Advances in Applied Science Research
ISSN: 0976-8610

Open access Short Communication

COVID-19 and Antisense Long Non-Coding RNA Related

Bortolini Marco*

Department of Microbiology, University of Trento, Italy

INTRODUCTION

For the immune system to effectively combat foreign infections, gene expression must be tightly regulated. Ferroptosis, a separate iron-driven form of programmed cell death, improves the activity of follicular helper T cells during infection. RNA regulation is a critical stage in the final expression of genes. This research sought to ascertain how the expression levels of the antisense lncRNAs A2M-AS1, DBH-AS1, FLVCR1-DT, and NCBP2AS2-1 and FLVCR1 correlated with the severity of COVID-19. Both COVID-19 patients and healthy, age and gender-matched controls were included in this investigation. The expression level of the antisense lncRNAs was assessed using RT-PCR. The FLVCR1 and A2M-AS gene expression was decreased in COVID-19 patients.

DESCRIPTION

They also showed increased expression of FLVCR1-DT, DBHAS1, and NCBP2AS2. NCBP2AS2 and FLVCR1-DT both showed a positive connection with interleukin-6 (IL-6). Between DBH-AS1 and FLVCR1-DT, there was a significant link in mortality, comorbidities, and mechanical ventilation. A2M-AS1, NCBP2AS2-1, FLVCR1, FLVCR1-DT, and both had a substantial negative connection. The antisense lncRNA expression level in COVID-19 patients was discovered to be unregulated, linked with the severity of the disease, and may be involved in the aetiology of the disease.

The prospective trial involved 180 patients, including 60 healthy, age and gender-matched controls and 120 COVID-19 patients. The participants were chosen from the records of confirmed coronavirus-19 patients treated at the El-Bagour Hospital between March and December 2021. A written consent form that had been accepted by the local ethical research committee in the faculty of medicine at Menoufia University was acquired from the participants before the study began and after it had been explained to them. A thorough history was collected of each participant, and a general examination was done to see if they had any systemic diseases. In addition, CRP, IL6, and D-dimer test data were taken into account. The gene expression of long was verified using real-time PCR.

Due to the heightened inflammatory response caused by the novel coronavirus SARS-CoV-2 that produces COVID-19, some patients may experience severe symptoms such acute respiratory distress syndrome, sepsis, coagulopathy, and even death. The lncRNA dopamine hydroxylase antisense RNA 1 (DBH-AS1), which has a polyadenylated tail and is approximately 2 kb in length, is translated from chromosome 9q34. Immune-related disorders are mostly brought on by dysfunctional dendritic cells (DCs), which are cells that deliver antigen. In December 2019, the severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) was identified as the infectious disease COVID-19's etiological agent. The ability of DBH-AS1 to control a number of cell cycle-related variables leads to increased proliferation and resistance to apoptosis. The virus that causes SARS, SARS-CoV-2, is a positive [1-5].

CONCLUSION

Estimating the expression levels of these lncRNAs in Coronavirus patients could be helpful in visualising and monitoring the treatment of these patients. According to an analysis of the ROC bend of these lncRNAs, A2M-AS1 and NCBP2AS2-1 had the best legitimacy to separate between serious and moderate Coronavirus contamination. Large-scale studies have shown that between 18.8% and 36.2% of COVID-19 patients have thrombocytopenia, and the present investigation indicated that both patient groups had significantly lower platelet counts than controls.

ACKNOWLEDGEMENT

The authors are grateful to the journal editor and the anonymous reviewers for their helpful comments and suggestions.

Received:	31-August-2022	**Manuscript No:**	AASRFC-22-14666
Editor assigned:	02-September-2022	**PreQC No:**	AASRFC-22-14666 (PQ)
Reviewed:	16-September-2022	**QC No:**	AASRFC-22-14666
Revised:	21-September-2022	**Manuscript No:**	AASRFC-22-14666 (R)
Published:	28-Sepember-2022	**DOI:**	10.36648/0976-8610.13.8.86

Corresponding author Bortolini Marco, Department of Microbiology, University of Trento, Italy, E-mail BortoliniMarico28@unibo.it

Citation Marco B (2022) COVID-19 and Antisense Long Non-Coding RNA Related. Adv Appl Sci Res. 13:86.

DECLARATION OF CONFLICTING INTERESTS

The authors declared no potential conflicts of interest for the research, authorship, and/or publication of this article.

REFERENCES

1. Mattick JS, Makunin IG (2006) Non-coding RNA. Hum Mol Genet 15: 17-29.
2. Yan H, Bu P (2013) Non-coding RNA in cancer. Essays Biochem 65(4): 625-639.
3. Matsui M, Corey DR (2017) Non-coding RNAs as drug targets. Nat Rev Drug Discov 16(3): 167-179.
4. Ren H, Wang Q (2021) Non-Coding RNA and Diabetic Kidney Disease. DNA Cell Biol 40(4): 553-567.
5. Esteller M (2021) Non-coding RNAs in human disease. Nat Rev Genet 12(12): 861-74.