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Variant Analytics of the Sars-Cov-2 Genome in South Karnataka Revealed Significance for Drug Resistance

Harishchander Anandaram

Centre for Excellence in Computational Engineering and Networking,

Amrita Vishwa Vidyapeetham, Coimbatore, Tamil Nadu, India

Abstract

The SARS-CoV-2 virus is the vital cause of the pandemic. Combating COVID-19 requires a vaccine design to identify the basic variant patterns, i.e., point mutations and Single Nucleotide Polymorphism (SNPs). Identifying possible variants in the genome of SARS-CoV-2 from a global perspective is the basis for creating a database of Mut.-SNP.-SARS-CoV-2.This study involves selecting the data of the SARS-CoV-2 genome in south Karnataka. The variant analysis resulted in 19 novel variants contributing to the mechanism of drug resistance.

Introduction

The repository syndrome of coronavirus had a higher transmission rate in the Middle East. The virus likely originated from bats with genetic diversity worldwide (Cui J et al., 2019). Phylogenetic analyses revealed associations between rhinolophid bats and their CoVs. Hence, host shifts have occurred in this group's recent history of evolution. These shifts may be due to either the virus's biological traits or the virus or the behavioural characteristics of the host (Vijaykrishna D et al., 2007). Due to the mortality of SARS-COV-2, an effective vaccine is a requirement for control. Hence, academia, industrial sectors, and the government are working

together to develop vaccines (Li Y et al., 2020). The lineage of B.1.1.7 in SARS-CoV-2 estimated a difference in reproduction numbers in the ranges from 0.4 to 0.7, and similarly, the increase ranges from 1.4 to 1.8 (Volz et al., 2021). The development of animal models to analyse the pathogenesis of SARS infection requires streamlining to initiate vaccine development.

The animal model data helped understand the SARS-CoV (Weiss & Navas-Martin, 2005). Several drugs like "arbidol, chloroquine, favipiravir, and redeliver" are undergoing clinical studies for treating COVID-19 (Dong L et al., 2020).

Efforts to develop potential vaccines against multiple strains of human coronavirus (CoV) infections such as MERS and SARS (Dhama K et al., 2020). The application of lipid peroxidation will affect the prognosis of patients with metabolic disorders. Still, obesity-associated pregnancy needs to be studied further in COVID-19 (Petrakis D et al., 2020).

Recent Studies on epidemiologic and virologic modelling reports confirm the rapid transmission. Critical knowledge gaps in SARS-CoV-2 include the relative incidence of symptomatic and asymptomatic infection (Furukawa NW et al., 2020).

Materials and Methods

Analytics

In the current study, "Reference-based Whole-genome Analytics" was implemented to identify the diversity of SARS-CoV-2 viruses globally based on mutations and polymorphisms.

Experiment

Quality Control provides a modular set of analyses to offer a fast impression of problems associated with the data.

Mapping

The process for aligning the sequencing reads on the reference genome.

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Quantification

A common practice to eliminate the duplicates of reads generated from PCR assumes the reads from the same cDNA molecule.

Validation

The variant calling process identifies single nucleotide variants (SNPs/SNVs), multiple nucleotide variants (MNCs), short insertion and deletions (indels), copy number variations (CNVs), and translocations present within the whole genome.

Filtration

The process consists of choosing highly confident variants.

Variants rate details

Chromosome	Length	Variants	Variants rate
NC_045512.2	29,903	19	1,573
Total	29,903	19	1,573

Figure 1. Variants rate details.

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Number variants by type

Type	Total
SNP	19
MNP	0
INS	0
DEL	0
MIXED	0
INV	0
DUP	0
BND	0
INTERVAL	0
Total	19

Figure 2. Number of variants by type.

Prediction

The Variant Effect Prediction process involves analysing, annotating, and prioritising genomic variants in the coding and non-coding areas.

Number of effects by impact

Type (alphabetical order)	Count	Percent
LOW	22	8.8%
MODERATE	17	6.8%
MODIFIER	211	84.4%

Figure 3. Several effects by impact.

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Result

Mutations are of different types. Among those mutations, SNPs are more common and occur very frequently. In the genome of South Karnataka (Karnataka_1), 19 variants occurred throughout the genome, and all variants are SNPs. The variants rate is 1573, which means one variant per 1573 bases (Figures 1-9).

Number of effects by functional class

Type (alphabetical order)	Count	Percent
MISSENSE	17	43.59%
SILENT	22	56.41%

Figure 4. Number of effects by functional class.

Of 19 variants, 84.4 % of the mutations are modifiers, meaning they have a higher impact ratio than moderate and low.

Regarding functional class effects, 43.59 % of the mutations are missense mutations that alter the protein to code, and the remaining are silent mutations that do not affect the gene's function.

Mutations: Classified according to the region of occurrence. On that note, around 83.6 % of the mutations occurred in the up and downstream areas. Most importantly, 15.6 % of the transformation happened in the exon region, which may cause potential changes in the function of the genes.

Out of 19 SNPs, Nucleotide T changed to C 14 times, which is assumed to have more significance.

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Number of effects by type and region

Type			Region		
Type (alphabetical order)	Count	Percent	Type (alphabetical order)	Count	Percent
downstream_gene_variant	95	38%	DOWNSTREAM	95	38%
intergenic_region	2	0.8%	EXON	39	15.6%
missense_variant	17	6.8%	INTERGENIC	2	0.8%
synonymous_variant	22	8.8%	UPSTREAM	114	45.6%
upstream_gene_variant	114	45.6%			

Figure 5. Number of effects by type and region.

