

Preliminary sequence-level analysis of SARS-CoV-2 variants: Identifying signature regions contributing to variant specificity

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ABSTRACT

Introduction: SARS-CoV-2, the virus responsible for COVID-19, has evolved into multiple variants with varying transmissibility, pathogenicity, and vaccine efficacy. These variants are defined by mutations in the viral genome, particularly in regions affecting host cell binding and immune evasion. Identifying these mutations is crucial for vaccine development and understanding variant-specific behavior. **Objective:** This study aims to perform a preliminary sequence-level analysis of various SARS-CoV-2 variants to identify specific genomic regions that contribute to the distinct characteristics of each variant. **Materials and Method:** Sequence data from several SARS-CoV-2 variants, including Alpha, Delta, and Omicron, were aligned using a manual approach. The alignment focused on comparing nucleotide sequences to identify conserved and variable regions that could serve as signature regions for each variant. Key nucleotide differences were analyzed to understand their potential impact on variant specificity. **Results:** The alignment revealed several key genomic positions where nucleotide variations were present among the SARS-CoV-2 variants. For example, significant differences in nucleotide composition were observed in the initial regions of the sequences, particularly between the Alpha variant and other SARS-related coronaviruses. These variations suggest potential signature regions that may influence the unique characteristics of each variant, such as increased transmissibility or immune evasion. **Conclusion:** This preliminary analysis identified signature regions within the SARS-CoV-2 genome that likely contribute to the specificity of different variants. These findings provide valuable insights into the functional differences between variants, although further research is required to fully understand their implications. Continuous monitoring and analysis of SARS-CoV-2 mutations are essential for managing the ongoing pandemic and preparing for future variants.