Sapovirus Translation Requires an Interaction Between VPg and the Cap

- 2 **Binding Protein elF4E**
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- 5 Myra Hosmillo^a, Yasmin Chaudhry^b, Deok-Song Kim^a, Ian Goodfellow^{b#} and
- 6 Kyoung-Oh Cho^{a#}
- 8 aLaboratory of Veterinary Pathology, College of Veterinary Medicine, Chonnam
- 9 National University, 300 Yongbong-dong, Buk-gu, Gwangju 500-757, Republic of
- 10 Korea; ^bDivision of Virology, Department of Pathology, University of Cambridge,
- 11 Addenbrooke's Hospital, Hills Road, Cambridge CB2 2QQ, UK.
- #Address correspondence to Ian Goodfellow, ig299@cam.ac.uk and Kyoung-Oh
- 14 Cho, choko@chonnam.ac.kr
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19 **ABSTRACT**

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Sapoviruses of the Caliciviridae family of small RNA viruses, are emerging pathogens that cause gastroenteritis in humans and animals. Molecular studies on human sapovirus have been hampered due to the lack of a cell culture system. In contrast, porcine sapovirus (PSaV) can be grown in cell culture making it a suitable model for understanding the infectious cycle of sapoviruses and related-enteric caliciviruses. Caliciviruses are known to use a novel mechanism of protein synthesis that relies on the interaction of cellular translation initiation factors with the virus encoded VPq protein that is covalently linked to the 5' end of the viral genome. Using PSaV as a representative member of the Sapovirus genus, we characterized the role of the viral VPg protein in sapovirus translation. As observed for other caliciviruses, the PSaV genome was found to be covalently linked to VPg and this linkage was required for the translation and the infectivity of viral RNA. The PSaV VPg protein was associated with the eIF4F complex in infected cells and bound directly to the eIF4E protein. As have been previously demonstrated for feline calicivirus, a member of the *Vesivirus* genus, PSaV translation required eIF4E and the interaction between eIF4E and eIF4G. Overall our study provides new insights into the novel mechanism of sapovirus translation suggesting that sapovirus VPg can hijack the cellular translation initiation mechanism by recruiting the eIF4F complex through a direct eIF4E interaction.

IMPORTANCE

Sapoviruses, of the *Caliciviridae* family, are one of the causative agents of viral gastroenteritis in humans. However, human sapovirus remains non cultivable in the cell culture hampering the ability to characterize the virus infectious cycle. Here, we show that the VPg protein from porcine sapovirus, the only cultivatable sapovirus, is essential for viral translation and functions via a direct interaction with the cellular translation initiation factor eIF4E. This work provides new insights into the novel protein primed mechanism of calicivirus VPg-dependent translation initiation.

INTRODUCTION

Sapoviruses belong to the *Caliciviridae* family and are recognized as cause of acute gastroenteritis worldwide (1–3). Based on the complete capsid sequence, sapoviruses are divided into five genogroups (GI-GV). Genogroups I, II, IV and V are known to infect humans, whereas the PSaV belongs to genogroup III. An increasing prevalence of sapovirus infections has been described highlighting their emerging role as a public health problem (2, 4). Despite this, limited studies on molecular mechanisms of the sapovirus infectious cycle have been conducted due to the lack of a cell culture system. PSaV, the prototype of the genus, has a permissive culture system (5, 6), making it a suitable model for understanding the

