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Computational Approaches for Predicting Site Directed miRNAs as Transcriptional Regulators Against HTLV-1 Virus Infection

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Abstract

Human T-cell leukemia virus type 1 (HTLV-1) is the first identified carcinogenic human retrovirus, with current estimates suggesting 5 to 10 million people are infected globally, likely an underestimation due to limited data. HTLV-1 transmission occurs mainly through direct contact with cell-rich body fluids such as blood, breast milk, and semen. In this study, we used computational tools (RNA22, RNAhybrid, and miRanda) to predict host microRNAs (miRNAs) that may interact with the HTLV-1 genome. These tools identify miRNA binding sites based on factors such as seed match, conservation, free energy, and site accessibility. Computational studies indicate that has-mir-4487 could be involved in HTLV-1 infection. This was followed by prediction of the binding sites of has-mir-4487 to the tax of HTLV-1 genome. In addition, structural predictions using MC-Fold and MC-Sym were carried out to make predictions of the three-dimensional structure of the miRNA and the target mRNA respectively. Molecular docking simulations were used to confirm the interaction profile between the miRNA and mRNA. All these findings point to the fact that hsa-miR-4487 might be able to bind directly to the mRNA of the HTLV-1 Tax gene, and thus directly suppress its translation and, as a result, reduce the level of Tax protein, which is a key regulator of viral transcription and replication.

Keywords: HTLV-1; Retrovirus; miRNA; RNA22; Docking complex; Tax

1. Introduction

Human T-cell leukemia virus 1, is the only type of oncogenic virus which has been identified so far. HTLV-1 effects 5-10 million people worldwide and lead to other fetal diseases such as adult T-cell leukemia (ATL) (Asigbee et al., 2025; Ernzen & Panfil, 2022). Despite being infected by over 10 million people around the globe, and causing life-threatening diseases in about 10 percent of infected persons, there is no vaccine or any other antiviral agent developed against HTLV-1 (Soriano & de Mendoza, 2024). HTLV-1 can be transmitted via three routes , it can be transmitted from mother to child during breast feeding, through sexual intercourse or through blood transfusion (Itabashi et al., 2023).

HTLV-1 has a single-stranded RNA genome measuring 8.5 kb in size. The viral particles are spherical in shape, with a diameter ranging from 80 to 100 nm (Kalinichenko et al., 2022). There are long terminal repeats (LTRs) at the 5 and 3 ends which surround the viral genome. HTLV-1 complex retrovirus that encodes not only the canonical structural and enzymatic genes (*gag, pro, pol,* and *env*) required for viral replication, but also a set of accessory genes that are critical to its pathogenesis. The LTRs of HTLV-1 contain key regulatory elements for viral transcription and integration (Lin et al., 2022; Maksimova, 2023). All genes, except Hbz, are transcribed from the sense strand. Tax is a crucial accessory protein that activates the 5′ LTR and is essential for viral transcription and T-cell transformation. Hbz, transcribed from the antisense strand, antagonizes Tax's activity, including its transcriptional activation. Together, Tax and Hbz maintain a regulatory balance vital for HTLV-1's persistence and oncogenicity (Ernzen & Panfil, 2022).

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MicroRNAs are small endogenous single-stranded RNA molecules, that are a part of a group of non-coding RNAs that are involved in the regulation of gene expression (George et al., 2024). miRNAs are 21 to 23 nucleotides in length and, are formed when hairpin loop-like miRNA precursors known as pre-miRNA get processed by the Dicer enzyme (RNase-III). MicroRNA can regulate the expression of the gene armed with mRNA and associated enzyme structures (Bouvier & Palese, 2008). MicroRNAs (miRNAs) function by binding to their target mRNAs, leading to either mRNA degradation or inhibition of translation. To predict the role of various miRNAs in a given cell process, a range of computational approaches has been utilized (Hassan et al., 2024; Li et al., 2010). There is a large number of bioinformatics tools available to perform miRNA analysis, including target prediction packages, like TargetScan and DIANA-microT, viral genome analysis packages, such as Geneious Prime and DNASTAR Lasergene, and differential expression packages, such as DESeq2 and EdgeR. These resources help to determine miRNA sequences and the deduction of their potential targets. Predicting human genes under the regulation of miRNAs that are simultaneously involved in viral replication, it is possible to explore the regulatory role of miRNAs in transcriptional activity during viral infection.

In the present study, a computational framework was employed to predict human miRNAs with the capacity to bind to *Human T-cell leukemia Virus type 1* (HTLV-1) genomic segments and potentially interfere with viral replication. A comprehensive set of human miRNAs was retrieved from publicly available databases and analyzed for potential interactions with the HTLV-1 genome using three established prediction algorithms: RNA22, miRanda, and RNA hybrid. To analyze the binding interactions between viral mRNA nucleotides and human miRNAs that could influence the start of viral replication, the resultant candidate miRNAs were put through molecular docking analyses. Furthermore, molecular dynamics (MD) simulations were conducted to evaluate the stability and conformational dynamics of the docked mRNA–miRNA complexes.

The findings from this in silico approach highlight the potential of specific human miRNAs to act as regulatory agents against HTLV-1 replication. Such miRNAs may serve as promising lead molecules for the development of RNA-based therapeutic interventions or vaccine candidates targeting HTLV-1 infection in future studies.

