Important Role for the Transmembrane Domain of Severe Acute Respiratory Syndrome Coronavirus Spike Protein during Entry

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The spike protein (S) of severe acute respiratory syndrome coronavirus (SARS-CoV) is responsible for receptor binding and membrane fusion. It contains a highly conserved transmembrane domain that consists of three parts: an N-terminal tryptophan-rich domain, a central domain, and a cysteine-rich C-terminal domain. The cytoplasmic tail of S has previously been shown to be required for assembly. Here, the roles of the transmembrane and cytoplasmic domains of S in the infectivity and membrane fusion activity of SARS-CoV have been studied. SARS-CoV S-pseudotyped retrovirus (SARSpp) was used to measure S-mediated infectivity. In addition, the cell-cell fusion activity of S was monitored by a Renilla luciferase-based cell-cell fusion assay. S

SVSV-Cyt, an S chimera with a cytoplasmic tail derived from vesicular stomatitis virus G protein (VSV-G), and S

SVSV-TMDCyt, a chimera with the cytoplasmic and transmembrane domains of mouse hepatitis virus, displayed wild-type-like activity in both assays. S

SVSV-TMDCyt, a chimera with the cytoplasmic and transmembrane domains of SVV-G, was impaired in the SARSpp and cell-cell fusion assays, showing 3 to 25% activity compared to the wild type, depending on the assay and the cells used. Examination of the oligomeric state of the chimeric S proteins in SARSpp revealed that S

SVSV-TMDCyt trimers were less stable than wild-type S trimers, possibly explaining the lowered fusogenicity and infectivity.

In the winter of 2002 to 2003, a new type of pneumonia, severe acute respiratory syndrome (SARS), emerged in Guangdong province, China. The etiological agent causing this disease was found to be an unknown coronavirus, which was named SARS coronavirus (SARS-CoV) (10, 18, 23, 30).

Among the structural proteins of SARS-CoV, the spike (S) protein is the largest, comprising 1,255 amino acids. Research on SARS and other coronavirus S proteins has shown that S is involved in receptor binding and membrane fusion and is a major determinant of the immune response and pathogenesis (12). The spike protein is a type I membrane protein and is anchored in the membrane of the virion. Peplomers, oligomers of two or three spike proteins (9), form the distinctive “corona” on the virus.

The main receptor for SARS-CoV has been identified as angiotensin-converting enzyme 2 (ACE-2) (20). ACE-2 is expressed in several tissues, among which are epithelia in the lung and small intestine (15). It has been shown that amino acids 318 to 510 of SARS-CoV S are sufficient to bind to ACE-2 (1, 44, 45). L-SIGN has been shown to function as an alternative receptor, albeit with a significantly lower affinity than ACE-2 (17). Another lectin, DC-SIGN, has been implicated in enhancement of infection by dendritic cell transfer, a process earlier described for other viruses such as human immunodeficiency virus (HIV) and hepatitis C virus (HCV) (16, 24, 49).

In most but not all coronaviruses, S is cleaved during viral maturation by a host cell protease to create the subunits S1 and S2 (11, 40). It is unclear at this moment whether this type of cleavage of the SARS-CoV spike protein occurs. Recently, however, evidence has emerged showing that SARS S is cleaved during entry of the virus rather than during maturation. Low-pH-dependent, endosome-resident cysteine proteases (i.e., cathepsin L) have been shown to be involved in SARS-CoV entry by cleavage of S. Specific inhibitors of cathepsin L block entry of SARS pseudotypes and also infection with SARS-CoV (36).

Coronavirus S proteins have been proposed to be class I viral membrane fusion proteins (4). Class I proteins contain a fusion peptide at or close to the N terminus of the integral membrane fragment of the spike protein, consisting of about 20 hydrophobic amino acids, that enters the target membrane to initiate fusion. Furthermore, the class I proteins contain two 4,3-hydrophobic heptad repeats (HR) (6, 8) and often an aromatic-rich domain within or close to the transmembrane domain (TMD), which anchors the protein in the viral membrane.

