

The Origin of SARS-CoV-2



Andersen et al have described the genomic structure of SARS-CoV-2. Notably, the virus has a receptor binding domain consisting of 6 amino acids which not only differentiates it from SARS-CoV but also confers it with ability to bind human or human-like Angiotensin Converting Enzyme-1 (ACE2) with high affinity. Computation studies showed that this receptor binding is not ideal, suggesting that the high affinity binding is a result of natural selection.

Further, a polybasic furin cleavage site on the highly variable spike protein is also unique to SARS-CoV-2. This site allows cleavage by proteases and determines viral host range but it's function in transmission and pathogenicity is unknown.

These features indicate that SARS-CoV-2 is not a laboratory manipulated virus but possibly a result of natural selection in an animal host like the pangolin or in humans following transmission from a zoonotic source. More data will be needed to prove either of the hypotheses.

Article: [Andersen et al, The proximal origin of SARS-CoV-2.](#)

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