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Infection with different strains of SARS-CoV-2 in patients with COVID-19

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Keywords: co-infection, SARS-CoV-2, spike glycoprotein, stop mutations

Abstract

Paper description:

- We examined the biological diversity of SARS-CoV-2 infection by investigating possible genetic variations of the spike glycoprotein in Iraqi patients with COVID-19.
- A 795 bp coding region within the viral spike (S) gene was amplified from 19
- Nucleic acid variations showed co-infection with two different viral strains. Most samples had three nonsense single nucleotide polymorphisms (SNPs). Network and phylogenetic analyses

indicated that all viral infections exhibited mixed evolutionary origins represented by multiple viral sources.

- Our findings indicate that defective SARS-CoV-2 relied on helper strains with intact spikes for infection. An alternative putative ACE2-independent viral infection route is also suggested.

Abstract: The biological diversity of SARS-CoV-2 was assessed by investigating the genetic variations of the spike glycoprotein of patients with COVID-19 in Iraq. Sequencing identified fifteen novel nucleic acid variations with a variety of distributions within the investigated samples. The electropherograms of all identified variations showed obvious co-infections with two different viral strains per sample. Most samples exhibited three nonsense single nucleotide polymorphism (SNPs), p.301Cdel, p.380Ydel and p.436del, which yielded three truncated spike glycoproteins, respectively. Network and phylogenetic analyses indicated that all viral infections were derived from multiple viral origins. Results inferred from the specific clade-based tree showed that some viral strains were derived from European G-clade sequences. Our data demonstrated the absence of single-strain infection among all investigated samples in the studied area, which entails a higher risk of SARS-CoV-2 in this country. The identified high frequency of truncated spike proteins suggests that defective SARS-CoV-2 depend on helper strains possessing intact spikes during infection. Alternatively, another putative ACE2-independent route of viral infection is suggested. To the best of our knowledge, this is the first report to describe co-infection with multiple strains of SARS-CoV-2 in patients with COVID-19.

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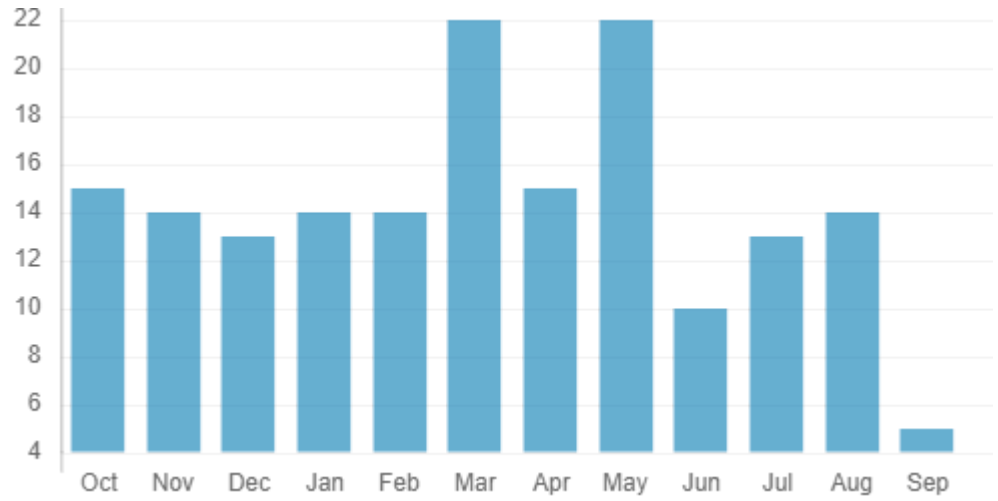

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Keywords: co-infection; SARS-CoV-2; COVID-19; spike glycoprotein; stop mutations

INTRODUCTION

Coronavirus disease 2019 (COVID-19) is a pandemic of a severe acute respiratory syndrome (SARS) caused by the novel coronavirus SARS-CoV-2 that was first reported in Wuhan, China in late 2019. These viral particles are attributed to the beta coronaviridæ family, which is responsible for the highest infectivity and pathogenesis in contemporary history [1,2]. Since its emergence as a newly identified pathogenic virus, SARS-CoV-2 has exhibited a rapid spread in a relatively short time scale with a catastrophic global pandemic sequel on healthcare systems and economies, with multifarious social aspects.

Despite preventive measures imposed by many governments around the world, a discrepancy in the cumulative mortality rates between states in America and even between western European countries by mid-June 2020 has been observed. This limitation in viral confrontation can be attributed to many causes, such as failure to adhere to measures of social distancing, the presence of concomitant chronic diseases strongly correlated to mortality (comorbidities), the preparedness of health systems to cope with the pandemic, and other related factors [3]. Despite the rapid progress of phylogenetic analysis and genetic mapping of SARS-CoV-2, the incidence of concomitant mixed infections

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