2. Methodology

2.1. Genome Sequence and Annotations Retrieval

The genomic sequence of *Human T-cell leukemia virus-1* with accession number (NC_001436.1) was obtained from the National Centre for Biological Information (NCBI) (https://www.ncbi.nlm.nih.gov/). CLC Genome WorkBench was used to download the complete annotated genome sequence of HTLV-1.

2.2. Mature miRNA Retrieval from miRbase

The miRbase database (http://www.mirbase.org/) is an accessible resource of previously reported miRNA sequences and annotations. (Kozomara & Griffiths-Jones, 2014). A total of 2654 human miRNAs were recovered from miRbase.

2.3. miRNA Target Site Prediction

Three tools, RNAhybrid (Kozomara & Griffiths-Jones, 2014), miRanda (Doench & Sharp, 2004), and RNA22 (Riffo-Campos Á et al., 2016), were utilized for the identification of potential human-derived miRNA targets in *Human T-cell leukemia virus 1* genome. This was carried out to locate miRNA targeting domains, which will enhance the resistance to HTLV-1 through RNAi.

2.3.1. RNA-hybrid

The first tool we used for our computational analysis is RNA-hybrid. RNA-hybrid is a tool for tracking down the minimum free energy for long and short miRNA. The role of miRNA is to modulate gene targeting by adhering to virus-targeted mRNAs (Macfarlane & Murphy, 2010). The inter-cross is carried out in domain mode, which means that the short sequence is hybridized with the best suited portion of the long sequence. RNA-hybrid works by recognizing outstanding small RNA to large RNA hybridization sites. The default parameters in the RNA hybrid were adjusted in such a way that it will predict the miRNA targeting sites in HTLV-1. Additionally, the GUULGe tool was used to predict the target sites of miRNAs (Gerlach & Giegerich, 2006).

2.3.2. miRanda

miRanda,which is computational tool for miRNA target prediction, was also utilized (Zhao & Xue, 2019). MiRanda uses criteria like the free energy of the RNA-RNA hybrid, the complementarity of the sequence, and cross-species conservation of the target to generate the results, which are a weighted total of match and mismatch scores for bases

that are paired and those with gap penalties. For each base complementarity, miRanda assigns values and penalties, including +5 for G≡C, +5 for A=U, +2 for G=U, and 3 for all other nucleotide matches, as well as +8 for gap opening and 2 for gap augmentation. The known target sites at the first eleven positions are multiplied by a scaling factor (in this case set at 2.0) in order to reproduce the observed 5′-3′ asymmetry. These and other factors are used to calculate the complementarity score between the miRNA and mRNA configurations, which is typically at 3′ UTR (Riffo-Campos et al., 2016).

2.3.3. RNA22

In contrasts to other computational tools, RNA22 (Li et al., 2004; Miranda et al., 2006), uses a pattern-based method together with an evaluation of the folding energy to uncover potential miRNA target sites without the need of a conservation filter for different animal kinds. Even without knowing the name of the targeted miRNA, it is still possible to identify plausible miRNA target sites. The initial step of this program is to examine the sequence of known mature miRNAs. Next, using pattern information from the miRNAs, it predicts the probable target sites. The virus's genome and miRNA served as the input to the RNA22 algorithm, which was available over the web at (cm.jefferson.edu/rna22/Interactive/). One unpaired base was permitted in the seed area with no cap on the number of G:U wobbles, and seed size of 7 was selected. Sensitivity and specificity levels were set at 63 and 61 percent, respectively. The minimum number of paired-up bases was set at 12, and the maximum folding energy was kept at roughly 14 kcal/mol.

2.4. RStudio and Ggplot2

The R language's integrated development environment (IDE), RStudio (https://rstudio.com), is typically used for computations and visualizations. The ggplot2 package was used to illustrate the graphical representations of miRNA predictions (https://cran.r-project.org/web/packages/ggplot2/index.html).

2.5. Conservation Analysis

CLC workbench is a bioinformatics software that enables comprehensive analysis of your NGS data, such as de novo assembly of whole genomes and transcriptomes and resequencing analysis (Krämer et al., 2014). We used CLC workbench for conservation analysis of HTLV-1 between different strains.

2.6. miRNA and mRNA model prediction

An online pipeline designated MC-Fold (https://major.iric.ca/MC-Fold/) and MC-Sym (https://major.iric.ca/MC-Sym/) generates 3D models of miRNAs. MC-Fold takes RNA sequence as an input and produce output in the form of secondary structure whereas A list of tertiary structures is the output of MC-Sym, which receives an input as a set of sequence and secondary structure (Biesiada et al., 2016). The NCBI-retrieved mRNA sequence was used as input for the RNA composer, which predicted the 3D structure of mRNA. Additionally, the miRNA and mRNA models were visualized and their graphical representations were displayed using the Chimera tool (Meng et al., 2006).

