Orenburg State Medical University Department of Microbiology, Virology, Immunology

Topic: Covid-19: features of the disease in India



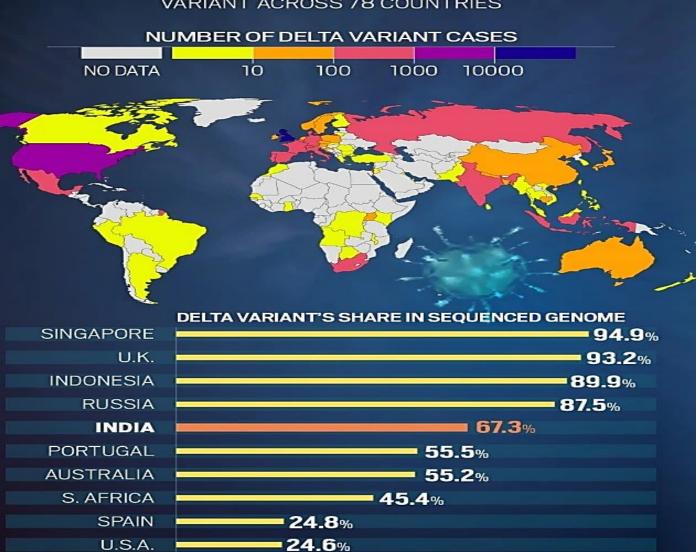
NAME:MUSKAN RASTOGI YEAR: 3rd year GROUP:312 Aznabaeva L. M., PhD, MD Aim: The purpose of this study presents the coronavirus spread in India, its characteristics along with the impact of various measures taken for it.

Materials and methods: Analysis of data from the National Center for Disease Control [CDC] and data from the Ministry of Health and Family Welfare.

Coronaviruses are large group of viruses that cause illness in humans and animals. Rarely, animal coronaviruses can evolve and infect people and then spread between people such as has been seen with MERS and SARS. The outbreak of Novel coronavirus disease (COVID-19) was initially noticed in a seafood market in Wuhan city in Hubei Province of China in midDecember, 2019, has now spread to 215 countries/territories/areas worldwide. WHO (under International Health Regulations) has declared this outbreak as a "Public Health Emergency of International Concern" (PHEIC) on 30th January 2020. WHO subsequently declared COVID19 a pandemic on 11thMarch, 2020.

GLOBAL SPREAD OF COVID-19'S DELTA STRAIN

MAPPING OF HIGHLY INFECTIOUS DELTA VARIANT ACROSS 78 COUNTRIES



INVASION of the CoVariants

The mutating coronavirus SARS-CoV-2 has spawned several variants that have scientists worried. Here's a lowdown on those detected in India's exploding second wave



B.1.1.7 UK variant

- Between 40 and 70% more infectious than other variants
- Raises death risk by about 60%
- · Vaccines seem to work against it



P1 Brazil variant

- More contagious than the initial coronavirus strain, can re-infect
- May be more virulent but further research needed
- E484K, 'escape mutation', helps the virus dodge antibodies



B.1.351 South Africa variant

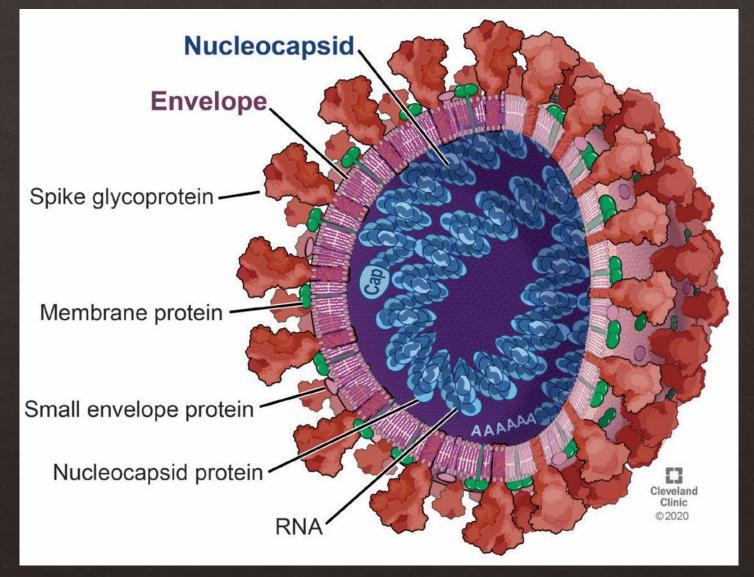
- Found in at least 20 countries, including the UK
- Mutation called N501 appears to make it more contagious
- Another mutation, called E484K, could help virus dodge a person's immune system and may affect how vaccines work