The S2 subunit of the spike protein contains two heptad repeats (HR1 and HR2) with a high affinity for each other, HR1 is located downstream of the (internal) putative fusion peptide, and HR2 is located just upstream of the transmembrane domain (see Fig. 1a). Upon onset of fusion, a conformational change takes place in the spike oligomer, and the HRs form a so-called six-helix bundle—three α-helices formed by HR1 and three antiparallel HR2 α-helices—thus bringing the fusion peptide and the TMD of the spike protein in close proximity (4). This structure represents the “postfusion" con-
The spike protein has an N-terminal signal sequence (SS), a putative fusion peptide (FP), two heptad repeats (HR), a transmembrane domain (TMD), and a C-terminal cytoplasmic domain (Cyt). The arbitrary border between S1 and S2 is indicated. The ACE-2 binding region is specified as part of S1. (b) Amino acid sequence of the transmembrane domain of SARS-CoV S (top), VSV-G (middle), and MHV S (bottom). The Trp-rich domain is depicted in a dark gray box, and the Cys-rich domain is light gray boxed. (c) Schematic representation of the wt S (Swt) and S chimeras (TMD), and a C-terminal cytoplasmic domain (Cyt). The arbitrary border between S1 and S2 is indicated. The ACE-2 binding region is specified as part of S1. (b) Amino acid sequence of the transmembrane domain of SARS-CoV S (top), VSV-G (middle), and MHV S (bottom). The Trp-rich domain is depicted in a dark gray box, and the Cys-rich domain is light gray boxed. (c) Schematic representation of the wt S (Swt) and S chimeras.

It is not known what conformational changes are occurring within the S protein to acquire the six-helix bundle. Since the native structure of the whole S protein has not been solved yet, in contrast to the HR1-HR2 complex (42, 47, 48), it remains unclear what other domains of S2 are involved in fusion. It has, however, become clear that, in contrast with other class I viral membrane fusion proteins, the N terminus of coronavirus S2 is not the fusion peptide, since it lacks the characteristic features described for fusion peptides. Rather, in coronaviruses the fusion peptide is an internal hydrophobic amino acid stretch. Putative coronavirus fusion peptides have been proposed (4) based on hydrophobicity plots and on peptide studies (32), but no conclusive evidence has been presented to date which points out the fusion peptide of coronaviruses.

Besides the HRs and the fusion peptide, another characteristic feature of the coronavirus S2 subunit is the length of its TMD. The TMD would comprise 34 amino acids, which is longer than predicted based on hydrophobicity plots and on peptide studies (32), but no conclusive evidence has been presented to date which points out the fusion peptide of coronaviruses.
plasmid pFLACE2. Subsequently, the T7 promoter of the plasmid was deleted by SpeI digestion and self-ligation (pCDNA3/FLACE2ΔSpeI). Then a cassette containing a T7 promoter, the Renilla luciferase gene, the 3′ nontranslated region (NTR) of hepatitis C virus, and a T7 termination signal (the fragment was originally obtained from plasmid pHCVwt-RLuc-3'T7R [C. B. E. M. Reusken, personal communication]) was cloned into this plasmid using the NotI and XhoI sites, yielding plasmid pFLACE2/T7rLuc.

Plasmid pBP9/CMVT7 contains a cytomegalovirus (CMV) promoter-driven T7 polymerase gene (7) followed by a simian virus 40 polyadenylation signal and was cloned using conventional cloning procedures.

