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Severe acute respiratory syndrome coronavirus Orf3a protein interacts with caveolin

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The orf3a (also called X1 or U274) gene is the largest unique open reading frame in the severe acute respiratory syndrome coronavirus genome and has been proposed to encode a protein with three transmembrane domains and a large cytoplasmic domain. Recent work has suggested that the 3a protein may play a structural role in the viral life cycle, although the mechanisms for this remain uncharacterized. Here, the expression of the 3a protein in various in vitro systems is shown, it has been localized to the Golgi region and its membrane topology in transfected cells has been confirmed. Three potential caveolin-1-binding sites were reported to be present in the 3a protein. By using various biochemical, biophysical and genetic techniques, interaction of the 3a protein with caveolin-1 is demonstrated. Any one of the potential sites in the 3a protein was sufficient for this interaction. These results are discussed with respect to the possible roles of the 3a protein in the viral life cycle.

INTRODUCTION

The aetiological agent for severe acute respiratory syndrome (SARS) was found to be a novel coronavirus (Ksiazek et al., 2003; Marra et al., 2003; Rota et al., 2003). Like other members of this viral family, the SARS coronavirus (SARS-CoV) has an approximately 30 kb, positive-sense RNA genome that contains 14 potential open reading frames (ORFs) (Marra et al., 2003; Rota et al., 2003). As well as the genes responsible for virus structure and RNA replication, coronaviruses also carry several putative accessory genes whose functions are poorly characterized. These genes are generally dispensable for growth in cell culture, but appear to play roles in viral pathogenesis in vivo (de Haan et al., 1999; Ortego et al., 2003; Paul et al., 1997; Wesley et al., 1991).

In addition to the genes found in other coronaviruses, the SARS-CoV genome also contains nine unique putative ORFs (Marra et al., 2003; Rota et al., 2003). The region between the S and E genes in the SARS-CoV genome contains a locus found frequently in other coronaviruses that has been proposed to be important for virulence and pathogenesis (Wesley et al., 1991; Vaughn et al., 1995; Zeng et al., 2004). In SARS-CoV, orf3a, also called X1 (Rota et al., 2003) or U274 (Tan et al., 2004b), is the largest of these ORFs and encodes a protein of 274 aa. It was predicted to contain an N-terminal signal peptide, followed by three transmembrane domains and a C-terminal cytoplasmic domain of approximately 150 aa (Zeng et al., 2004). The 3a protein was localized to the plasma membrane and perinuclear regions of infected or transfected cells (Tan et al., 2004a).

The 3a protein is associated with virus particles produced following infection of Vero E6 or CaCo2 cells (Ito et al., 2005; Shen et al., 2005) and assembles into virus-like particles when co-expressed with the M and E proteins in insect cells (Shen et al., 2005). It is O-glycosylated (Oostra et al., 2006), interacts with the M, E and S structural proteins (Tan et al., 2004b) and forms inter-chain disulfide linkages with the S protein (Zeng et al., 2004). The protein is released in membranous structures from transiently expressing, as well as SARS-CoV-infected, cells (Huang et al., 2006) and the deletion of its gene reduces virus growth (Yount et al., 2005). Convalescent sera from SARS patients contain antibodies to the 3a protein (Tan et al., 2004a). In addition to a proposed structural role, the 3a protein may also have regulatory functions. The ectopic expression of 3a induces apoptosis in Vero E6 cells (Law et al., 2005) and upregulates the expression of fibrinogen in A549 lung epithelial cells (Tan et al., 2005). Recently, the 3a protein has been shown to possess ion-channel activity selective for monovalent cations and was proposed to belong to the viroporin class of proteins (Lu et al., 2006).

