Identification of Regional Differences in Proinflammatory Cytokine Concentrations in Chronic Heart Failure Due to Chagas Cardiomyopathy: A Key Element in the Comprehension of the Disease

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Background: Despite the existing evidence suggesting an important role of cytokines in the development of heart failure (HF), the origin of its production remains unclear. It may be produced by the heart or by extracardiac sites. The purpose of this study is to investigate if the serum concentrations of proinflammatory cytokines in patients with HF due to Chagas' Cardiomyopathy (CC) are higher than in normal controls and if there are regional differences in the concentrations of cytokines.

Methods: The population consisted of patients with heart failure due to CC (n=25, age 52±15.6) and controls (n=25, age 53±17.6), left ventricular ejection fraction (LVEF) 29±7.6%. B-type natriuretic peptide (BNP) 514±431 pg/ml and normal individuals (n=25; age 53±7.6; y; 6 male; 16 female; 44±6.8 pg/ml), submitted to right and left heart catheterization. Blood samples were drawn from the aorta, coronary sinus and supra-hepatic vein. Serum cytokines were measured by the ELISA sandwich technique; Nitric oxide (NO) was analyzed by the Griess method; BNP was analyzed by ELSIA (Bioelisa); patients were also submitted to 2-D echocardiogram. 6-min walking test and quality of life questionnaires.

Results: Serum concentrations of TNF-alfa and gamma-interferon were significantly higher in patients than in controls (119±3.6 versus 115±8.3; p=NS); NO was undetectable. Conclusions: For the first time, a transmyocardial cytokine gradient was demonstrated in patients with HF. This evidence suggests that the heart is the main site of relative production of cytokines in patients with HF and contributes for a better understanding of the immune activation process in patients with HF due to CC.76

Nitric Oxide Regulation of Myocardial Contractility and Calcium Cycling: Independent Impact of Neuronal and Endothelial Nitric Oxide Synthases

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Background: Linkage Identifies 10q24-26 as a locus for dilated cardiomyopathy (DCM), a major cause of heart failure (HF). By localizing disease mutations, this method has been widely used. Successful human disease localization, however, is dependent on polymorphism between human and mouse genomic sequences. We sought to describe the sequence, genomic structure and expression of human N-RAP and determine whether the mutations cause DCM or hypertrophic cardiomyopathy (HCM).

Methods: The population consisted of patients with heart failure due to CC (n=25, age 52±15.6) and controls (n=25, age 53±17.6), left ventricular ejection fraction (LVEF) 29±7.6%. B-type natriuretic peptide (BNP) 514±431 pg/ml and normal individuals (n=25; age 53±7.6; y; 6 male; 16 female; 44±6.8 pg/ml), submitted to right and left heart catheterization. Blood samples were drawn from the aorta, coronary sinus and supra-hepatic vein. Serum cytokines were measured by the ELISA sandwich technique; Nitric oxide (NO) was analyzed by the Griess method; BNP was analyzed by ELSIA (Bioelisa); patients were also submitted to 2-D echocardiogram. 6-min walking test and quality of life questionnaires.

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