61 infectious cycle and molecular mechanisms of sapovirus translation and 62 replication. Sapoviruses have a small single-strand positive-sense RNA genome of 63 64 approximately 7.3 to 7.5 kb, predicted to contain two or three open reading 65 frames (ORF) (7, 8). ORF1 encodes 7 non-structural proteins (NS), and the 66 major capsid protein (VP1). The NS5 region encodes the VPg protein, which in other caliciviruses has been found to be covalently linked to the 5' terminal of 67 68 murine norovirus (MNV) and feline calicivirus (FCV) viral RNA (9, 10). PSaV 69 ORF2, the equivalent of the FCV ORF3, is thought to encode a minor structural 70 protein that by analogy with other caliciviruses may also play are role in viral 71 replication (11, 12). Sapovirus ORF3 is present in some strains of the virus but 72 function is as yet to be known (7). 73 As with all positive sense RNA viruses, sapovirus translation initiates immediately 74 upon cell entry with the viral genome acting as an mRNA template. The 75 expression of viral proteins is frequently subject to regulation at the level of the 76 initiation of mRNA translation. There are at least 12 eukaryotic translation 77 initiation factors (eIF) recruited during the initial stage of protein synthesis (13). 78 Among these, a cap-binding complex (eIF4F) binds to the 5' end of the cellular 79 mRNAs and recruits other factors to form a highly stable ribonucleoprotein complex for protein synthesis (13, 14), eIF4F is a heterotrimeric complex 80 81 consisting of a cap binding protein eIF4E, scaffold protein eIF4G and an RNA 82 helicase eIF4A. During the translation initiation process, eIF4E binds to the 7-

methyguanosine cap structure of the host mRNA and then recruits and activates eIF4G and eIF4A. eIF4A unwinds the mRNA at the 5' end and facilitate ribosome binding (13), eIF4G acts as the cornerstone for the multi-subunit eIF4F complex linking mRNA cap and ribosomal subunit via eIF4E and eIF3 binding domains respectively (15). Many RNA viruses have developed unique mechanisms to usurp the host cell translation machinery for viral protein synthesis. Cap-independent translation is well characterized in the Picornaviridae, where internal ribosomal entry site (IRES)-mediated translation is used (16). Recently, another cap-independent translation mechanism primed by a viral encoded protein has been characterized in caliciviruses. Like picornavirus, calicivirus genomes do not possess a 5' cap structure; instead a viral protein genome (VPg) is covalently linked to the 5' end of the genome (17, 18). Recent studies have demonstrated a critical role for VPg in caliciviruses viral protein synthesis (9) as treatment of FCV or MNV VPq-linked RNA with proteinase K abrogated translation and infectivity (9, 10). The Norwalk virus VPg protein also interacts with eIF3 (19, 20). FCV VPg-dependent translation is directly coupled with the interaction of VPq with the cap binding protein eIF4E and eIF4E is functionally required for FCV translation (9). MNV translation is not affected by depletion of eIF4E nor by the separation of the eIF4E binding domain from eIF4G, but shows a functional requirement for eIF4A (9). This suggests that within the *Caliciviridae* family, the functional requirements for eIF4F components differ (9, 21–23).

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The mechanism of translation initiation used by sapoviruses is currently unknown. Therefore to characterise the role of sapovirus VPg in initiation of viral protein synthesis, we performed a series of biochemical and *in vitro* studies. We have demonstrated that the linkage of VPg to the PSaV genome is required for the translation and infectivity of viral RNA. We also show a clear role for a VPg-eIF4E interaction in PSaV translation indicating that PSaV is functionally similar to FCV. These results contribute to a more detailed understanding of sapovirus translation and the role of PSaV VPg protein during initiation of viral protein synthesis.

MATERIALS AND METHODS

Virus, cells and reagents. The PSaV Cowden strain was obtained from Dr. K.O. Chang (Kansas State University) and is a tissue culture adapted strain recovered from the full-length infectious clone pCV4A (24). PSaV permissible LLC-PK1 cells were transduced with lentiviruses expressing the bovine viral diarrhea disease virus (BVDV) Npro protein to produce an IFN-deficient cell line, which allows more efficient virus replication (M.Hosmillo, F. Soorgeloos, R. Hiraide, I.Goodfellow and K-O. Cho, submitted for publication). IFN-deficient LLC-PK1 derived transduced cells expressing BVDV NPro (LLC-PK-Npro) were used to propagate the PSaV in Eagle's minimal essential medium (EMEM) supplemented

with 200 μ M glycochenodeoxycholic acid (GCDCA, Sigma), 2.5% fetal calf serum and 1% penicillin/streptomycin (P/S) at 37°C with 5% CO₂.

Antisera to PSaV VPg and capsid were generated by immunization of New Zealand white rabbits with purified recombinant VPg and virus, respectively. Antisera against eIF4E, eIF4A and eIF4G1 were purchased from Cell Signaling Technology.