The 3a protein may modulate the trafficking properties of the SARS-CoV spike (S) protein (Tan et al., 2005). As well as the presence of tyrosine-sorting (YXXΦ) and diacidic motifs in its cytoplasmic region (Tan et al., 2004b), the 3a
protein was also shown to contain putative binding sites for caveolin-1 (Cai et al., 2003). The caveolins (1, 2 and 3) are 21–24 kDa proteins that form the major structural component of caveolae, which are membrane microdomains implicated in the uptake of small molecules through glycosyolphosphatidylinositol (GPI)-anchored receptors (Rothberg et al., 1992; Anderson, 1998). Caveolin-1 appears to play a direct role in caveolar biogenesis through its ability to form oligomers (Sargiacomo et al., 1995; Schlegel & Lisanti, 2000) and its interaction with cholesterol (Murata et al., 1995). Caveolae have also been proposed as sites for signal transduction (Razani et al., 2000), virus entry into cells (Pelkmans et al., 2001) and virus assembly (Brown et al., 2002). The caveolar localization of various signalling molecules provides a compartmental basis for their subsequent regulated activation and also explains the cross-talk between different signalling pathways (Lisanti et al., 1994). Many signalling molecules bind to and are regulated by caveolin-1 (Li et al., 1996; Okamoto et al., 1998; Smart et al., 1999). The signalling pathways include the extracellularly regulated kinase (ERK) and inducible nitric oxide synthase (iNOS) pathways, two critical pathways involved in cell survival, proliferation and response to viral infection (Garcia-Cardenas et al., 1997; Engelman et al., 1998, 1999; Felley-Bosco et al., 2002). Caveolin also regulates the cell cycle through transcriptional repression of cyclin D1 (Hulit et al., 2000) and a p53-dependent mechanism (Galbiati et al., 2001).

In view of the presence of caveolin-1-binding motifs in the SARS-CoV 3A protein (Cai et al., 2003) and the importance of caveolae in cell signalling, the cell cycle and virus uptake, we explored the interaction between caveolin-1 and the 3a protein. We show here the subcellular localization of the 3a proteins and their interaction with caveolin-1 by using various biochemical, genetic and biophysical methods.

**METHODS**

**Materials.** All common reagents were from Sigma unless stated otherwise. COS-1 cells were obtained from the ATCC (Manassas, VA, USA), whilst Madin–Darby canine kidney (MDCK) and HT29 cells were obtained from the National Animal Cell Repository (National Centre for Cell Sciences, Pune, India). All cell lines were cultured at 37 °C in 10% CO_2_ in complete Dulbecco’s modified Eagle’s medium (DMEM) containing 5% fetal bovine serum (FBS). Anti-haemagglutinin (HA) tag and anti-enhanced GFP (EGFP) were from Santa Cruz Biotechnology, and anti-caveolin from Becton Dickinson Biosciences. Antibodies to 3a were prepared in rabbits immunized with a purified His<sub>c</sub>-cyto3a protein (aa 125–274) expressed in *Escherichia coli*.

**Plasmid constructs.** The orf3a gene (nt 25 268–26 092) of the SARS-CoV genome (GenBank accession no. NC_004718) was provided by Dr Vincent Chow (National University of Singapore). Fragments corresponding to the full 3a or its cytoplasmic domain (aa 125–274) were cloned into the expression vector pSGI-HA to give pSGI-3a-HA and pSGI-cyto3a-HA. The pSGI-HA vector was derived from pSGI (Jameel et al., 1996) by inserting annealed oligonucleotides carrying the HA epitope at the 3’ end of the multiple cloning sites, placing the HA tag at the C terminus of the 3a proteins. Mutants of 3a with deletions of individual caveolin-1-binding motifs were constructed by PCR-based mutagenesis of pSGI-3a-HA. These included single mutants Δ1 (aa 69–77; nt 205–231), Δ2 (aa 107–114; nt 319–341) and Δ3 (aa 141–149; nt 421–447) and the double mutants Δ1 + Δ2 and Δ2 + Δ3. The 3a cytoplasmic domain containing a deletion of the third potential caveolin-1-binding domain (ΔCyto3a) was made by PCR amplification. All mutants were confirmed by DNA sequencing. For yeast two-hybrid assays and microscopy, the 3a fragments were cloned into plasmids pGBK7 (as *NcoI–BamHI* fragments) and pEYFP-N1 (as *EcoRI–BamHI* fragments), respectively. The 3a gene was cloned into plasmid pDsRed-N1 as an *EcoRI–BglII* fragment. The caveolin–1 gene (Schlegel & Lisanti, 2000) was cloned into plasmids pGAD17 (as an *NcoI–BamHI* fragment) and pEYFP-N1 (as an *EcoRI–BamHI* fragment) for two-hybrid assays and microscopy, respectively. The primer sequences, PCR conditions and cloning details are available upon request.

