



## SARS-CoV-2 evolution, its variants and effects-a review

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### SUMMARY

Animals are helpful for people in art, food, tool, trade, magic, traditional and modern-medicine and role as a bioindicators. Human who have contact with fauna with domestic and wild animals can be at risk for diseases. Pathogen may be passed fauna to *Homo sapiens* as well as *H. sapiens* to *Homo sapiens* with aerosol, contact, infected droplet, oral, and vector. Coronaviruses has of single-stranded RNA virus, and enveloped. Coronaviruses are divided into 4 genera viz. “Alphacoronavirus”, “Betacoronavirus”, “Gammacoronavirus” and “Deltacoronavirus”. *Betacoronavirus* may originate from bats. SARS-CoV-2 is identified in bat species as well as Malayan Pangolin. Study revealed that SARS-CoV-2 most probably originate from recombination both “bat” and “pangolin” virus. As the COVID-19 disease enters in 2020, it is critical to keep a watch for novel strains and local ailment occurs. The SARS-CoV-2 evolution can provide it more infectious through mutations that enhance binding or increase affinity to host cells.

**Keywords:** COVID-19, Pangolin, Bat, Betacoronavirus

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### INTRODUCTION

In December 2019, unique pneumonia was documented in Wuhan, China and might be transferred from wildlife to “human” and “human” to “human”. The SARS-Cov-2 show a phylogenetic relation with “SARS-like coronavirus” and this virus was new, different and unique coronavirus. This ailment was detected with SARS-Cov-2 (Adil, 2021). Xu *et al.* (2020) and Jiang *et al.* (2020) also documented as a “SARS-Cov-2” related to lineage “SARS-CoV”. Wu *et al.* (2020) study demonstrate the phylogenetic contrast between SARS-Cov-2 and SARS, and between these virus recognize 380 amino acid changeovers, which may cause pathogenic and functional divergence of SARS-Cov-2. Paraskevis *et al.* (2020) study showed that SARS-Cov-2 not-mosaic and its almost half genome lineage within “*Betacoronavirus*” and these genomic characteristics indicated its high virulence in humans.

### EVOLUTION OF SARS-COV-2

Animals are useful for people in art (Barrett and Sommerstein, 2003), food (Altaf and Umair, 2020; Tariq, 2020; Haidar and Bashir, 2021), tool, trade (Khan *et al.*, 2020), magic, traditional (Altaf *et al.*, 2017) and nano-medicine (Zainab, 2021) and role as a

bioindicators (Sidra *et al.*, 2019; Khan *et al.*, 2021). Human who have contact with fauna with domestic and wild animals may be at risk for “zoonotic diseases”. Pathogen can be passed on from fauna to *Homo sapiens* and *Homo sapiens* being to *Homo sapiens* with aerosol, contact, infected droplet, oral, and vector (Altaf, 2020). Coronaviruses has of single-stranded RNA virus, and enveloped. Coronaviruses are divided into 4 genera viz. “Alphacoronavirus”, “Betacoronavirus”, “Gammacoronavirus” and “Deltacoronavirus”. “Betacoronavirus” may originate from bats. SARS-CoV-2 is identified in bat species as well as Malayan Pangolin. Study noted that SARS-CoV-2 most probably originate from recombination both “bat” and “pangolin” virus (Paraskevis *et al.*, 2020; Zhang *et al.*, 2020).

#### VARIANTS OF SARS-COV-2

COVID-19 pandemic arrive in second year after spreading, it's very important to keep a lookout for unique, growing and emergent strains and limited virus's outbreak. Due to evolution in SARS-CoV-2, essence it's infectious by emerging mutations that rise affinity or improve binding to host cells, whereas seepage mutation in SARS-CoV-2 help it avoid to immune responses and it have severe implications for therapeutics and vaccines and can harmfully effect the mortality and cruelty of the disease. Scientists during this pandemic various vaccine are rolled out, in these year virus will be exposed for the new modification, selection, pressure for meets evolution modes of virus (Srivastava *et al.*, 2021).

#### Indian Variant

Due to COVID-19, mortality rate originate very unequal globally. With population of 1.3 billion people of India, the mortality rate comparatively lowest from other countries where they have high infectious rates. They basic element of pathogenesis and virulence is continuously changing isolates, in genetics compositions. In this study main point was to analyze and compare the amount of differences in genome of Indian isolates (n ¼ 2525) with isolates and Wuhan-1 strain, with those countries they show higher mortality rates such as USA, France, Belgium, and Italy. The another main point of this study was to analyze the basic mutation influence collaboration with angiotensin, which converting panel of neutralizing monoclonal antibodies and enzyme 2 (ACE2). But in India dominancy of N439K mutation in receptor binding motif (RBM) did not reported, as relate to worldwide sequester (0.54%). This research authorizations by large scale observing of Indian quarantines as SARS-CoV-2 virus and its estimated that this virus mutation and progress may appear in impulsive way (Alai *et al.*, 2021).

#### UK Variant

Mohandas *et al.* (2021) study the UK variant SARS-CoV-2 virus formerly using D614G variant in hamster model and shedding using “VOC 202012/01 UK variant”, and its observation showed that the viral RNA dropping through nasal wash significantly. In hamster model identify the transmission of SARS-CoV-2, by aerosol, direct contact, and fomite routes. Through comparing the spreading of UK Variants in many ways, for understanding the highly viral RNA molting from nasal cavity routed

in Syrian hamsters and the infected hamster with UK variant could increase the spreading competency of the variant.