Recombinant SARS spike expression. VeroE6R cells were seeded into 35-mm wells (0.5 × 10^5 cells/well) and 16 h later transfected with 2 μg of DNA per 35-mm plate using Lipofectamine (Invitrogen) according to the manufacturer’s protocol. A typical labeling experiment was performed as follows. Cells were starved 18 h posttransfection (hpt) for 30 min in RPMI 1640 without Met and Cys and were subsequently labeled metabolically with RPMI 1640 without Met and Cys plus [35S]Cys and [35S]Met (ICN Biomedicals Inc.). After a 2-h labeling, the medium was removed and replaced by chase medium (DMEM plus 10% FCS and extra [2,5-fold] Met and Cys) and pBp9/CMVT7 using Lipofectamine 2000 (Invitrogen) using the manufacturer’s protocol. A C-type reverse transcriptase activity kit (Innovagen, Sweden) was used to correct for the amount of retrovirus particles per ml of supernatant used to transduce target cells. Briefly, 2 × 10^5 cells were transduced with SARSpp retrovirus supernatants were purified with a 20% sucrose cushion (SW41 rotor, 2 h, 25 krpm). Pellets containing SARSpp were resuspended in PBS. Prior to immunoprecipitation, 1% sodium dodecyl sulfate (Sds) was added to the samples to solubilize the SARSpp. Immunoprecipitations were performed as previously described, using an anti-SARS-CoV polyclonal antiserum. Immunoprecipitates were resuspended in Laemmli loading buffer (19) without dithiothreitol and kept at room temperature or incubated 5 min at 80°C prior to loading of the samples on a 4% polyacrylamide gel.

RESULTS

Expression of SARS-CoV (Frankfurt) S protein and chimeras. The SARS-CoV (strain Frankfurt) S protein-encoding sequence was cloned into pcCMV, yielding pcCMV-Swt. In addition, several chimeras were constructed to investigate the role of the TMD and the cytoplasmic domain of S in membrane fusion activity and infectivity. In chimera Ssw0-Cys, the cytoplasmic tail of SARS-CoV S was replaced by its vesicular stomatitis virus G protein (VSV-G) counterpart. In Ssvsv-TMDCys, the transmembrane and cytoplasmic domains of SARS-CoV S were replaced by the VSV-G transmembrane and cytoplasmic domains. In Smvh-TMDCys, the transmembrane and cytoplasmic domains of SARS-CoV S were replaced by the MHV-A59 S transmembrane and cytoplasmic domains (see Fig. 1c).

First, expression and maturation of wild-type (wt) S and the S chimeras was studied. After transfection of VeroE6R cells with the proper plasmids, pulse-chase labeling was carried out. Cell lysates were subjected to immunoprecipitation with an S-specific antibody and subsequent EndoH digestion to check the maturation. At the start of the chase (Fig. 2a, lanes 0), the majority of wt S and S chimeras was EndoH sensitive (bands marked S_{EndoH}) indicating that most of the S proteins had not passed the endoplasmic reticulum. However, a small portion of all S variants already had become EndoH resistant (bands marked S_{EndoH}).

Transport of S and the S chimeras to the plasma membrane was confirmed by a biotinylation experiment. Surface proteins of S-transfected 293T cells were biotinylated, and cell lysates were subjected to immunoprecipitation with anti-S antibody. Subsequently, Western-blot analysis was carried out using
reached titers of 10^6 to 10^7. To check whether the infectivity of RD114, the envelope of a feline endogenous retrovirus, depended on the infection method (with or without spinoculation) (see Fig. 3a). Control particles, pseudotyped with depending on the infection method (with or without spinoculation) (see Fig. 3a). Control particles, pseudotyped with