**In vitro synthesis, transfection and detection.** For *in vitro* protein expression, a coupled transcription–translation system (TNT; Promega) was used according to the manufacturer’s instructions, programmed with DNA from pSGI-HA-based plasmids as described previously (Jameel et al., 1996). Transfections of animal cells, carried out with 5 μg plasmid DNA per 60 mm dish and Lipofectin (Invitrogen), and Western blotting were performed as described previously (Kar-Roy et al., 2004).

**Immunofluorescence, subcellular localization and fluorescence resonance energy transfer (FRET) assays.** Cells grown on coverslips to 40–50% confluence were transfected in antibiotic- and serum-free DMEM. Six hours post-transfection, the medium was removed and replaced with complete DMEM containing 5% FBS. Around 48 h post-transfection, the cells were washed with PBS, fixed with 2% paraformaldehyde for 15 min at room temperature and observed directly in the case of fluorescently tagged proteins, or stained with antibodies and imaged as described previously (Kar-Roy et al., 2004). For subcellular localization, cells were co-transfected to express the required protein and a relevant fluorescent subcellular marker (Living Colours Subcellular Localization Vector set; Clontech). For FRET analysis, COS-1 cells were transfected as described above with 3a–enhanced cyan fluorescent protein (ECFP) (full-length, cyto or Δcyto) and caveolin–1–enhanced yellow fluorescent protein (EYFP) expression plasmids. Image acquisition and FRET assays were as described previously (Kar-Roy et al., 2004). The percentage FRET efficiency was calculated by using the formula

\[
\text{FRET efficiency} = \frac{\text{ECFP intensity before photobleach}}{\text{ECFP intensity after photobleach}} \times 100
\]

**Preparation and analysis of microsomes.** The preparation of microsomal membranes from transfected cells, *in vitro* translation in the presence of canine pancreatic membranes (Promega) and protease protection of the translocated 3a protein were carried out essentially as described previously (Zafurrullah et al., 1999).

**Triton solubility, alkaline carbonate extraction and caveolar fractions.** The extraction of Triton X-100-soluble proteins and alkaline carbonate extraction were performed as described previously (Schlegel et al., 1999). Transfected COS-1 cells were fractionated in the presence of Triton X-100 to isolate caveolar fractions as described previously (Cherukuri et al., 2004; Sargiacomo et al., 1993). Various fractions (20 μl each) were separated by SDS-PAGE and analysed by Western blotting.
Yeast two-hybrid assays. The 3α and caveolin-1 genes in the pGBK7T and pGADT7 two-hybrid vectors, respectively, were used. Expression of the relevant fusion proteins was checked in vitro by using a TNT system (Promega). The yeast two-hybrid analysis was carried out essentially as described previously (Kar-Roy et al., 2004; Tyagi et al., 2004). The specificity of the interaction was tested as growth on plates containing 20 mM 3-amino-1,2,3-triazole (3AT). The filter-lift and liquid β-galactosidase assays were carried out as described previously (Kar-Roy et al., 2004; Tyagi et al., 2004).

