Cryo-electron microscopy structure of the SARS-CoV spike glycoprotein provides insights into an evolution of unique coronavirus spike proteins

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27 **Abstract**

28 The current outbreak of Coronavirus Disease 2019 (COVID-19) by a novel
 29 betacoronavirus severe acute respiratory syndrome coronavirus 2 (SARS-
 30 CoV-2) has aroused great public health concern. Coronavirus has a history of
 31 causing epidemics in human and animals. In 2017 an outbreak in piglets by a
 32 novel coronavirus was emerged designated as swine acute diarrhea
 33 syndrome coronavirus (SADS-CoV) which is originated from the same genus
 34 of horseshoe bats (*Rhinolophus*) as Severe Acute Respiratory Syndrome CoV
 35 (SARS-CoV) having a broad species tropism. In addition to human cells, it
 36 can also infect cell lines from diverse species. Coronavirus host range is
 37 determined by its spike glycoprotein (S). Given the importance of S protein in
 38 viral entry to cells and host immune responses, here we report the cryo-EM
 39 structure of the SADS-CoV S in the prefusion conformation at a resolution of
 40 3.55 Å. Our study reveals that SADS-CoV S structure takes an intra-subunit
 41 quaternary packing mode where the NTD and CTD from the same subunit
 42 pack together by facing each other. The comparison of NTD and CTD with
 43 that of the other four genera suggests the evolutionary process of the SADS-
 44 CoV S. Moreover, SADS-CoV S has several characteristic structural features,
 45 such as more compact architecture of S trimer, and masking of epitopes by
 46 glycan shielding, which may facilitate viral immune evasion. These data
 47 provide new insights into the evolutionary relationships of SADS-CoV S and
 48 would extend our understanding of structural and functional diversity, which

49 will facilitate to vaccine development.

50

51 Introduction

52 The risk of major coronavirus (CoV) epidemics in the previous two
 53 decades comprising SARS in 2003, Middle East Respiratory Syndrome
 54 (MERS) in 2012, SADS in 2017, and the latest 2019 outbreak of human-
 55 infecting virulent strain of SARS-CoV-2 have claimed a large number of
 56 human lives and livestock. They have shared features of pathogenicity, origin
 57 from bats [1-3]. The typical crown-like spike proteins on its surface gives it its
 58 name coronavirus. They belong to subfamily *Coronavirinae*, family
 59 *Coronaviridae*, order *Nidovirales*, and grouped into four genera including
 60 alpha- (α), beta- (β), both CoVs infecting mammals, gamma- (γ) CoVs
 61 infecting birds, and delta- (δ) CoVs infecting mammals and birds [4]. The
 62 genome of CoV is the second largest of all RNA viruses containing a positive-
 63 sense, 27-32 kb in length single-strand RNA (+ssRNA) [5]. CoVs bring about
 64 subclinical or respiratory syndrome, central nervous system (CNS) infections,
 65 gastrointestinal ailments in humans, and animals [6, 7]. These infections are
 66 accountable for 30% of the respiratory illnesses, atypical pneumonia [3, 8],
 67 and show a tendency for interspecies transmission, which happened rather
 68 often during CoV evolution and shaped the diversity of CoVs [9].

69 Porcine CoVs are chief health concerns of the pigs that causes
 70 considerable enteric and respiratory infections causing agents of swine. A
 71 novel CoV instigating SADS (also called as SeACoV and PEAHV) emerged
 72 since August 2016. It is associated with HKU2-related *Rhinolophus* bat CoV

73 with death rate up to 90% in piglets of 5 days or younger in Guangdong
74 territory pig breeding farms and accounted for the killing of around 25 000
75 piglets [10]. SADS-CoV has a position with the class α -CoVs, and it is
76 enveloped +ssRNA virus [2, 6, 11]. The intracellular entry of SADS-CoV relies
77 on a precise interaction amid virion and the host cell. The disease is initiated
78 by the interplay of the viral particle with specific cell surface S trimmer [12].

79 CoVs from various genera display evident serotypes, for the most part,
80 because of the dissimilarity of their envelope-anchored diversified S proteins.
81 S protein is of around 1300 amino acids, has a place with class I viral
82 combination protein, including SARS-CoVs, human immunodeficiency virus
83 (HIV) envelop glycoprotein 160 (gp160), influenza virus haemagglutinin (HA),
84 paramyxovirus F and Ebola virus glycoprotein [13]. The S protein includes
85 three sections: a large ectodomain, a single-pass transmembrane anchor, and
86 a small intracellular tail. The ectodomain comprises of an N-terminal receptor-
87 binding domain (RBD) viral attachment and entry subunit S1 (approximately
88 700 amino acids) forming a crown-like structure and a membrane-fusion C-
89 terminal subunit S2 (approximately 600 amino acids) leading to an assembly
90 of architecture, i.e., CTD is sandwiched by its NTD [14]. In addition, CTDs
91 with the assistance of S1 retains a “lying down” inactive state, which transits
92 to “stand up” active state on the S trimer for efficient receptor binding [7, 15-
93 17].

