

## DIFFERENTIAL GENE EXPRESSION IN *Trypanosoma cruzi* STRAINS FROM CHAGASIC PATIENTS

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The majority of the individuals with positive serology for Chagas disease are asymptomatic (indeterminate form). After several years, 10-40% of these patients develop lesions of the heart (cardiac form) or digestive system (digestive form). The variability of symptoms has been mainly attributed to the genetic diversity of *T. cruzi* strains. One possibility to explain the distinct pathogenicity of the strains is the differential expression of particular genes. In a previous report, we demonstrated that despite the genetic heterogeneity of *T. cruzi* strains, DNA microarrays bearing predominantly ESTs of the CL Brener strain – the reference organism of the genome project - are a valid tool for comparative genomics and analysis of gene expression in this parasite (Baptista *et al.* 2004). In the present study DNA microarrays were used for comparative gene profiling of strains isolated from individuals presenting the indeterminate and cardiac forms of Chagas disease (three strains of each group derived from the same endemic area). To identify DNA sequences differentially expressed between the two groups we used as premise to select the genes up regulated or down regulated in the 3 cardiac strains when compared with the 3 asymptomatic strains. For statistical analysis of the data, we developed a method called BayBoots, a non-parametric Kernel and Bayesian Bootstrap (Vêncio *et al.*, submitted). We concluded that 10 probes were up regulated in the cardiac strains and 4 probes, up regulated in the asymptomatic strains. Fifty percent of the sequences had no similarity in public databases. The differential transcription of the genes was investigated by Northern blot. One of the probes encoding the sequence of one component of the mitochondrial electron-transport chain showed cardiac/asymptomatic microarray hybridization ratios of 20-30. Studies are in progress to characterize this component. It is anticipated that the genetic markers differentially expressed may be of potential use in diagnostic/prognostic tests and could assist the understanding of the pathogenesis of Chagas disease. **Support: FAPESP and CNPq**