RESULTS

Expression of the 3α proteins

The genes for full-length 3α protein, its cytoplasmic domain and various mutants with deletions in potential caveolin-1-binding motifs were cloned and verified by sequencing (Fig. 1a, b). Following cloning into the pSGI-HA vector, all constructs expressed proteins of the expected size in a coupled transcription–translation system (Fig. 1c). Expression was also tested in transfected COS-1 cells followed by either Western blotting or indirect immunofluorescence (IFA). Whilst high levels of 3α–HA expression were observed in transfected cell lysates (Fig. 2a), the Cyto3α–HA protein could not be detected by Western blotting (not shown). When transfected cells were observed by IFA, large numbers were repeatedly found to express 3α–HA, but very few cells expressed Cyto3α–HA (Fig. 2b). This was the case with multiple transfections, using different plasmid preparations and transfection reagents, suggesting that either the Cyto3α–HA plasmid was poorly transfected or the protein was degraded rapidly. The 3α–HA protein localized prominently to the perinuclear region; smaller amounts were also present on the plasma membrane. The Cyto3α–HA protein was, however, restricted to the perinuclear region, with none found at the plasma membrane.

Subcellular localization of the 3α protein

In COS-1 cells co-transfected to express 3α and an organelle-specific marker, the 3α protein was found to localize predominantly to the Golgi (Fig. 2c), but not to the endoplasmic reticulum or mitochondria (not shown). Three transmembrane domains are predicted in the 3α protein. To determine its topology on intracellular and extracellular domains, 3α deletion mutants were generated and tested in yeast two-hybrid assays and in mammalian cells.

Fig. 1. Orf3a constructs used in this study. (a) The 3α protein (274 aa) is shown with its predicted transmembrane regions (grey boxes) and caveolin-binding motifs (black boxes). The various 3α deletion mutants used in this study are shown as lines, with breaks indicating the deleted regions. Numbers represent amino acid residues. (b) The amino acid sequence of the 3α protein is shown with the predicted transmembrane regions (underlined) and potential caveolin-binding motifs (bold, upper case). (c) In vitro coupled transcription–translation to confirm protein expression from the indicated pSGI-HA constructs. In the first panel (lanes 1–5), the arrow indicates the full-length protein; the arrowhead indicates the product of in vitro translation from an internal AUG codon. Size markers (kDa) are shown on the left of each panel.
plasma membranes, we carried out trypsin-digestion experiments. The 3a–HA proteins were expressed in vitro in the presence of canine microsomal membranes and the vesicles were subjected to trypsin digestion to evaluate protection of the translocated proteins. Whilst the 3a–HA protein sedimented with the vesicles, it was not protected from trypsin digestion (Fig. 3a; lanes 4–6). In contrast, similarly synthesized and processed yeast α-factor was protected from trypsin digestion in the absence, but not in the presence, of NP-40 (Fig. 3a; lanes 1–3). The status of translocated 3a–HA was also analysed by using microsomes prepared from transfected COS-1 cells. Again, no trypsin protection was observed (Fig. 3b). This suggests that the 3a protein either associates with the cytoplasmic face of membranes or inserts into membranes with a topology that places most of it outside the vesicles.

**Colocalization of 3a and caveolin-1**

There are three predicted caveolin-1-binding sites in 3a (Fig. 1b). To address whether 3a and caveolin-1 colocalize in cells, we carried out biochemical fractionations. Lysates from co-transfected cells were separated into Triton X-100-soluble and -insoluble fractions. The 3a–HA protein

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**Fig. 2.** Expression and subcellular localization of the 3a protein. (a) COS-1 cells were transfected with pSGI-HA vector (lane 1) or pSGI-3a-HA (lane 2) and the cell lysates were subjected to Western blotting with either anti-HA or anti-3a antibodies as described in Methods. (b) COS-1 cells were transfected with pSGI-HA (vector), pSGI-3a-HA or pSGI-Cyto3a-HA and the cells were stained for IFA with either anti-HA or anti-3a. (c) COS-1 cells were co-transfected with pSGI-3a-HA and pEYFP-Golgi. Cells were stained for 3a–HA expression with anti-HA and anti-rabbit–Alexa 594 antibodies, and imaged as described in Methods. The pseudocoloured images are shown individually and merged to show colocalization of 3a with the Golgi marker. Bars, 5 μm (b, c).