94 The envelope trimeric S protein is vital for identifying host tropism and
95 transmission limits. It intercedes receptor binding to approach host cell cytosol
96 utilizing acid-dependent proteolytic cleavage of S protein by a cathepsin,
97 TMPRRS2, or additional protease ensued by fusion of the membrane [18, 19].
98 CoVs utilize an assortment of receptors and triggers to initiate fusion [12].
99 Receptor binding is fundamental to host-pathogen interaction and
100 pathogenesis. Numerous α -CoVs, for example, human CoV (HCoV-229E),
101 utilize aminopeptidase N (APN) as its receptor, SARS-CoV, HCoV-NL63 and
102 SARS-CoV-2 employ angiotensin-converting enzyme 2 (ACE2), and MERS-
103 CoV ties to dipeptidyl-peptidase 4 (DPP4). However, receptor investigation of
104 SADS-CoV demonstrated that none of the known CoV receptors, i.e., APN,
105 ACE2 and DPP4, is crucial for cell entry that shows the divergence and
106 significance of S protein in SADS-CoV infection [10]. Along these lines,
107 considering the clinical indications of this advancing virus, there is an
108 essential need for primary and practical comprehension of SADS-CoV to
109 expand mechanisms of viral entry and pathogenesis in pigs.

110 Notwithstanding the significance of the S protein in viral entry and host
111 immunity, high-resolution structural details of this large macromolecular
112 machine have been hard to acquire. In this study, a cryo-EM structure of
113 SADS-CoV S glycoprotein at 3.55 Å resolution is determined.
114 Correspondingly in the present investigation of SADS-CoV, we portrayed the
115 general structure of the S protein and the organization of its structural

116 components. In light of the structures and functions of these essential
 117 components, we detail the evolutionary perspective of SADS-CoV S in
 118 comparison with S proteins from different CoV genera. In our study, SADS-
 119 CoV S forms a “lying down” conformation following the transition from inactive
 120 to an active state, and ACE2 is not the receptor of SADS-CoV. The structural
 121 alignment suggests that SADS-CoV S is located between α -CoV and β -CoV
 122 clade. Hence, our results extend the understanding of critical structural and
 123 evolutionary insights into SADS-CoV S, comprising the CTD/RBD essential
 124 for receptor recognition and viral entry. This study provides the
 125 epidemiological and evolutionary information of this novel CoV in China,
 126 which is deteriorating economically important swine industry, and highlights
 127 the urgency to develop effective measures to control SADS-CoV.

128

129

130

131 **Results and discussions**

132 **Overall structure of SADS-CoV spike protein**

133 In order to investigate the role of SADS-CoV S in its invasion, we aimed
 134 to solve the high-resolution structure of SADS-CoV S. Ectodomain of SADS-
 135 CoV S was expressed, and purified from media of insect cells after 3 days of
 136 infection by baculovirus. A fusion peptide of general control protein GCN4 at
 137 the C-terminal end of S was used to promote the protein to form a trimer [20]
 138 (**Fig. 1A**). The size-exclusion chromatography (SEC) result showed that the
 139 protein sample is a trimer in the solution and the purity of more than 95%
 140 examined in SDS-PAGE analysis (**Fig. S1A, S1B**). The protein displayed high
 141 homogeneity in cryo-EM screening and was then diluted to 0.63 mg ml⁻¹ for
 142 the data collection. Cryo-EM micrograph movies were collected on a Gatan
 143 K2 direct electron detector mounted on an FEI Titan Krios electron
 144 microscope (**Fig. S2**). Following reference-free 2D classification of the S
 145 protein, we determined a three-dimensional (3D) structure of the SADS-CoV
 146 S trimer at 3.55 Å resolution judged by the gold-standard Fourier shell
 147 correlation (FSC) criterion of 0.143 (**Fig. 1B, 1C and Table 1**). The resolved
 148 atomic structure of prefusion SADS-CoV S ectodomain covers almost all of
 149 the key structural elements, as shown in **Fig. 1A** except residues 81-101 of
 150 NTD and residues 999-1068 of HR-C (**Fig. 1D, Fig. S3**). Forty-five (15 on
 151 each subunit) N-linked glycans spread over the surface of the whole S trimer
 152 with another 15 predicted but not observed. In addition, the protein trimer is

