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SARS-COV-2 Lineage B.1.1.7: Origin, Spread, Symptoms and Countermeasures

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Abstract: ***A new strain of SARS-COV-2 virus was reported by United Kingdom on December 14,2020. It was detected in the Southeast part of England in October 2020 from the samples taken the month before during the COVID pandemic. The new strain which quickly began to spread at a rate of about 56% more than the original strain is known as SARS-COV-2 VOC 202012/01 (i.e. the first Variant of Concern from 2020, December) or lineage B.1.1.7. The variant is currently in 137 countries with701235cases reported. The variant B.1.1.7. carries a mutation in the RBD (Receptor binding domain) of the spike protein at position 501, where amino acid Asparagine (N) has been replaced with Tyrosine (Y), known as the N501Y mutation. This amino acid substitution in the spike RBD is the defined cause for the increased rate of infection greater than any other strains of the Novel Coronavirus, as it's known for increasing the binding affinity between the spike RBD and the human Angiotensin Converting Enzyme 2 (ACE-2).***

Keywords: SARS-COV-2, Lineage B.1.1.7, Variant of Concern, N501Y mutation

1. Introduction

Corona viruses are positive sense enveloped single-stranded RNA, that belongs to family Coronaviridae[4]. Coronaviruses cause illnesses such as common cold, Middle East respiratory syndrome (MERS) and severe acute respiratory syndrome (SARS). Coronavirus that caused disease COVID-19 was reported in December 2019 from the city of Wuhan in the Hubie province in China[3]. The virus is currently known assevere acute respiratory syndrome coronavirus 2 (SARS-CoV-2). COVID-19 was declared as a global pandemic by World Health Organisation (WHO) on 11thMarch 2020 and heretofore has caused grievous death of more than 3 million people worldwide[5,6].

Naming

The variant was initially known as the UK Variant or the Kent Variant sometimes. Scientifically, the variant erstwhile was known as the first Variant Under Investigation (VUI – 202012/01) in December 2020 by Public Health England (PHE), but was changed to Variant of Concern (VoC-202012/01) following the report made by Meera Chand and her colleagues, which was published by PHE[7,8]. The name Lineage B.1.1.7 was described in a report written by Andrew Rambaut and co-authors on behalfof COVID-19 Genomics UK (COG-UK) Consortium[9].

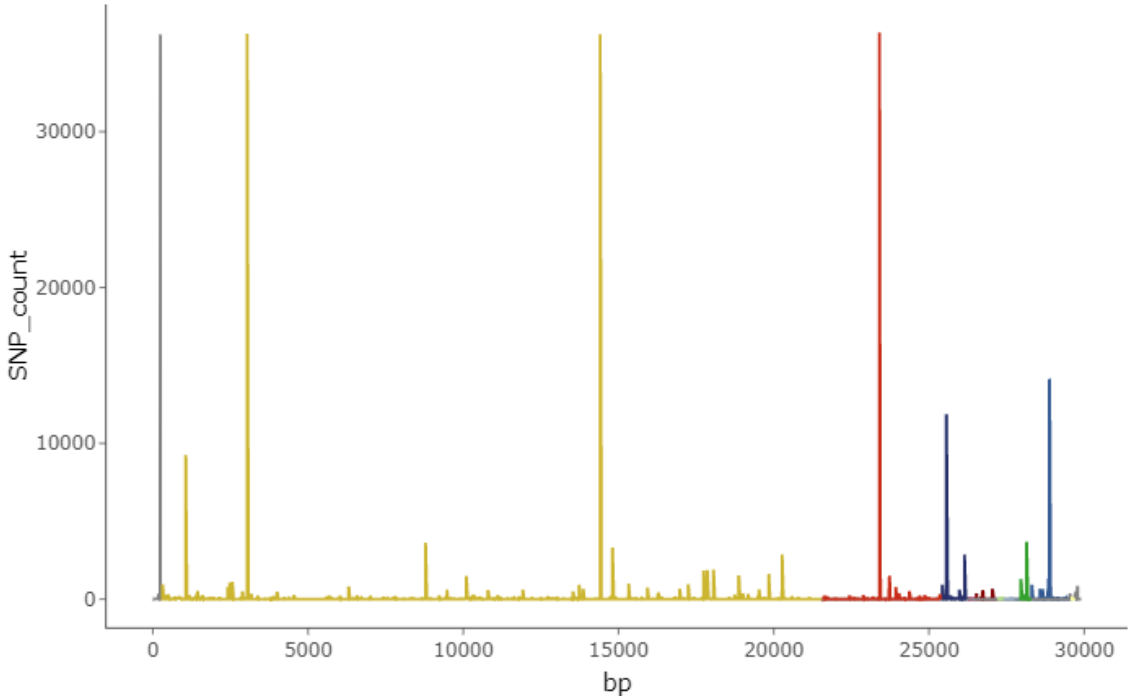
Detection

The earliest reports from the samples collected in Kent and Greater London, respectively indicated the presence of genomes belonging to lineage B.1.1.7 dates back to the month of September 2020, were submitted to the GISAID (sequence accessions EPI_ISL_601443 and EPI_ISL_581117, respectively) during which it was spreading at low-levels[2,8,9]. The variant inclined attention towards itself in the late November when the cases in the Kent (UK) didn't decline despite the nationwide restrictions. The Public Health England (PHE), discovered it's spread in London and Essex, when a cluster belonging to this lineage was discovered[2,8].

