Journal of science faculty at Sirte University
JSFSU
2021
Peer-review Periodical Journal

جامعة سرت
Sirte University
1989

ISSN INTERNATIONAL STANDARD SERIAL NUMBER

eISSN: 2789-858X

SCIENTIFIC JOURNAL FOR THE FACULTY OF SCIENCE – SIRTE UNIVERSITY

SJFSSJ

DOI: 10.37375/issn.2789-858X - Indexed by Crossref, USA

VOLUME 3 ISSUE 2 OCTOBER 2023

Bi-annual, Peer- Reviewed, Indexed, and Open Accessed e-Journal

Legal Deposit Number@NationaL Library (Benghazi): 990/2021

1.02/2022

jsfsu@su.edu.ly
journal.su.edu.ly/index.php/JSFSU

Scientific Journal for the Faculty of Science-Sirte University Vol. 3, No. 2 (2023) 44-50

Scientific Journal for the Faculty of Science-Sirte University

Journal home page: http://journal.su.edu.ly/index.php/JSFSU/index

DOI: 10.37375/issn.2789-858X

Prediction and Analysis of Targeting Libyan Severe Acute Respiratory Syndrome Corona Virus 2 isolates by Micro-RNA

Marwa E. Elwash, Asma S. Alilish, Saad Aboulkasem, Maab M. Aldeeb and Mona M. Aborwis

Genetics and Biotechnology Department, Science Faculty, Misurata University, Libya.

DOI: https://doi.org/10.37375/sjfssu.v3i2.1595

ARTICLE INFO:

Received: 14 July 2023

Accepted: 09 October 2023

Published: 26 October 2023

Keywords: COVID-19, pandemic, miRNAs, bioinformatics prediction

A B S T R A C T

The COVID-19 pandemic has caused widespread concern, and extensive studies have been conducted to discover an effective therapy for the virus, some of these studies have demonstrated that host miRNAs have antiviral properties and may enhance the treatment of individuals with COVID-19. Host miRNAs are important regulators of virus replication and translation by binding directly to viral RNA. Investigating the interaction between miRNA and SARS-CoV2 can reveal novel therapeutic approaches against this virus. The study analyzed the genomes of seven Libyan SARS-CoV2 isolates and the Wuhan reference strain and used bioinformatics prediction to identify human mature miRNAs that interact with the virus. The study found that 142 lung miRNAs could interact with the viral RNA, and identified several miRNAs with multiple binding sites, including hsa-mir-197-5p and hsa-mir-286-3p. The study also identified miR-138-5p and miR-574-5p as potential therapeutic targets, as they have the ability to bind to the 3'UTR of IFN and ACE2 genes in the host cell. However, the interactions between miRNA and mRNA identified in this study require further experimental validation to confirm their therapeutic potential.

1 Introduction

SARS-CoV2 is an enveloped, positive-sense, single-stranded RNA virus that belongs to the family of coronaviruses. The virus primarily infects the respiratory tract and can cause severe respiratory illness ranging from mild cold-like symptoms to severe acute respiratory syndrome and death. COVID-19 has a high transmission rate and mortality rate, making it a significant threat to global public health. The outbreak of the novel coronavirus disease (COVID-19) caused by (SARS-CoV2) has rapidly spread worldwide, resulting in a global health crisis. Despite extensive efforts by the scientific community, there is currently no specific treatment or vaccine available for COVID-19 (Agarwal *et al.*, 2015). Therefore, there is an urgent need to identify potential therapeutic targets and develop effective treatments against SARS-CoV2. MicroRNAs (miRNAs) are small non-coding RNAs that play a crucial role in regulating gene expression in eukaryotes. Recent studies have shown that host miRNAs can regulate the replication and translation of viral RNA by directly binding to viral RNA (Discovery & Alam, 2021). Investigation into the interaction between miRNAs and SARS-CoV2 can reveal novel therapeutic approaches against this virus. MicroRNAs are small RNA molecules that regulate gene expression by binding to the 3' untranslated region (UTR) of target messenger RNAs (mRNAs), leading to their degradation or translational repression. Recent studies have shown that host miRNAs can also regulate viral replication and translation by direct binding to viral RNA in infected cells(Agarwal *et al.*, 2015).