153 stabilized by 30 pairs (10 on each subunit) of disulfide bonds (**Fig. S4**). The S
154 trimer shows a dome-like shape, with three S1 heads forming a crown-like
155 structure and sitting on top of a trimeric S2 stalk (**Fig. 1D, 1E, and Movie S1**).
156 The trimer spike has a length of 143.2 Å from S1 to S2 and a width of 111.3 Å
157 and 61.4 Å at S1 and S2, respectively (**Fig. 1E**). Three S1-CTDs are located
158 at the top center of the S trimer arranged as a small triangle, whereas three
159 S1-NTDs are located on the lower and outer side of S1-CTDs arranged as a
160 big triangle. This architecture, i.e., CTD sandwiched by its own NTD and the
161 adjacent NTD, comes into being one side of the big triangle (**Fig. 1F**). The
162 cleavage site of S1 and S2 subunits locates between residues 544 (Val) and
163 545 (Arg). The central helicase N (CH-N) and C (CH-C) of S2 from each
164 subunit form a six-helix bundle in the core of S trimer. Heptad repeats N (HR-
165 N) contains four helices connected by three loops locked between the S1 and
166 S2 subunit at the outside of the S2 stalk, while part of the HR-C is missed in
167 the structure (**Fig. 1G**). Each monomeric subunit of S1 contains two major
168 domains, S1-NTD and S1-CTD which are used to bind attachment sialic acid
169 receptors or protein receptors and play a vital role in the CoV entry, and two
170 subdomains, SD1 and SD2 whose function are not very clear (**Fig. 1H-1I,**
171 **Movie S1**).

Fig. 1. The 3.55 Å cryo-EM structure of SADS-CoV S in the prefusion conformation.

(A). Representative 2D class averages in different orientations of SADS-CoV S trimer.

177 (B). Gold-standard FSC curves of SADS-CoV S. The resolution was
178 determined to be 3.55 Å, and a horizontal yellow indicates the 0.5 cut-off
179 value dashed line.

180 (C). Schematic drawing of SADS-CoV S. S1: receptor-binding subunit. S2:
181 membrane-fusion subunit. NTD: N-terminal domain of S1. S1-CTD: C-terminal
182 domain of S1. SD1-3: subdomain 1-3. FP: fusion peptide. CH-N and CH-C:
183 central helices N and C. HR-N and HR-C: heptad repeats N and C. Tag:
184 GCN4 trimerization tag followed by His 6 tag.

185 (D). Final cryo-EM density map of SADS-CoV S colored according to the local
186 resolution.

187 (E). Cryo-EM structure of SADS-CoV S in the prefusion conformation. Each of
188 the monomeric subunits is colored in green, cyan and magenta, respectively.

189 (F). Same as (E), but the dome is rotated 90 degrees to show the top view of
190 the trimer, the CTDs arrange as a small triangle and is indicated by a black
191 triangle. The two adjacent NTDs sandwich one CTD to form one side of a big
192 triangle, which is indicated by a gray triangle.

193 (G). Cryo-EM structure of the SADS-CoV S monomeric subunit. The structural
194 elements are colored in the same way as in panel (A).

195 (H-I). Structures of S1-NTD (cyan) and S1-CTD (green), the putative RBM
196 loops are indicated by a dashed cycle.

197

198 **Structural evolution of coronavirus spike protein**

199 The S protein from all the four different genera of the CoVs packs a
200 crown-like structure by three monomeric subunits, which can be divided into
201 two packing modes: the cross-subunit packing mode and the intra-subunit
202 packing mode [21]. Our SADS-CoV S structure takes an intra-subunit
203 quaternary packing mode where the NTD and CTD from the same subunits
204 pack together by head to head. In SADS-CoV S, the three NTDs from different
205 subunits are located at the vertices of the big triangle formed by the S1
206 subunits and sandwich the CTDs to the center of the triangle. As a result, the
207 putative receptor-binding moieties located on the top of CTDs are also
208 wrapped at the center of the crown-like trimer (**Fig. 2A**). Accordingly, the
209 geometry of SADS-CoV S resembles the prefusion structures of other α - and
210 δ -genera with the intra-subunit packing mode and is more compact than those
211 of β - and γ -genera that use the cross-subunit packing mode (**Fig. 2A-2E**).
212 Interestingly, although SADS-CoV belongs to the α -genera, its spike protein
213 doesn't have the domain 0, which is commonly found in other α -genera CoVs,
214 e.g., NL63-CoV and PEDV (**Fig. 2F-G**) [20].

215 Different from the receptor-binding inactive state of these structures
216 whose all three CTDs in “lying down” positions (**Fig. 2A-2E**), the previous
217 study captured several β -CoVs S which contain one or two, even all three
218 CTDs in “stand up” positions [7, 15, 17, 22, 23]. The engagement of the CTDs
219 of SARS S trimer helps it to keep one or more CTDs in the “stand up” position
220 and facilitate the binding of ACE2 or neutralizing antibodies. If all the three

221 CTDs are in the “lying down” position, it is not possible to bind ACE2 due to
 222 the partial binding sites are hidden and steric clashes between binding
 223 factors. This kind of conformation represents an inactive state (**Fig. 2H**). The
 224 CTDs in our structure keep a “lying down” state, and the receptor-binding
 225 moieties are partially concealed. It needs to “stand up” on the spike trimer and
 226 release the steric clash for efficient receptor binding. The linker between
 227 CTDs and S1 subdomains works as a hinge to facilitate the conformation
 228 change of CTDs from “lying down” to “stand up”, furthermore, transit the
 229 receptor-binding inactive state to active state (**Fig. 2F**).