FIG. 2. Expression and maturation of S and S chimeras. (a) CMV-driven S expression plasmids were transfected into VeroE6R cells. After a 24-h incubation, cells were pulsed for 2 h with [35S]Met-Cys and chased for the indicated periods (in hours). After the chase, cells were lysed and and the S proteins were immunoprecipitated with anti-SARS serum. Samples were analyzed on an 8% PAA gel. Endo H-resistant S (S_{Res}) and EndoH-sensitive S (S_{Sens}) are indicated. Lanes: 1, SWT; 2, S_{VSV-Cyt}; 3, S_{VSV-TMD-Cyt}; 4, S_{MHV-TMD-Cyt}; 5, VSV-G. (b) Cell surface expression of S was demonstrated by biotinylation of S proteins. Transfected 293T cells were incubated with sulfo-NHS-LC-biotin 24 h posttransfection. Subsequently, S-specific immunoprecipitation was carried out, followed by Western blot analysis using HRP-conjugated streptavidin. Bands were visualized by chemiluminescence. S-specific bands are indicated. Lanes: 1, SWT; 2, S_{VSV-Cyt}; 3, S_{VSV-TMD-Cyt}; 4, S_{MHV-TMD-Cyt}; 5, mock.

horseradish peroxidase (HRP)-conjugated streptavidin. Figure 2b shows that the S chimeras were biotinylated at least to the same extent as wt S (S_{WT}), indicating that the S chimeras were transported to the plasma membrane in the same manner as the wt S protein.

Synthesis and characterization of SARS-CoV pseudotyped retrovirus. Next, we wanted to investigate the potential of S and the chimeras to mediate the infection of a cell. To do this, a SARS pseudotype system based on the retrovirus MLV was used. SARSpp were analyzed for their ability to transduce permissive VeroE6R cells. Since the particles contain a GFP-encoding RNA, the number of transduced cells could be measured by FACS analysis. Titers of 10^7 to 10^9 were reached, depending on the infection method (with or without spinoculation) (see Fig. 3a). Control particles, pseudotyped with RD114, the envelope of a feline endogenous retrovirus, reached titers of 10^7 to 10^9. To check whether the infectivity of the SARSpp was dependent on the SARS-CoV S protein, a neutralization assay was done with sera of several SARS patients, a SARS-specific rabbit serum, and control sera. Figure 3b shows that the infectivity of the SARSpp was specifically inhibited by the SARS receptor ACE-2- and S-expressing cells, and that interaction between cells expressing these two molecules results in fusion. In contrast with this observation, we were unable to observe any syncytia in VeroE6R cells infected with SARS-CoV (results not shown).

In SARS patients, syncytia in lung tissue have been observed (18). These syncytia are most likely due to the fact that the infected cells express the SARS-CoV spike and the SARS receptor ACE-2 and that interaction between cells expressing these two molecules results in fusion. In contrast with this observation, we were unable to observe any syncytia in VeroE6R cells infected with SARS-CoV (results not shown). We investigated whether the SARS-CoV S protein was able to induce cell-cell fusion in vitro, as has been previously observed by Li et al. (20) by overexpressing ACE-2 and SARS-CoV S. 293T cells were transfected with either pFLACE2/T7rLuc or pFR-CMV-S and pBp9/CMVT7. pFAACE2/T7rLuc encoded CMV promoter-driven ACE-2 and a Renilla luciferase gene under a T7 polymerase promoter. In the case of fusion between ACE-2- and S-expressing cells, Renilla luciferase could be synthesized. Consequently, the Renilla luciferase activity represented the level of cell fusion. Twenty-four hours posttransfection, the cells were mixed and incubated for 17 to 20 h. Microscopic examination of the cells was carried out, and small syncytia were observed (results not shown). Cells were lysed, and the luciferase activities and protein concentrations of the samples were determined.

Figure 6 shows the results obtained with this cell-cell fusion assay. The values of the chimeric S proteins are given relative to that for wt S and are corrected for non-S-related background luciferase activity. Consistent with the results obtained with the SARSpp, S_{VSV-Cyt} and S_{MHV-TMD-Cyt} displayed 50 to 60% of the activity of wt S, indicating that the cytoplasmic domain is not important for fusion and that the TMD and cytoplasmic
The domain of MHV can be used by the SARS-CoV S protein. The result obtained with S\textsubscript{SVSV-TMDCyt} was remarkably different from the result found with SARSpp S\textsubscript{SVSV-TMDCyt}. The cell-cell fusion value measured for this chimera was around 25%, while the infectivity of S\textsubscript{SVSV-TMDCyt}-containing SARSpp was only about 5% (5 times lower), indicating that the TMD of S is less important for the cell-cell fusion activity than for the infectivity of the SARSpp.

