Identification of miRNA-21 from SARS-CoV-2 genome sequence.

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Abstract

Introduction: Severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) is an enveloped RNA virus that's diversely found in humans and is known to infect the neurological, respiratory, enteric, and hepatic systems. The majority of SARS-CoV-2 patients have minor symptoms, but they can deteriorate quickly, especially in the elderly or those with underlying disorders such as chronic lung or cardiovascular disease. There is currently no viable treatment for SARS-CoV-2 patients. Because there are no specific SARS-CoV-2 vaccinations or medications, it is critical to recognize and treat the condition as soon as possible. Interestingly, microRNAs (miRNAs) are important post transcriptional regulators of nearly every organic process which is taking place within the cell. The present study aims to identify the miRNA-21 from SARS-CoV-2 genome sequences available in public genomic databases.
Materials and methods: A computational study on miRNA-21 in SARS-CoV-2 genome sequence was identified using NCBI (National Centre for Biotechnology Information) database. The secondary structure of miR-21 was obtained from the RNAfold web server.
Results: After the careful evaluation of the secondary structure, SARS-CoV-2 genome sequence was obtained with a minimum free energy of -34.60 kcal/mol.
Conclusion: In conclusion, it was found that miR-21 acts as an effective therapeutic target and as a specific biomarker and can help in the diagnosis of SARS-CoV-2. Our study results can provide a theoretical basis for use by other researchers to accelerate the study of SARS-CoV-2. This study shows that miRNAs-21 play a significant role in viral control of several cellular processes seen during the viral infection.

Keywords: miRNA-2, SARS-CoV-2, Bioinformatics, Innovative technique.

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Introduction

Severe Acute Respiratory Syndrome Coronavirus 2 (SARS-CoV-2) is an enveloped RNA virus that's diversely found in humans and they're known to infect the neurological, respiratory, enteric, and hepatic systems. The past few decades have seen endemic outbreaks within the sort of Middle East Respiratory Syndrome Coronavirus (MERS-CoV). Yet again, we see the emergence of another outbreak of a replacement strain called the SARS-CoV-2 virus. The foremost recent outbreak was initially presented as pneumonia of unknown etiology during a cluster of patients in Wuhan, China [1].

The epicenter of infection was linked to food and exotic animal wholesale markets within the city. SARS-CoV-2 is very contagious and has resulted in a rapid pandemic of COVID-19. As the number of cases continues to rise, it's clear that these viruses pose a threat to public health. COVID-19 attacks the body directly from the airborne droplets or from transfer of the virus from your hands to your face. The virus travels to the back of your nasal passages and mucosa in the back of your throat. It attaches to the cell, begins to multiply and moves into lung tissue. From there, the virus can spread to other body regions [2].

Nowadays, human-to-human transmission is considered the most sort of transmission. Individuals who remain asymptomatic could also transmit the virus. Transmission occurs by the spread of aerosols through coughing or sneezing. The majority of SARS-CoV-2 patients have minor symptoms, but they can deteriorate quickly, especially in the elderly or those with underlying disorders such chronic lung or cardiovascular disease. There is currently no viable treatment for SARS-CoV-2 patients. Because there are no specific COVID-19 vaccinations or medications, it is critical to recognize and treat the condition as soon as possible **[3]**.

Interestingly, microRNAs (miRNAs) are small, noncoding RNAs with regulatory functions, which play a crucial role in many human diseases **[4]**. Various studies show that miRNAs can act as both oncogenes and as tumor suppressor genes. Germline, somatic mutations and polymorphisms can contribute to cancer proneness. miRNA expression levels have diagnostic and prognostic implications, and therapeutic agents that are promising and are currently under investigation [5]. Our team has extensive knowledge and research experience that has translate into high quality publications [6-25].

The study aims in identifying the miRNA which can act as an effective therapeutic target and as a specific biomarker and can help in the diagnosis of SARS-CoV-2.

Materials and Methods

In this study we used the bioinformatics approach to identify the miRNAs in the SARS-CoV-2 genome sequence, where the data was collected from publicly accessible databases.

Computational method

Human genome sequence data was obtained through the National Center for Biotechnology Information (NCBI) web portal for International nucleotide sequence database consortium.

The search term keyword "SARS-CoV-2 genome sequence in *Homo sapiens*" was used to extract the SARS-CoV-2 genome sequence using this free search engine. Human mature miRNA were selected out of many entries from miRbase.

After removing the low-quality and redundant sequences, a local nucleotide database was formed for SARS-CoV-2 specific genome sequences. The previously mentioned nucleotide data set was looked for in the homolog among the miRNAs dataset. The mature miRNAs were used as a source to search for similar genome sequences.

The FASTA formats of all sequences were processed and mature miRNA sequences were aligned against the unique genome sequences. Genome sequences were aligned to reference pre-miRNA sequences.