Cap analogue (m7 G(5')ppp(5')G, Promega), elastatinal (Calbiochem), proteinase K (Ambion) and [35S] Methionine (PerkinElmer) were purchased. Recombinant 4E-BP1 was a kind gift from Simon Morley (University of Sussex) and the recombinant FMDV Lb protease was provided by Tim Skern (University of Vienna). The elF4E expression plasmid was the kindly received from Stephen Curry (Imperial College London). Recombinant elF4E was first purified with His tag by affinity chromatography on a Hitrap chelating column (GE Healthcare). To ensure a functional elF4E protein, purified elF4E was then additionally purified via m7-GTP Sepharose column (GE Healthcare) using a salt gradient elution to avoid possible contamination with cap analogue (9).

Expression and purification of recombinant PSaV VPg. The cDNA encoding PSaV VPg was PCR amplified from a full-length clone pCV4A using primers VPg-F (5'- GCG ACC ATG GCG AAA GGG AAA AAC AAA CGC) and VPg-R (5'

-TTA CTC GAG TCA CTC ACT GTC ATA GGT GTC ACC). PCR amplicons were cloned into pProEX HTc digested with Ncol and Xhol (underlined) and the resulting constructs were verified by sequencing.

VPg containing plasmid was expressed in B834 (DE3) *E. coli* strain. A large scale recombinant protein production was performed in an autoinducible ZYP media containing antibiotics, and cultured for 2 d at 37°C with shaking. Cell pellets from the bacterial culture were resuspended in a lysis buffer containing 20 mM Tris-HCl pH 7.5 and 500 mM NaCl, and one tablet of EDTA-free protease inhibitor (Roche). Following resuspension, the pellets were digested and sonicated. The lysates were collected and loaded onto a 5 mL HisTRAP HP column (GE Healthcare) and His-tagged VPg proteins were eluted in 500 mM imidazole. To prepare the untagged VPg protein, His-tag from VPg were digested by tobacco etch virus protease (kindly provided by Jeong-sun Kim, Chonnam National University) at 18°C overnight and purified again by HisTrap HP column. The final recombinant untagged VPg protein was concentrated and snap frozen in liquid nitrogen before storage at -80°C.

VPg-dependent *in-vitro* **translation**. Mock or PSaV were inoculated in LLC-PK-Npro cells at m.o.i. of 10 TCID50/cell. At 12, 24 and 48 h post infection, cells were harvested and total RNA were extracted using GenElute total RNA extraction kit (Sigma). *In vitro* translation reactions using Flexi rabbit reticulocyte

lysate (RRL, Promega) was performed as previously described (9) using 40 µg ml⁻¹ mock or PSaV RNA and 12.5 µg ml⁻¹ in vitro transcribed control RNAs. Capped control dicistronic mRNAs containing either foot and mouth disease virus (FMDV) or porcine teschovirus-1 (PTV)-IRES were synthesized in vitro from plasmids pGEM-rluc/FMDV/fluc or pGEM-CAT/PTV/LUC provided by Graham Belsham (Technical University of Denmark) respectively (25). Control capped PSaV RNA were in vitro transcribed from pCV4A containing the full-length PSaV genome. Transcribed RNAs were then capped using ScriptCap m7-G capping system (Epicentre Biotechnologies). In reactions that required the addition of cap analogue, 4E-BP1, Lb protease and eIF4E, recombinant proteins were preincubated at 30°C for 15 min prior to the addition of RNA. Complementation with recombinant eIF4E after eIF4E sequestration or depletion was carried out for additional 5 min before incubation of the RNA template. After the incorporation of RNA, in vitro translation was performed at 30°C for 90 min and terminated with equal volume of tris buffer containing 10 mM EDTA and 100 ng ml⁻¹ RNASe A (Ambion). Translated proteins were resuspended in 5x SDS sample buffer and resolved on 12.5% polyacrylamide gels. Pretreatment of RNAs was carried out by incubation of RNA in 10 mM Tris, pH 8.0, 1.0 mM EDTA, 0.1M NaCl and 0.5% SDS in the presence or absence of 10 µg ml⁻¹ proteinase K for 30 min at 37°C. Pretreated RNAs were immediately purified by GenElute RNA clean up protocol (Sigma). Protein synthesis levels were quantitated from dried gels using a Packard Instant Imager

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(Canberra, Packard, UK). X-ray films were developed after 4-24 h incubation at room temperature.

