عنوان مقاله:

Exploring transcription factors in Echinococcus granulosus

محل انتشار:

بیستمین کنگره بین المللی میکروب شناسی ایران (سال: 1398)

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خلاصه مقاله:

Introduction and Objectives: Recent advantages in Next-generation RNA sequencing (RNA-seq) in Echinococcus species has developed a revolutionary opportunity for an in-depth, genome-wide view of cestodes transcriptome and considerably more advantages in the detection of novel transcripts, allele-specific expression, and alternative splicing in compare with other methods. The rate of transcription of genetic information from DNA to messenger RNA is controlled with transcription factors (TF) by binding these proteins to a specific DNA sequence. Materials and Methods: All proteins sequences of E. granolusus (10,273) was collected from the published genomes of E. granulosus (PRJEB121) in WormBase ParaSite. The FASTA format file was manually uploaded in Animal Transcription Factor DataBase (AnimalTFDB) tool to explore the most comprehensive and accurate information for E. granulosus TFs and cofactors. In order to identify transcription factor in any species, AnimalTFDB does the give-and-take best-hit BLAST between the human and other species with the conditions set as e-value<=1e-4, coverage> =50%, identity> =30%. Results: Exploring the whole proteins sequences of E. granolusus was classified into 379 transcription factors into 56 Family. Interestingly, three TFs, zf-C2H2, Homeobox, and zf-H2C2-2 have the most domain number with 77, 57, and 24 respectively. These TF Family has less domain number in comparison to other organisms, especially the model helminths organism Caenorhabditis elegans with 100 and 86 for zf-C2H2, Homeobox respectively. However, no significant zf-H2C2_2 TFs was predicted in C. elegans. Conclusion: Most zoonotic such as Echinococcus species are regularly exposed to a variety of intermediate and definitive host stress conditions. Therefore, they have developed multipurpose systems like transcription factors for accurate signaling transduction. Therefore, identification of these critical regulatory factors could provide fundamental importance to elucidate nature .biology of parasitic helminths

کلمات کلیدی:

Echinococcus granulosus, Next-generation sequencing, RNA-seq

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