

Systems Biology Research Symposium

Oral Presentation Session

Grand Ballroom
Tuesday, June 5th
7:00-8:30pm

Gene Network Analysis During Early Cellular Infection by *Trypanosoma cruzi*

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Gene network analysis of cellular infection by *Trypanosoma cruzi* will facilitate the identification of molecular signatures caused by this human pathogen and will advance the understanding of the global molecular pathogenesis involved in Chagas disease, thus allowing development of new means for intervention. We studied the global regulation of cellular gene transcription during the early process of infection. We analyzed the expression of all cellular genes in a human epithelial cell line during the early entry process of *T. cruzi*. Our results indicate that during early trypanosome entry into a human epithelial cell, the trypanosome regulates the expression of approximately 0.4% of the genes of the cell. We identified the early genes and their known upstream 'regulators' and downstream 'targets' by signal network analysis. Our transcriptome level results were verified by Real-Time PCR. A novel selected biological pathway was identified which will facilitate a deeper understanding of the parasite's infection process. Moreover a set of cellular genes, which are required for trypanosome infection as evidenced by RNA-interference, was also identified. Furthermore, we identified the cellular genes that the trypanosome silences in order to evade the innate immune response and rapidly establish itself intracellularly. Our results identified the early cellular signature in a human epithelial cell caused by *T. cruzi* entry.

Key words: *Trypanosoma cruzi*, gene network analysis, transcriptome, gene regulation, cellular infection