Immunoprecipitation. Products from IVT reactions were incubated with protein A agarose beads and antibodies against MNV NS7, PSaV VPg or VP1 in radioimmunoprecipitation assay buffer (RIPA, 50 mM Tris pH 8.0, 150 mM NaCl, 1% NP-40, 0.5% sodium deoxycholate, 0.1% SDS) buffer. The mixture was centrifuged, washed with RIPA buffer 3 times and the immunoprecipitated proteins were then evaluated by autoradiography.

Avicel-based plaque assay. Total RNA extracts (10 μ g) from mock or PSaV infected cells were pretreated with and without proteinase K as above. Treated or mock-treated RNA were transfected into LLC-PK-Npro using lipofectamine 2000 as per the manufacturer's instructions (Invitrogen). After 4 h, the cells were washed and overlaid with 1.3% Avicel cellulose (FMC Health and Nutrition) in EMEM supplemented with 2.5% FBS, 0.225% sodium bicarbonate and 1.0% penicillin/streptomycin. Plates were incubated at 37°C for 4 days. After incubation, the Avicel mixture was removed, and cells were fixed and stained with 1.6% methylene blue and with 33.3% formaldehyde solution in 1x PBS for 30 min. Plates were washed with distilled water until the desired staining intensity was achieved. Infectious virus titer was quantified by plaque assay method.

Cap-sepharose purification for eIF4F complex. Cell lysates were prepared from either mock or PSaV infected (m.o.i of 10 TCID50/cell) LLC-PK-Npro cells in cap-sepharose lysis buffer (100 mM KCl, 0.1 mM EDTA, 10% glycerol, 2 mM MgCl₂, 20 mM HEPES pH 7.6) and ribonuclease treated for 15 min at room temperature. Cytoplasmic extracts were centrifuged and incubated with m7-GTP sepharose (GE Healthcare) overnight at 4°C. eIF4F enriched complex was precipitated and washed 2 times with lysis buffer. Bound proteins were eluted in 2x reducing buffer, resolved by SDS-PAGE and analysed by immunoblot.

ELISA-based initiation factor capture assay. An ELISA-based capture assay was performed as described previously (26). Briefly, purified PSaV VPg (1 μ g) was coated onto 96-well plates (NUNC immunosorb) overnight at 4°C. The wells were then blocked with 2% BSA in tris-buffer saline (TBS). Hela cell lysates or recombinant eIF4E were diluted in 2% BSA in TBS with 0.05% Tween-20 and was incubated for 2 h at 4°C with previously coated wells. The association to eIF4E, eIF4A and eIF4G was detected using specific primary antibodies. Secondary HRP conjugated antibodies were added, and signals were developed with TMB substrate. Reaction was stopped with H₂SO₄ and the optical density was determined at 450 nM.

Pull down assay. His-tagged PSaV VPg was immobilized on HisPur cobalt resin

(Pierce) and incubated with either recombinant eIF4E or ribonuclease-treated cell lysates on the rotator for 4 h to overnight at 4°C, respectively. Proteins interacting with His-tagged VPg were pulled down by centrifugation and sequentially washed 3 to 5 times in lysis buffer. Bound proteins were eluted with 400 mM imidazole. Binding to eIF4F components or recombinant eIF4E was analysed by western blot.

eIF4E siRNA-based functional assay. Confluent cell culture of LLC-PK-Npro were transfected with either siRNA against non-specific target (100 pmol) or eIF4E (100 pmol) using Lipofectamine 2000 following manufacturer's instructions. Cells were then infected at an m.o.i. of 1 TCID50/cell. Unabsorbed viruses were removed after 4h, and infected cells were maintained in EMEM with 2.5% FBS and 200 μ M GCDCA. The virus titer was analysed 24 h post infection by RT-qPCR using specific PSaV primers targeting viral protease, 5'-CAACAATGGCACAACAACG-3' (forward) and 5'-ACAAGCTTCTTC ACCCCACA-3' (reverse).