The TMD of SARS-CoV S is less critical for the infectivity of SARSpp in cells expressing human ACE-2 at a high level than in VeroE6R cells. There are several possible explanations for the difference we observed between the SARSpp assay and the cell-cell fusion assay (see Discussion). One of them is the fact that the ACE-2 molecules in the two assays were not the same: human ACE-2 (cell-cell fusion) versus ACE-2 of the African green monkey (VeroE6R cells in SARSpp assay). Also, the expression levels of ACE-2 may differ in the two assays. The expression level of human ACE-2 in the cell-cell fusion is probably very high, whereas the ACE-2 expression level in VeroE6R cells is lower. It has been shown by Simmons et al. (37) that S-transfected 293T cells do not fuse with VeroE6 cells. Therefore, we decided to use the 293T cells transiently expressing ACE-2 in the SARSpp assay in order to be able to fairly compare cell-cell fusion activity and SARSpp infectivity. Transduction of the ACE-2-transfected cells was carried out 24 h posttransfection, and GFP expression was measured 72 h posttransduction. Figure 7 shows the relative infectivity of the SARSpp containing S chimeras compared to the wild type. The dramatic lack of infectivity of the S\textsubscript{SVSV-TMDCyt} SARSpp, as observed with VeroE6R cells, was less pronounced in the ACE-2-transfected cells (3 versus 10% relative infectivity). However, the influence of the TMD and cytoplasmic domain of VSV-G on infectivity was still quite substantial. In addition, the SARSpp displaying one of the other two chimeras, S\textsubscript{SVSV-Cyt} and S\textsubscript{SMHV-TMDCyt}, had a much higher infectivity than wild-type S-containing SARSpp. In summary, the influence of the TMD on infectivity is more pronounced than that on cell-cell fusion.

The TMD of SARS-CoV S is important for S trimer stability. It has been shown before that SARS-CoV S oligomerizes into dimers and trimers (39, 39, 46, 52). We investigated the oligomeric state of the S chimeras S\textsubscript{SVSV-Cyt}, S\textsubscript{SVSV-TMDCyt}, and S\textsubscript{SMHV-TMDCyt} in the SARSpp by immunoprecipitation of S after purification of SARSpp. Samples were run on SDS-PAGE (4%) gels under reducing conditions.

FIG. 3. Characterization of SARSpp. (a) Titer determination of SARS and control pseudotypes. Pseudotypes were prepared as described in Materials and Methods. To determine the titer, VeroE6R cells were transduced and the percentage of GFP-positive cells was determined by FACS. The total amount of GFP-positive cells represented the amount of infectious units (IU), provided that the percentage of positive cells did not exceed 10%. Black bars represent infection without a centrifugation step, and white bars represent infection with a centrifugation step. (b) Neutralization assay with SARS S-specific sera shows that the infectivity of SARSpp is S specific. Prior to titer determination, SARSpp and control RD114pp were incubated with the indicated sera for 45 min. Titers were calculated as for panel a. White bars, SARSpp values; black bars, RD114pp values. Serum numbers: 1, DMEM; 2, normal human serum 640; 3, normal human serum 641; 4, rabbit anti-SARS Marburg University; 5, goat anti-RD114 79S756; 6, human serum Hku 1a; 7, human serum Hku 1b; 8, human serum Hku 2; 9, human serum London; 10, human serum Delleith. Values are means from three independent experiments. (c) Maturation of S in SARSpp. Maturation of S in the SARSpp was examined by Western blotting of EndoH- or EndoF-treated SARSpp using a rabbit anti-SARS serum for detection. *, EndoH-resistant S; **, S digested by EndoF.
nonreducing conditions, with half of the sample being incubated at 80°C and the other half at room temperature. The results are shown in Fig. 8. When the samples were not heated, a smear of protein bands was visible, probably representing the heterogeneity of glycosylation of S. After incubation of the sample for 5 min at 80°C (39), three distinctive bands, most likely representing S trimers, dimers, and monomers, were visible for wt S and all three chimeras. However, the ratio between the three forms in S-VSV-TMDc was different from the ratio observed in Swt and the two other chimeras. Quantification of the bands by phosphorimaging and QuantityOne software (Bio-Rad) showed that the percentage of trimers of S-VSV-TMDc is only half of the percentage of trimers seen in the other three samples, suggesting that the S-VSV-TMDc trimers were less stable at 80°C than wt S protein. Moreover, Fig. 2b showed an extra S-specific band, most likely an S oligomer. Also on this blot, the S-VSV-TMDc oligomer band is weaker than the oligomer band in the other lanes. Since S-VSV-TMDc contains the TMD of VSV-G, this result suggests that the coronavirus S TMD is involved in stabilization of the S trimer.

