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LNCRNA TMEVPG1 EXPRESSION AND IFN γ CORRELATES WITH HIGHER DISEASE SEVERITY AND OCCLUSION RATE ACCORDING TO GENSINI SCORE IN PATIENTS WITH CORONARY ARTERY DISEASE

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Background: In this study, we investigated the associations of circulating long non-coding RNA (lncRNA) Tmevpg1, transcription factor T-bet and IFN-γ cytokine relative expressions with severity and occlusion rate of coronary artery disease (CAD) patients.

Methods: Sixty-four patients suspected of CAD who underwent coronary angiography were consecutively enrolled in this study and divided into four group CAD 2, 3, 4 patients (N = 48) and CAD1 or controls (N=16) according to coronary angiographic results and Gensini Score. Blood samples of all participants were collected. Quantitative polymerase chain reaction (qPCR) was used to measure lncRNA Tmevpg1, transcription factor T-bet and IFNG cytokine expressions in whole blood samples. Serum interferon gamma (IFN-γ) was evaluated using enzyme-linked immunosorbent assay (ELISA). Gensini Score was used to assess the disease intensify and occlusion rate of CAD patients.

Results: LncRNA Tmevpg1 relative expression in CAD patients was upregulated compared with that in controls (P<0.003). LncRNA Tmevpg1 relative expression was remarkably associated with Gensini Score (P<0.01). Additionally, IFNG expression and IFN-γ serum levels were significantly increased (P<0.001), while, T-bet expression was not significantly increased. (P=0.06).

Conclusion: lncRNA Tmevpg1 and INF-γ expression correlated with higher disease severity, elevated inflammation and occlusion rate in CAD patientS.

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