

HOST RESPONSE TO TRYPANOSOMA CRUZI: TRANSCRIPTOME ANALYSIS OF A CARDIOMYOCYTE MURINE MODEL

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Trypanosoma cruzi is a parasite able to invade and infect a wide variety of cell types and host species. One of the main targets in the mammalian host is the cardiac tissue, and one of the main pathologic alterations is cardiac failure by cardiomegalia. We are studying the transcriptome changes on a murine cardiomyocyte model by microarray analysis. Previous analyses using a Genechip[®] microarray, containing about one third of the genome, provided a startpoint for the transcriptome description. In order to gain further insights, we performed experiments using a whole-genome microarray, with more time points (n=7), and evaluating the host response to trypomastigotes derived from Vero cells (blood trypomastigote-like) and from TAU medium (metacyclic trypomastigote-like). With these data, we were able to identify a large number of differences in gene expression, significantly increasing the actual knowledge about whole-transcriptome host cell response to *Trypanosoma cruzi* infection. More important, a smaller, but extremely interesting, set of genes was identified, related to the differences in host response to blood and metacyclic trypomastigotes, including genes related to TNF- α and TGF- β pathways. The influence of these differences in infectivity will be evaluated.

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