230 It is noteworthy that stronger interactions in the SADS-CoV S trimer may
 231 become obstacle conformational change and dissociation of S1-CTD in the
 232 prefusion process (**Fig. S5**). Moreover, to probe the intrinsic mobility of the
 233 CTD/RBD of S trimer in the apo form (or to see whether the CTD/RBD of S
 234 trimer can spontaneously expand to an open state), we performed 2000 ns-
 235 long coarse-grained (CG) molecular dynamics (MD) simulations [24]. A Martini
 236 CG model was initially generated using the “lying down” state structure (**Fig.**
 237 **S6**). The center-of-mass distances between every two CTDs/RBDs across the
 238 simulations (**Fig. S6**) indicated that all the three CTDs/RBDs were stabilized
 239 in a “lying down” state similar to the structure observed in this study, i.e. the
 240 distance differences calculated from simulations and crystal structure were
 241 less than 5 Å. Although we did not find apparent expanding of the CTDs/RBDs
 242 from a “lying down” state to a “stand up” state during the simulations, it did not

243 rule out the co-existence of the two states in the apo form. Because such a
244 large conformational transition may happen over long time scales (ms to s),
245 far beyond the simulations performed here. Taken together, these simulation
246 results may explain the homogeneity of SADS-CoV S observed in our 3D
247 classification and that the different S1-CTD conformations are invisible in our
248 results (**Fig. 1B**).

249 For the NTDs, the core structure consists of two six-stranded antiparallel
250 β -sheet layers stacked together, which takes the same galectin fold as human
251 galectins and the NTDs from the other genera. Besides the core structure,
252 NTD of SADS-CoV S1 also has a loop (residues 133-150) formed as a partial
253 ceiling-like structure that resembles the partial ceiling of γ -CoV rather than the
254 other α - and δ -coronavirus which do not have a ceiling-like structure, or the β -
255 CoV which has a reinforced ceiling-like structure (**Fig. 2I-M**). Based on the
256 structural similarity between the NTDs from four different CoVs genera, the
257 sugar-binding site in SADS-CoV S1-NTD might also be located in the pocket
258 formed between the core structure and the partial ceiling (**Fig. 2I**). Compared
259 with other CoVs, the structure of the subdomain under the core domain of
260 SADS-CoV S1-NTD has the same situation as the partial ceiling-like structure
261 (**Fig. 2I-M**). The previous study gave the idea that NTDs from the four genera
262 form an evolutionary spectrum in the order of α -, δ -, γ - and β -genera, with α -
263 CoVs NTD probably being the most ancestral [21]. Our structure has also
264 unexpectedly consistent with this conclusion. Furthermore, we propose that

265 the structural evolution of SARS-CoV S1-NTD is more likely to located
266 between the other α -CoVs, δ -CoVs, and γ -CoVs.

267 For the CTDs, despite there are dramatic sequential differences between
268 SARS-CoV S1-CTD and other CTDs, all of them share similar structural
269 topology (**Fig. 2N-R**). Unlike the other CTDs of α -CoVs and δ -CoVs which
270 have a more compact core β -sandwich structure containing two β -sheet
271 layers, our CTD resembles the γ - and β -CoVs which just has one layer β -
272 sheet and several α -helix and coil structures with a loose packing (**Fig. 2N-R**).
273 Based on the structural comparison of the CTDs of all the four genera, all the
274 other α -CoVs and δ -CoVs use the loops located on the top of the β -sandwich
275 of CTDs as its receptor binding motif (RBM). As a result, we propose that
276 SARS-CoV also uses these loops on the CTD as its RBM (**Fig. 2N-P**).
277 Moreover, the CTDs of γ -CoVs evolve to get extended loops, and the β -CoVs
278 obtain an insertion domain which contains RBM under the host immune
279 pressure, these receptor-binding moieties also located on the top of core
280 domain (**Fig. 2Q-R**). Previous studies have shown that the core structures are
281 two layers β -sandwiches for α - and δ -CoVs CTDs, weakened β -sandwiches
282 for γ -CoVs CTDs, and single β -sheet layer for β -CoVs CTDs. The RBMs are
283 three short discontinuous loops for α - and δ -CoVs CTDs, two reinforced loops
284 for γ -CoVs CTDs, and a single continuous insertion domain for β -CoVs CTDs.
285 The CTDs from different genera give an evolutionary spectrum, using α - and
286 δ -CoVs CTDs as ancestral, γ -CoVs CTDs as the transitional structure and β -

287 CoVs CTDs the downstream structure, but the evolutionary direction could go
288 either way [21]. Hence, we propose that the SADS-CoV S1-CTD located
289 between the other α -, δ -CoVs, and β -CoVs CTDs on the evolutionary
290 spectrum (**Fig. 2N-R**).