Corresponding author: **E-mail:** saad_libya@ymail.com

Bioinformatics prediction is a computational approach used to predict the interaction between two or more biological molecules, such as proteins, DNA, RNA, and miRNA. In the case of miRNA-virus interaction, bioinformatics prediction is used to identify potential binding sites between host miRNAs and viral RNA (Identify *et al*., 2020). The prediction is based on the sequence complementarity between miRNA and RNA, particularly in the seed region (positions 2-8) of the miRNA. The seed region is the most important region of miRNA for target recognition and binding, and it requires perfect or near-perfect complementarity with the target RNA to initiate the miRNA-mediated gene silencing process (Identify *et al*., 2020). There are several software programs and databases available for miRNA target prediction, including TargetScan, miRanda, and RNAhybrid, among others. These programs use algorithms to predict the most likely binding sites between miRNA and RNA based on sequence complementarity, thermodynamic stability, conservation, and other factors. However, it is important to note that bioinformatics prediction is not always accurate, and experimental validation is required to confirm the predicted miRNA-virus interactions.

Therefore, bioinformatics prediction should be considered as a preliminary step in identifying potential miRNA-virus interactions, and not as conclusive evidence of their existence(Chauhan *et al*., 2022; Nieto-d *et al*., 2021).

The genomic similarity between SARS-CoV2 and mRNAs suggests the presence of micro-RNA binding sites that could potentially reduce virus expression and translation. Given the lack of specific treatments available for COVID-19 patients, exploring the role of cellular miRNAs in SARS-CoV2 pathogenesis could lead to the development of promising therapeutic options.

Our study is one of the first conducted in Libya to investigate the interaction between human miRNAs and Libyan SARS-CoV2 isolates. However, current treatment options for SARS-CoV-2 remain limited in their safety and efficacy. In this study, we aimed to identify lung epithelial miRNAs that could potentially regulate virus replication and expression in Libyan SARS-CoV2 isolates, as well as host miRNAs that could regulate ACE2 and TMPRSS2.

2 Materials and Methods

2.1 Retrieving SARS-CoV2 Genome Sequences

Seven nucleotide sequences of Libyan SARS-CoV2 isolates were downloaded as FASTA files from National Center for Biotechnology Information (NCBI), with accession numbers (MW018435, MW018429, MW018431, MW018436, MW018428, MW018434, MW018432). These seven viral genomes were detected in Libyan SARS-CoV2 positive nasopharyngeal samples in June 2020 Virus strain isolated in Wuhan, China (NC-045512.2) was also retrieved and considered as the reference viral sequence in this study (Yao *et al*., 2019).

2.2 Obtaining Human miRNAs Sequences

All human mature miRNA sequences were accessed from the miRBase database version 22.1 (Siniscalchi *et al., 2021)*. This study only analyzed high-confidence mature miRNAs that have been reported to have target binding sites or have a role in viral host interaction in peer-reviewed original articles in previous studies.

2.3 MiRNAs Expression in Human Lung Tissue

Selected miRNAs were again filtered to analyze only high-confidence miRNAs that express in the lung epithelial cells which are the main target of the SARS-CoV2. Lung micro-RNA expression data were extracted from the Human miRNA Tissue Atlas (https:// ccb-web.cs.uni-saarland.de/tissueatlas). This is a web-based repository of experimental data collection by microarray analysis for the detection of 1997 microRNAs in 61 tissue biopsies of different human organs (Young *et al*., 2022).

The miRNA that was not found in Human miRNA Tissue Atlas database, was obtained from the Cancer Genome Atlas lung adenocarcinoma (TCGA-LUAD) project utilizing only the matched normal tissue specimen (Zealy *et al*., 2017), this database is available from the TCGA Research Network database: (https://portal.gdc.cancer.gov/projects/TCGA-LUDA)

2.4 RNA-RNA Interaction Analysis:

To find miRNAs that can bind to viral RNA, two freely available online tools were used as Insilco screening:

RNA Hybrid (https://bibiserv.cebitec.uni-bielefeld.de/rnahybrid), using a cut off parameter for free energy of binding (mfe) ≤ -25kcl/mol (Wong & Saier, 2021), and 150 binding site

per RNApar, no other parameters were modified. The miRNA that binds with the viral genome with 100% seed site complementary was considered (the size of seed 7mer) from nucleotide 2 to nucleotide 8 in the 5` of miRNA sequence.

RNA22 Version 2 (https://cm.je_erson.edu/rna22/Interactive), this prediction tool used to identify microRNA region elements (MREs) in the viral genome to miRNAs that showed considered targets in the RNA hybrid tool results. Only significant miRNA- MRE prediction ($P<0.05$) with a seed size of 7 nucleotides and no unpaired base were registered (Wong & Saier, 2021).

