DIFFERENTIAL GENE EXPRESSION ANALYSIS OF PRIMARY CULTURE OF SKELETAL MUSCLE CELLS INFECTED WITH *TOXOPLASMA GONDII* TACHYZOITES

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Microarray analysis is a powerful technique to investigate changes in gene expression occurring during an infectious process. This work aims to study the interaction between a host cell using skeletal muscle cells from primary culture infected with tachyzoites of *Toxoplasma gondii.* We have selected genes modulated in the infectious process using two different analysis methods (Li-Wong and gcRMA). Comparative analysis with previously published work (BLADER *et al.* 2001) showed a good correlation between both datasets. We have observed 42 differentially expressed genes (DEG) at 30 minutes, 95 (DEG) at 4 hours and 631 (DEG) at 24 hours of infection, after a selection based in statistical (5% FDR) and fold change (>=1.75) criteria. The comparison between the selected genes and gene interaction information were used to select several protein networks modulated during the infection, including vesicles and vesicle mediated transport, inflammatory response and apoptosis genes. These data provide new insights into the *Toxoplasma* infection, in particular with cells where the cystogenesis *in vivo* occur.