P. 120

DIFFERENTIALD PROTEIN PROFILES OF *TRYPANOSOMA CRUZI* STRAINS ISOLATED FROM ASYMPTOMATIC AND SYMPTOMAC PATIENTS WITH CHAGAS DISEASE

Rocío del Pilar Niño Moyano[1], Clara Isabel González Rugeles[2], Rodrigo Gonzalo Torres Sáeza

Grupo de Bioquímica e Ingeniería de Proteínas[1], Grupo de Inmunología y Epidemiología[2] Molecular, Universidad Industrial de Santander

Trypanosoma cruzi is a protozoan kinetoplastid parasite responsible for Chagas disease. This important disease affects 18 million people in Latin America. Currently, a few hundred thousand of seropositive individuals are estimated to live in the USA, Europe and Asia. Moreover, Chagas disease is characterized by an acute phase followed by a long chronic phase. During this disease, 70% of T. *cruzi*-infected individuals remain asymptomatic, whereas the remaining 30% suffers Chagas cardiomyopathy. Drugs for the treatment of *T. cruzi* infection are inadequate, and vaccines are lacking. On the other hand, prognostic values of these alterations in the variability of symptoms, and geographical differences in the distribution of the chronic forms of Chagas disease, have been attributed to diversity of *T. cruzi* strains. Many investigations have determined that gene expression in *T. cruzi* is mainly regulated at post-transcriptional level. Alternatively, proteome analyses have been used for the generation of protein maps from different parasite forms. One explanation for different phenotypes and pathogenesis induced by *T. cruzi* strains may be attributed to differential expression of some particular proteins. In this work, we have investigated this hypothesis, analyzing proteome profiles of two strains of *T. cruzi*. For this aim, we used 2D-gel electrophoresis, determining protein expression profiles of two *T. cruzi I* strains isolated from asymptomatic (strain MF) and symptomatic patiens (with cardiac form of Chagas disease (strain LQ)). For protein identifying of differentially expressed proteins between these two strains, we carried out image analysis, using PD-Quest Image Software analysis (Biorad). 273 and 305 spots were displayed respectively in the strains LQ and MF gels. The two strains share the presence of 242 spots; determining differences in protein expression and spot intensity of proteome images.