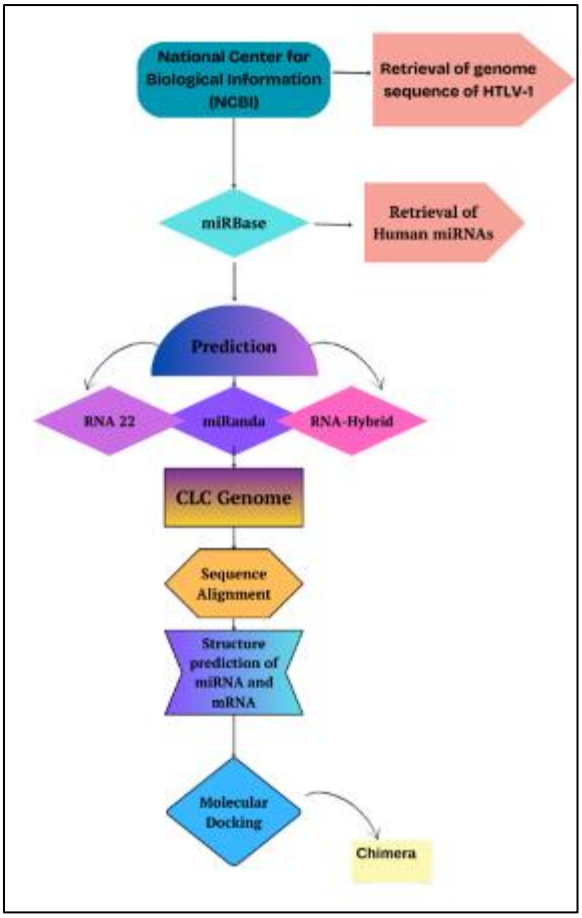

Figure 1 Overview of our research project

2.7. Docking Analysis of Mature miRNA with Target mRNA

The HDock algorithm was employed to check the interactive profile between miRNA and mRNA that was based on flexibility and scoring of docking algorithm (Schneidman-Duhovny et al., 2005). HDock utilizes a geometry-oriented docking algorithm designed to recognize transformations that yield good molecular shape complementarity. Docking results were further assessed using the visualization tools in UCSF Chimera 1.10.1 and Discovery Studio (4.1). Figure 1 shows the steps of our suggested methodology.

3. Results and discussion

3.1. miRNA and genome analysis result

The first step in understanding the biology of miRNAs is to identify their sequence (Saif et al., 2019). Several aspects of miRNA-target interactions were revealed through research and testing, resulting in precise predictions of targeted mRNAs. Analysis of miRNA target recognition provided insights into the principles of miRNA–mRNA duplex formation, including the interactions of hsa-miR-3652, hsa-miR-4487, hsa-miR-765, and hsa-miR-766-5p with the HTLV-1 genome. A deeper knowledge of the role of miRNAs and the prevalence of HTLV-1 might be shown by targeting proteins based on projected miRNAs. The genomic structure of HTLV-1 has been illustrated in (Figure 2).

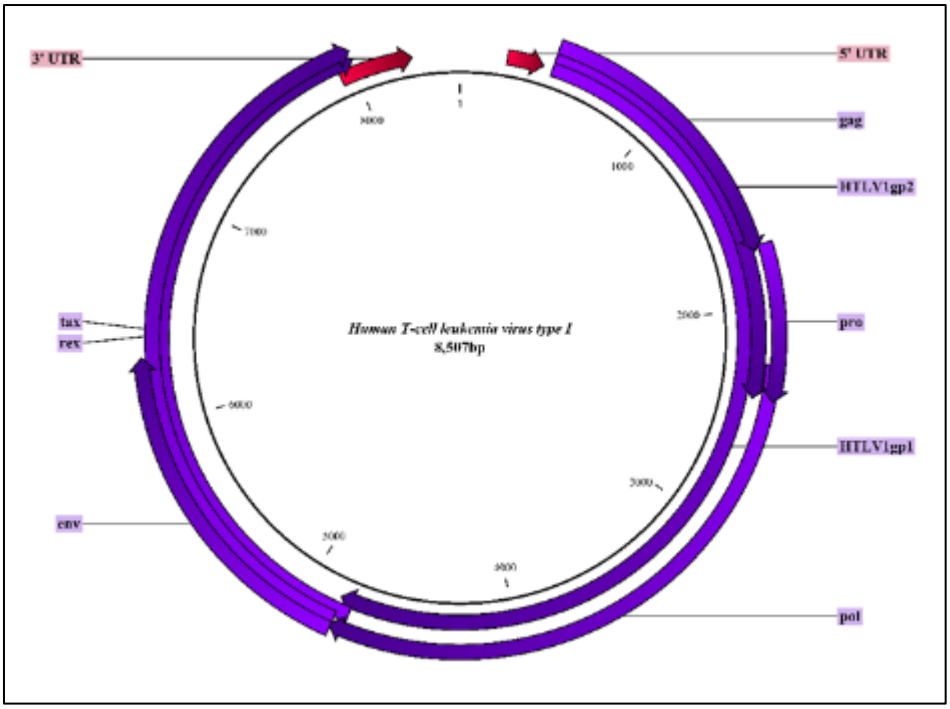

Figure 2 Human T-cell leukemia virus-1 genome

3.2. miRNA target sites prediction results

According to several studies miRNAs lower the expression of their corresponding target proteins in a variety of ways. The sequestering of mRNA from the translational machinery, reduced ribosome occupancy, induced decapping, induced deadenylation, altered cap protein binding, and RNA degradation are all examples of this. It is widely documented that microRNAs cause the expression of their targets to decline. However, not all functional microRNA interactions result in a decrease in the target gene's expression (Mohr & Mott, 2015). In our computational studies, based on microRNA-mRNA complementarity, we predicted and assessed target sites for 2654 human-derived miRNAs from miRBase (hairpin and genomic position). hsa-mir-3652 (Chr12: 103930425-103930555), hsa-mir-4487 (Chr11: 47400970-47401042), hsa-mir-765 (Chr1: 156936131-156936244), and hsa-mir-766-5p (ChrX: 119646738-119646848) are the genomic positions of four predicted miRNAs.

