

OMICRON or B.1.1.529: Are We Going back to Point Zero

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According to an statement from Director-general of the World Health Organization Dr. Tedros Adhanom Ghebreyesus "Omicron is spreading at a rate we have not seen with any previous variant," in conjunction with the data reported by worldometer on December 15, 2021, indicating a total of 5,342, 179 deaths so far from the coronavirus COVID-19 outbreak; and 272, 146, 299 confirmed cases in 222 countries and territories worldwide, while the fatality rate is still being assessed. This new variant of concern (VOI); SARS-CoV-2 -B.1.1.529 or "Omicron" is being discussed at every level since November 26, 2021, suggestive of potentially more transmissible, and confer resistance to therapeutics, or partially escape infection- or vaccine-induced immunity. This new variant though first reported by South Africa has been isolated in Netherland couple of days ago around third week of November 2021. Currently, as reported by WHO, Omicron accounts for 90% of COVID-19 cases in South Africa and is a growing problem in Europe; has been reported from approximately 80 countries, and at least thirty seven (37), U.S. states.

In line with Merriam Webster, this name "Omicron" is the 15th letter of the Greek alphabets that means small "O". Traditionally, the WHO uses Greek letters to name variants, for easy communication instead of complicated scientific code numbers. WHO best practices for naming new diseases to avoid names that may cause offence to any culture, society, nation, region, profession or ethnic group(s).

"The Technical Advisory Group on SARS-CoV-2 Virus Evolution (TAG-VE)", is an independent group of experts that periodically monitors and evaluates the evolution of SARS-CoV-2 and evaluates if certain genetic changes, mutations and combinations of mutations are appearing that might alter the behaviour of the virus. On November 26, 2021, the TAG-VE was convened to assess the SARS-CoV-2 variant: B.1.1.529, after detailed phylogenetic analysis and correlating taxonomic characterization with evolutionary changes among similar group of organisms. This new variant was given scientific name SARS-CoV-2: B.1.1.529 that represents its lineage, origin and the chain of evolution from SARs-CoV-2, to alpha, beta, theta.....and now omicron.

Paul et al reported in 2020, SARS-CoV-2 is a member of Betacoronavirus of subgenus Sarbecovirus. A unique strain of RNA viruses that have not been previously observed in humans. The virus has wide host adaptability and is capable of causing severe diseases in humans, masked palm civets, mice, dogs, cats, camels, pigs, chickens, and bats, typically causes respiratory and gastrointestinal sickness in both humans and animals. Comparing the novel 2019 coronavirus to other human coronaviruses (HCoV) and known animal coronaviruses; directed scientists to explore more about how this virus infects and insight into potential regions for testing and diagnosis.

As mentioned above, this SARS-CoV-2 is a RNA virus and its RNA transcript encodes multiple genes. These target regions are very useful for real-time reverse transcription PCR (RT-PCR) testing and helped diagnosing multiple variants. These regions code for the replicase complex ORF1ab, the spike protein (S), viral envelope (E), membrane (M), and the nucleocapsid proteins (N). This rareness of the region is the key in deciding the target sites for SARS-Co-V-2 genome amplification techniques. Accompanied by SARS-CoV and MERS-CoV, there are many other coronaviruses that are known for their pathogenicity, including four other human coronaviruses HCoV-OC43, HCoV-HKU1, HCoV-NL63, and HCoV-229E. These viruses are important contributor to the global occurrences of other respiratory infections, like common cold.

A lot of the first reported cases of Omicron variant infection seem to be of mild nature, but there are potential overlapping symptoms of mild COVID-19, with infection like flu, common cold etc. That is why, any test for SARS-CoV-2 should be specific enough to not catch these genetic relatives. In case of flu, which is caused by four different types of influenza viruses, overlapping of symptoms is possible, but due to immensely different genetic makeup and coding regions, there is a lower risk of cross reactivity and miss-diagnosis.