291

292 **Fig. 2. Structural evolution of coronavirus spike protein.**

293 (A). The architecture of the SADS-CoV S1 subunit. Three subunits are shown
294 as different colors; one of the NTD and CTD indicated as magenta, the

295 receptor-binding moieties are shown as wheat and indicated by cycles.

296 (B-E). The architecture of the four coronavirus genera S subunit. (B): α -CoVs

297 S-trimer, NL63-CoV, PDB: 5SZS; (C) δ -CoVs S-trimer, PdCoV, PDB: 6BFU; γ -

298 CoVs S-trimer, IBV, PDB: 6CV0; β -CoVs S-trimer, SARS-CoV, PDB: 5X58.

299 (F). Structures of S1 monomer from SADS-CoV. A red frame indicates the

300 linker between the CTD and SD1. The NTD, CTD, and receptor-binding

301 moiety are indicated by a black arrow, respectively.

302 (G). Structures of S1 monomer from NL63-CoV, the additional domain 0 is

303 indicated by a dotted cycle.

304 (H). Structures of S1 monomer from SARS-CoV. The left panel shows the S1

305 subunit in a “lying down” state, while the right panel shows the S1 subunit in a

306 “stand up” state. The conformational change of the subunits from “lying down”

307 to “stand up” help the trimer to expose receptor-binding moieties and then

308 switch inactive state to active state.

309 (I-M). Structures of NTDs from different genera. The core structures and

310 subdomain (dotted rectangle) of NTDs are labeled, respectively. Partial ceiling

311 and ceiling are indicated by a black arrow. The sugar-binding site or putative

312 sugar-binding site in sugar-binding NTDs are indicated by a red star. (I):

313 SADS-CoV S1-NTD; (J): NL63-CoV S1-NTD (PDB: 5SZS); (K): PdCoV S1-

314 NTD (PDB: 6BFU); (L): IBV S1-NTD (PDB: 6CV0); (M): SARS-CoV S1-NTD

315 (PDB: 5X58).

316 (N-R). Structures of CTDs from different genera. The RBM loops and putative

317 RBM loops are indicated by dotted cycles, while the extended RBM loops and
318 RBM subdomain are indicated by a black arrow. (N): SADS-CoV S1-CTD; (O):
319 NL63-CoV S1-NTD (PDB: 5SZS); (P): PdCoV S1-CTD (PDB: 6BFU); (L): IBV
320 S1-CTD (PDB: 6CV0); (M): SARS-CoV S1-CTD (PDB: 5X58).

321

322 **Structural alignment between the S of SADS-CoV, SARS-CoV and SARS-** 323 **CoV-2**

324 The phylogenetic analysis based on the whole genome and N gene of
325 eight SADS-CoVs and other CoVs showed that all the sequences of SADS-
326 CoVs clustered with bat coronavirus HKU2 to form a well-defined branch and
327 belong to the α -genera [25]. However, surprisingly/interestingly, the
328 phylogenetic analysis of the S genes showed that the S gene cluster can be
329 divided into two groups: α -CoV-1 and α -CoV-2. All of the SADS-CoVs and bat
330 coronavirus HKU2 belong to α -CoV1 which group with the β -CoVs to form the
331 half evolutionary branch of CoVs, whereas the other α -CoVs cluster to the α -
332 CoV-2 [11, 25]. The structural alignment of the SADS-CoV S trimer by Dali
333 analysis (<http://ekhidna2.biocenter.helsinki.fi/dali/>) implies that SADS-CoV S
334 has a relative conservation with that of β -CoVs, as reflected by the generally
335 high Z-scores and high RMSD (**Table S1**). In addition, the Dali analysis of
336 CTD showed that SADS-CoV S CTD is relatively poorly conserved with β -
337 CoVs, as reflected by the generally low Z-scores and high RMSD. However, it
338 shares roughly identical core folding with other β -CoVs, i.e., HKU9, SARS-

339 CoV, MERS-CoV, HKU1 and OC43 (**Table S2**). Taken together, these results
340 are consistent with that of the sequence alignment.