3.2.1. RNA-hybrid Analysis

The first method used is RNA-hybrid, which detects sites in 30 UTRs that may create a thermodynamically favorable duplex with a certain miRNA. The predicted binding sites for miRNAs are evaluated using the minimal free energy (MFE) method by RNA-hybrid. Figure 3 demonstrates that locations with MFEs of -35 to -40 kcal/mol and nucleotide positions of 0–2000 bp are the most commonly targeted. Furthermore, the best-predicted target sites are found in the genes gag, pro, pol, enc, rex, and tax.

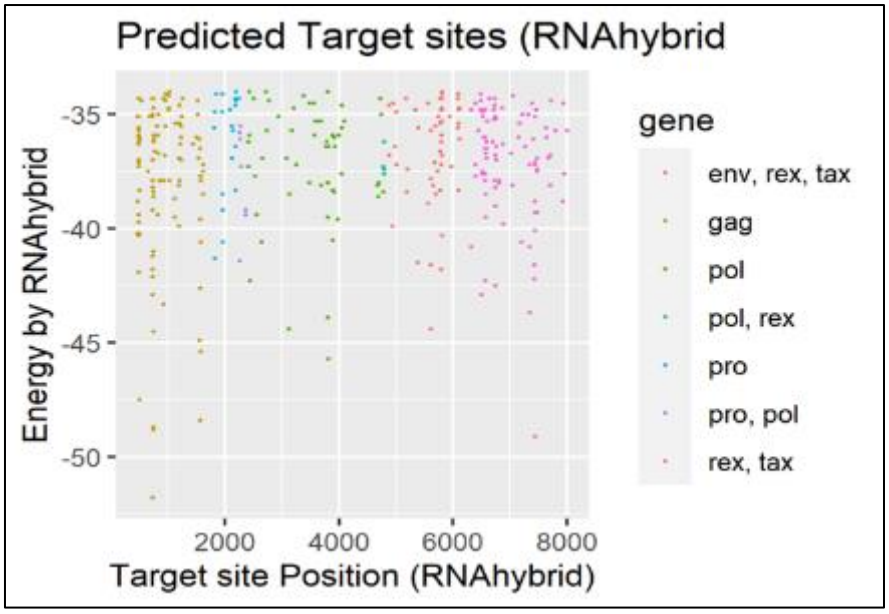

Figure 3 Target sites for miRNAs binding to HTLV-1 genome predicted by RNA-hybrid algorithm. The color dots represent binding to genes coding the relevant proteins

3.2.2. miRanda Analysis

The data was analyzed using MiRanda according to the similarity of miRNA-mRNA sequences, free energy (between 18 and 33 kcal/mol), and score (between 140 and 185). Figure 4 illustrates that places with a free energy of -30 to -35 kcal/mol and a range of nucleotide position 0-8000 bp have the most frequent targeting. Moreover, genes gag, pro, pol, enc, rex, and tax have been of great predictive value to target locations.

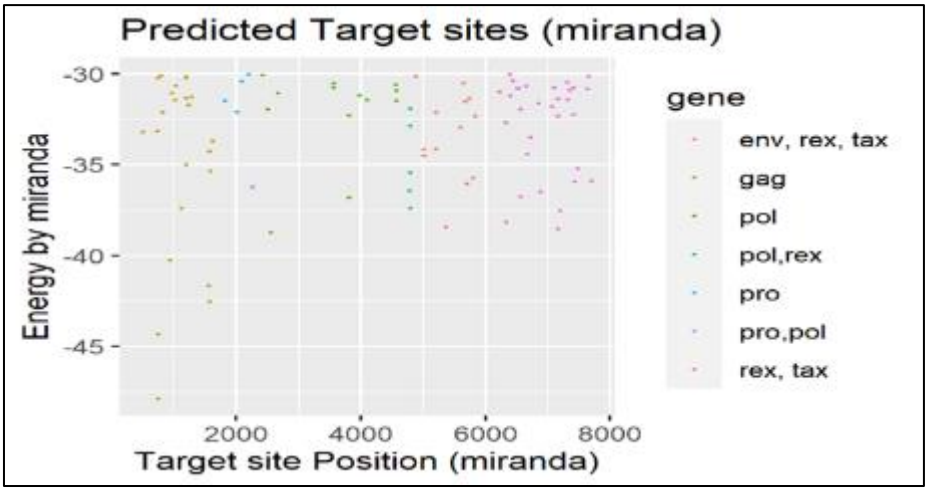

Figure 4 Target sites for miRNAs binding to HTLV-1 genome predicted by miRanda algorithm. The color dots represent binding to genes coding the relevant proteins

3.2.3. RNA22 Analysis

Rna22 is a tool for identifying microRNA binding sites and their corresponding heteroduplexes. RNA22 is resistive to noise, does not rely on cross-species conservation, and, unlike other approaches, detects possible microRNA binding sites in the sequence of interest before identifying the targeted microRNA (Miranda et al., 2006). Figure 5 illustrates commonly targeted sites with folding energies ranging from 30 to 35 kcal/mol and nucleotide positions ranging from 0 to 8000 bp. Furthermore, the best predicted target sites are found in genes gag, pro, pol, enc, rex, and tax.

