TWO-DIMENSIONAL DIFFERENCE GEL ELECTROPHORESIS IN MYOCARDIUM FROM PATIENTS WITH CHRONIC CHAGAS DISEASE AND OTHER NON-INFLAMMATORY CARDIOMYOPATHIES

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Chronic Chagas disease cardiomyopathy (CCC), caused by *Trypanosoma cruzi*, has a shorter survival than clinically similar cardiomyopathies showing less inflammatory phenomena. We have used proteomic analysis to compare the protein expression in heart samples from patients with CCC and other non-inflammatory cardiomyopathies (NIC). The global analysis of cardiac proteins requires a high-resolution technique to separate individual proteins from complex mixtures, which can be achieved by the application of the DIGE method (Two-dimensional Fluorescence Difference Gel Electrophoresis). In this method, samples are prelabelled with fluors and multiplexed within the same gel, along with an internal standard. We evaluated different protein loading methods, used at the isoelectric focusing, to detect a higher number of spots with lower labeling variation. Sample loading by paper-bridge at the cathode side of the IPG-strip (3-11 NL) improves the gel resolution (> 95% of similarity between fluorophores) and the number of detected spots (2062) as compared to cup-loading at the cathode side (2039), cup-loading at the anode side (1864) and rehydratation loading (2041). We next analyzed the differential expression of myocardium proteins from 5 patients with CCC and 5 patients with NIC, using DIGE. In this study, we found 894 spots present in all the samples. From these 157 are differentially expressed ($p<0.05$, t-test), 78 have increased and 78 decreased levels in the heart from patients with CCC as compared to patients with NIC. Molecular identification of the differentially expressed proteins is in process. We believe that results might help to understand the pathogenesis of CCC. **Supported by**: FAPESP and CNPq.