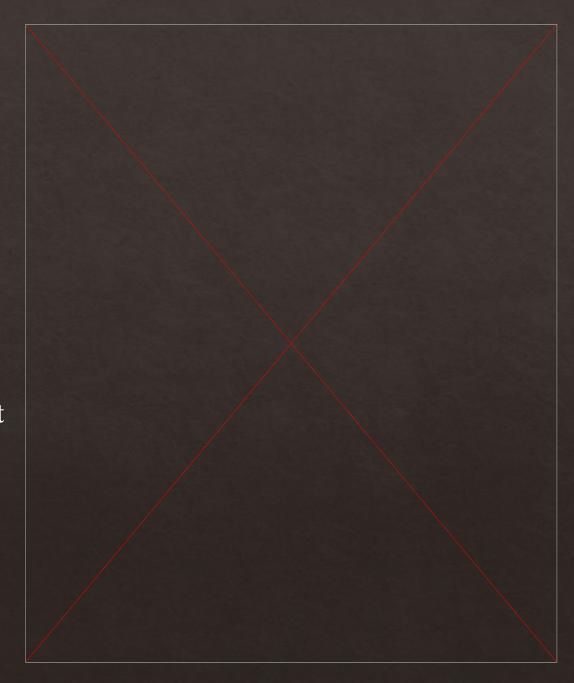
B.1.617 Double Mutant

- E484Q mutation is similar to another variant, the E484K, found in fast-spreading Brazil and South Africa regions
- Includes L452R mutation, which helps the virus escape our body's natural immune response
- This variant has been detected in at least 10 other countries, including the US, the UK, Australia, and New Zealand

The SARS-CoV-2 is a novel member of coronavirus family. Coronavirus are enveloped positive sense single strand RNA viruses (genome size 36–42 kb, diameter: 60–140 nm) having surface projections resembling a crown under the electron microscope. This crown like appearance is the basis behind the name, Coronavirus. These viruses are zoonotic pathogens; they originate in wild animals and spill over from wildlife into humans causing disease

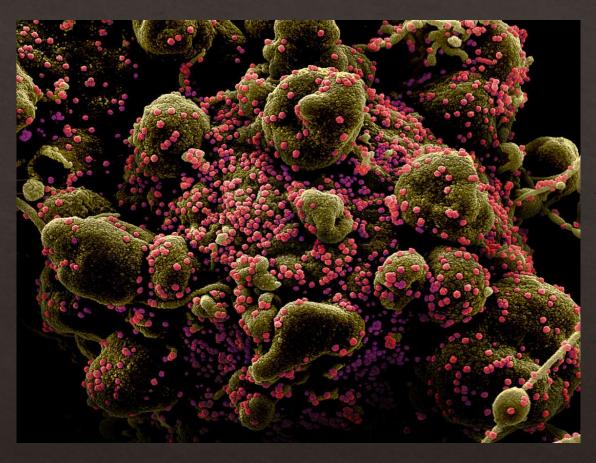


The B.1.617 variant of the virus, which has in part been blamed for India's explosive outbreak, has been dubbed a triple mutant variant since it is split into three lineages. The B.1.617.2, the Delta variant, does have increased transmissibility, which means it can spread easier between people. Experts believe the B.1.617 variant is driving the huge wave in infections. Delta (B.1.617.2 lineage)-The fourth variant of concern, B.1.617.2 also referred to as the Delta variant was initially identified in December 2020 in India and was responsible for the deadly second wave of COVID-19 infections in April 2021 in India.