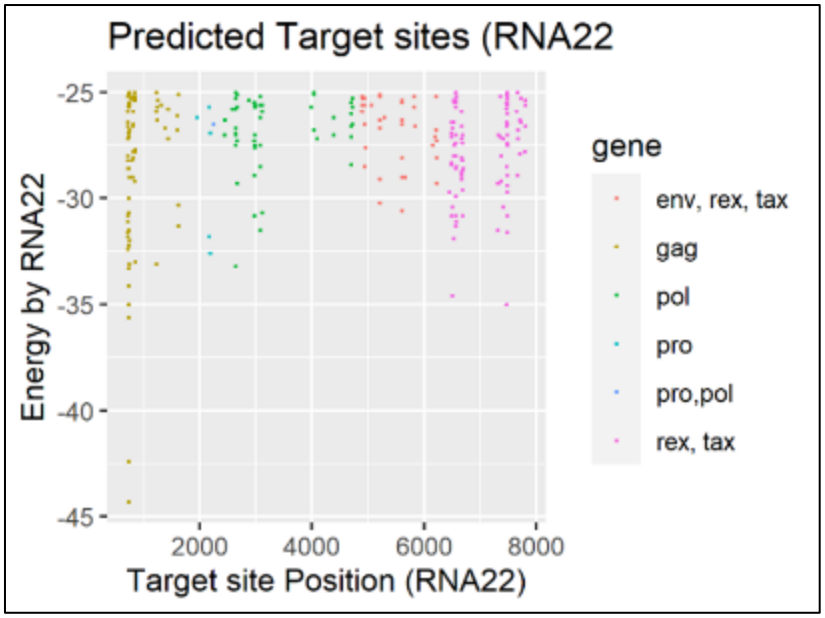

Figure 5 Target sites for miRNAs binding to HTLV-1 genome predicted by RNA22 algorithm. The color dots represent binding to genes coding the relevant proteins

3.2.4. Common miRNA

RNA22, miRanda and RNAhybrid identified 487, 338 and 953 miRNAs that have potential binding sites to the genome of the HTLV-1 and the four most frequent hsa-mir-3652, hsa-mir-4487, hsa-mir-765 and hsa-mir-766-5p, respectively. Moreover, 129 miRNAs were shared in RNA22-miRanda and 234 miRNAs were shared in RNA22-RNAhybrid predictions and 222 miRNAs were shared in RNAhybrid-miRanda predictions respectively in a union graph analysis (Figure 6). Table 2 has reported the common miRNA, as predicted by all the three algorithms. In addition, we have identified several proteins by genes in the HTLV-1 genome, including Env, Gag, Rex, Tax and P8 that have potentially played a critical role in cellular functionality of the HTLV-1(Gross & Thoma-Kress, 2016). Tax has been found to play a direct role in HTLV-1 virus replication cycle (Matsuoka and Jeang, 2011). (Matsuoka & Jeang, 2011). Hsa-mir-4487 and tax mRNA, therefore, may have an interaction that prevents the replication cycle of HTLV-1 and consequently inhibit the infection of HTLV-1.

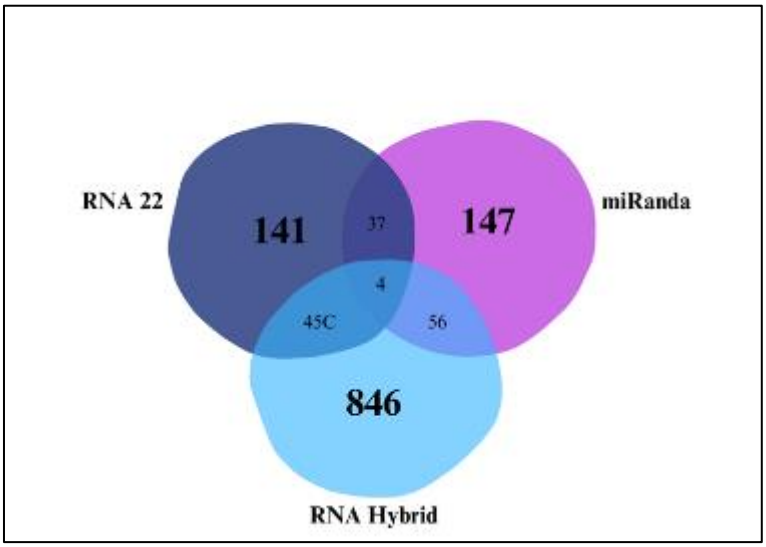

Figure 6 The Venn diagram of miRNAs predicted to bind to HTLV-1 genome by all three different tools: RNAhybrid, RNA22, and miRanda. Four common miRNAs were identified in the intersection graph: hsa-mir-3652 , hsa-mir-4487, hsa-mir-765 and hsa-mir-766-5p respectively