**Fig. 3.** Membrane topology of the 3a protein. (a) The yeast α-factor (lanes 1–3) or 3a–HA (lanes 4–6) proteins were synthesized in vitro in a T7 coupled transcription–translation system in the presence of canine pancreatic membranes. The microsomes were pelleted and subjected to trypsin digestion as described in Methods, and the proteins were detected by SDS-PAGE and fluorography. Lanes: 1 and 4, untreated; 2 and 5, with trypsin; 3 and 6, with trypsin and NP-40. Arrows indicate the undigested protein bands. (b) COS-1 cells were transfected with pSGI-3a-HA; the microsomes were prepared and treated with trypsin as described in Methods and the proteins were detected by Western blotting with anti-3a antibodies. Lanes: 1, untreated; 2, with trypsin; 3, with trypsin and NP-40. The 3a–HA band is indicated.
localized to the soluble fraction that also contained about 40–50 % of the endogenous caveolin-1 and a small fraction of caveolin-1–EGFP (Fig. 4a). The control EGFP–protein was found mainly in the soluble fraction. We then isolated caveola-enriched membrane fractions by sucrose-gradient ultracentrifugation of Triton X-100 lysates prepared from 3a–HA-expressing cells. Endogenous caveolin was present in two regions of the gradient: the top half, which represents cholesterol-rich membrane domains (rafts), and the bottom half, which represents non-raft membrane fractions (Fig. 4b). The 3a–HA protein was found in the same non-raft fractions as endogenous caveolin-1 (Fig. 4b). Proteins attached to the surface of membranes are solubilized easily by alkaline carbonate extraction, whereas integral membrane proteins remain insoluble. On alkaline carbonate extraction, caveolin as well as caveolin-1–EGFP were found mainly in the insoluble fraction, which also contained about 20 % of the 3a–HA protein (Fig. 4c). Thus, 3a and caveolin-1 were found to colocalize, based on confocal microscopy in three different cell lines (MDCK, HT29 and COS-1) that express variable amounts of caveolin-1. Extensive colocalization of caveolin-1 and 3a was observed as punctate, perinuclear staining, shown earlier to be in the Golgi region (Fig. 5a). This was also true for all the 3a mutants that lacked either one or two of the three potential caveolin-1-binding sites (Fig. 5b). The Cyto3a–HA protein also showed similar distribution but when aa 141–149, comprising the third potential caveolin-binding motif of 3a, were deleted, there was a dramatic change in its distribution (Fig. 5c). Instead of punctate staining, the ΔCyto3a–HA protein showed a diffuse cytoplasmic distribution (Fig. 5c) and did not colocalize with caveolin-1. These results suggest that the presence of just one of the three potential caveolin-1-binding motifs is sufficient for the characteristic subcellular distribution of 3a and its colocalization with caveolin-1.

**Yeast two-hybrid analysis of the caveolin-1–3a interaction**

To assess any direct interaction between caveolin-1 and 3a, we used the yeast two-hybrid system as described in Methods. A representative set of plates is shown in Fig. 6(a). All transformants grew on non-selective yeast extract/peptone/glucose (YPD) plates. Single transformants and all co-transformants containing activation domain (AD)–caveolin-1 grew on SD/Leu− (L−) plates; similarly, those containing binding domain (BD)–3a grew on SD/Trp− (T−) plates and the co-transformants grew on SD/Leu Trp− (LT−) plates. Co-transformants that contain interacting protein pairs can transactivate the HIS3 gene, resulting in growth on SD/Leu−Trp−His− (LTH−) plates. The growth of AD–caveolin/BD–3a co-transformants on the LTH− plate is indicative of an interaction between the two proteins. The transformants were also grown on LTH− plates in the presence of 20 mM 3AT to further confirm the specificity and strength of the interactions. All co-transformants that grew on LTH− plates also grew on the 3AT plates. Colonies were transferred to a nitrocellulose filter and a β-galactosidase filter assay was carried out. The presence of β-galactosidase activity only in the positive control and AD–caveolin/BD–3a co-transformants further confirmed the caveolin-1–3a interaction. The same analysis was repeated with AD–caveolin-1 and either BD–cyto3a or BD–Δcyto3a co-transformants (Fig. 6b). The results showed interaction of caveolin-1 with the cyto3a protein; this binding was lost when the caveolin-binding motif in cyto3a (aa 141–149) was removed (Fig. 6b). A semiquantitative liquid β-galactosidase assay also confirmed these results (not shown).