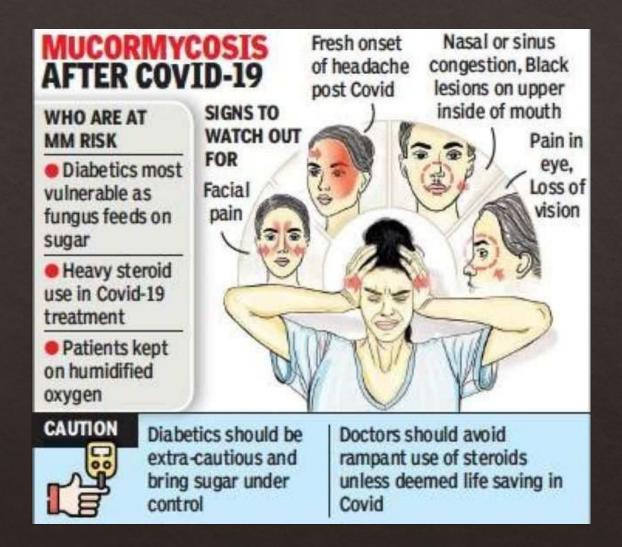


Double mutant: The double mutant variant, scientifically known as B.1.617, is a combination of E484Q and L452R mutations of the SARS-CoV-2 that cause COVID-19. As per reports, the variant is becoming increasingly common in India, but how many states have it in circulation remains unclear. So far, it has been detected among the positive cases in Maharashtra, Delhi and Punjab. Moreover, it has also been found in approximately 20% of samples from Maharashtra.

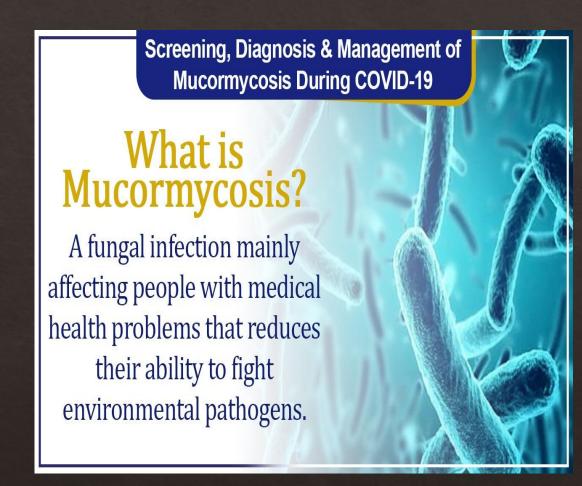
Triple mutant: This is the latest threat to the population of India as its detection coincides with the horrific rise in COVID-19 cases this month. This third mutation has emerged from the aforementioned B.1.617 strain and has been named B.1.618 or the Bengal strain. It has been found in circulation among the samples collected from Maharashtra, Delhi, West Bengal and Chhattisgarh.



Coronavirus disease 2019 (COVID-19) caused by severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) has been associated with a wide range of opportunistic bacterial and fungal infections. Both Aspergill us and Candida have been reported as the main fungal pathogens for co-infection in people with COVID-19. Several cases of mucormycosis in people with COVID-19 have been increasingly reported world-wide, in particular from India.



- The primary reason that appears to be facilitating Mucorales spores to germinate in people with COVID-19 is an ideal environment of low oxygen (hypoxia), high glucose (diabetes, new-onset hyperglycemia, steroid-induced hyperglycemia), acidic medium (metabolic acidosis, diabetic ketoacidosis), high iron levels (increased ferritins) and decreased phagocytic activity of white blood cells (WBC) due to immunosuppression (SARS-CoV-2 mediated, steroid-mediated or background comorbidities) coupled with several other shared risk factors including prolonged hospitalization with or without mechanical ventilators.
- Mucormycosis is an uncommon but a fatal fungal infection that usually affects patients with altered immunity



Conclusion. In our work, we analyzed various information resources of India. Due to the fact that so many events are happening in India right now, it becomes necessary that we study the current situation in India using data analysis methods and develop various plans for the future that can be useful to Indian administrators and medical professionals.diabetes mellitus (DM) has been the most common risk factor linked with mucormycosis in India.

THANKS FOR YOUR ATTENTION!

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