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Commentary

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An Overview 0f Characteristics of SARS-Cov-2 And COVID-19 And Therefore the Proximal Origin of SARS-Cov-2

Akhila Sabbineni*

Coronaviruses area unit a various cluster of viruses infecting many alternative animals, and that they will cause delicate to severe metastasis infections in humans. In 2002 and 2012, severally, 2 extremely unhealthful coronaviruses with animal disease origin, severe acute metastasis syndrome coronavirus (SARS-CoV) and geographic area metastasis syndrome coronavirus (MERS-CoV), emerged in humans and caused fatal respiratory disorder, creating rising coronaviruses a replacement public health concern within the ordinal century [1]. At the tip of 2019, a unique coronavirus selected as SARS-CoV-2 emerged within the town of metropolis, China, and caused a deadly disease of surprising virus infection. Being extremely transmissible, this novel coronavirus sickness, conjointly called coronavirus sickness 2019 (COVID-19), has unfold quick everywhere the planet [2,3]. it's irresistibly surpassed respiratory illness and MERS in terms of each the quantity of infected individuals and therefore the abstraction vary of epidemic areas.

The proximal origin of SARS-CoV-2

Our comparison of alpha- and betacoronaviruses identifies 2 notable genomic options of SARS-CoV-2: (i) on the premise of structural studies7,8,9 and organic chemistry experimentS [3,4] SARS-CoV-2 seems to be optimized for binding to the human receptor ACE2; and (ii) the spike supermolecule of SARS-CoV-2 encompasses a purposeful polybasic (furin) cleavage website at the S1–S2 boundary through the insertion of twelve nucleotides8, that to boot light-emitting diode to the anticipated acquisition of 3 O-linked glycans round the website.

Differences between SARS-CoV-2 and SARS-CoV

According to the principle of international commission on virus classification, the coronavirus identification primarily depends on the similarity of the aminoalkanoic acid sequences of the seven domains encoded by ORF1ab, as well as ADRP, nsp5, and nsp12–16. thanks to the very similar (more than 90%) aminoalkanoic acid sequences within the seven domains, each SARS-CoV-2 and SARS-CoV belong to the taxonomic group Coronavirinae within the family Coronaviridae of the order Nidovirales and area unit classified as SARS-like species, though they're classified into completely different clusters.

the previous belongs to the bat-like coronavirus cluster and therefore the latter to the respiratory illness cluster. Biological process analysis showed that SARS-CoV-2 encompasses a longer branch length compared to its nearest relatives, as well as bat-SL-CoVZC45 and bat-SL-CoVZXC21; moreover, it's genetically completely different from SARS-CoV. SARS-CoV-2 has solely 79.5 and 400th similarity with SARS-CoV and MERS-CoV, severally, indicating an outsized genetic distance. At constant time, the S-protein similarity between SARS-CoV and SARS-CoV-2 is additionally comparatively low at 76.5%. Mutations within the receptor-binding domain of SARS-CoV-2.

The receptor-binding domain (RBD) within the spike supermolecule is that the most variable a part of the coronavirus genome1,2. Six RBD amino acids are shown to be important for binding to ACE2 receptors and for deciding the host vary of SARS-CoV-like viruseS. With coordinates supported SARS-CoV, they're Y442, L472, N479, D480, T487 and Y4911, that correspond to L455, F486, Q493, S494, N501 and Y505 in SARS-CoV-2. 5 of those six residues take issue between SARS-CoV-2 and SARS-CoV. On the premise of structural studies associate degreed organic chemistry experiments SARS-CoV-2 appears to own an RBD that binds with high affinity to ACE2 from humans, ferrets, cats and alternative species with high receptor homology7

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***Corresponding authors:** Akhila Sabbineni, Department of Microbiology, Andhra University, Vishakapatnam, Andhrapradesh, India;
E-mail: sabbineni21Akhii@gmail.com

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Author Affiliation

Department of Microbiology, Andhra University, ,Vishakapatnam, Andhrapradesh, India