Conclusion In conclusion, diagnostic model was established to distinguish no calcification and combination group from control group, which could provide useful laboratory information for risk assessment of cardiovascular disease patients.

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THE RELATIONSHIP STUDIES BETWEEN THE PROFILING OF BLOOD BIOMARKER AND THE CT IMAGING CHARACTERISTICS ON CORONARY ATHEROSCLEROSIS

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Background and Objective Studies showed that the metabolic disorder of lipid and inflammatory factor in blood might lead to the injury of endothelium, and then generate artherosclerosis gradually. It is difficult to distinguish plaque characteristics and composition by imaging characteristics. The authors aim to evaluate the risk degree of cardiovascular disease by analysing blood related gene expressing profile, cytokines profile and lipid metabolism profile.

Material and Methods Up to 205 imaging characteristics were analysed by Dual source CT. Subjects were divided into group A (control group without plaque), group B (calcification group) and group C (none calcification group, and combination group). Using GeXP technology to analyse cardiovascular disease related gene expression profile in peripheral blood including IL-β, IL-6, IL-8, IFNγ, MCP-1, VWF, MTHFR, L-Selectin, TNFα, Ubiquitin, MCSF, ICAM-1, ID_2, HMOX-1 and LDL-R. 10 items of cytokines expression profile were detected by liquid chip method including IL-1β, IL-2, IL-4, IL-6, IL-8, IL-10, IFNγ, MCP-1, TNFα and GM-CSF. The variations of blood lipid and hsCRP level were evaluated on Hitachi automatic analyser.

Results Compared with control group, the level of systolic blood pressure, GLU, TC, TG, APOB, APOC2 and hsCRP increased in group C ($p<0.05$). Discriminant analysis showed that 85.7% of group C cases were correctly classified. These seven items yield an AUC (area under curve) of 0.720 in discriminating group C patients from control group with sensitivity of 60.5% and specificity of 76.8%. There was no significant different item between calcification group and control group. Multi-PCR systems for analysing 17 genes were set up. The within-run and between-run CV values were 3.69–2.53% and 4.40–13.40%, respectively. The authors detected 15-gene expression profile in plaque group and control group, and found expression of IL-1β, IL-6, IL-8, MCP1 increased in group C (without diabetes) compared with control group ($p<0.05$). Peripheral blood cytokine levels showed that IL-6 of group C increased significantly compared with control group. IL-6 yields an AUC of 0.592 in discriminating group C patients from control group with sensitivity of 78.0% and specificity of 39.7%. A diagnostic model was set up by IL-6 combined with biochemical items, which yield an AUC of 0.746 in discriminating group C from control group with sensitivity of 78.0% and specificity of 65.1%.