The variant possesses 13 other lineage defining mutations along with the N501Y and Del 69-70 respectively. Del 69-70 (the deletion in the amino acid Histidine and Valine at position 69 and 70) causes the failure of S-gene target (SGTF) in the at least one of the three RT-PCR based assays (i.e. Thermo Fisher Taq Path COVID-19 assay) performed[8,9,19].

Mutation

As a general rule mutations occur in viruses. Mutations occur during RNA replication. Viruses encoding RNA in their genome such as the SARS-CoV-2 and influenza are penchant to mutations, compared to the ones with DNA. The fate of newly emerging mutations is determined by natural selection. The mutations that possess advantages with respect to replication, transmission or escaping the immune system are favoured. Over the course of the spread of SARS-CoV-2, it was an essentiality to keep a check on the mutations occurring. Since the start of the pandemic the SARS-CoV-2 has shown a sluggish rate of mutation. Despite of such rate, there are more than 12000 catalogued mutations[10,11]. Mutations can vary from a single letter change in the genome to deletions or insertions in the long sequence. There are several major mutations such as N501Y, A222V, E484K, K417N etc. that were spotted in a confined region or at several places at once, as they caused major alterations in the way the virus responded and its contagiousness[12,13].



Mutation in B.1.1.7 strain:
The strain B.1.1.7 indicated a higher molecular evolution than the other strains of the virus. It contains 23 mutations in its genome among which 14 are non-synonymous, 6 are synonymous and 3 are deletions. The strain has caught major attention towards itself through the increased transmissibility in humans[8,14].

***-N501Y*:**
According to the research published by Rambaut *et al.* (2020), the mutation N501Y (a change from ASPARAGINE to TYROSINE in amino-acid position 501), found in the spike's protein RBD (Receptor binding domain), which is one of the six contact amino acids, plays a crucial role in binding affinity of RBD on the spike to the ACE-2(Angiotensin converting enzyme) in humans[9]. In an experiment performed by Jadson C. Santos and Geraldo A. Passos (2020), in silico tools were used to mutagenize the virus's RBD with Y501 mutation, at the protein level, it was found that that, the WT (wild type) was subside in comparison to the mutated strain showing a greater affinity to the human ACE-2 receptor[14].

It was found in the research that greater interactions were taking place in the B.1.1.7 lineage and the ACE-2 receptor. The usual distance of 3.5 angstrom between the hydrogen bond of K353 of ACE-2 and Y501 of spike RBD was reduced. Furthermore, interactions were increased between the ACE-2 and the supplementary residues like N500, G502, V503. Thus, the mutant strain resulted in increased hydrogen and apolar bonds of the Y501 site along with the supplementary sites, with the ACE-2 K353 and Y41 residues which accounted for the stable interaction[14,15].

-Del 69-70:
The deletion of the 69th and 70th amino acid in the N-terminal domain (NTD) of the spike (McCarthy *et al.* 2020), has also been concluded to be the cause of increase transmissibility or prevarication to the human immune response as it has been found in multiple lineages which accounted for RBD mutation[16].

2. Symptoms

Top symptoms reported by patients in United Kingdom

Symptom	Variant	Original strain
Cough	34%	27%
Fatigue/weakness	32%	29%
Headache	34%	30%
Muscle aches	26%	20%
Sore throat	23%	19%
Fever	23%	20%
Loss of taste	16%	19%
Loss of smell	14%	19%

Difference presented between the strains iswithin the margin of error.
Source: Office for National Statistics (ONS), United Kingdoms[17].

3. Vaccines

Oxford-AstraZeneca ChAdOx1 nCoV-19 (AZD1222) exhibited a promising result against the U.K. variant or B.1.1.7 strain, as published in *THE LANCET*. The research came to a conclusion that the clinical efficacy of vaccine was 81.5% for non-B.1.1.7 lineages and 70.4% for B.1.1.7 lineages. The vaccine ChAdOx1 caused a reduction in the duration of shedding as well as viral load, which bolstered the reduced viral infection[18].Other vaccines like BioNTech-Pfizer mRNA based COVID-19 vaccine BNT162b2 is also to be effective against B.1.1.7 strain[20].

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