(4) coronary collaterals to the infracted region. The myocardial perfusion was evaluated by myocardial perfusion grade (MBG). All the patients were divided into good perfusion group (MBG $\geq$2, n=137) and poor perfusion group (MBG $\leq$1, n=31) according to post intervention MBG. The MPV, white blood cell (WBC) count, and so on were compared. And the correlative factors were analyzed to find out the predictors of myocardial perfusion post PPCI.

RESULTS The MPV (11.2±1.4 fL vs. 9.5±1.3 fL, P <0.001) and WBC count (11.1±1.0 ×10^9/L vs. 10.1±1.3 ×10^9/L, P <0.001) were higher in poor perfusion group comparing with the good perfusion group. Multivariate logistic regression analysis showed that MPV (OR 0.42, 95% CI 0.28-0.61, P <0.001) and WBC count (OR 0.59, 95% CI 0.39-0.90, P =0.015) were the predictors of poor myocardial perfusion after PPCI. MPV was also correlated with post PPCI MBG (r = -0.607, P<0.001) and LVEF (r = -0.621, P <0.001).

CONCLUSIONS In STEMI patient receiving PPCI, higher pre-intervention MPV and WBC count means poor myocardial perfusion, and higher MPV also indicates worse left ventricular systolic function post PPCI.

GW26-e4776
A new cooperative approach in treatment of acute myocardial infarction in China

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OBJECTIVES Acute myocardial infarction (AMI) is the most serious type of coronary heart disease that affect the life and health of people, but < 30% of all of the patients with AMI have been treated effectively and timely in China. Delayed treatment has been considered as a leading cause of death and severe outcomes. This study aimed to evaluate a new regional cooperative emergency model in improving the first medical contact-to-balloon time and the therapeutic effects on patients with ST-elevation myocardial infarction (STEMI).

METHODS A new regional cooperative emergency model was established in some regions of Zhenjiang, Jiangsu province in China. A retrospective analysis of 458 STEMI patients before and after the model used in these regions was performed. Patients were divided into two groups in terms of before or after the regional cooperative rescue model used: model group (n=285) and control group (n=173). The first medical contact-to-balloon (FMC-to-B) time, door-to-balloon (D-to-B) time, referral time, cardiac function, mean cost, days of hospitalization, and major adverse cardiac events (MACE) were analyzed.

RESULTS The mean FMC-to-B time, D-to-B time and referral time of the model group were 97 ± 20, 22 ± 8, 61 ± 17 min, respectively, these parameters were significantly lower than the corresponding indexes of the control group (211 ± 27, 105 ± 14, 101 ± 19 min). Six months after the patients were discharged from the hospital, the left ventricular ejection fraction (LVEF) of the model group increased but left ventricular end-diastolic dimension (LVED) was decreased when compared with control group. These results also showed that mean costs (43813.0 ± 2731.0 vs 50471.0 ± 5264.0 CNY) and days of hospitalization (7.85 ± 3.15 vs 11.02 ± 4.06 days) were reduced. The incidence rate of MACE in the model group was 8.2%, which was lower than the rate of 16.8% in the control group.

CONCLUSIONS Regional cooperative emergency model may decrease the FMC-to-B time, which could improve the cardiac function, therapeutic effect on patients with AMI, and decrease financial burden of patients.

GW26-e1305
Platelet aggregation influenced by the loading-dose of multiple anti-platelet therapy in patients with acute myocardial infarction

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OBJECTIVES Due to the severity of acute myocardial infarction (AMI) and cardiovascular interventions, many patients should be prescribed multiple anti-platelet therapy to reduce platelet aggregation. We aimed to explore the influence of the loading-dose of multiple anti-platelet drugs on the inhibition of platelet aggregation in patients with AMI.

METHODS The present study included 84 patients who were initially diagnosed with AMI. Patients were divided into 3 groups randomly:

AC group (aspirin 0.3g plus clopidogrel 0.3g), ATG group (aspirins 0.3g plus ticagrelor 0.18g), and ACTF group (triple therapy with aspirins 0.3g, clopidogrel 0.3g and tirofiban 0.15ug/kg/min). Adenosine diphosphate(ADP)-induced platelet aggregation was measured using the multiplate analyzer at the time of initial diagnose of AMI, 2 hours after taking loading-dose of anti-platelet therapy, and the second morning.

