Occurrence of differential alternative splicing in the transcriptome of mice hearts infected with two populations of *Trypanosoma cruzi*

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Since the description of Chagas disease, caused by the protozoan parasite *Trypanosoma cruzi*, the mechanism underlying the parasite tissue tropism has yet to be revealed. Our group has previously shown that different strains of *T. cruzi* (JG and Col1.7G2) had a differential tissue tropism in BALB/c mice upon infection., being JG preferentially found in hearts and Col1.7G2 in other tissues of these animals, especially in the rectum. Transcriptome sequencing (RNA-seq) of mRNA extracted from BALB/c infected hearts (groups: JG, Col1.7G2 and an equivalent mixture of both strains) was compared to non-infected mice and showed a predominance of upregulated genes in Col1.7G2-infected animals. In the other side, JG-infected mice had a great number of downregulated genes. Curiously, the mixture-infected group showed both cases simultaneously. Alternative splicing is a RNA processing in which different exons and introns of the same pre-mRNA may be skipped or retained to produce different mature mRNAs, largely expanding the transcriptome repertoire. Thus, the aim of this study was to evaluate the occurrence of differential alternative splicing in the transcriptome of mice infected with both *T. cruzi* strains. For initial analyses of the transcriptomes, the quality of sequences was accessed with the FastQC software. Subsequently, we performed alignment against the mouse reference genome using the splice-aware aligner, STAR. After alignment, the program Multivariate Analysis of Transcripts Splicing (rMATS) was used for recognition of the main types of alternative splicing patterns namely exon skipping (ES), mutually exclusive exons (MXE), alternative 5′ splice site (A5SS), alternative 3′ splice site (A3SS) and intron retention (RI). Our present result showed that intron retention and exon skipping have less inclusion level in Col1.7G2 and mixture-infected group mice when compared to the control group and only alternative 3′ splice site prevailed in mice hearts with mixed infection. Comparing JG infected mice with the control group only exon skipping have higher inclusion level in the infected group over the others events. In conclusion, we have shown that, in the experimental model of Chagas disease, different *T. cruzi* strains can remodel the splicing pattern of the host and this may be relevant for disease development and the parasite tissue tropism.