**DISCUSSION**

The entry of SARS-CoV is an essential step in the viral life cycle. It is evident that the S protein is crucial in this process. It binds to the cellular receptor, and it is responsible for fusion of the viral and cell membranes, giving the viral RNA access to the cytosol.

In this paper, the role of the strongly conserved transmembrane domain of SARS-CoV in virus entry has been investi-

**FIG. 7.** SARSpp infectivity in 293T cells transfected with human ACE-2. 293T cells were transfected with pHACE2/T7rLuc. Twenty-four hours later, the cells were transduced with SARSpp and incubated for 3 days. Transduced cells were scored by FACS analysis, and the infectivity of the chimeric S-containing SARSpp was plotted as a percentage of that of wild-type S-containing SARSpp. Columns: 1, mock; 2, S-VSV-Gc; 3, S-VSV-TMDc; 4, S-MHV-TMDc; 5, Swt.

**FIG. 8.** Examination of the oligomeric state of S in SARSpp. 35S-labeled SARSpp were concentrated through a sucrose cushion, and the particles were resuspended. Half of the sample was subjected to an 80°C incubation step. Both treated and untreated samples were run on a 4% polyacrylamide gel under nonreducing conditions and were made visible by phosphorimaging. S monomers, dimers, and trimers are indicated, as are the marker bands. Lanes: 1, S-VSV-Gc; 2, S-VSV-TMDc; 3, S-MHV-TMDc; 4, Swt.
erved in infected lung tissue (18). It is unclear why syncytium formation is observed only in particular cases. It might be related to the level of ACE-2 and S expression or to the lower affinity of the African green monkey ACE-2 for the S protein. Indeed, recent results have shown that a change of only a few residues in ACE-2 can result in a great difference in affinity for SARS-CoV S (21). Possibly, other factors might be involved, such as the need for a coreceptor.

Replacement of the S cytoplasmic domain with the VSV-G cytoplasmic domain had a mild effect on the activity of S both in the SARSpp assay and in the cell-cell fusion assay. This confirms a previous report on MHV fusion, based on syncytium formation, in which it was shown that the VSV-G cytoplasmic tail can replace the S tail without inhibiting fusion activity (3).

The S_{SVSV-TMD\text{Cyto}} chimera, in which the SARS-CoV S TMD and cytoplasmic domain have been replaced by those originating from MHV, shows fusion activity with a slight reduction (50 to 60% activity). This shows that the TMD of MHV can serve as a membrane anchor for SARS-CoV S. Clearly, the strong sequence conservation of the coronavirus S TMD ensures that its function is also conserved.