Then the aligned portion was expressed as a candidate pre-miRNA sequence. The secondary structure was then obtained using RNAfold which provided the miRNA expressed in the COVID-19 genome sequence which helped in target prediction, which was done using target scan.

Results

The miRNA identification was performed through computational approach and it is more economical than other methods. After the collection of databases from NCBI and careful evaluation of the secondary structure, hsa-miR-21 was identified in the SARS-CoV-2 genome sequences. The mature sequence was found using an RNAfold is

UGUCGGGUAGCUUAUCAGACUGAUGUUGACUGUUG AAUCUCAUGGCACAACACCAGUCGAUGGGCUGUCU GACA and the minimum free energy were found to be -34.60 kcal/mol. Figure 1 representing the secondary structure of the identified hsa-miR-21

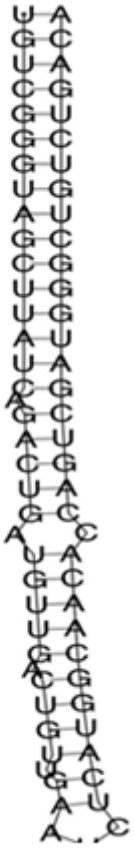

Figure 1. *Representing the secondary structure of the identified hsa-miR-21.*

In addition, miRNA target analysis has been analyzed by the target scan online computational tool to identify hsa-miR-21 (Figure 2).

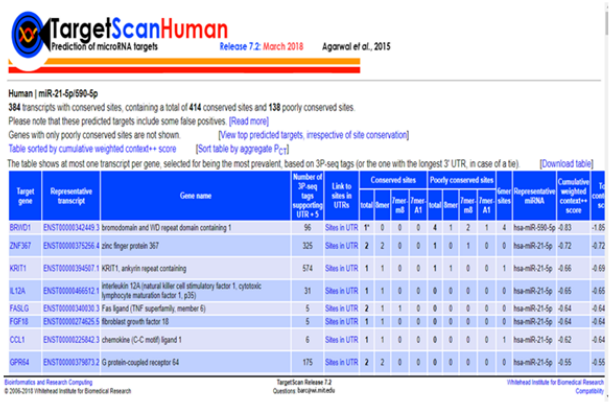

Figure 2. *Representing the target gene of hsa-miR-21.*

Discussion

In the present study has-miRNA-21 in SARS-CoV-2 genome sequences were identified using computational finding and bioinformatics. The identified hsa-miR-21 for SARS-CoV-2 may be used as diagnostic, prognostic and therapeutic targets.

MiRNAs are small, non-coding RNAs with 22 nucleotides that are needed for the translation of mature messenger mRNAs to proteins. Most miRNAs are transcribed into primary miRNAs (pri-miRNAs), precursor miRNAs (pre-miRNAs) and then finally mature miRNAs [26]. MiRNAs show activated gene expression under certain conditions. In many cases, miRNAs interact with the 3' UTR of target mRNAs for suppression and interaction of miRNAs with other regions such as 5' UTR. These miRNAs play a major role in cell proliferation, differentiation, growth and apoptosis. When a virus or any pathogen infects a person, the first immune response is from innate immunity. The miRNAs can also regulate the functions of the various immune cells such as the dendritic cells, epithelial cells, monocytes, granulocytes, and macrophages [27].

MicroRNAs (miRNAs) are important post-transcriptional regulators of nearly every organic process which is taking place within the cell [28]. Thus, miRNAs have rapidly emerged as promising targets for the advancement of novel therapeutics [29].

The coronavirus disease 2019 (COVID-19) pandemic which is caused by the virus called Severe Acute Respiratory Syndrome Coronavirus 2 (SARS-CoV-2) has infected over 59.69 million people worldwide and has led to the deaths of over 1.4 million of the overall world population. The virus was first detected in late-2019 in Wuhan, China, and has spread across the world to 191 countries [30]. Over the past 13 months, much has been discovered about the novel virus; its capacity to infect human host cells, its varying effects on infected individuals and also the dynamics of its transmission from one person to another person [31].

The COVID-19 pandemic is spreading across the world at an alarming rate. It has caused more infections and deaths as compared to SARS or MERS. It's deemed that SARS-CoV-2 is more infectious than SARS or MERS. Elderly and immune compromised patients are at the high risk of fatality. The rapid spread of the disease warrants intense surveillance and isolation protocols to stop further transmission of the disease. No confirmed medication or vaccine has been developed till now. Current treatment strategies are aimed towards symptomatic care and oxygen therapy. Prophylactic vaccination is required for the prevention of COV-related epidemics [32].

Conclusion

It can be concluded that hsa-miR-21 is identified as target miRNA for SARS-CoV-2. Our study results can provide a theoretical basis for use by other researchers to accelerate the study of SARS-CoV-2. This study shows that miRNAs play a significant role in viral control of several cellular processes seen during the viral infection. The activity of the miRNAs-21 can determine the severity of SARS-CoV-2.

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Conflict of Interest

The authors declare no conflict of interest.

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