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Letter to Editor

The New Covid-19 – A Bioweapon or Natures' Balancing Act

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Abstract

The Coronavirus has caused the most devastating pandemic till date. Various discussions have been done on the origin of the virus and after genetic studies, researchers tell that it's due to zoonotic transmission and natural selection. After and during the first wave researchers have been working on vaccines to combat its spread and have been successful to a great extent. However, the virus has been mutating and producing new variants. These being more infectious and equipped in escaping the host immune mechanisms and thus reducing the efficacy of the vaccination drives. This is the first study from this area which notifies the prevalence of different variants found circulating in the population in and around Firozabad district of Uttar Pradesh, India. These being variants of concern and variants of interest are very significant and indicate the need for whole genome sequencing of all positive samples. Also this district being close to Agra which holds an International significance and attracts tourists, it is important to stop further spread of the virus and a knowhow of the variants will be useful in immunology and vaccination outcomes.

Keywords – Bioweapon, Covid19, genome sequencing, mutations, vaccination, variants

The most negative word for the years 2020 and 2021 perhaps is "positive". The Covid 19 virus has caused the most fatal pandemic of the century. The first wave of the infection caught the population off guard and unprepared. Many theories of it being a bioweapon were put forward [1, 2]. Some debated that it was the result of an accidental leak from a laboratory at Wuhan. [3] However, there are studies that contradict both these views and on comparison of the alpha and beta Coronavirus on the basis of biochemical [4-6] and structural properties [5,7,8] the SARS-CoV-2 is known to optimise for binding to the human receptor ACE2 (Angiotensin converting enzyme 2) and its spike protein bears a functional polybasic cleavage site at the S1–S2 boundary [8]. The Receptor Binding Domain (RBD) on the spike protein besides being very variable has a high affinity to ACE2 from humans which is a result of natural selection thus evident of Covid -19 not being a bioweapon or a manipulated organism [9]. Genetic studies show that SARS-CoV-2 has not been derived from any previous virus and no reverse-genetic systems have been used [10,11]. Evidence-based studies show that there were no signs of human manipulation which rules out theories of laboratory leak [12].

With the onset of the epidemic, a probability of involvement of animals was put forward due to the proximity of the lab to the Huanan market in Wuhan [4,13]. Studies show that the RaTG13 from a *Rhinolophus affinis* bat has an overall 96% (appx.) similarity to SARS-CoV-2 [7,13] but its spike diverges in the RBD suggesting it may not bind efficiently to human ACE2 and bats may act as a reservoir host for its progenitor. Besides, Coronaviruses similar to SARS-CoV-2 showing strong similarity in RBD were found in Malayan pangolins [14]. However, the genome of RaTG13 bat virus is the closest to SARS-CoV-2. These are clear evidences of natural selection in animal hosts.

In natural outbreaks, besides humans the animals also get affected and so also has happened during the Covid -19 pandemic. Relating to the origin of the disease, consumption of wild animals is not only a culture of Western China but also an industry worth 76 billion dollars and hence close interaction of population to wildlife [12].Therefore, there is a strong possibility of the virus jumping from the animals to humans i.e. zoonotic transfer and human to human transfer following it and requires further studies. A detailed study is required among animals too otherwise the virus may be a harbinger of destruction of life beyond our imagination.

The devastating Covid19 pandemic has accounted for more than 4.5 million deaths [15] till date and taken the entire human population aboard for the worst experience of their lives. The uglier picture is of the virus undergoing mutations [16] and producing new variants which may compromise the vaccination drives and Monoclonal Antibody therapies [17]. In the Microbiology Department at Autonomous State Medical College, Firozabad, U.P., India, Rtpcr was done from the samples of suspected cases and those which were diagnostically SARS-CoV-2–positive with amplification of the targeted region crossing the threshold before 25 cycles were subjected to whole genome sequencing. Sequencing reads were mapped using SARS-CoV-2 reference genome (NCI_045512.2). The variant class, amino acid changes and other relevant annotations were added to the variants. Phylogeny and clade classification was performed using the Pangolin 3.1.4 and Nextclade 1.1.0 program respectively. The 11 positive samples showed the presence of 4 Delta (B.1.617.2 lineage), 6 Kappa (B.1.617.1 lineage) and 1 Alpha, V1(B.1.1.7 lineage) variant. The Delta (B.1.617.2 lineage) variant is known to be about four times more infectious than the original virus having impacts on neutralisation for antibody therapies [17]. The Kappa (B.1.617.1 lineage) variant besides having mutation L452R which is also present in Delta also has a mutation E484Q which is different from others and both have been found in India [17, 18]. Although, Alpha (B.1.1.7 lineage) variant is the only one that has one mutation on RBD and was found in the U.K. [18] it is known to increase viral transmission [19].

This is the first report of Covid 19 variants from this part of U.P. India and Firozabad being very close to Agra which has forever been an attraction for international tourists is very important as these variants are known to have not only increased infectivity, transmission and binding to ACE receptors but also have change in antigenicity, immune escape mechanisms and decrease in susceptibility to Monoclonal antibodies. The Delta and Alpha being variants of concern (VOC) and the Kappa being variant of interest (VOI) [20]. These variants maybe a hindrance in mass vaccination outcome and Covid 19 treatment. However, more studies are required to be done along with continuous monitoring, surveillance and whole genome sequencing of the positive samples.

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