341 Based on the phylogenetic analysis, we compared the CTDs of SADS-
342 CoV, SARS-CoV and SARS-CoV-2 by the sequence and structure. The whole
343 SADS-CoV S ectodomain is only approximately 30% sequence identity when
344 compared with the SARS-CoV and SARS-CoV-2, which obstructs structural
345 alignment between SADS-CoV, SARS-CoV and SARS-CoV-2. Especially
346 there is no significant homologous CoV S CTD found in the PDB when the
347 SADS-CoV S CTD sequence as the inquiry. Interestingly, the SADS-CoV S
348 CTD is smaller (about 130 residues) than other CoV CTD (about 170
349 residues) (**Fig. 3A**). To further investigate the differences between the S of
350 SADS and other CoVs, and deduce the hypothesis of SADS pathogenic
351 mechanisms, we focused on CTD and performed structural alignments using
352 the complexes of CTD (SARS-CoV-2)-ACE2, CTD (SARS-CoV)-ACE2, CTD
353 (NL63-CoV)-ACE2 (**Fig. 3B-3D**) and the CTDs of SARS-CoV-2, SARS-CoV
354 and SADS-CoV (**Fig. 3E**). Surprisingly, although SARS-CoV-2, SARS-CoV
355 and SADS-CoV CTD do not share significant sequence homology and belong
356 to a different family of CoVs (**Fig. 3A**), they share roughly identical
357 organization and core folding (**Fig. 3E**). Notably, SADS-CoV uses the variant
358 loop region as its RBM, which is consistent with the insertion domain of
359 SARS-CoV and SARS-CoV-2 CTDs that is formed by two β sheets and
360 several loops (**Fig. 3E**). Meanwhile, compared with the β -CoVs SARS-CoV-2

and SARS-CoV, the α -CoV NL63 also use its loops to bind ACE2. Although the loops of SADS-CoV and NL63 CTDs share a structural similarity, SADS-CoV cannot use the ACE2 as its receptor. These features imply that both of the variant sequence and the local structure of these loops are combined to determine the receptor binding specificity.

Fig. 3. Comparison of the RBD domain of SADS-CoV, SARS-CoV, and SARS-CoV-2.

(A). Sequence alignment on CTD of SADS-CoV, SARS-CoV and SARS-CoV-2.

(B-D). Structures of SARS-CoV-2 CTD complex with ACE2 (B), SARS-CoV-CTD complex with ACE2 (C), NL63-CoV-CTD complex with ACE2 (D). CTD is colored green and ACE2 is colored gray.

(E). Structural alignment of SARS-CoV-2 (colored gray and red), SARS-CoV

(colored gray and purple) and SADS-CoV CTD (colored green). Red and purple ribbons indicate the ACE2 binding motif (insertion domain).

Immune evasion strategies by SADS-CoV S

As a protein located on the surface of the virus, the S proteins mediate viral entry into host cells and also undergo the immune pressure from the immune system of the host at the same time. The structure of SADS-CoV S provides some hints on the immune evasion strategies of SADS-CoV.

On the one hand, the SADS-CoV S has a classical compact structure as other α -CoVs, which uses the intra-subunit packing mode (**Fig. 2A-2B**). As a result, this kind of architecture can maximally reduce the surface area of the S protein to the immune system. Moreover, all of the NTDs and CTDs in a “lay down” station (closed conformation) can further reduce immune pressure (**Fig. 2F**). Nevertheless, the NTDs and CTDs still have the chance to expose for receptor binding. Furthermore, they can also be selected as single- or two-RBD system [4]. Based on the structural alignment of these structures, we speculate that SADS-CoV uses the two-RBD system for which the NTD is used as the attachment receptor-binding domain and the CTD is used as the protein receptor-binding domain. Upon infecting host cells, S1-CTD would need to switch to an open conformation (“stand up”) to render the putative RBM loops accessible to the host receptor. This closed-to-open mechanism

396 can minimize the exposure of the putative RBM loops to the immune system
397 [4].

398 On the other hand, as one of the immune evasion strategies, masking of
399 epitopes by glycan shielding is usual in CoV evolution [26]. Our map shows
400 that fifty N-linked glycans are spreading over the surface of each S subunit.
401 They are mainly located on the surface of S1 rather than on S2 like HCoV-
402 NL63 (**Fig. 4A**). In contrast to that, HCoV-NL63 S evades host immune
403 surveillance mainly by glycan shielding its S2 epitopes, SADS-CoV spike
404 appears to evade host immune surveillance mainly by glycan shielding its S1
405 epitopes [26]. In addition, unlike the other α -CoV and δ -CoV whose putative
406 sugar-binding sites are surrounded by glycans, most of the SADS-CoV N-
407 linked glycosylation sites are located on the CTD (**Fig. 4A-4B**). As a result,
408 the putative sugar-binding sites on the NTD are shielded, not by glycans, but
409 by the partial ceiling-like structure on the top of the core structure. As a
410 comparison, this feature is consistent with BCoV-S1-NTD [27]. Unlike the
411 HCoV-NL63 receptor-binding residues interacting with domain A belonging to
412 the same protomer, SADS-CoV CTD uses a loop (residues 321-328) to
413 interacting with NTD from the same S1. Both use N-linked glycosylation
414 (residue Asp358) to make them buried and not available to engage the host
415 cell receptor (**Fig. 4C**) [26]. Taken together, SADS-CoV has several unique
416 structural features that may facilitate viral immune evasion.

Fig. 4. N-linked glycan distribution on the surface of SADS-CoV S.

(A). Distribution of observed N-linked glycosylation sites on the one-dimensional structure of SADS-CoV S. Ψ indicates N-linked glycosylate sites.

