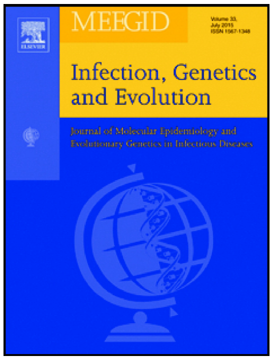

RNA-seq in kinetoplastids: A powerful tool for the understanding of the biology and host-pathogen interactions

Luz Helena Patino, Juan David Ramírez

PII: S1567-1348(17)30045-X
DOI: doi: 10.1016/j.meegid.2017.02.003
Reference: MEEGID 3065

To appear in: *Infection, Genetics and Evolution*

Received date: 18 October 2016
Revised date: 1 February 2017
Accepted date: 2 February 2017

Please cite this article as: Luz Helena Patino, Juan David Ramírez , RNA-seq in kinetoplastids: A powerful tool for the understanding of the biology and host-pathogen interactions. The address for the corresponding author was captured as affiliation for all authors. Please check if appropriate. Meegid(2017), doi: 10.1016/j.meegid.2017.02.003

RNA-Seq in kinetoplastids: A powerful tool for the understanding of the biology and host-pathogen interactions

Luz Helena Patino[a], Juan David Ramírez[a]*

[a] Grupo de Investigaciones Microbiológicas-UR (GIMUR), Programa de Biología, Facultad de Ciencias Naturales y Matemáticas, Universidad del Rosario, Carrera 24# 63C-69, Bogotá, Colombia

*Corresponding author:
Address: Carrera 24 # 63C - 69, Bogotá, Colombia
Telephone number: +57-1-297 0200 Ext: 4033
E-mail address: juand.ramirez@urosario.edu.co

Abstract

The kinetoplastids include a large number of parasites responsible for serious diseases in humans and animals (*Leishmania* and *Trypanosoma brucei*) considered endemic in several regions of the world. These parasites are characterized by digenetic life cycles that undergo morphological and genetic changes that allow them to adapt to different microenvironments on their vertebrates and invertebrates hosts. Recent advances in ´omics´ technology, specifically transcriptomics have allowed to reveal aspects associated with such molecular changes. So far, different techniques have been used to evaluate the gene expression profile during the various stages of the life cycle of these parasites and during the host-parasite interactions. However, some of them have serious drawbacks that limit the precise study and full understanding of their transcriptomes. Therefore, recently has been implemented the latest technology (RNA-seq), which overcomes the drawbacks of traditional methods. In this review, studies that so far have used RNA-seq are presented and allowed to expand our knowledge regarding the biology of these parasites and their interactions with their hosts.

Keywords: transcriptome, transcriptomics, RNA-Seq, microarrays.