3 Results

3.1 Libyan SARS-CoV$_2$ Isolates Have Numerous Human miRNAs Binding Sites

The miRBase database version 22.1 was used to identify human mature miRNAs with direct binding sites on different coronavirus isolates from different geographical regions worldwide (Table 1). Only 228 high confidence miRNAs were identified based on the criteria in miRBase. From these high confidence ones, 219 were found expressed in lung epithelial cells according to the human microRNA Atlas database and TCGA-LUAD project. The study focused on miRNAs showing interactions with perfect matching in the seed region with free energy $\Delta G \leq 25$kcal/mol. A total of 142 miRNAs were sorted out by RNA hybrid tool. According to the results, there were 38 miRNAs with more than three binding sites on the seven analyzed Libyan coronavirus 2 isolates. Among them, eight showed more than 7 target hits, namely: (hsa-mir-149-3p, hsa-mir-103-3p, hsa-mir-4676-5p, hsa-mir-143-5p, hsa-mir-3619-5p, hsa-mir-296-3p, hsa-mir-885-3p, hsa-mir-197-5p). Notably, the hsa-mir-197-5p and hsa-mir-286-3p revealed the greatest number of interactions (12 and 11 sites respectively) with SARS-CoV2 (table 2).

The position of binding sites on the analyzed SARS-CoV2 for high confidence lung miRNAs was also explored and it was noticed that the predicted targets occurred in various locations in the genome, including genes encoding structural proteins as well as non-structural proteins coding genes (Nsps). In this study, out of the four structural protein genes (E, M, N, S) in COVID-19 genome, S gene is the most targeted gene as it is the largest structural gene followed by N gene and then M gene. Only one high-confidence human miRNA (hsa-mir199a-3p) targets E gene.

Out of the 16 Nsps of SARS-CoV2, RNA hybrid tool predicted (most targets on Nsp3 and Nsp2 then Nsp4, Nsp6-10). No hits were predicted on Nsp1, Nsp5 and Nsps11-16; again, the numbers of targeting sites appeared to be correlated with the gene length.

Additionally, the predicted targets of the human miRNAs on viral genomes were not restricted to gene bodies; three miRNA (hsa-mir-4684-3p, hsa-mir-4786-3p and hsa-mir-3614-5p) were found targeting 5` untranslated region with ΔG -27, -30.1 and -30,1 respectively. No high confidence miRNA was predicted to target viral 3` UTR with 100% complementary in seed site region and $\Delta G \leq 25$ kcal/mol in this study. The target sequence identified by two predictive tools RNA hybrid and RNA22 were then filtered to consider only the position targets that were validated by both tools in all seven tested COVID strains. This selection yielded 11 high confidence lung miRNAs with more validated targets (table 3). Four targeted (ORF1ab), which encoding 5` viral replicase, one target spike protein which responsible for attachment to ACE2 receptor for host cell entry, one targeted (ORF7a) which encoding transmembrane protein involved in apoptosis induction and five miRNA targeted N gene which responsible for form viral nucleocapsid.

3.2 miRNAs Viral Genome Interaction and mRNA Entry Receptor Interaction

Given that viral entry is crucial for the infectivity and pathogenesis of SARS-CoV2, this research investigated the ability of predicted miRNAs (53 miRNAs) that have been reported to target the 3'UTR of host receptor proteins ACE2 and TMPRSS, as well as their upstream regulator IFN genes, to bind to SARS-CoV2 genomes.

Remarkably, the binding prediction tool revealed that hsa-mir-138-5p, which can bind to the 3'UTR of the INF-beta gene, has six binding sites on SARS-CoV2. Additionally, hsa-mir-574-5p, which binds to the 3'UTR of the ACE2 gene, has four binding sites in the viral genome.

Table (1): Description of Libyan SARS-CoV2 isolates that analyzed in this study

Isolates	Gene-Bank Accession number	Gender	Age	Origin	Date	Super spreader cluster
1	MW018435	F	50	Tripoli	04 June 2020	SS_1
2	MW018429	F	35	Tripoli	19 June 2020	SS_1
3	MW018431	F	40	Tripoli	15 June 2020	SS_1
4	MW018436	ND	ND	Sabha	ND	SS_1
5	MW018428	M	47	Tripoli	ND	SS_1
6	MW018434	M	4	Tripoli	ND	SS_1
7	MW018432	M	47	Tripoli	13 June 2020	SS_1

*F: Female, M: Male, ND: no data available.