(B). Distribution of observed N-linked glycosylation sites on the three-dimensional structure of the SADS-CoV S. Blue sphere indicates N-linked glycosylate sites.

(C). Distribution of observed N-linked glycosylation sites in monomeric S1 (colored as panel A).

427 **Table 1. Data collection and refinement statistics.**

Dataset	SADS-CoV S ectodomain
Data collection	
EM equipment	FEI Titan Krios
Voltage (kV)	300
Detector	K2 Summit
Pixel size (Å)	1.04
Electron dose (e ⁻ /Å ²)	60
Defocus range (µm)	-1.8 ~ -2.5
Reconstruction	
Software	RELION 3.0
Particle Numbers	35,000
Symmetry	C3
FSC threshold	0.143
Final resolution (Å)	3.55
Map-sharpening <i>B</i> factor (Å ²)	-152
Model building	
Software	Coot 0.8.9
Refinement	
Software	Phenix-1.18rc1
CC_mask	0.78
Bond lengths (Å)	0.007
Bond angles (°)	1.389
Validation	
Clashscore	5.90
Rotamers outliers (%)	1.57
Ramachandran plot	
Favored (%)	89.85
Allowed (%)	8.89
Outliers (%)	1.26

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432 **Methods**

433 **Protein expression and purification**

434 SADS-CoV spike glycoprotein (virus strain GDS04; GenBank No.:
435 ASK51717.1) gene was synthesized with codons optimized and inserted into
436 pFastBac vector (Life Technologies Inc.). The ectodomain of SADS-CoV spike
437 protein without the transmembrane anchor and intracellular tail (residues 18-
438 1068) was expressed by the Bac-to-Bac insect cell system (Invitrogen). To get
439 the trimer ectodomain protein, we added a GCN4 trimerization tag followed by
440 a TEV cleavage site and an 8×His-tag at the C terminal of the S protein. The
441 cells were harvested by centrifugation at 4,000×g and remove the cells. Then
442 the supernatant was loaded to Ni-NTA (Nitrilotriacetic acid) resin (Invitrogen)
443 affinity-purified by the C-terminal 8×His-tag. Spike protein was finally purified
444 using Superose 6 HR10/300 column (GE Healthcare) pre-equilibrated with
445 buffer containing 20 mM HEPES (pH 7.5) and 150 mM NaCl, 1 mM DTT and
446 concentrated with a centrifugal filter (Amicon Ultra) to approximately 1 mg/ml
447 and divided into aliquots, flash-frozen in liquid nitrogen.

448 **Cryo-EM sample preparation and data acquisition**

449 Purified S protein was diluted to 0.63 mg ml⁻¹ with buffer containing 20 mM
450 HEPES pH 7.5, 100 mM NaCl and 2 mM DTT. A 4 µl volume of sample was
451 applied to a glow-discharged Quantifoil copper grid and vitrified by plunge
452 freezing in liquid ethane using a Vitrobot Mark with a blotting time of 3 s. Data
453 collection was performed on a Titan Krios microscope operated at 300 kV and

454 equipped with a field emission gun, a Gatan GIF Quantum energy filter and a
455 Gatan K2 Summit direct electron camera in super-resolution mode, at CBI-
456 IBP. The calibrated magnification was 130,000 $\times$ in EF TEM mode,
457 corresponding to a pixel size of 1.04 Å. The automated software SerialEM
458 was used to collect 1,000 movies at a defocus range of between 1.8 and 2.3
459 μ m. Each exposure (10 s exposure time) comprised 32 sub-frames amounting
460 to a total dose of 60 electrons Å⁻² s⁻¹.

461

462 **Image processing**

463 Micrograph movie stacks were corrected for beam-induced motion using
464 MotionCor2 [28]. The contrast transfer function parameters for each dose
465 weighting image were determined with Gctf [29]. Particles were initially auto
466 picked with Gautomatch without template and extracted with a 256-pixel by
467 256-pixel box. Reference-free 2D-class average was performed using
468 RELION [30], and the well-resolved 2D averages were subjected to another
469 iteration particle auto picking as a template with Gautomatch. After iterative
470 2D-class average in RELION, only particles with best-resolved 2D averages
471 were selected for initial model generation and 3D classification using RELION.
472 The classes with identical detailed features were merged for further auto-
473 refinement with a sphere mask, and post-processed with 3-pixel extension
474 and 3-pixel fall-off around the entire molecule, to produce the final density
475 map with an overall resolution of 3.55 Å. Chimera and PyMOL

476 (<https://pymol.org/>) were used for graphical visualization [31].

477

478 **Model building**

479 *Ab initio* modeling of the spike protein was performed in Coot [32], using
480 structure predictions calculated by Phyre2 [33], the partial structure modeled
481 by EMBuilder [34], and the reference model (PDB: 5X58). Map refinement
482 was carried out using Phenix.real_space_refine [35], with secondary structure
483 and Ramachandran restraints. Cryo-EM data collection, refinement and
484 validation statistics were listed in Table 1.