3.3. Target site conservation analysis

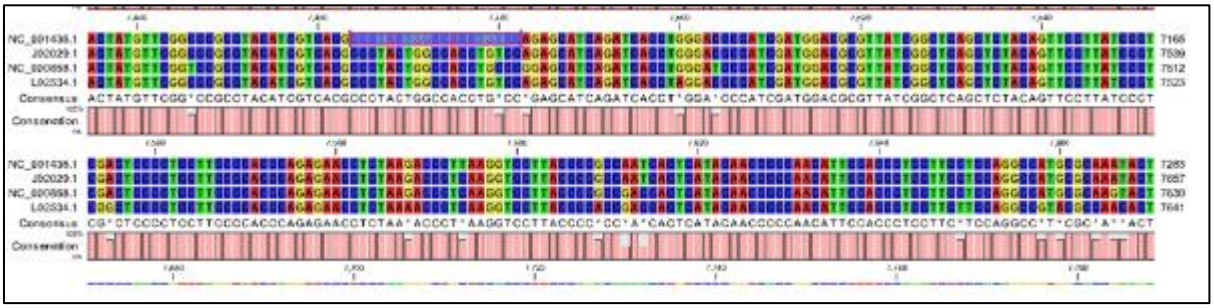

Figure 7 The pattern of target-site conservation in distinct HTLV-1 strains. The target sites are indicated in blue, with bars indicating the extent of conservation at each location. Predicted proteins are involved in the HTLV-1

MiRNA targets are abundant in genes involved in translation regulatory pathways because conserved miRNA target sites are frequently enriched in the 5′ ends of protein-coding genes' 3′ UTRs. (Xiong et al., 2019). Our findings revealed that distinct HTLV-1 strains had conserved nucleotides. This pattern of conservation in Figure 7, shows improved accuracy and reliability of projected miRNAs in other strains.

3.4. HTLV-1–encoded viral proteins and their contribution to the infection process

Our results show that multiple proteins are involved in binding of miRNAs to the HTLV-1 genome.

3.4.1. Env

The Env protein plays a pivotal role in HTLV-1 infectivity by mediating efficient cell-to-cell transmission. It is synthesized as a highly glycosylated precursor that undergoes proteolytic cleavage to generate two functional subunits: the surface (SU) and the transmembrane (TM) proteins. These subunits are subsequently transported to the cell membrane, where they contribute to viral assembly and budding (Hoshino, 2012; Jones et al., 2011). The SU subunit specifically interacts with host cell receptors, including Glut-1, NRP-1, and heparan sulfate proteoglycans (HSPGs), to facilitate membrane fusion between the virus and target cells. Moreover, Env is critically involved in the formation of the virological synapse (VS), thereby enhancing direct cell-to-cell viral spread. Collectively, these functions underscore the indispensable role of Env in both in vitro and in vivo HTLV-1 transmission (Mazurov et al., 2010; Saito et al., 2014).

3.4.2. Gag

The initial protein synthesized by HTLV-1 is a group-specific antigen (Gag, p55), which is a polyprotein. Gag polyprotein is then transported to the inner face of the plasma membrane after undergoing post-translational modifications and myristoylation (Gross & Thoma-Kress, 2016; Lairmore et al., 2011). It is then cleaved to three major functional domains by viral proteins: matrix (MA, p19), capsid (CA, p24), and nucleocapsid (NC, p15). The Gag targeting, membrane association and Env incorporation require the matrix domain. The capsid domain assembles itself into the structural inner core of the virion whereas the nucleocapsid domain attaches to the viral genomic RNA in the inner core. These assembly and budding processes cannot be effectively regulated in space and time to enable efficient HTLV-1 replication and transmission (Gross & Thoma-Kress, 2016; Martin et al., 2016).

3.4.3. Rex

Beyond the well-characterized role of Tax, the regulatory protein Rex is also essential for HTLV-1 propagation. Evidence for its importance comes from two independent lines of research. First, studies using a proviral clone lacking Rex demonstrated a marked impairment in viral transmission within host organisms (Lairmore et al., 2011). Second, the T-cell line C8166-45, which is naturally deficient in Rex, has been shown to neither release viral particles nor maintain infectivity (Paré et al., 2005). Collectively, these observations underscore the pivotal role of Rex in facilitating the export of unspliced and partially spliced viral transcripts, thereby ensuring the efficient production of structural proteins and successful viral dissemination (Lairmore et al., 2011).

3.4.4. Tax

Tax is inarguably the most important viral accessory protein that is engaged in transformation. Tax is a versatile protein that is involved in the control of a variety of pathways and cellular processes. This one viral protein can regulate the expression of viral genes, induce NF-κB signaling pathways, deregulate cell cycle, disrupt apoptosis and cause genomic

instability. The combination of these processes leads to cellular transformation and oncogenesis by the virus. (Ernzen & Panfil, 2022).

3.5. Structure prediction of hsa-mir-4487

The mir-4487 hsa genes are the important ones in our study. The miRNA acts as a guiding signal to the fundamental pairing with the target mRNA to repress its production. Depending on the extent of compatibility between miRNA and mRNA target, the paired miRNAs of mRNA target gene mutation is through transcription repression. In Figure 9, expected 3D structures of hsa-mir-4487 are represented.

