Natural variations within the glycan shield of SARS-CoV-2 impact viral spike dynamics

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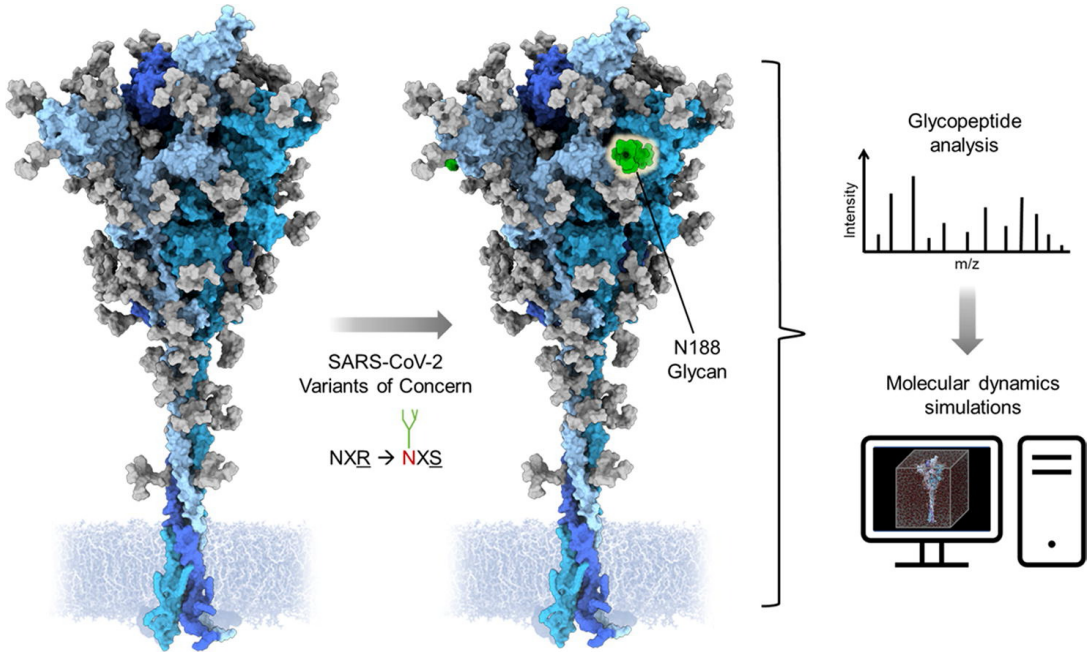
The effectiveness of current protection against SARS-CoV-2 infection whether acquired spontaneously or by vaccination, is altered by SARS-CoV-2 variants. Determining the effect of mutations on the antigenic surface is made easier by understanding the shape of the viral spike. One type of mutation which can drastically affect the antigenic surface is the introduction / deletion of glycosylation sites, which can affect the antigenic structure in ways that go beyond just shielding. We examine the glycosylation of a recombinant viral spike of the P.1 (Gamma) strain, which has three more N-linked glycan sites than the comparable the Wuhan strain. In this study, we ascertain the site-specific glycosylation of Gamma strain and determine the dynamics using molecular dynamic (MD) simulations. The N188 glycosylation site is observed to be novel in the gamma strain and the resulting Man 5 glycan occupies a cavity in the NTD, which affects the dynamics of this domain, according to structural modelling and molecular dynamics. These findings point to a mechanism by which mutations that change viral glycosylation sites influence the antigenic surface's structural composition.



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Bibliographic references:

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