A Mechanistic Basis for the Analysis of SARS-CoV-2 Omicron Variant Severity

New COVID-19 variants are caused by structural changes in the antibody-RBD complex of the SARS-CoV-2 protein. Thus, identifying regions in this complex where mutations are less prone is crucial in identifying areas of the protein that are less likely to evade antibodies, which can set a blueprint for future vaccine creation.

Dataset

- Data obtained from GISAID of 8,377 patients worldwide that had COVID-19 Omicron variant
- Used data of Spike protein mutations and patient severity

Study Procedure

1. **Mutation M**
   - # of Patients with M
   - # of Patients without M

2. \[ \text{RMSD} = \sqrt{\frac{\sum_{i=0}^{N} [m_i * (X_i - Y_i)^2]}{M}} \]

3. \[ \Delta \Delta G = \Delta G_{\text{Wild Type}} - \Delta G_{\text{Mutant}}, \text{ where} \]
   \[ \Delta G_{\text{folding}} = \Delta H - T\Delta S \]

4. \[ Z = \frac{W_{DDG}}{W_{DDG} + W_{SE}} Z_{DDG} + \frac{W_{SE}}{W_{DDG} + W_{SE}} Z_{SE} \]

Results & Applicability

- Comparison of \( \Delta \Delta G \) values in the Receptor Binding Domain
- Mutated RBD has DDG values consistently above 0 in comparison to the wild type \( \rightarrow \) isolated mutations have destabilizing implications

Mutated RBD (A) shows red (electronegativity) in greater proportion
- Mutations decrease electrostatic potential, which means that the vaccine binding is looser

1. Results prove that this set of mutations induces structural implications on SARS-CoV-2 virus
   a. These mutations can be targets of reduced vaccine evasion

2. For any virus which we have patient and genomic data, we can apply this strategy to create more targeted vaccines

All graphics generated by researcher unless cited otherwise.