Table (2): MiRNAs with more than 3 binding site on the four SARS-CoV2 genomes

N	miRNA ID	Number of binding sits	N	miRNA ID	Number of binding sits
1	Hsa-miR-199a-3p	5	20	Has-miR-365a-5p	6
2	Hsa-miR-93-5p	5	21	Has-miR-550a-5p	4
3	Hsa-miR-135a-3p	4	22	Has-miR-3065-3p	4
4	Hsa-miR-3619-5p	9	23	Has-miR-3130-3p	4
5	Hsa-miR-330-3p	5	24	Has-miR-4676-5p	8
6	Hsa-miR-103a-3p	8	25	Has-miR-4687-5p	4
7	Hsa-miR-3189-3p	4	26	Has-miR-17-5P	5
8	Hsa-miR-17-3p	5	27	Has-miR-214-3p	4
9	Hsa-miR-3194-5p	5	28	Hsa-miR-197-5p	12
10	Hsa-miR-29c-3p	5	29	Has-miR-5001-3p	7
11	Hsa-miR-4684-3p	4	30	Hsa-miR-494-5p	6
12	Hsa-miR-29a-3p	5	31	Has-miR-15b-5p	5
13	Hsa-miR-143-5p	9	32	Hsa-miR-323b-5p	7
14	Hsa-miR-4786-3p	6	33	Hsa-miR-296-3p	11
15	Hsa-miR-6834-5p	4	34	Hsa-miR-323b-5p	7
16	Hsa-miR-760	5	35	Hsa-miR-296-3p	11
17	Hsa-miR-107	7	36	Hsa-miR-885-3p	11
18	Hsa-miR-574-5p	4	37	Hsa-miR-149-3p	8
19	Has-miR-29b-3p	5	38	Has-miR-138-5p	6

Table (3): MiRNAs that binds in the same position in the two prediction tools

Human miRNA	Target position (RNA hybrid)	Mfe And P-value	Lung repression copy per million	miRNA-mRNA paring
Has-miR-4676-5p	4762	-27.7 P = 0.05	20،31631	AAACCATCTCACTTGCTGGTTC || |||||: :||||:|| AGTGACAGAGTGG-TGACCGAG
Has-miR-4687-5p	440	-30.0 P = 0.03	16228،47	AACTGC-ACCTC--ATGGTCA |||| |||| |::|:|| CGGACGGGGGAGGTTGTCGGT
Has-miR-197-5p	3010	-31.7 P = 0.007	29739	ATATGTATTGTTCTTTCTACCCT : :|:||::||:|||||| GGAGGGTGACGGGAGAGATGGG C
Has-miR-138-5p	23100	-25.8 P = 0.05	3.23564	TGGAAAAACTCAAAACACTAGTT :|| ||| ||||:||: GCCGGACTAAGTGTTGTGGTCGA
Has-miR574-5p	27719	-25.1 P = 0.004	2494،975	TAACACTT-TGC-TTCACACTCA |||||: ::| ||||||| TGTGTGAGTGTGTGTGTGTGAGT
Hsa-miR-3189-3p	29099	-26.4 P = 0.05	7.56629	GTGGTCCAGAACAAACCCAAGGA |: :||| || ||||||| GATGGGGT--AGTCTGGGTTCCC
Hsa-miR-3619-5p	29440	-25.3 P = 0.01	3,82595	ACTGTTACTCTTCTTCCTGCTGC |||: ||: :|| |||||| CGACG-TGGTCGGACGGACGACT
Hsa-miR-514a-3p	2499	-26.6 P = 0.001	0,20335	ACTTCCCACAGAAGTGTTAAC || | |||||||||:|| AGATGAGTGTCTTCACAGTTA
Hsa-miR-502-5p	28436	26.3- P = 0.008	2,45825	AAATTCCCTCGAGGACAAGGCGT T ||| |: |||||:| TGCCAGGATGT--GAGTTCCGTAC
Hsa-miR-4684-3p	29476	-25.8 P = 0.05	4,00759	ATTTCTCCAAACAATTGCAACA ||||| ||||||| TGCAGAGGTGGCTGAACGTTGT
Hsa-miR-219a-1-3p	29506	26.1- P = 0.05	1,064817	ATGAGCAGTGCTGACTCAACTCA :| || | |||||||| GCCCTG-CAGGTCTGAGTTGAGA

4 Discussion

The potential role of miRNAs in regulating host-virus interactions during infections. Host cells can use miRNAs to limit viral replication by targeting viral genomes or transcripts directly or indirectly by modulating host factors involved in the immune response. However, long-standing viral infections can lead to a balance between host and virus, where viruses adapt to coexist with host cells by utilizing mRNA machinery. For example, in HBV infection, the virus-encoded HBx protein up-regulates the expression of miR-125, which inhibits viral replication and allows the virus to evade immunoreceptors and keep host cells alive (Shimakami *et al*., 2012).