#### Pakistani Variant

Scientists declared detection of S clade and GH strains and G614 variant from Pakistan justifying large-scale of whole-genome sequencing of strains dominant in different areas and help in explore their genetic diversity and also understand evolution of virus. Meanwhile SARS-CoV-2 appears from china, including Pakistan and spread globally. The “SARS-CoV-2” genome sequence has played an essential role for understanding the diversity of genome and evolution of virus during pandemic. While from Pakistan unparalleled number of full genomes sequences data of SARS-CoV-2 has been recorded in NCBI and GISAID is exceptional. In Pakistan it reported the genomic characterization, phylogenetic analysis and the sequencing, of SARS-CoV-2 strains which isolated from patients. Two19B (S)-clade were closely associated with Oman and India viruses. In recent genome sequences study generally mutation were detected in twenty nine amino acid, in which four novels and fifteen missense mutation. Especially mutation D614G (aspartic acid to glycine) found in spike protein from GH clade sequences. The characteristics of D614 mutation carried in G614 variant and it's very infectious and spread very rapidly globally (Umair *et al.*, 2021).

#### US Variant

Incredibly, in the “SARS-CoV-2” genome detected numerous changes of encoding “amino acid” accruing in single Nucleotide 37 Variations (SNVs), as major mutates of “SARS-CoV-2” genomes with pattern 38 RNA enzymes. In October 2020 research listed 39 three main variants. These shown that fourteen key mutations in which 40 were found with several associations amongst 14 different predominant signs. In U.S these 41 signs probably signify SARS-CoV-2 evolutionary lineages as well as also expose evidence of 42 evolution such as in 2020 summer mutational burst, similarly its lead to a household new 43 variant, and a develop towards higher mutational capacity within viral isolates, but with intermittent 44 mutation loss. During ending of “2020” show about growth of novel 45 low frequency mutations replacements in spike protein and on near putative furin cleavage site hyper mutational glutamine 46 residue present. Lastly, the data show that 47 known variants present and also containing B.1.1.7, which has developed extra 48 “spike mutations”. This research outcomes show that, major viral sequences are energetically 49 progressing with time, with passage of time mutational spurts and undiminished mutation buildup. The 50 is great level of surviving variation, although it have low frequencies and in the 51 spike mutation encoding region ability of challenging in super-spreader proceedings and it is similar to serial 52 Initiator events in evolution (Tasakis *et al.*, 2021).

#### Italy Variant

The 2<sup>nd</sup> wave of “SARS-CoV-2” has hit very hard in Italy's, in which 100,000 deaths and more than three million cases, and this number increase ten-fold time noted in August 2020. In Italy between 2020 to 2021 after analyzing the 6515 SARS-CoV-2

sampled sequence it's noted that how diverse lineages developed multiple times independently even with strictly lockdown restrictions. In November 2020, "virus lineage B.1.177" turn into the dominant variant during that time cases at peaked and in a day 40,000 cases were reported, but this is being switched by the "B.1.1.7" variant of concern in January 2021. From December to onwards in Italy suddenly increasing another lineage P.1 utmost expected caused by a single introduction (Di Giallonardo *et al.*, 2021).

#### Iran Variant

Starting pandemic due to rapidly spreading of SARS-CoV-2 all over the world from December 2019, rapidly after its occurrence, with now more than "one million" deaths around the world. In February Iran was first country along with other countries provoked with quickly spreading of virus, while immediately no whole-genome tracking of "SARS-CoV-2" performed in Iran. During March-July 2020 from different geographical locations of Iran research done on 50 whole sequences of genome of viral isolates for easily understanding this issue. Continuously analyzing on genetic diversity, origins and transmission dynamics indicated that in Iran at least two introductions of the virus, and it creating two Group defined as "B.1\*" and "B.4". Almost on 26 December 2019, first entry of virus arisen, as recommended by the time to the most universal ancestor, followed by a rapid public transmission, led to dominance of "B.4" lineage in initial epidemic till the end of June. In mid may regularly dominance of "B.4" lessening possibly happen during other entries of other virus followed by surge of "B.1\*" lineages. Unusually, the virus variation tracking showed that increasing frequency of D-614-G mutation, along with B.1\* lineages, and its continuously shown till October 2020. According to D-614-G possible role of increased infection and spreading of the virus, as well as the current high frequency of the disease and "dominance" of this lineage may drive the country into a serious health condition. Therefore, data informs for allowing for tougher prohibition schemes stopping the frequency of better disaster in future (Fattahi *et al.*, 2020).

#### CONCLUSION

After outbreak of SARS-CoV-2, continuously threaten on years to human lives. Although variety of vaccines have been develop or still processing to develop the vaccine against this virus, but with high spreading capability and quickly spreading of genetic variants recommend that the current controlling measures may be arrived. Moreover, quickly spreading of "SARS-CoV-2" variants might avoid "immune responses" of healthier patients and weaken the vaccines being under development. It is needed that all countries should cooperate and work collectively so that all over the world spreading of this virus should be controlled. Research should be lead to study the influence of the variation of these viruses and work should be done to make helpful and defended vaccination of this variant, such as novel vaccines pursuing the significant novel variant "501Y.V2" should at least be officially ready immediately.

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