Omics approaches for the study of Chagas Disease

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Chagas disease is caused by the protozoa parasite Trypanosoma cruzi, being an important cause of morbidity and mortality in South and Central Americas. As an early branched eukaryote, T. cruzi has several peculiar characteristics, mainly related to its gene expression regulation, which occurs largely post transcriptionally. Aiming to deepen and enlarge the scientific knowledge about its molecular biology, focusing in the parasite, host-parasite relationship and Chagas disease causality, we have initiated an extensive project of high-throughput characterization of T. cruzi molecular biology, using novel technologies, as micro arrays, liquid chromatography coupled to mass spectrometry and next generation sequencing, in order to obtain broad maps of diverse representations of biological information, producing an “omics” view of the parasite and the disease associated. A large dataset comprising results from genomics, transcriptomics, proteomics, interatomics and ribonomics approaches is being constructed, which provides several clues and targets for further specific researches. Besides that, a coding region collection of all T. cruzi genes, named ORFeome, is being produced and will provide an invaluable tool for high throughput functional characterization. The advent of next-generation sequencing enables the analysis of several aspects of gene expression regulation, which, influenced mainly by the broadness and precision of the data obtained, allows us to construct a better representation of how gene expression regulation works post transcriptionally. Nevertheless, the main benefit of these “omics” datasets is their integration into a broader, more holistic, representation of how biological systems work, in what is now called Systems Biology. This is a relative new field, of actual relevance, with several challenges, which will be solved by the integration of biological, mathematical, statistical and computational experiences.

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