New Genome Study Reveals that Omicron will Outcompete Delta Variant for Next 4-5 Months Globally

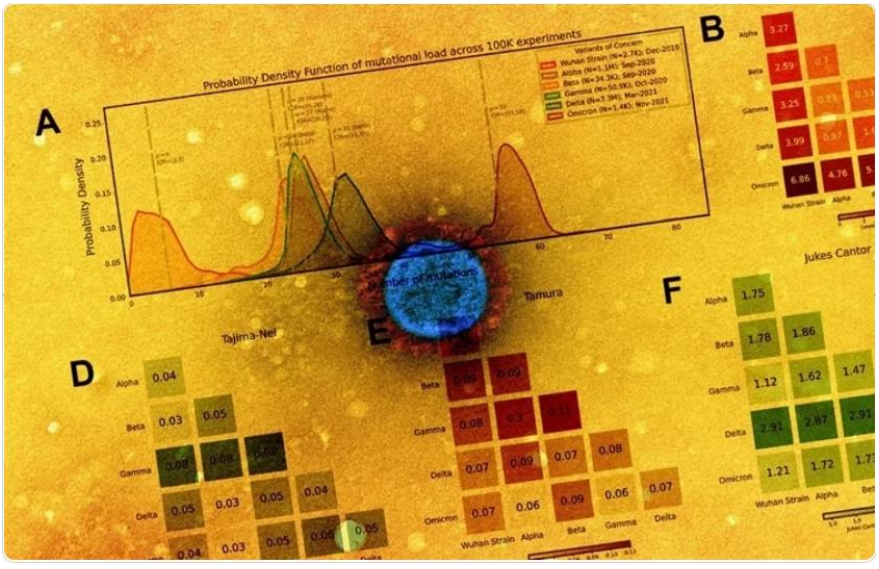
Since the onset of the COVID-19 pandemic, several severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) variants of concern (VOC) have emerged, leading to repeated surges in cases, deaths, and hospitalizations throughout the world. Classification of these variants by the Phylogenetic Assignment of Named Global Outbreak Lineages (PANGO) nomenclature shows that although they have descended from a common ancestor, they are not direct descendants of one another.

The PANGO lineages that have been corresponded to the VOCs include Alpha variant (B.1.1.7 and Q lineages), Beta variant (B.1.351 and descendant lineages), Gamma variant (P.1, which is a descendant of B.1.1.28, and descendant lineages), Delta variant (B.1.617.2 and AY lineages), and Omicron variant (B.1.1.529 and BA lineages).

All the variants were reported to have evolved from the B.1 lineage, while Alpha, Gamma, and Omicron also have B.1.1 as an additional parent lineage. However, these classifications do not describe the degree of distinctiveness between the variants or provide insights into the genetic properties of the variants.

The evolution of SARS-CoV-2, like all other viruses, occurs via the mutation of its genome; these mutations alter the amino acid sequences of the viral proteins. The mutations can be either positively or negatively selected based on their impact on viral fitness. Mutations in several regions, such as the N-terminal domain (NTD) of the Spike glycoprotein and receptor-binding domain (RBD), improved viral fitness. Although much attention has been given to individual mutations at the amino acid level, limited attention has been given to the nucleotide sequence level.

A new study hypothesized that the emergence of more immune invasive or transmissible variants of SARS-CoV-2 was associated with increased genetic distinctiveness from the original or previous strains.

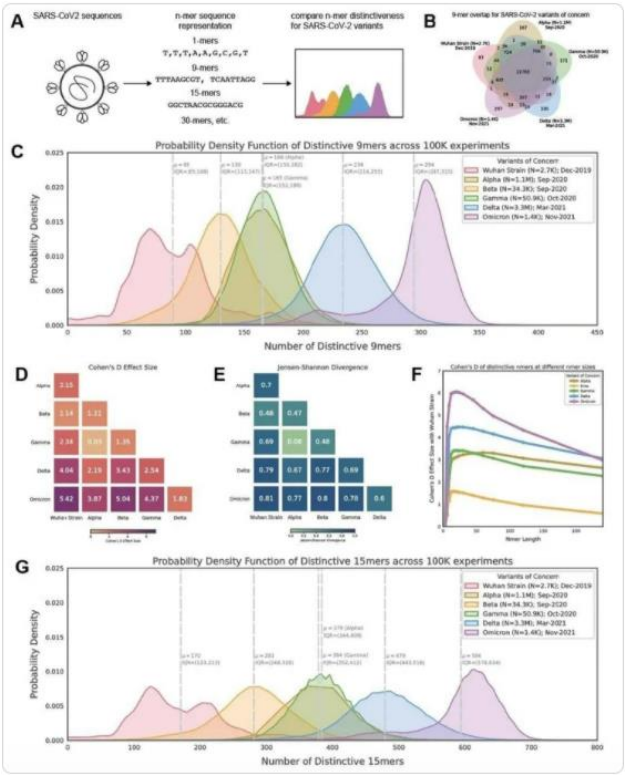


To test the hypothesis, the study introduced a new methodology that quantifies the number of distinct nucleotide n-mers (of various sizes) in VOCs to estimate the degree of viral evolution.

