial infarction by 3.200