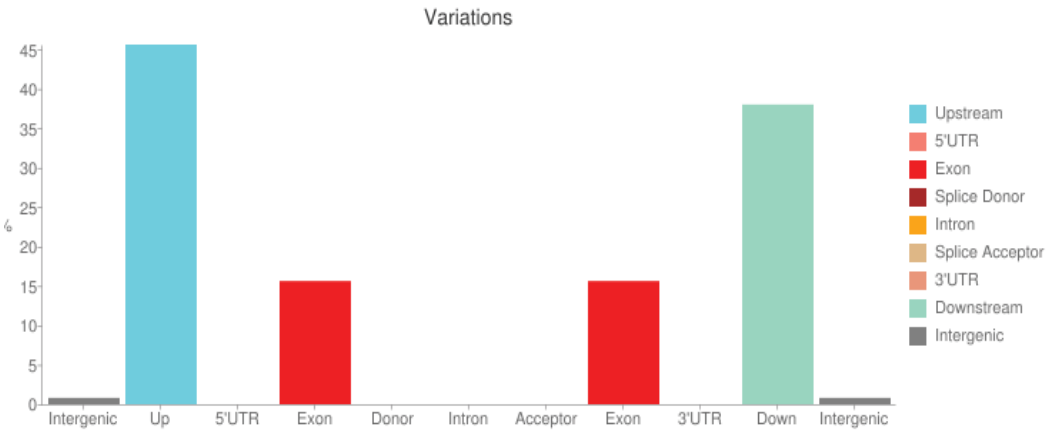

Figure 6. Variations.

Base changes (SNPs)

	A	C	G	T
A	0	0	3	1
C	0	0	0	14
G	0	0	0	1
T	0	0	0	0

Figure 7. Base change.

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Nucleotide G changed to A 3 times, T to A 1 time, and T to G 1 time. In the below-mentioned figure, single-nucleotide variation leads to different codons were illustrated. It describes 19 mutations in the Karanataka_1 genome (South Karnataka) that change the original to the mutated codons.

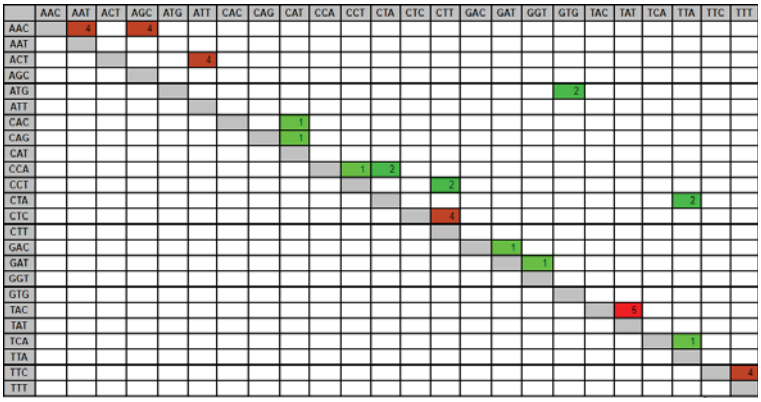

Figure 8. Single-nucleotide variation leads to a different codon.

The below figure explains how one nucleotide variation leads to a change in the amino acids. Here, significant mutations are amino acid L(Leucine) is mutated into P(Proline) four times, S(Serine) is mutated into N(Asparagine) four times, I(Isoleucine) mutate into T(Threonine) four times.

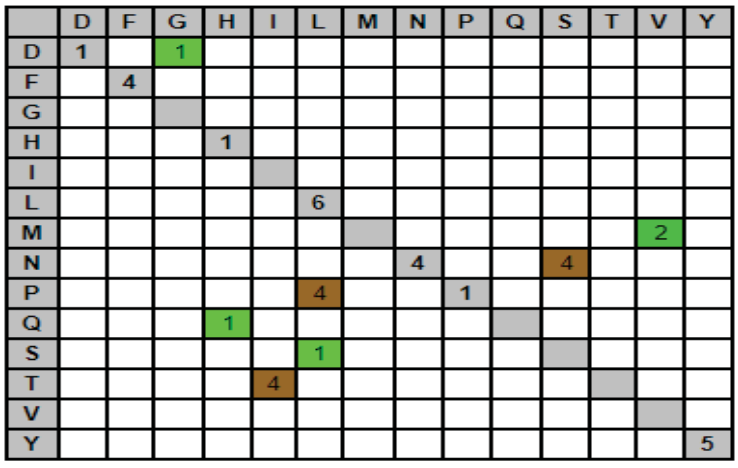

Figure 9. One nucleotide variation leads to a change in the amino acids.

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Conclusion

This study found the variants, i.e., the number of mutations and the associated SNPs in the SARS-CoV-2 genome from South Karnataka in India. Approximately 11 to 19 mutations traced in the genome were virulent. Mutation statistics do not show much variation in South Karnataka, containing 13 and 16 similar transformations in the respective reference genome. In South Karnataka, the variants have a lower differential rate. A further detailed study of the mutation is necessary to pinpoint the significant difference in the variant rates. Still, functional effects are not likely to affect much if the variant rates are low.

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