In the case of SARS-CoV2, several studies have predicted cellular miRNAs targeting the viral genome, but few have had experimental validation (Hardin & Xiao, 2022; Li *et al*., 2022). This study focused on high-confidence lung miRNAs interacting with Libyan SARS-CoV2 isolates using bioinformatics prediction. The study identified several miRNAs with multiple binding sites, suggesting that these miRNAs may be sequestered during SARS-CoV2 replication, leading to a reduction in their availability, which could disrupt normal pathways regulated by the mRNA (Li *et al*., 2022).

The study identified several miRNAs that may have potential therapeutic applications, including miR-197-5p, which has been associated with defense mechanisms against certain viruses and has been reported to play a vital role either as an oncogene or tumor suppressor in different cancers (Jain *et al*., 2019). MiR-138-5p was predicted to target the IFN beta and ACE genes, and it has experimental evidence of having an antiviral role during HIV infection and acting as a tumor suppressor gene for many types of cancers (Xu *et al*., 2020). Additionally, miR-138-5p targets the EZH2 gene, whose inhibition induces a potent antiviral state and suppresses infection by DNA and RNA viruses.

5 Conclusions

The study found that several lung miRNAs, including has-mir-138-5p and has-mir-197-5p, have the potential to interact with Libyan SARS-CoV2 genomes, with miR-138 also having a potential role in regulating ACE2 expression. However, further in-vitro and in-vivo experiments are needed to validate the potential antiviral activity of these miRNAs.

Disclaimer: The article has not been previously presented or published and is not part of a thesis project.

Conflict of Interest: There are no financial, personal, or professional conflicts of interest to declare.

References

Agarwal, V., Bell, G. W., Nam, J., & Bartel, D. P. (2015). Predicting effective microRNA target sites in mammalian mRNAs.

Arbuckle, J. H., Gardina, P. J., Gordon, D. N., Hickman, H. D., Yewdell, J. W., Pierson, T. C., Myers, T. G., & Kristie, T. M. (2017). Inhibitors of the histone methyltransferases EZH2/1 induce a potent antiviral state and suppress infection by diverse viral pathogens. MBio, 8(4), 1–14.

Chauhan, N., Jaggi, M., Chauhan, S. C., Yallapu, M. M., Valley, G., & Valley, R. G. (2022). Fighting the invisible enemy with microRNAs. Expert Review of Anti-Infective Therapy. HHS Public Access. 19(2), 137–145.

Di, D., & Molecolare, M. (2020). MECHANISMS OF MIR-3189-3P-MEDIATED ANTITUMORAL ACTIVITY IN BREAST CANCER.

S.-R. D., & Alam, T. (2021). miRCOVID-19 : Potential Targets of Human miRNAs in.

Girardi, E., López, P., & Pfeffer, S. (2018). On the importance of host MicroRNAs during viral infection. Frontiers in Genetics, 9(OCT), 1–17.

Hardin, L. T., & Xiao, N. (2022). MiRNAs: The Key Regulator of COVID-19 Disease. International Journal of Cell Biology, 2022(i).

D., Arisan, E. D., Dart, A., Grant, G. H., Arisan, S., Cuhadaroglu, S., Lange, S., & Uysal-onganer, P. (2020). The Prediction of miRNAs in SARS-CoV-2 Genomes : Host Responses and Virus Pathogenicity-Related KEGG Pathways Significant for Comorbidities.

Jain, N., Roy, J., Das, B., & Mallick, B. (2019). miR-197-5p inhibits sarcomagenesis and induces cellular senescence via repression of KIAA0101. Molecular Carcinogenesis, 58(8), 1376–1388.

JC Lovejoy, CM Champagne, L de Jonge, H. X. and S. S. (2008). A Neuron-Specific Host MicroRNA Targets Herpes Simplex Virus-1 ICP0 Expression and Promotes Latency. International Journal of Obesity, 32(6), 446–456.