When both the TMD and cytoplasmic tail of S were replaced with those of VSV-G, a remarkable reduction in fusion activity was observed in the SARSpp assay, using VeroE6R cells, resulting in <5% activity. This shows the importance of the TMD for SARSpp entry into VeroE6R cells. However, the cell-cell fusion assay showed a different result. There was 20 to 30% activity in this assay, showing a significant discrepancy between the two assays. By using ACE-2-transfected 293T cells instead of VeroE6R cells in the SARSpp assay, the S_{SVSV-TMD\text{Cyto}} chimera exhibited 10% activity. The reason for the difference in infectivity between the two cell lines may be found in the difference in receptor expression level and affinity (human versus African green monkey ACE-2), which may result in a changed fusion activity. Another reason might be that the TMD is less important for S-mediated cell-cell fusion than for S-mediated infectivity.

Based on the three experiments described here, we conclude that S_{SVSV-TMD\text{Cyto}} has a significantly lower activity than wild-type S. We and others have reported earlier that the Cys-rich domain of the TMD is important for fusion (3, 5), which might explain the lowered activity of the S_{SVSV-TMD\text{Cyto}} chimera, lacking the Cys-rich domain. Also, the highly conserved Trp-rich region in gp41 is not present in the S_{SVSV-TMD\text{Cyto}} chimera, which might be an additional explanation for the lowered activity of S_{SVSV-TMD\text{Cyto}}. Another possible explanation for lowered S_{SVSV-TMD\text{Cyto}} activity may be the lower stability of the S_{SVSV-TMD\text{Cyto}} trimer. It has been suggested before that the oligomeric state of S may be important for fusion activity (22). At this point we do not know if the stability of S trimers is directly linked to membrane fusion activity, but this interesting option cannot be ruled out at this time.

As mentioned before, the TMD of coronaviruses is highly conserved. It consists of a N-terminal tryptophan-rich domain, a central hydrophobic domain, and a C-terminal cysteine-rich domain. A tryptophan-rich domain, located close to the TMD of HIV gp41, has been described to be important for HIV fusion (35), in particular on the level of pore dilation (26). Since we do not know where exactly the TMD of SARS-CoV S starts, it could be that the tryptophan-rich domain of coronavirus S in fact precedes the actual transmembrane part and that this domain can partition into interfacial regions of membranes, as has been described for the Trp-rich juxtamembrane domain in gp41 and has been proposed to occur in viral fusion proteins in other virus families through regions enriched in aromatic residues (29, 41). Moreover, a recent study on SARS-CoV S has identified the “pretransmembrane” region (i.e., the Trp-rich domain) as a membrane-active region, possibly involved in membrane fusion, in analogy with the HIV gp41 Trp-rich domain (14). In addition, Sainz et al. (33) propose that the coronavirus S Trp-rich region, after the HR six-helix bundle has formed, aligns with the fusion peptide, thus creating an extended hydrophobic stretch that aids the lipid flow, thereby establishing a fusion pore. Finally, it has been suggested that the Trp-rich region in gp41 might also be involved in prefusion trimerization (31), which might be related to the S trimerization and the S_{SVSV-TMD\text{Cyto}} trimer instability we observed.

The cysteine-rich domain has been shown to be necessary for fusion of MHV, as evidenced by mutational analysis (3, 5). Some of these Cys residues are palmitoylated, arguing for a strong membrane association (3), although it is not clear whether this region is located within the membrane. It has been shown that the cysteine residues are involved in the transition from hemifusion to fusion during MHV-S-mediated cell-cell fusion (5), a situation reminiscent of the role that acylated cysteine residues have been described to play in influenza virus hemagglutinin-mediated membrane fusion (34). In addition, for MHV, deletion of three of the seven cysteines in the TMD results in a defect in cell-cell fusion but not in virus-cell fusion (50). Despite these reported effects of the cysteine residues on the membrane fusion activity of coronavirus S proteins, there is no model by which the mode of action of these residues during fusion can be explained.

To better understand the membrane fusion process of SARS-CoV, we are currently further investigating the function of these Trp-rich and Cys-rich domains in SARS-CoV S.

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