



# Genetic Evolution of the Novel Coronavirus

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## Abstract

The SARS CoV2 is a positive sense RNA virus which causes COVID-19, that is now causing the fourth wave of infections across the world in many countries. Many new mutants and variants of this virus, also called the Novel Coronavirus, have now evolved. Many factors like animal- man conflict, overcrowding and non-adherence of people worldwide to the COVID- appropriate protocols have led to the genetic evolution of the virus by way of mutation and recombination. These factors should hence be studied well and have been discussed in this article.

**Keywords:** Novel Coronavirus; Mutation; Recombination

## Introduction

The Novel Coronavirus is now raging across the world as the third wave in most regions and the fourth wave in some countries. The outbreak was first reported in December 2019 in Wuhan province in China [1]. The causative agent is the positive sense RNA virus, SARS-CoV2. It was initially adapted to bats and then had jumped across species barriers to infect pangolins and man. Coronaviruses can be classified into 4 types:  $\alpha$ -coronavirus,  $\beta$ -coronavirus,  $\delta$ -coronavirus, and  $\gamma$ -coronavirus. Some common human coronaviruses, like HKU1, NL63, OC43 and 229E, infect humans and only cause mild respiratory disease, whereas MERS-CoV and SARS-CoV1 had caused devastating severe acute respiratory infection in the recent past [1]. SARS and MERS were highly fatal infections and hence maybe less transmissible. Coronaviruses continuously change their structure by means of mutation, deletion, and/or insertion mutations. The most genetically variable part in SARS-CoV and SARS-CoV-2 genome is the RBD or Receptor Binding domain in the S protein of the virus [1,2]. On the contrary, the highest rate of significant amino acid substitutions is found in its nucleocapsid viral protein, but it is lowest in the envelope protein. This implies that envelope protein

is more stable and less diverse [1]. The coronaviruses that have, till now, caused outbreaks, epidemics or pandemics are SARS-CoV1, MERS and now SARS-CoV2. The estimated mean incubation period of the SARS-CoV-2 virus is 5.1 days. In general, all the 3 emerged coronaviruses have more or less similar mean time of incubation period, which is around 5 days. More accurately, it is 5.1 in SARS-CoV-2 (ranging from 4.5 to 5.8 days), 5 days in SARS (ranging from 2 to 14 days), and 7 days in MERS (ranging from 2 to 14 days) [1]. The ACE-receptor binding ability of SARS-CoV2 is about ten times that of SARS-CoV1.

Evolution-wise, the novel coronavirus is closely related to coronaviruses derived from five wild animals, like *Paguma larvata* (masked civet), *Paradoxurus hermaphroditus* (Asian palm civet), Civet, *Aselliscus stoliczkanus* (Stoliczka's trident bat) and *Rhinolophus sinicus* (Chinese rufous horseshoe bat), and is in the same branch of the phylogenetic tree [3]. The genome sequence homology between SARS-CoV-2 and other viruses have been studied lately. It is found to be 79% homologous with SARS-CoV1, but is more homologous to the BatCoV RaTG13 which belongs to SARS-like bat coronaviruses [1]. The evolutionary analysis results thus show that the Novel coronavirus or SARS-CoV2 is most similar to the Bat

coronavirus isolate RaTG13 (GenBank No.: MN996532), with 96.2% sequence homology in the whole genome [3]. Other groups suggest that pangolin, mink, snake, turtle may be potential intermediate hosts for the virus. In fact, the Omicron variant is thought to arise from recombination of parent strain of SARS-CoV2 with deer coronaviruses and also possibly the mink coronaviruses [4]. It may be so that the SARS-CoV 2 virus emerged via bat and then pangolin hosts and then the infection spilled over to humans.

The Omicron variant is very different from the parent strain of the Novel coronavirus. In contrast to the other strains; it infects mainly the upper airways. Omicron variant has in its genome, over 50 new mutations, mostly in the spike protein, in comparison to the strain that started the pandemic [5]. Scientists think now that the Omicron variant may have been accumulating mutations slowly for over 1 year, and it is also thought that it went on spreading between different animals before it made a switchover or jumped species barriers again to infect mainly humans [5]. Some of the evolved mutants are behaviour wise so different that they are called Variants of concern (VOC).

Recently, genetic recombinations have also been detected between BA.1 and BA.2 subvariants of the omicron variant, and also between Delta VOC and Omicron VOC (Deltacron). This needs to be studied more. Genetic recombination in SARS-CoV2 may be commoner than previously thought. The major reason for recombination in all Coronaviruses can occur at the replication step in the viral life cycle, when more than one variants or subvariants/sublineages incidentally exist in the same person or in a family. During replication, a set of subgenomic RNAs is formed, thus increasing the homologous recombination rate among the closely related genes from different lineages of coronaviruses or other viruses by template switching. Also, circulating coronaviruses in multiple host species may contribute to increase in the frequency of such recombination events [6].

## Discussion

Continuous conflicts between man and animals has led to the ongoing genetic evolution of the SARS-CoV2. Coronaviruses continuously modify their structures by way of mutation, deletion, and insertion mutations. The most genetically variable part in genome of SARS-CoV1 and SARS-

CoV-2 is the RBD (Receptor-Binding domain) in the S (spike) protein. In fact, some locations in S protein sequence may even be related to positive selection [1]. Other things like overcrowding in public places and non-adherence to COVID appropriate behavior have only led to further generation of mutants and recombinant strains of the virus. Very soon India might encounter the fourth wave of COVID infections, as per scientific predictions. Hence the Indian Government is now focusing on the five-fold strategy for COVID management and control which is test, track, treat, vaccination and adherence to COVID- appropriate behaviour [7]. However, it is also a fact that the newer variants and mutants will tend to be milder and less fatal, as this imparts stability and fitness to the virus. Time will tell the exact future of the pandemic and how many more waves of infection are to be seen.

## Conclusion

The Novel Coronavirus is naturally prone to get mutated and evolved genetically. External factors can further facilitate its genetic evolution.

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