Data in Brief 20 (2018) 978–980

Contents lists available at ScienceDirect

Data in Brief

journal homepage: www.elsevier.com/locate/dib

Data Article

Differential expression analysis of transcriptome data of *Trypanosoma brucei* RBP6 induction in procyclics leading to infectious metacyclics and bloodstream forms *in vitro*

Huafang Shi, Kiantra Butler [1], Christian Tschudi [*]

Department of Epidemiology of Microbial Diseases, Yale School of Public Health, 60 College Street, New Haven, CT 06520, USA

ARTICLE INFO

Article history:
Received 25 July 2018
Accepted 27 August 2018
Available online 1 September 2018

ABSTRACT

We used an *in vitro* system based on the inducible expression of the RNA binding protein 6 (RBP6) to monitor transcriptome changes during the differentiation of *Trypanosoma brucei* from non-infectious procyclics to infectious metacyclics and from metacyclics to bloodstream forms. This data file describes the bioinformatics analysis of 20 distinct RNA-Seq samples, with four biological replicates each, highlighting differential transcript abundance. Additional functional annotation analysis using Gene Ontology is also presented. Complete raw data files were deposited at the NCBI Sequence Read Archive – SRA at http://www.ncbi.nlm.nih.gov/Traces/sra/sra.cgi with accession numbers: SRP153824, SRP153562, and SRP152737.

DOI of original article: https://doi.org/10.1016/j.molbiopara.2018.07.011
* Corresponding author.
E-mail addresses: huafang.shi@yale.edu (H. Shi), nhw7@cdc.gov (K. Butler), christian.tschudi@yale.edu (C. Tschudi).
[1] Present address: Division of Scientific Resources, National Center for Emerging and Zoonotic Infectious Diseases, Centers for Disease Control and Prevention, 1600 Clifton Road, Atlanta, GA 30329, USA.

https://doi.org/10.1016/j.dib.2018.08.169

Specifications Table

Subject area	Biology
More specific subject area	Molecular Parasitology
Type of data	Tables and raw data
How data was acquired	High-throughput sequencing carried out by The Yale Center for Genome Analysis (YCGA) using an Illumina HiSeq 2500.
Data format	Raw, analyzed
Experimental factors	RNA isolation, cDNA library construction and sequencing
Experimental features	Total RNA was extracted from time course samples. Library preparation and sequencing was performed by YCGA. Analysis was carried out in-house.
Data source location	New Haven, Connecticut, USA
Data accessibility	RNA-Seq data from this study have been submitted to the NCBI Sequence Read Archive – SRA at http://www.ncbi.nlm.nih.gov/Traces/sra/sra.cgi with accession numbers: SRP153824, SRP153562, and SRP152737.
Related research article	A single-point mutation in the RNA-binding protein 6 generates *Trypanosoma brucei* metacyclics that are able to progress to bloodstream forms in vitro Huafang Shi, Kiantra Butler[1] and Christian Tschudi* Department of Epidemiology of Microbial Diseases, Yale School of Public Health, 60 College Street, New Haven, Connecticut 06520, USA. [1] Present address: Division of Scientific Resources, National Center for Emerging and Zoonotic Infectious Diseases, Centers for Disease Control and Prevention, 1600 Clifton Road, Atlanta, GA 30329, USA. *Corresponding author at: Department of Epidemiology of Microbial Diseases, Yale School of Public Health, Boyer Center for Molecular Medicine 136C, 295 Congress Avenue, New Haven, Connecticut 06536, USA. Tel.: +1 203 785 7332. E-mail: christian.tschudi@yale.edu Molecular and Biochemical Parasitology, 224 (2018) 50-56.

Value of the data

- This is the first transcriptome analysis of *Trypanosoma brucei* differentiation from procyclics to metacyclics and from metacyclics to bloodstream forms.
- The differential expression analysis provides a data source for the understanding of how *Trypanosoma brucei* becomes infectious.
- The transcriptome changes might in the future lead to a better understanding how metacyclic to bloodstream form differentiation is orchestrated.

1. Data

This data consists of 20 high-throughput sequencing samples with four biological replicas each of wild-type RBP6 and mutant RBP6 (Q109K) induced for 6 and 5 days, respectively. In addition, metacyclics from the mutant RBP6 induction were transformed into bloodstream forms over an 11-day period. Raw data is available through NCBI's Sequence Read Archive through the direct link http://www.ncbi.nlm.nih.gov/sra? with accession numbers: SRP153824, SRP153562, and SRP152737.

2. Experimental design, materials, and methods

2.1. Experimental design

RBP6 (Tb927.3.2930) was inducibly expressed in the *Trypanosoma brucei* Lister 427(29-13) procyclic strain as described [1,2]. Metacyclics were purified at room temperature on zirconia/silica beads columns [3]. Purified metacyclics were cultured in bloodstream form conditions at 37 °C.

Total RNA was prepared from 2×10^7 procyclics, purified metacyclics, and bloodstream form cells with the TRIzol reagent (Invitrogen) according to the manufacturer's instructions. Four independent samples, i.e., biological replicas, were prepared from each life cycle stage and from each time point in a time course and isolation of poly(A)$^+$ mRNA, library preparation and sequencing on an Illumina HiSeq. 2500 platform were performed at the Yale Center for Genome Analysis. 75 nt long reads were mapped to the *T. brucei* 11 megabase chromosomes (GeneDB version 5) using the Lasergene 14.1.2 software package from DNASTAR as described [1]. Reads assigned per kilobase of target per million mapped reads (RPKM) was used for normalization and only open reading frames were used for the calculation of RPKM values. Differential gene expression analysis was done with the Lasergene software package from DNASTAR [1] and the Gene Ontology (GO) enrichment tool on the TriTrypDB webserver (http://tritrypdb.org/) was used to analyze the differentially expressed genes for functional annotation and GO terms were condensed by submitting to REVIGO [4].

Acknowledgments

This work was supported by the National Institutes of Health (http://www.nih.gov) [Grant numbers AI028798 and AI110325].

Transparency document. Supporting information

Transparency document associated with this article can be found in the online version at https://doi.org/10.1016/j.dib.2018.08.169.

Appendix A. Supporting information

Supplementary data associated with this article can be found in the online version at https://doi.org/10.1016/j.dib.2018.08.169.

References

[1] R. Christiano, N.G. Kolev, H. Shi, E. Ullu, T.C. Walther, C. Tschudi, The proteome and transcriptome of the infectious metacyclic form of Trypanosoma brucei define quiescent cells primed for mammalian invasion, Mol. Microbiol. 106 (2017) 74–92.

[2] N.G. Kolev, K. Butler, G.A. Cross, E. Ullu, C. Tschudi, Developmental progression to infectivity in Trypanosoma brucei triggered by an RNA-binding protein, Science 338 (2012) 1352–1353.

[3] K. Butler, E. Ullu, N.G. Kolev, C. Tschudi, Synchronous expression of individual metacyclic variant surface glycoprotein genes in Trypanosoma brucei, Mol. Biochem. Parasitol. 200 (2015) 1–4.

[4] F. Supek, M. Bosnjak, N. Skunca, T. Smuc, REVIGO summarizes and visualizes long lists of gene ontology terms, PLoS One 6 (2011) e21800.