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**Scientific Literacy Background Essay (Part 1)**
**BIOL - 293 - Dr. Christina Steel**
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The SARS virus predates prior to its ambitious presence it contributes to modern day. Within a quarter of a century, three highly communicable and deleterious coronaviruses have materialized, "namely SARS-CoV, MERS-CoV and SARS-CoV-2 (Zhu, 2020)." Everchanging, these viruses, specifically SARS-CoV-2, have proven their ability to mutate at an exceeding rate and transmit swiftly from host to host. By increasing the understanding of how SARS-CoV-2 mutates, we can improve the effectiveness of current treatments and remedies for the future.

Initially we will discuss the mutation of certain amino acids. Discussing changes about these amino acids contributes to the alteration of a spike protein in dramatic cases. L452R is an alteration of amino acid #452, Leucine. This leucine switched with an arginine amino acid. This alteration may seem insignificant, however this change in polarity from non-polar to polar has a dramatic effect on the protein structure. Leucine is a hydrophobic amino acid with an isobutyl side chain, generally buried within folded proteins (Baldwin and Lapointe, 2003). This would mean leucine is typically a backbone structure that adds to the length of the protein without changing the shape much. Arginine is one of the lowest called amino acids, making its rareness much greater than other other amino acids (Baldwin and Lapointe, 2003). This is very important as the structure of the protein changes angle due to the polarity of the amino acid. The consequent spike protein could then be altered.

N501Y amino acid change incorporates Tyrosine into the #501 spot Asparagine. Asparagine is a polar molecule with an amide group with a relative neutral charge. That being said, it is beneath many other amino acids in a chain. Tyrosine is a nonpolar molecule with an aromatic group. Similar to L452R, this change would significantly change the structure of the protein synthesized. P681H works likewise to both of these mutations. Proline #681is a nonpolar cyclic compound found often at the ends of loops or or turns (Baldwin, 2003). This amino acid shows a turn in the protein structure and so it is important to the shape of the amino acid. Histidine is a positively charged, polar compound serving a role in stabilizing the folded structures of proteins. When histidine replaces proline, the nonpolar to polar change has a great effect on the shape of the protein.

Polypeptide change E484K involves amino acids glutamic acid at position #484 and lysine. Glutamic acid is a polar molecule and has a carboxyl group at its end. Lysine is a polar molecule however basic, making it positively charged and highly reactive. Baldwin (2003) goes on to state that Lysine partakes in numerous reactions at active center enzymes. Although both molecules are polar so the protein may not be altered geometrically severely, however the basic

properties of lysine could definitely lead to significant changes. E484Q involves the amino acid mutation of glutamic acid at the previously mentioned position mutating to glutamine. Glutamine is a polar but neutral molecule that is the amide of glutamic acid (Baldwin, 2003). This makes glutamine relatively unreactive and would definitely change the outcome of the protein structure, but only slightly, because of glutamine being polar.

**References**

Baldwin, T. & Lapointe, M. (2003). *The Chemistry of Amino Acids.* The Biology Project [Online], Available: http://www.biology.arizona.edu/biochemistry/

Zhu, Z., Lian, X., Su, X. et al. (2020). *From SARS and MERS to COVID-19: a brief summary and comparison of severe acute respiratory infections caused by three highly pathogenic human coronaviruses.* Respir Res 21, 224. https://doi.org/10.1186/s12931-020-01479-w

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