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Editorial

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Evolution of Microbes: A lesson from Severe Acute Respiratory Syndrome – Coronavirus SARS-CoV

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In England, the first case of human coronavirus was identified in 1965 as human CoV (B814), which directly infects the upper respiratory tract of humans. In 2002, a suspected flu-like case initially regarded as an unknown coronavirus (β genera) which is from bats and eventually emerged to infect humans through palm civet cats (*Paguma larvata*) as the intermediary host in Guangdong province of China. The virus was later named as SARS-CoV, which resulted in 8422 cases in China and Hong Kong and caused 900 deaths accounting for 11% mortality rate (Walls *et al.,* 2020).

World Health Organization (WHO) alerted case of an infectious diseases from unknown viruses towards the end of 2019, which emerged from Wuhan city, Hubei province, central China (WHO, 2019). The symptoms were reflective of respiratory illness like viral pneumonia and cough, dyspnea, and fever (WHO, 2019; Wu *et al.,* 2020). The unknown virus was later identified as a new Beta type of coronavirus (β-CoV) strain in December 2019 using performed high throughput sequencing (Lu, 2020; Wu *et al.,* 2020). This novel CoV strain was found to be parallel genetically to the existing bat strains of severe acute respiratory syndrome (SARS-SL-CoVZC45 and SL-CoVZXC21) which has 88% homology, SARS-CoV-1 with 79.5% homology, and Middle East respiratory syndrome (MERS) having 50% homology coronaviruses (Guan *et al*., 2020). This unknown strain of 2019 eventually declared as novel β-CoV strain, a new type of SARS-CoV-2 virus by the International Committee on Taxonomy of Viruses (ICTV) and WHO officially. This nomenclature was due to its genetic similarity with previous CoV strains. SARS-CoV-2 directly infects the organs of the upper respiratory tract (sinus, nose, and throat) and lower respiratory tract (windpipe and lungs) of humans. However, there were other CoV family strains before the evolution of SARS-CoV-2 (Wu *et al*., 2020).

COVID-19 was an infection engendered by SARS-CoV-2 which evolved from the SARS-CoV wild-type virus and many novel variations have developed during the COVID-19 pandemic and ongoing episodes in Europe and Africa like Ghana. Some of the new mutants of SARS-CoV-2 were termed as Variants of Concern (VOC) which are divided into five categorises and are presented as: (i) Alpha (B.1.1.7), (ii) Beta (B.1.351), (iii) Gamma (P.1), (iv) Delta (B.1.617.2), and (v) Omicron (B.1.1.529) according to World Health Organization (WHO, 2019). These five variants of SARS-CoV-2 have demonstrated a substantial pathogenicity level and dynamic transmissible rate. There are other variants which are regarded as new variants of SARS-CoV-2 due to their uniqueness in causing diseases. Some of the uniqueness associated with their infection are severity of sickness, transmissibility, diagnostic and immunological escapes. These variants of SARS-CoV-2 were categorised as variations of interest (VOI) (Lu *et al.,* 2020).

Considering the COVID-19 outbreak, SARS-CoV-2 has experienced genetic mutations in the S protein and receptor-binding protein (RBD) region of the virus thereby, altering the existing characteristics of the virus, which includes pathogenicity, transmission rate, immune evasion, testing and vaccine failure. Experimentally, it has been shown that SARS-CoV-2 that was developed from the wild strain of SARS-CoV through a single mutation (D614G), demonstrated enhanced rate of transmission but decreased illness severity (Wu *et al.,* 2020). Also, evaluation of SARS-CoV-2 and its VOC revealed that there are many alterations in the S protein and RBD of the spike protein in a recent novel VOC Omicron thereby accounting for the high rate of transmission and relatively mild disease severity (Walls *et al.,* 2020). Enhanced and multiple symptoms (such as fever, cough, myalgia (tiredness), diarrhea, sputum production, headache, dyspnea, rhinorrhea, nausea, sneezing, and sore throat) are products of the genetic alterations of the virus genome. Evolution of SARS-CoV-2 has demonstrated the threats that can emerge from microorganisms which could eventually put the nations of the world at risks of future pandemic.

Omicron has currently spread to all nations of the world due to the genetic changes in the S protein and receptor-binding domain (RBD) of the virus spike protein. The genetic mutation has responsible for the variant having high transmissible rate but decreased severity of illness. The two sublineages of Omicron which are Omicron BA.1 and BA.2 varies from each other due to the difference in the patterns of mutation. The genetic variation in these sublineages may account for the higher frequency and transmissibility of sublineage BA.2. It should be noted that continuous study of the genome of new variants or circulating variants and comparative study of the genetic alterations, epidemiology,

and presentations of SARS-CoV-2, VOC, and their sublineage clinically will be valuable. Understanding of the virus evolution will undoubtedly aid in the control of diagnosis, transmission, prevention, and treatment of the coronavirus-infected patients (Hillary *et al*., 2023).

The occurrence of SARS-CoV-2 variants suggests serious responses that should involve understanding new mechanism of infection, transmission strategies and reapproaching the development of vaccines and drugs to overcome the current and prevent a future pandemic from SARS-CoV-2 variants. More attention should be placed to prevention strategies to restrict the transmission of this virus and possibly, new variants.

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