Figure 8 The predicted 3D structures of premature and mature hsa-mir-4487. The pink violet color represents immature miRNA and Cyan color represents mature miRNA

Table 1 Precursor and mature sequence of most potential miRNA

miRNA	Precursor miRNA	Mature miRNA
hsa-mir-4487	ACUGUCCUUCAGCCAGAGCUGGCUGAAGGGCAGAAGGGAACUGUCCUUCAGCCAGAGCUGGCUGAAGGGCAGA	AGAGCUGGCUGAAGGGCAG

Table 2 Common miRNA predicted by RNA-Hybrid, miRanda and RNA22 tools

RNA22-miRanda	miRanda-RNA Hybrid	RNA Hybrid-RNA22
hsa-miR-10526-3p	hsa-miR-10526-3p	hsa-miR-10526-3p
hsa-miR-11181-3p	hsa-miR-11181-3p	hsa-miR-11181-3p
hsa-miR-3130-3p	hsa-miR-3130-3p	hsa-miR-3130-3p
hsa-miR-30b-3p(a)	-	-
-	-	hsa-miR-3135b(a)
hsa-miR-3202	hsa-miR-3202	hsa-miR-3202
hsa-miR-3652	hsa-miR-3652	hsa-miR-3652
hsa-miR-4260	hsa-miR-4260	hsa-miR-4260
hsa-miR-4313	hsa-miR-4313	hsa-miR-4313
hsa-miR-4450	hsa-miR-4450	hsa-miR-4450

hsa-miR-4467	hsa-miR-4467	hsa-miR-4467
hsa-miR-4478	hsa-miR-4478	hsa-miR-4478
hsa-miR-4487	hsa-miR-4487	hsa-miR-4487
hsa-miR-4492	hsa-miR-4492	hsa-miR-4492
hsa-miR-6133	hsa-miR-6133	hsa-miR-6133
hsa-miR-615-5p(a)		
hsa-miR-637	hsa-miR-637	hsa-miR-637
-	hsa-miR-658(a)	-
hsa-miR-6748-5p	hsa-miR-6748-5p	hsa-miR-6748-5p
hsa-miR-6880-5p(a)	-	-
hsa-miR-6884-5p(a)	-	-
hsa-miR-6887-5p	hsa-miR-6887-5p	hsa-miR-6887-5p
hsa-miR-765	hsa-miR-765	hsa-miR-765
hsa-miR-766-5p	hsa-miR-766-5p	hsa-miR-766-5p
hsa-miR-7847-3p(a)	-	-
hsa-miR-877-5p(a)		--