Ke, X., Zeng, X., Wei, X., Shen, Y., Gan, J., Tang, H., & Hu, Z. (2017). MiR-514a-3p inhibits cell proliferation and epithelial-mesenchymal transition by targeting EGFR in clear cell renal cell carcinoma. American Journal of Translational Research, 9(12), 5332–5346.

Li, C., Wang, R., Wu, A., Yuan, T., Song, K., Bai, Y., & Liu, X. (2022). SARS-COV-2 as potential microRNA sponge in COVID-19 patients. BMC Medical Genomics, 15, 1–9.

Mosca, N., Castiello, F., Coppola, N., Trotta, M. C., Sagnelli, C., Pisaturo, M., Sagnelli, E., Russo, A., & Potenza, N. (2014). Functional interplay between hepatitis B virus X protein and human miR-125a in HBV infection. Biochemical and Biophysical Research Communications, 449(1), 141–145.

Nieto-d, M., Soto, A., Muñoz-galdeano, T., & Reigada, D. (2021). In Silico and In Vitro Analyses Validate Human MicroRNAs Targeting the SARS-CoV-2 3 - UTR.

Orsten, S., Baysal, Yabanoglu-Ciftci, S., Ciftci, T., Azizova, A., Akinci, D., Akyon, Y., & Akhan, O. (2021). MicroRNA expression profile in patients with cystic echinococcosis and identification of possible cellular pathways. Journal of Helminthology, 95.

Reyes-p, P. R., Paul, S., Alberto, L., Bravo, V., Estrada-meza, C., Arturo, R., Alburquerque, A., Pathak, S., Banerjee, A., Bandyopadhyay, A., Chakraborty, S., & Srivastava, A. (2020). Since January 2020 Elsevier

Shimakami, T., Yamane, D., Jangra, R. K., Kempf, B. J., Spaniel, C., Barton, D. J., & Lemon, S. M. (2012). Stabilization of hepatitis C virus RNA by an Ago2-miR-122 complex. Proceedings of the National Academy of Sciences of the United States of America, 109(3), 941–946.

Siniscalchi, C., Di Palo, A., Russo, A., & Potenza, N. (2021). Human MicroRNAs Interacting With SARS-CoV-2 RNA Sequences: Computational Analysis and Experimental Target Validation. Frontiers in Genetics, 12(June), 1–8.

Wong, N. A., & Saier, M. H. (2021). The sars-coronavirus infection cycle: A survey of viral membrane proteins, their functional interactions and pathogenesis. In International Journal of Molecular Sciences (Vol. 22, Issue 3).

Xu, K., Shi, J., Mo, D., Yang, Y., Fu, Q., & Luo, Y. (2020). miR-219a-1 inhibits colon cancer cells proliferation and invasion by targeting MEMO1. Cancer Biology and Therapy, 21(12), 1163–1170.

Yadav, R., Chaudhary, J. K., Jain, N., & Chaudhary, P. K. (2021). Role of Structural and Non-Structural Proteins and Therapeutic Targets of SARS-CoV-2 for COVID-19. Cells, 10(4), 821.

Yang, C. Y., Chen, Y. H., Liu, P. J., Hu, W. C., Lu, K. C., & Tsai, K. W. (2022). The emerging role of miRNAs in the pathogenesis of COVID-19: Protective effects of nutraceutical polyphenolic compounds against SARS-CoV-2 infection. International Journal of Medical Sciences, 19(8), 1340–1356.

Yao, Q., Chen, Y., & Zhou, X. (2019). The roles of microRNAs in epigenetic regulation. Current Opinion in Chemical Biology, 51, 11–17.

Young, M., Crook, H., Scott, J., & Edison, P. (2022). Covid-19: virology, variants, and vaccines. BMJ Medicine, 1(1).

Zealy, R. W., Wrenn, S. P., Davila, S., Min, K. W., & Yoon, J. H. (2017). microRNA-binding proteins: specificity and function. Wiley Interdisciplinary Reviews: RNA, 8(5), 1–8.

Zhang, Q., Miao, S., Han, X., Li, C., Zhang, M., Cui, K., Xiong, T., Chen, Z., Wang, C., & Xu, H. (2018). MicroRNA-3619-5p suppresses bladder carcinoma progression by directly targeting β-catenin and CDK2 and activating p21. Cell Death and Disease, 9(10).

SCIENTIFIC JOURNAL FOR THE FACULTY OF SCIENCE – SIRTE UNIVERSITY

Scientific Journal Impact Factor

TOGETHER WE REACH THE GOAL

jsfsu@su.edu.ly

journal.su.edu.ly/index.php/JSFSU