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SARS-Cov-2 Genomic Variations Among Isolates from Jordanian Patients

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Abstract: ABSTRACT Severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) is a highly infectious viral disease that emerged in late 2019 and rapidly deployed globally, Jordon as the most countries of the world has been affected and suffered from COVID-19 Pandemic, In the current study, we track the SARS-CoV-2 mutation and evolution, through conducting multiple alignments and phylogenetic analysis for isolated strains in Jordan. Twenty-one amino acid sequences of SARS-CoV-2 whole-genome and their Spike protein were used in the phylogenetic analysis and alignment. Amino acid sequences were selected from 28 Jordanian isolates retrieved from the global initiative on sharing all influenza data (GISAID) (https://www.gisaid.org/). These sequences were analyzed in comparison with SARS-CoV-2 isolate Wuhan-Hu-1 (Reference strain) using the BLAST tool, MAFFT online server, Guidance, BioEdit and CoVsurver Application for detection the mutations , phylogenetic analysis and multiple alignments. It was found that the evolution of SARS-CoV-2 whole-genome not more than 0.07% from reference strain while the spike protein variant not more than 0.08%, it was detected numerous of mutations (N_G204R; N_M234I; evolved variants of SARS-CoV-2 likelihood increasing transmissibility or pathogenicity of COVID-19 infection; thus, Keywords: COVID-19; SARS-CoV-2; spike protein; Jordan; Coronavirus; mutation; sequence analysis. INTRODUCTION China, were admitted to hospitals suffering from SARS have the same pneumonia symptoms; later, the World Health Organization (WHO) named the virus COVID-19 [1-2]. COVID-19 is a member of the Betacoronaviruses family, such as Respiratory Syndrome coronavirus (SARS-CoV) and the Middle East Respiratory Syndrome coronavirus (MERS-CoV) [3]. According to WHO, SARS has a mortality rate of 10%and MERS has mortality rates of 30%, while COVID-19 has a 2% mortality rate [3]. It is brought about by Severe-Acute-Respiratory- SyndromeCorona-Virus-2 (SARS-