

**Correlates of SARS-CoV-2 Variants on Deaths, Case Incidence and Case Fatality Ratio among the Continents for the Period of 1 December 2020 to 15 March 2021**

**Authors:** Wajdy J. Al-Awaida, Baker Jawabrah Al Hourani, Samer Swedan, Refat Nimer, Foad Alzoughool, Hamzeh I. Al-Ameer, Sara F. Al-Tamam, Raqad Alashgar, Omar Al

**Abstract:** The outbreak of coronavirus disease 2019 (COVID-19), by the severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2), has quickly developed into a worldwide pandemic. Mutations in the SARS-CoV-2 genome may affect various aspects of the disease including fatality ratio. In this study, 553,518 SARS-CoV-2 genome sequences isolated from patients from continents for the period 1 December 2020 to 15 March 2021 were comprehensively analyzed and a total of 82 mutations were identified concerning the reference sequence. In addition, associations between the mutations and the case fatality ratio (CFR), cases per million and deaths per million, were examined. The mutations having the highest frequencies among different continents were Spike\_D614G and NSP12\_P323L. Among the identified mutations, NSP2\_T153M, NSP14\_I42V and Spike\_L18F mutations showed a positive correlation to CFR. While the NSP13\_Y541C, NSP3\_T73I and NSP3\_Q180H mutations demonstrated a negative correlation to CFR. The Spike\_D614G and NSP12\_P323L mutations showed a positive correlation to deaths per million. The NSP3\_T1198K, NS8\_L84S and NSP12\_A97V mutations showed a significant negative correlation to deaths per million. The NSP12\_P323L and Spike\_D614G mutations showed a positive correlation to the number of cases per million. In contrast, NS8\_L84S and NSP12\_A97V mutations showed a negative correlation to the number of cases per million. In addition, among the identified clades, none showed a significant correlation to CFR. The G, GR, GV, S clades showed a significant positive correlation to deaths per million. The GR and S clades showed a positive correlation to number of cases per million. The clades having the highest frequencies among continents were G, followed by GH and GR. These findings should be taken into consideration during epidemiological surveys of the virus and vaccine development.