The Emerging Strains of SARS-CoV-2 and Current Vaccine Strategies: A Systemic Review

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INTRODUCTION Severe Acute Respiratory Syndrome Coronavirus 2 (SARSCoV-2) is a single-stranded positive-sense Ribonucleic Acid (RNA) virus that has burst upon the world, causing millions of deaths worldwide. Inadequate public health measures cause the virus to evolve more rapidly, acquiring several mutations Though the virus has a "Proofreading" activity, several lineages and clades have been established based on the characteristic given mutation . The natural mutation most probably occurs due to a chance event called the "Founder effect" that either helps the virus survive or be culled out from the population . Since March 2020, the S:pD614G variant was predominant worldwide.

DIFFERENT CLADES OF SARS-COV-2 The SARS-CoV-2 virus is classified into seven major clades based on its marker mutation, namely S and L, later splitting L into G and V, and then G into GH, GR, and GV [13]. The S clade strains refer by nucleotide changes at positions C8782T and T28144C (NS8: Sp.L84S). The L clade strain is the wild version of the genome with no mutations. The V clade was designated by clustered co-occurring mutations at G11083T (NSP6: Sp.L37F) and G26144T (ORF3a: Sp.G251V). The mutation in nucleotides at C241T, C3037T, A23403G, and the amino acid change S-D614G was referred to as G clade. Additional G28882A mutation with amino acid changes in the N protein N:pG204R and ORF3a:pQ57H (G25563T) refer to GR and GH clade, respectively [2,14]. An additional mutation in the spike protein along with the S:pD614G, the nutation at position C2.

TRANSMISSIBILITY OF THESE NEW VARIANTS Several mathematical modeling studies mainly determine transmission probability. The European variant although does not account for a second wave but its transmissibility arose due to the lower restriction in traveling. And after Europe, it became the dominant variant in America indicating a higher transmission rate. Early reports showed that the new variant VOC 202012/1 is 75% more transmissible than the other circulating variants with a R0 estimation of 0.39-0.93 for SARS-CoV-2 . However, R values generated using different mathematical models based on mutational characteristics also propose a higher transmissibility rate. The South African variant 501Y.V2 also has a higher transmissible rate (56%) than the three main circulating variants three main variants (B.1.1.54, B.1.1.56, and C.1) in South Africa . But no data was found for the diverge novel P.

CONCLUSION The world is now facing the most alarming pandemic of this century involving SARS-CoV-2 that has caused immense death. Unremitting mutation if SARS-CoV-2 has once again put the world in a dire situation. Several important mutations caused the virus to transmit faster and reduced binding affinity with the neutralizing antibody, challenging some of the detecting methods. This current study describes the overall mutations of SARS-CoV-2 in different geographical regions, their transmissibility. This study also describes current vaccination strategies along with alternative detection methods that can be useful in detecting different strains of SARS-CoV-This data could help identify differently distributed variants after sequencing and detecting them in a precise manner. The overall study will also aid in understanding the mutations as well as their different clades and lineages.