RESULTS There were no significant differences in demographic characteristics among groups, including age, risk factors and sex. In the ADP-induced platelet aggregation ratio, there were not statistically significant among groups at the time of initial diagnose of AMI. However, there was significant difference between before and after the administration of anti-platelet drugs (53.3%±11.2% vs 27.9%± 8.5%, p<0.05) in all patients. The platelet aggregation ratio of triple therapy groups was significantly lower than dual anti-platelet therapy, both at the time of 2h after administration drugs and the second morning(14.3%±6.3% vs 23.5%±9.4%, p<0.05; 16.4%±8.5% vs 33.5%± 9.4%). Compared with AC group, ATG group had a significantly lower platelet aggregation ratio at the time of 2 hours after administer drugs (26.4%±7.8% vs 20.6%±4.5%, p<0.05). There were no significant differences between AC group and ATG group at the second morning (32.5%±6.4% vs 34.5%±7.3%, p=0.3).

CONCLUSIONS Addition tirofiban to conventional dual anti-platelet therapy can reduce drastically platelet aggregation ratio for the patients with AMI. Compared to aspirin combination with clopidogrel, aspirin plus ticagrelor had better inhibiting effect in 2 hours after administration.

GW26-e1416
Peripheral blood based discrimination of Coronary Heart Disease from healthy people by genome-wide gene expression profiling in Chinese Han people

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OBJECTIVES The polygenic inheritance and the dependence on environmental factors pose a challenge for the diagnosis and treatment of coronary heart disease (CHD). We hypothesized that a molecular diagnostic assay using easily accessible peripheral blood would greatly assist in the screening and diagnosis of CHD. In order to validate this a microarray analysis was carried out, the results indicated that there were some genes had differential expression. We discussed the function of these differential genes in the process of the occurrence and development of CHD and further evaluated their diagnostic potential in CHD.

METHODS A total of 26 subjects (n=26) were recruited in this study including 13 CHD and 13 healthy people. The total mRNA of the subjects were isolated from leukocyte in the peripheral blood within 4 hours after collection, and were reversed-transcribed to cDNAs as soon as possible. We constructed 2 pools of 3 subjects (3 CHD and 3 healthy people) for microarray screening with Affymetrix GeneChip® Scanner 3000 to discover new biomarkers and candidate genes. The results were analyzed with SAM, GO, KEGG. The other samples were used for RT-PCR to confirm the microarray on the next step. Randomly selected three candidate genes from the results of microarray for RT-PCR: CYP4F3 acted as up-regulated group, IL13RA1 acted as normal expression group, MED6 acted as down-regulated group. The results of RT-PCR was analyzed by 2$^{-\Delta\Delta Ct}$ method.

RESULTS The results of microarray were analyzed by Affymetrix Expression Console Software. With the choice criterion of p$\leq$0.05, logFC$\geq$1 or logFC$\leq$-1, there were 300 differential genes being selected, among them 30 genes had over expression and 270 genes had low expression. Analyzed by GO showed these 300 genes belonged to 105 cellular components, and involved in 295 biological processes and participated in the regulation of 212 molecular functions. Analyzed by KEGG showed that these genes took part in 75 gene pathways. The results of RT-PCR analyzed with 2$^{-\Delta\Delta Ct}$ method showed that compared to healthy people, the expression of CYP4F3 gene was 2.06 ± 0.57 (p=0.004), the expression of IL13RA1 gene was 0.96 ± 0.05 (p=0.870), and the expression of MED6 gene was 0.62 ± 0.12 (p=0.002). All the results obtained from RT-PCR were in accordance with the results of microarray.

CONCLUSIONS The microarray can be used as the foundation of exploring the pathogenic gene for coronary heart disease, and the differential expression of CYP4F3 or MED6 may take effect on the process of the occurrence and development of coronary heart disease. It can be conjectured that these findings may serve to identify new