عنوان مقاله:

In silico analysis of the substitution mutations and evolutionary trends of the SARS-CoV-۲ structural proteins in Asia

محل انتشار:

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خلاصه مقاله:

Objective(s): To address a highly mutable pathogen, mutations must be evaluated. SARS-CoV-۲ involves changing infectivity, mortality, and treatment and vaccination susceptibility resulting from mutations.Materials and Methods: We investigated the Asian and worldwide samples of amino-acid sequences (AASs) for envelope (E), membrane (M), nucleocapsid (N), and spike (S) proteins from the announcement of the new coronavirus ۲۰۱۹ (COVID-۱۹) up to January ۲۰۲۲. Sequence alignment to the Wuhan-۲۰۱۹ virus permits tracking mutations in Asian and global samples. Furthermore, we explored the evolutionary tendencies of structural protein mutations and compared the results between Asia and the globe.Results: The mutation analyses indicated that ۵.۸۱%, ۷۰.۶۳%, ۲۶.۵۹%, and ۳.۳۶% of Asian S, E, M, and N samples did not display any mutation. Additionally, the most relative mutations among the S, E, M, and N AASs occurred in the regions of ۵۰۸ to ۶۳۵ AA, ۷ to ۱۴ AA, ۶۶ to ۸۸ AA, and ۱۶۴ to ۲۰۵ AA in both Asian and total samples. D۶۱۴G, T۹I, I۸۲T, and R۲۰۳M were inferred as the most frequent mutations in S, E, M, and N AASs. Timeline research showed that substitution mutation in the location of ۶۱۴ among Asian and total S AASs was detected from January ۲۰۲۰.Conclusion: N protein was the most non-conserved protein, and the most prevalent mutations in S, E, M, and N AASs were D۶۱۴G, T۹I, I۸۲T, and R۲۰۳M. Screening structural protein mutations is a robust approach for developing drugs, vaccines, and more specific diagnostic tools.

کلمات کلیدی:
Asia, COVID-۱۹, Evolutionary analysis, Genome-wide mutations, mutations, SARS-CoV-۲