**FRET for caveolin-1–3a interaction**

To confirm these protein–protein interactions further in vivo, we carried out FRET assays. COS-1 cells were co-transfected with vectors expressing 3a–ECFP and caveolin-1–EYFP, as already shown in Fig. 5(a). To measure FRET, we followed an acceptor photobleach protocol, wherein the mean fluorescence intensities from the donor (ECFP) and acceptor (EYFP) fluorophores were recorded before and after the photobleach.
after EYFP photobleaching (Siegel et al., 2000; Xia & Liu, 2001). Two different areas within the same cell, one showing colocalization and another where no colocalization was observed, were subjected to FRET analysis. As expected, the 3a–ECFP and caveolin-1–EYFP proteins colocalized in transfected cells (Fig. 7a, upper panels). On simultaneous scanning of the two fluorophores, there was an increase in cyan (donor) fluorescence following bleaching of the yellow (acceptor) fluorophore (middle panels); this was also monitored in real time (lower panel). Similar measurements were also made in cells expressing caveolin-1–EYFP together with either Cyto3a–ECFP (Fig. 7b) or Δ3Cyto3a–ECFP (Fig. 7c). Multiple FRET measurements were carried out in more than one region of the same cell, with similar results. The mean fluorescence intensities were determined for each FRET measurement and the efficiency was calculated. Whilst there was efficient FRET between caveolin-1–EYFP and either 3a–ECFP or Cyto3a–ECFP, none was observed with Δ3Cyto3a–ECFP (table in Fig. 7). Thus, FRET analysis further confirmed direct binding of caveolin-1 to the 3a protein.

DISCUSSION

Several unique ORFs were predicted in the SARS-CoV genome (Marra et al., 2003; Rota et al., 2003). As this virus shows increased virulence compared with other human coronaviruses (Holmes, 2003; Navas-Martin & Weiss, 2003), it is reasonable to hypothesize a role for the unique SARS-CoV proteins in its pathogenesis, virulence or disease outcomes. The 3a protein is the product of the largest unique ORF in the SARS-CoV genome and is expressed during infection of human patients, as well as by cells in culture (Zeng et al., 2004; Tan et al., 2004a; Yu et al., 2004).

By using 3a expression constructs, we show that a protein of the predicted size of approximately 34 kDa is expressed...
in transfected animal cells and localizes to the plasma membrane and Golgi region. This is in agreement with other reports (Tan et al., 2004b; Yuan et al., 2005). Whilst the cytoplasmic domain of 3a (aa 125–274) is not present on the plasma membrane, it still localizes to the Golgi. In another study, a cytoplasmic region of 3a that included aa 147–274 fused to EGFP did not show perinuclear localization, but was distributed throughout the cell in a pattern similar to EGFP (Yuan et al., 2005). This suggested that, besides the transmembrane region, aa 125–147 of 3a were also critical for its characteristic subcellular distribution. This region contains a putative caveolin-1-binding site, YDANYFVCW (aa 141–149). In addition, two other caveolin-1-binding sites, WQLALYKGF (aa 69–77) and YLYALIYF (aa 107–114), were predicted within the 3a protein (Cai et al., 2003). By using an N-terminally myc-tagged protein, Tan et al. (2004b) demonstrated the topology of the 3a protein to be such that its N terminus is extracellular and its C terminus is cytoplasmic. This would place the N terminus in the lumen of microsomal vesicles and leave the C terminus exposed to trypsin in our protection experiments. With 17 predicted trypsin-cleavage sites on the 3a protein, its complete digestion with this topology would result in fragments too small to be seen on the gels in Fig. 3. Alternatively, a reverse topology would produce a protected fragment of about 150 aa; this was clearly not observed. Thus, our results confirm earlier findings (Tan et al., 2004b).