Study

The study involved calculating and quantifying the number of distinctive n-mers for SARS-CoV-2 sequences from the original reference strain (PANGO lineage A) and five VOCs, Alpha, Beta, Gamma, Delta, and Omicron, that were obtained from the GISAID database. In addition, the number of amino acid mutations for the sequences obtained from GISAID were determined and compared to the original Wuhan-Hu-1 strain of SARS-CoV-2.

Multiple sequence alignment (MSA) was carried out for the sub-sampled SARS-CoV-2 genomes to calculate the phylogenetic distance. Finally, the distinctiveness of n-mers for a specific SARSCoV-2 lineage was calculated using an alternative metric, A*(1-B).



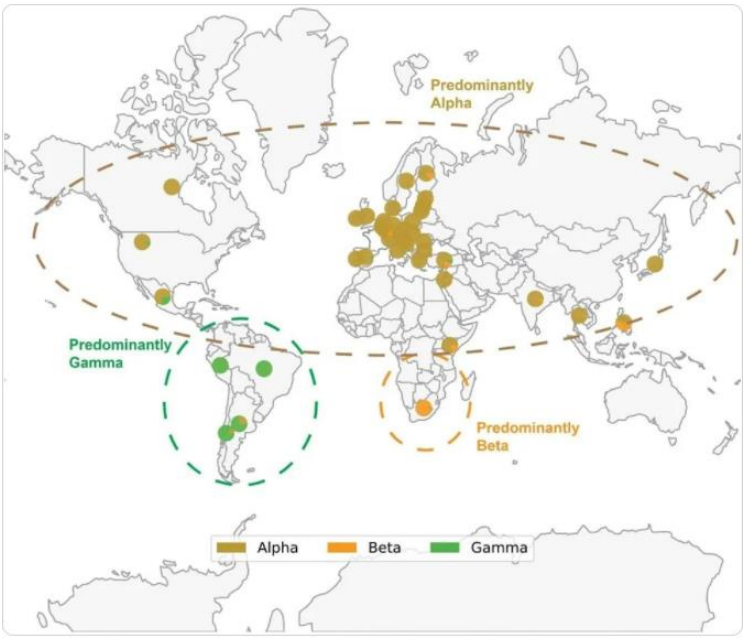
Results

The results reported that from each genome, a distinctive nucleotide 9-mers (DN9s) were derived that was present in a given lineage but absent from all others. The number of DN9s corresponded to the time of emergence and was found to be highest for Omicron, followed by Delta, Alpha, Gamma, and finally Beta variant. The Omicron sequence was also found to have more DN9s than all other VOCs.

Omicron was indicated to be the most highly mutated VOC, while the phylogenetic distance between Gamma from Alpha and Beta was the most notable. The results also suggest that the newly emerging SARS-CoV-2 variants were genetically distinct from the original strain and that they comprised unique nucleotide sequences that resulted in the distinctiveness. The distinctiveness was also found to increase within a lineage with evolutionary time.

The current study thus provides a new methodology that will help the researchers identify and assess the distinctiveness of any new SARS-CoV-2 variants compared to the previous ones. However, further research is required to determine whether this method will be able to classify lineages as VOCs earlier

than the time taken currently, how vaccination would impact the SARS-CoV-2 genomic diversity, and also determine whether SAR-CoV-2 infection would progress towards seasonality or endemicity.



Limitations

The study had certain limitations. First, since the number of Omicron sequences available in the GISAID database is currently low, it can lead to oversampling. Second, apart from nucleotide 9-mers, protein-coding nucleotide n-mers or amino acid n-mers should also be considered in the determination of genomic diversity. Third, the study can be sensitive to the lineage composition in the complement group. Finally, further research is required regarding the relationship between genomic distinctiveness metrics with phylogenetic depth and evolutionary time.

Source:

https://www.news-medical.net/news/20211229/Omicron-will-outcompete-Delta-variant-for-next-4-5-months-globally-Genome-study.aspx