The Variants of SARS-CoV-2 are in relation to the amino acids mutated structures. Here we will review the changes to the amino acid structure and chemistry. This will describe where the variants are seen, and their effect on the vaccines currently available**.** Many of these mutations are found on the spike proteins (Howes, 2021.)

E484K is the name of the deletion where Glutamic Acid ($C_5H_9N_1O_4$) deletion to Lysine ($C_6H_{14}N_2O_2$) at the 484 position. Glutamic Acid is non-essential amino acid that forms proteins. The structure of Glutamic Acid is a Negative Charged Side Chain. Changed to Lysine which is a Cationic side chain. Lysine attaches to the central carbon of the amino acid back bone. This mutation is found in the Beta variant, and the Gamma variant. This mutation is an escape mutation. (Freud, 2022.) This mutation happens at the same point that the e484q, shows similar effects.

E484Q is the name of the mutation where Glutamic Acid ($C_5H_9N_1O_4$) mutated to Glutamine ($C_5H_{10}N_2O_3$) in the 484 position. The structure of Glutamic Acid is an amide side chain. Glutamine structure is an amide side-chains. This is a spike mutation, found in the Delta variant.

N501Y is the name of the mutation where Asparagine ($C_4H_8N_2O_3$) mutated to Tyrosine ($C_9H_{11}N_1O_3$) in the 501 position. Asparagine structure is an amide side-chains, its structure changes to aromatic side chain. Seventeen amino acid swaps and one deletion in various viral proteins, this receptor binding domain RDB. This can increase the binding recognition to further mutate. This mutation is found in the Alpha, Beta and Gamma variant. For the Gamma variant vaccines do not show to be affective to it. Vaccines are shown to be less effective towards this Beta variant. The mutations in the Alpha variant work together to spike the binding to the ACE2. The pathogens bind strongly to human cells and spread fast though out the body (Freud, 2022)

P681H is the name of the mutation where Proline $C_5H_9N_1O_2$ mutated to Histidine ($C_6H_9N_3O_2$). The structure of Proline is aliphatic side-chains that mutates to a cationic side chain. This mutation is found in the Delta variant. These mutations help the virus escape the immune system.

L452R is the name of the mutation where Leucine $C_6H_{13}N_1O_2$ exchanged to Arginine $C_6H_{14}N_4O_2$ at position 452. This swap happens in the receptor binding domain. Leucine is branched-chain amino acid, one of the hydrogens attached to the alpha carbon. Leucine is a aliphatic side chain, changed to cationic side chain. This mutation is found in the Epsilon, and Delta variant. The Epsilon can bind much stronger. Vaccines aren't less affective towards this Epsilon variant.

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