25TH NATIONAL & 11TH INTERNATIONAL ANNUAL CONGRESS
ON RESEARCH AND TECHNOLOGY OF IRANIAN MEDICAL SCIENCES STUDENTS
URMIA UNIVERSITY OF MEDICAL SCIENCES, URMIA, IRAN

Long COVID: Further Advances in Our Understanding of the Role of Specific Chemokines (*CCR5*, *CCR6*, *CCR9*, *and* CCL3) in Pediatrics

Hamidreza Farhadirad[1], Nasir Arefinia[2*], Zohreh-Al-Sadat Ghoreshi[3], Fateme Sadeghzade[1]

[1]Student Research Committee Jiroft University of Medical Sciences Jiroft Iran
[2]Bio Environmental Health Hazard Research Center, Jiroft University of Medical Sciences, Jiroft, Iran
[3]School of Medicine, Jiroft University of Medical Sciences, Jiroft, Iran

OPEN ACCESS

***Corresponding Author:**
Bio Environmental Health Hazard Research Center, Jiroft University of Medical Sciences, Jiroft, Iran

Citation:
Farhadirad H, Arefinia N, Ghoreshi ZAS, Sadeghzade F. The Long COVID: Further Advances in Our Understanding of the Role of Specific Chemokines (CCR5, CCR6, CCR9 and CCL3) in Pediatrics. *Iranian biomedical journal*. Supplementary (12-2024): 332.

ABSTRACT

Introduction: ARS-CoV-2 infection (COVID-19) is a major pandemic that has caused significant mortality and morbidity worldwide. About 80% of patients had mild or moderate disease, and 5% of patients with severe disease developed severe disease. Long COVID-19, also known as post-COVID-19 syndrome, is a condition in which individuals continue to experience symptoms for weeks or months after recovering from COVID-19. There is a lack of sufficient data on the risk factors for post-COVID-19 sequelae in children. This study aimed to evaluate the long-term effects of severe COVID-19 on promotor methylation and expression genes, including *CCR5*, *CCR6*, *CCR9*, and *CCL3* in children.

Methods and Materials: Clinical data and blood samples from 94 long COVID patients and 25 healthy subjects were collected. Promotor methylation and mRNA expression of *CCR5*, *CCR6*, CCR9, and *CCL3* genes in these patients and control group were assessed through methylation-specific PCR and real-time PCR assay.

Results: Our result indicated that promotors of CCR5 (p = 0.01) and CCL3 (p = 0.006) in convalescence COVID-19 children were hyper-methylated compared to the healthy control group. Subsequently, *CCR5* and *CCL3* transcripts decreased compared to the control group (p = 0.01). In addition, *CCL3* transcript in children with convalescent COVID-19 decreased compared to the control group (p = 0.008). However, we did not observe any significant modification in the transcript levels of *CCR6* (p = 0.7) and *CCR9* (p = 0.46) in children with convalescent COVID-19 compared to all the control groups.

Conclusion and Discussion: The *CCR5* and *CCL3* promoter region DNA methylation and the subsequent decrease in the expression of these genes were possibly correlated with long-term COVID-19 occurrence in children. Our study revealed additional data on the SARS-CoV-2-mediated inflammatory response.

Keywords: CCR5 receptor antagonists, Chemokine CCL3, Methylation

[DOI: 10.61186/ibj.25th-11th-IACRTIMSS]