The 3a protein was predicted to be a transmembrane protein (Zeng et al., 2004) and subsequent studies on its topology (Tan et al., 2004b) and O-glycosylation (Oostra et al., 2006) have supported this prediction. Whilst our results confirm the membrane topology of 3a, alkaline carbonate extraction reproducibly showed only about 20% of the protein in the insoluble fraction. This, together with its complete solubility in Triton X-100, suggests that the 3a protein may have an unusual membrane insertion. The pestivirus Erns (Fetzer et al., 2005) and infectious bronchitis virus 3a (Pendelton & Machamer, 2005) are examples of proteins that are neither stripped easily with alkaline carbonate like peripheral membrane proteins, nor bound tightly like integral membrane proteins.

The Cyto3a protein (aa 125–274) is devoid of any predicted transmembrane domain, but still localized to the Golgi. It is possible that this accumulation is on the cytoplasmic face of the Golgi, possibly due to its interaction with another Golgi-associated protein.
caveolin-binding site is predicted within the Cyto3a protein and caveolin is localized prominently to the Golgi. We carried out three different cell fractionation procedures to show that the 3a protein co-fractionated with both endogenous caveolin-1 and an ectopically expressed caveolin-1–EGFP fusion protein. Furthermore, by using fluorescent-protein-tagged caveolin and 3a, we demonstrated colocalization of these proteins in transfected cells. Deletion of any one or two of the three potential caveolin-1-binding motifs had no effect on this. Together with the distribution pattern of the Cyto3a and Δ3Cyto3a proteins, this suggests that one caveolin-binding motif is sufficient for the characteristic subcellular distribution of the 3a protein and its colocalization with caveolin-1.

By using a yeast two-hybrid approach, we showed a direct interaction between caveolin-1 and 3a. The 3a cytoplasmic domain was sufficient for this interaction. This was further confirmed by using FRET, a non-radiative energy-transfer method that is critically dependent upon the distance and dipole orientations of the donor and acceptor fluorophores, and is taken as evidence of an interaction between them (Xia & Liu, 2001). The interaction between caveolin-1 and 3a was directed by the potential caveolin-binding motifs in the latter protein, as its deletion in the Cyto3a background led to a loss of the FRET signal. Furthermore, no direct interaction was seen in either the yeast two-hybrid or FRET assays between the caveolin-1 and Δ3Cyto3a proteins.

There are two broad roles assigned to caveolin-1. One is a structural role wherein the protein is a major component of caveolae; these membrane microdomains are involved in...
non-clathrin-mediated virus uptake into cells (Pelkmans et al., 2001; Anderson et al., 1996). Caveolin has been shown to be associated with the assembly of respiratory syncytial virus and to be incorporated into virus particles during assembly (Brown et al., 2002). Whilst preliminary results suggest that caveolin-1 might also associate with SARS-CoV particles, direct evidence for a role of the 3a protein is lacking (data not shown). Through its interaction with caveolin-1, the 3a protein may regulate virus uptake, as well as the trafficking of structural proteins to the plasma membrane or endomembranes, which are the sites for coronavirus assembly and release (Lai & Holmes, 2001).

Caveolins also function as general negative regulators to inhibit the basal activity of many signalling proteins by sequestering these into caveolae (Razani et al., 2000); the sequestration and inhibition cease on activation of signalling (Okamoto et al., 1998; Smart et al., 1999). Loss of caveolin-1 expression activates the Ras–MAPK pathway and transforms NIH 3T3 cells (Galbiati et al., 2001). Caveolin-1 also regulates nitric oxide production in cells by binding nitric oxide synthases (NOS) (Garcia-Cardena et al., 1997; Felley-Bosco et al., 2002). Nitric oxide is genotoxic and a key regulator of cellular damage, and has been shown to inhibit SARS-CoV replication (Akerstrom et al., 2002). Whilst preliminary results suggest that caveolin-1 might also associate with SARS-CoV proteins. Putative caveolin-binding sites in SARS-CoV proteins. Acta Pharmacol Sin 24, 1051–1059.


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