عنوان مقاله:

Identification of G-quadruplex-forming Sequences in Nucleocapsid Gene of SARS-CoV-۲ Variants of Concern : An In Silico Analysis

محل انتشار:

مجله منابع ژنتیک, دوره 10, شماره 1 (سال: 1403)

تعداد صفحات اصل مقاله: 8

نویسنده:

Saeedeh Ghazaey Zidanloo - Department of Cell and Molecular Biology, Faculty of Science, Kosar University of Bojnord, Bojnord, Iran

خلاصه مقاله:

The severe acute respiratory syndrome coronavirus ۲ (SARS-CoV-۲), as an enveloped RNA virus, has resulted in a global health threat. Recent studies emphasized that G-quadruplex structures are intrinsic obstacles to genome replication and targeting them in viral genomes could be a novel antiviral strategy to develop antiviral agents. The genomic RNA of SARS-CoV-۲ codes for ۲۹ proteins. One of them is the nucleocapsid protein with multiple functions, which is crucial for several steps of the viral life cycle. Here, we have analyzed putative G-quadruplex sequences (PQSs) in the Nucleocapsid gene of SARS-CoV۲ and its variants of concern using a bioinformatics tool. The results showed that the number, position, and G-scores of PQSs were similar in Wuhan-hu-۱ and Alpha, Beta, and Gamma variants. The main difference was observed in the Delta variant, in which a PQS was deleted at position ۶۳۰ of the gene, which is the top-ranked highly conserved G-quadruplex. The Omicron variant had this PQS back at position ۶۲۱ as it had acquired several mutations. In addition, there is also a unique R۲۰۳M mutation, in the N protein of the Delta variant that leads to increased RNA packaging, replication, and severe COVID-۱۹. We proposed that the R۲۰۳M mutation has led to G T substitution and loss of the top-ranked highly conserved PQS in the N gene of the Delta variant. Therefore, due to the loss of this important PQS or indeed an obstacle to viral replication, the Delta variant could exhibit .higher reproduction and pathogenicity than other variants of concern

کلمات کلیدی:

G-quadruplex, Nucleocapsid gene, SARS-CoV۲, Variants of concern

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