08687 - Sessão de Cartazes I

C.03 - Identification and mapping of Schistosoma mansoni v10 Long Non-Coding RNAs Associated with Oocyte Differentiation Using Public Bulk and Single-Cell RNA-Seq Data

Caio Felipe Freire de Sousa[1,2], T. Souza-Lopes[1,2], A.C. Tahira[1], Sergio Verjovski-Almeida[1,3]
[1]Laboratório de Ciclo Celular, Instituto Butantan (São Paulo, Brasil), [2]Programa Interunidades de Pós-Graduação em Bioinformática, Universidade de São Paulo (São Paulo, Brasil), [3]Departamento de Bioquímica, Instituto de Química, Universidade de São Paulo (São Paulo, SP)

INTRODUCTION: Schistosomiasis, caused by Schistosoma mansoni in the Americas, remains a major health issue with more than 700 million people at risk of infection due to the limitations of Praziquantel, the only available drug, and resistant strains are already reported. LncRNAs regulate essential parasite biology, including reproduction, making them promising therapeutic targets. Previous studies used incomplete genome versions and limited data. OBJECTIVES: This study aims to generate a comprehensive lncRNA catalog by mapping public RNA-Seq data to the improved version 10 S. mansoni genome. We will identify, annotate, and infer potential lncRNA functions across life stages, focusing specifically on their role in oocyte differentiation. MATERIALS AND METHODS: Public RNA-Seq data underwent quality control and STAR alignment to the v10 genome. A hierarchical transcriptome assembly (Ryūtō, StringTie) and annotation (GffCompare) were performed. LncRNA candidates were identified by assessing coding potential (FEELnc, CPC2, CPAT). Functional inference will use differential expression (DESeq2) and co-expression networks (WGCNA). Proximity to histone marks near the 5' transcription start site will help confirm the genomic location of lncRNA candidates. Single-cell RNA-Seq analysis (STARsolo, Seurat) for ovarian cells and experimental validation (WISH) will be integrated in the future. DISCUSSION AND RESULTS: A robust v10 transcriptome was constructed, identifying 14,450 lncRNAs, many novel compared to previous annotations. Preliminary differential expression analyses revealed stage- and sex-specific expression patterns, including 190 newly detected and differentially expressed lncRNAs. Future analysis will integrate bulk, single-cell, and proximity to histone marks to precisely postulate and test a set of lncRNA roles within ovarian cell populations during differentiation. CONCLUSION: This work delivers a robust v10 lncRNA resource for S. mansoni. Subsequent research focusing on multi-omic analysis of ovarian cells and validation will significantly advance understanding of lncRNA function in parasite reproduction, paving the way for identifying novel anti-schistosomal drug targets.

Keywords: parasitology, transcriptomics, neglected diseases
Supported by: Fapesp

08125 - Sessão de Cartazes II

C.04 – PROJECT/PMBQBM - HTLV-1 infection and progression to HAM/TSP: in silico analysis of epitopes and drugs as new therapeutic perspectives

Evely Dantas Borges Lopes[1,2], Aline Cristina Andrade Mota Miranda Mascarenhas[1,2]
[1]Departamento de Bioquímica e Biofísica, Universidade Federal da Bahia (Bahia, Brasil), [2]Departamento de Bioquímica e Biofísica, Programa Multicêntrico de Pós-graduação em Bioquímica e Biologia Molecular (Bahia, Brasil)

INTRODUCTION: HAM/TSP is a progressive neurological disorder characterized by muscle weakness, spasticity, and bladder control issues, affecting approximately 3% of those infected, with a higher prevalence in Brazil. Drug therapies for HAM/TSP are used to reduce inflammation and control disease progression. In recent years, new drugs have been evaluated as therapeutic alternatives. OBJECTIVES: Evaluating drugs for the HAM/TSP treatment targeting different molecular pathways and identifing potential linear and conformational epitopes in HTLV-1 regulatory proteins associated with HAM/TSP manifestation. MATERIALS AND METHODS: The three-dimensional structures of molecular targets and drugs, used in the treatment of HAM/TSP, will be identified from scientific databases. The structures of molecular targets will be obtained from the PDB database, while ligands will be selected from PubChem, DrugBank, and ZINC 15. Molecular docking will be performed using AutoDockTools 1.5.7 and GOLD and molecular targets and ligands will be prepared. Molecular dynamics simulations will be conducted in CHARMM-GUI, and trajectory analyses will be performed using VMD. Epitope prediction will be carried out using complete HTLV-1 genome sequences available in public databases through the online tool IEDB 2.21. Additionally, MOE and SPARTAN software will be used for pharmacophore modeling. DISCUSSION AND RESULTS: Unveil new therapeutic targets and provide a deeper understanding of the clinical manifestation, treatment, pathogenesis, and a novel perspective on the repurposing of existing drugs targeting HAM/TSP. CONCLUSION: The findings of this study may contribute to the HAM/TSP understanding, enabling the development of more effective therapeutic strategies. Furthermore, it is expected to open new avenues for drug repurposing and optimization, as well as, the design of novel molecules.

Keywords: HAM/TSP, Molecular docking, Epitopes