485

486 **ACCESSION NUMBER**

487 The Cryo-EM structure of SADS-CoV S has been deposited into EMDB with
488 accession numbers of EMD-30071. Coordinates and structure factors have
489 been deposited in the Protein Data Bank (PDB) under accession number
490 6M39.

491

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503

504 **Competing interests:** The authors have declared that no competing interests
 505 exist.

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507 **AUTHOR CONTRIBUTIONS**

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641 **Fig. S1. Expression and purification of SADS-CoV S.**

642 A. The size-exclusion chromatogram (SEC) of SADS-CoV S gives three
643 peaks and the elution volumes of which are indicated by red, green and cyan,
644 respectively. Data from a Superose 6 10/300 column are shown in the black
645 line.

646 B. The samples from different peaks were checked by SDS-PAGE analysis
647 and the sample from peak 2 (green) is used to analyze further.

648

Fig. S2. Cryo-EM data processing flow chart of SADS-CoV S.

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659 **Fig. S3. SADS-CoV S structure cryo-EM map (A) and representative**

660 **density (B).** The map is colored by protomer and blue density indicates

661 observed glycosylation sites.

662

663 **Fig. S4. The distribution of 10 pairs disulfide bond on each subunit (236-**

664 **246, 287-292, 279-302, 343-399, 333-361, 592-614, 597-603, 698-708, 886-**

665 **897, 936-945).**

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668 **Fig. S5. Structural comparison between SARS-CoV spike S1 domain (A)**
 669 **and SADS-CoV spike S1 domain (B).**

670 S1-NTD, S1-CTD, SD1 and SD2 are colored by cyan, green, gray and red,
 671 respectively. In the native state, only interactions between S1-CTD and S1-
 672 NTD of neighbor monomer are visible in SARS-CoV S (dotted circle in panel
 673 A). S1-CTD is dissociated from S1-trimer when binding ACE2 in the prefusion
 674 state. While in SADS-CoV spike, three interaction regions are visible in the
 675 native state (dotted circles in panel B), including S1-CTD and S1-NTD of
 676 neighbor monomer, internal S1-CTD and S1-NTD, S1-CTD trimer.

677

678

Fig. S6. Molecular dynamics of simulations on SADS-CoV S trimer.

(A) The initial and final coarse-grained models of SADS-CoV S trimer from the simulations. The three RBDs were highlighted in green, orange and purple, respectively.

(B) The center-of-mass distances between every two RBDs in the simulations.

691 **Table S1. The results of the SADS-CoV S structure comparison by Dali**
692 **service.**

No	PDB ID- Chain	Z Score	RMSD	Description
1	6nb4-A	28.6	4.6	MERS-CoV S complex with human neutralizing LCA60 antibody Fab fragment (state 2)
2	6nzk-A	27.4	5.4	Human coronavirus OC43 attachment to sialic acid receptors
3	5xlr-A	26.2	5.0	Structure of SARS-CoV spike glycoprotein
4	6cs2-B	25.6	7.5	SARS Spike Glycoprotein - human ACE2 complex, Stabilized variant, all ACE2-bound particles
5	6cv0-A	25.3	6.3	Cryo-electron microscopy structure of infectious bronchitis coronavirus spike protein
6	6jx7-A	25.1	7.4	Cryo-EM structure of spike protein of feline infectious peritonitis virus (strain UU4)
7	5x59-B	24.9	6.1	Prefusion structure of MERS-CoV spike glycoprotein, three-fold symmetry
8	5i08-A	22.9	4.4	Prefusion structure of a human coronavirus HKU1 (isolate N5) spike protein

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698 **Table S2. The results of the SADS-CoV S RBD structure comparison by**
699 **Dali service.**

No	PDB ID- Chain	Z score	RMSD	Description
1	5gyq-A	6.8	2.9	Putative receptor-binding domain (RBD) of bat-derived coronavirus HKU9 spike protein
2	6cs2-B	3.4	3.3	SARS Spike Glycoprotein - human ACE2 complex, Stabilized variant, all ACE2-bound particles
3	5x59-B	7.0	3.2	Prefusion structure of MERS-CoV (isolate the United Kingdom/H123990006/2012) spike glycoprotein, three-fold symmetry
4	5xlr-A	5.7	3.4	Structure of SARS-CoV spike glycoprotein
5	5i08-A	5.5	3.4	Prefusion structure of a Human coronavirus HKU1 (isolate N5) spike protein
6	6cv0-A	4.3	3.4	Cryo-electron microscopy structure of infectious bronchitis coronavirus spike protein
7	6nzk-A	4.2	3.2	Structural basis for Human coronavirus OC43 attachment to sialic acid receptors
8	6atk-E	3.2	3.1	Crystal structure of the human coronavirus 229E spike protein receptor-binding domain in complex with human aminopeptidase N

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