

TREML4 gene expression evaluation as a biomarker in cardiovascular disease

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INTRODUCTION: Cardiovascular diseases (CVD) are the major cause of mortality in the world. The atherosclerosis has been identified as the basis for the development of these diseases. The *TREML4* gene is a surface protein belonging to the family of Triggering receptor expressed on myeloid cells, involved in developing of CVD. **OBJECTIVE:** This study analyzed the gene expression of *TREML4* in patients stratified according to the degree of atherosclerotic lesion, in order to identify a new potential biomarker of CVD. **MATERIAL AND METHODS:** RNA from peripheral blood was obtained from 70 patients undergoing coronary angiography in the catheterization sector in hospitals of Natal. The severity of coronary artery lesions was estimated by Friesinger score. The analysis of mRNA expression was performed by relative quantification by real-time PCR TaqMan system. **RESULTS AND DISCUSSION:** The subject was stratified in patients without lesion (n=23; 31%), low lesion (n= 22; 31%), intermediate lesion (n=17, 24%), and major lesion (n=8; 11%). *TREML4* mRNA gene expression between Friesinger score groups were not significant, when considering all individuals ($p>0.05$). However, after exclude the patients without *TREML4* expression, it was observed an increased of this gene according to severity of coronary atherosclerotic burden ($p<0,05$). **CONCLUSIONS:** Even though the limited results of this study, it is possible to demonstrate a direct correlation between the *TREML4* expression and the different levels of lesion atherosclerotic.

Keywords: *TREML4*; atherosclerosis; Friesinger score.

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