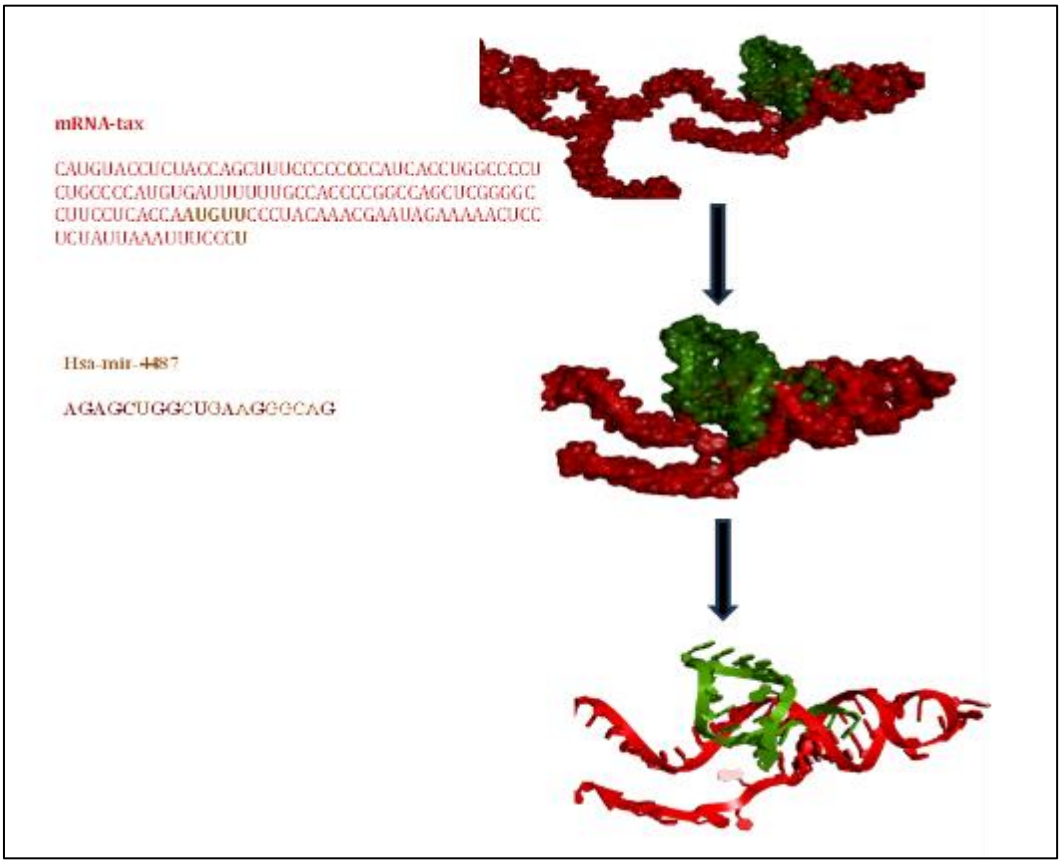

Figure 9 Docking Complex of has-mir-4487

3.6. Molecular Docking Analysis

According to our predictions and literature data, miRNA and the mRNA encoding the tax protein was used in docking procedure to verify the binding conformation of hsa-miR-4487 with mRNA of tax. The hsa-miR-4487 and mRNA 3D structures of tax were examined in detail to clarify the importance of different nucleotides to the bound form. The docking complex has a score of -403 which is the best docking scoring value with the best geometric shape complementarity. Fig. 10 has demonstrated the detailed docking scoring values. The interactions of the non-coding RNAs (e.g. lncRNA; miRNA) with the receptor molecules contain an essential regulatory role in different biological processes (Zhang et al., 2021; Zhao et al., 2023). Thus, their interactive profiles have been predicted by several computational approaches (Sun et al., 2022; Wang et al., 2022). The dynamic interaction of hsa-mir-4487 and hsa-mir-4487 mRNA was studied in detail and our findings reveal that several nucleotides of hsa-mir-4487 interact with the mRNA of Tax. Guanine and adenine (GA) nucleotides 2 and 3 and guanine (G) position 4 were closely interacting with the target mRNA of tax, formed close interactions with the target mRNA of tax. Similarly, cytosine and guanine (CG) at positions 5 and 7, followed by guanine (G) at position 8, also exhibited strong interactions with the receptor. In addition, uracil (U) at position 10 and adenine (A) at position 12 were found to be directly involved in binding with mRNA of tax. Further interactions were observed at the terminal region, where guanine (G) at positions 14 and 19 participated in stabilizing the complex. These results suggest that different regions in mRNA of Tax serve as potential receptor sites, with nucleotides recognizing motifs such as GA, CG, U, and G-rich regions, thereby facilitating stable binding with hsa-mir-4487 (see Fig. 11). According to the docking results, hsa-miR-4487 binding to mRNA-tax may halt the protein's translation and potentially stop HTLV-1 infection. Of undoubtedly, more thorough clinical research is needed to validate our computational predictions.

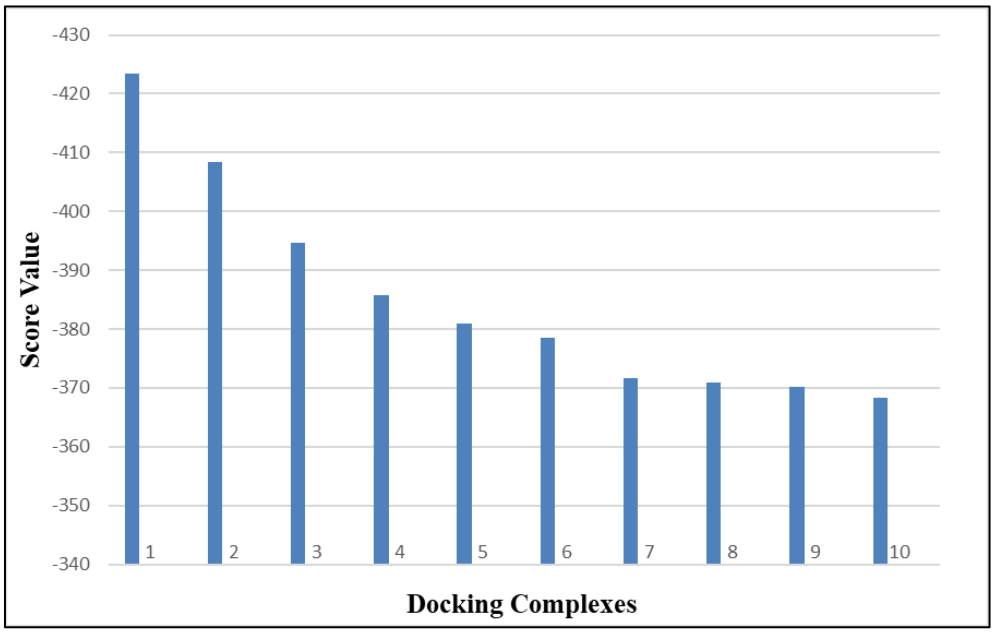

Figure 10 Docking Score values of top complexes 10

4. Conclusion

miRNA-based therapy is a new promising approach including computational modeling against different diseases such as cardiovascular and neurological disorders, tumorigenesis, and viral infections (Ying et al., 2021). The current research represents an in-silico method for detecting miRNAs aimed at silencing the HTLV-1 genome. Our results show that has-mir-4487 exhibits very good binding complementarity with the HTLV-1. Furthermore, several proteins have been predicted as useful targets for the mumps therapeutics. Overall, the tax protein was predicted as having a significant role in the HTLV-1 infection because it is the most important viral accessory protein. In addition, the docking results showed a binding pattern of has-mir-4487 against the mRNA of the tax protein. Our results explore the nucleotide interaction profiles which may play an important role in the inhibition activity of the tax gene transcription. The present work proposes a systematic approach to find the miRNAs by using miRNA target prediction algorithms and aims to silence the virus that affects humans by RNA interference. The identification of therapeutic miRNAs may be ranked among the most revolutionary and exciting therapeutic discoveries for pharmaceutical industry, after successful

completion of several phases of clinical trials. Additionally, a better understanding of miRNA-lncRNA interactions (Wang et al., 2022) will lead in the future to the design of miRNAs based chemical scaffolds and novel vaccines

Compliance with ethical standards

Disclosure of conflict of interest

No conflict of interest to be disclosed.

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