Current SARS-CoV-2 PCR diagnostics seems continue to detect this new variant, omicron. According to WHO, several labs have indicated that for one widely used PCR test, one of the three target genes is not detected (called S gene drop-out or S gene target failure or SGTF) and this test can therefore be used as marker for this variant, pending sequence confirmation. This method is grounded on rapid screening for SGTFs by PCR (RT-PCR) to point out potential cases of Omicron infection by gene amplification and sequencing. Virus that displays SGTFs have a higher probability to be Omicron (although SGTFs are not exclusive to Omicron) based on a mutation (69–70 deletion) that reduces SGTF amplification in some of the currently available PCR assays. Using this approach, this variant has been detected at faster rates than previous heaves in infection, suggesting that this variant may have a growth benefit. Tulio de Oliveira, the director of South Africa's Centre for Epidemic Response and Innovation aid that the most concerning difference between Omicron and other known variants is that it has a "very unusual constellation of mutations". Those roughly 50 mutations of note include over 30 on the virus's spike protein, including ten mutations on a key protein (the ACE2 receptor) that helps the virus infect humans three of them D614G, N501Y and K417N are considered more potent— while the Delta variant has two mutations on the ACE2 receptor, and the Beta variant has three.

As stated by WHO, a variant, with genetic changes that might affect virus transmissibility, disease severity, immune escape, diagnostic or therapeutic escape; while causing significant community transmission or multiple COVID-19 clusters, in numerous countries with rising number of cases over time, or other obvious epidemiological impacts to advocate an emerging risk to global public health is designated as SARS-CoV-2-VOI (variant of Interest). While a variant, that matches the definition of a VOI and, through a comparative assessment, has been demonstrated to be linked with one or more of other changes at a global level of public health significance; OR increase in virulence or change in clinical disease presentation; OR decrease in effectiveness of preventive measures or available diagnostics, vaccines, therapeutics is designated as SARS-CoV-2 VOC (variant of Concern).

Overall, the WHO currently lists 5 Variants of Concern (VOC) i.e. Omicron (B.1.1.529), identified in southern Africa in November 2021; Delta (B.1.617.2), which emerged in India in late 2020 and spread around the world, Gamma (P.1); which emerged in Brazil in late 2020; Beta (B.1.351), which emerged in South Africa in early 2020; Alpha (B.1.1.7), which merged in Britain in late 2020; and two Variants of Interest (VOI) i.e., Mu (B.1.621), which emerged in Colombia in early 2021, and Lambda (C.37), which emerged in Peru in late 2020.

It is not easy to tell the difference between different viruses just on the basis of symptoms. Like for example symptoms of the delta COVID variant are similar to that of the alpha COVID strain (B.1.1.7) but are found to cause more cold-like symptoms. Alpha COVID strain develops fatigue, headache, sore throat, fever or loss of taste and smell, while COVID symptoms linked to the omicron variant have been described as "extremely mild" by doctors in South Africa who first raised the alarm over the new strain. They say that the patient didn't have a sore throat, but more of a "scratchy throat", no cough or loss of taste or smell —symptoms that until that time have been associated with previous strains of the coronavirus.

Herewith winter season, influenza and multiple variants of SARS-COV-2 around, the prevalence of current Omicron variant has rapidly jumped sevenfold with 43 reported cases in the US alone as of December 11, 2021. According to the CDC, this highly mutated variant of the coronavirus could inflame the pressure on a health system already stressed almost everywhere, as the delta variant continues its own surge. Current data indicates that the Delta variant is dominant around the world, but researchers are closely watching other VOCs including Omicron.

It's a natural phenomenon, just like flu virus, we are going to see variants coming up like this omicron continuously. As per CDC, the recent emergence of the Omicron variant (B.1.1.529) further emphasizes the importance of vaccination, boosters, and general prevention strategies needed to protect against COVID-19. The vaccines that we have for COVID-19 are expected to protect against severe illness, hospitalizations, and deaths due to infection with the Omicron variant. However, development and prognosis of infections in people including those who are fully vaccinated can be different depending on individual's immune response. The best way is to keep continue using all recommended standard precautionary measures and see what we will find out as we will find more about this variant.

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