The porcine sapovirus RNA is linked to VPg. Based on data obtained on other
genera of the Caliciviridae, sapovirus RNA is predicted to be VPg-linked (Fig.
1A). To date, however, no experimental evidence for the formation of VPg-linked
sapovirus RNA has been described. To determine if VPg is linked to the PSaV
genome, we examined lysates and purified RNAs from infected LLC-PK-Npro
cells for the presence of VPg by western blot. It is important to note that we used
interferon deficient LLC-PK-Npro cells to infect mock or PSaV for total RNA
extractions to enable us to harvest the sufficient amount of viral RNA that
facilitate an in vitro translation reaction. Using this cell line, our previous studies
showed a 100-fold increase in virus replication and thus, these cells were
consequently used for virus propagation (M.Hosmillo, F. Soorgeloos, R. Hiraide,
I.Goodfellow and K-O. Cho, submitted for publication). This cell line shall be
referred to as LLC-PK-Npro throughout the manuscript.
Cell lysates harvested from PSaV infected cells showed the presence of a fully
processed form of VPg (15 kDa) and two VPg containing precursors from
polyprotein which based on their molecular weights, corresponded to NS4-VPg
(46 kDa) and NS4-VPg-NS6-7 (85 kDa) (Fig. 1B). To determine which form of
VPg is linked to the viral genome, we examined purified RNA isolated from mock
and PSaV infected cells for the presence of VPg after ribonuclease treatment.
western blot analysis revealed that only the fully processed form of VPg is linked

to PSaV genome (Fig. 1B) as observed for MNV (9). This confirms that like the other *Calicivirus* genera, the genome of PSaV, a member of the *Sapovirus* genus is also covalently linked at the 5' end.

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Porcine sapovirus VPg is required for infectivity and the translation of viral RNA. To characterize the translation initiation of PSaV, RRL were used to examine the ability of the VPg-linked RNA to translate in vitro. Total RNA was extracted from either mock or PSaV infected cells and used to program RRL for in vitro translation reactions. The translation profile from PSaV RNA showed several additional proteins compared with that of RNA from mock infected cells (Fig. 2A). These additional proteins were predicted to be of viral origin as the viral RNA used to produce these proteins increased during the course of infection. To determine if the additional protein products were in fact PSaV specific, immunoprecipitations were performed using antisera specific to several PSaV proteins. Using antibodies against the PSaV VPg and capsid protein (VP1), proteins corresponding to predicted molecular weights of VP1 and precursor forms of VPg were immunoprecipitated (Fig. 2B). As expected, no significant levels of PSaV viral proteins were immunoprecipitated with antisera to the MNV NS7 protein, although a small amount of the capsid protein was often detected due to the high levels of expression (Fig. 2B).

To determine if PSaV translation is VPg-dependent, we examined the effect of proteinase K (Pk) treatment on the translation profile of RNA. As controls, we used RNAs isolated from either mock infected cells and capped in vitro transcribed RNA of a dicistronic construct, expressing the CAT protein in a capdependent manner and the fluc protein dependent on FMDV-IRES structure. In addition, we used capped in vitro transcribed full-length PSaV RNA. Following Pk treatment, RNA samples were confirmed to be intact before subjecting to in-vitro translation and transfection (Fig. 2C). The translation of VPg-linked PSaV RNA was abrogated by prior treatment with Pk (Fig. 2D), confirming that VPg linkage is necessary for viral translation in vitro. To further confirm the role of VPg in PSaV translation during replication in cells, we then examined the effect of Pk treatment on PSaV RNA infectivity. We measured the specific infectivity of Pk or mock treated PSaV RNA in permissive LLC-PK1 cells. Without Pk pretreatment, PSaV RNA yielded up 1.6 x 10⁵ pfu/µg of total RNA but this was markedly reduced to 8 pfu/µg after Pk treatment (Fig. 2E).

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Porcine sapovirus VPg is associated with cellular translation initiation factors during virus infection. Previous studies on FCV and MNV translation revealed the association of VPg with cellular translation initiation factors during viral replication in cell culture (9, 10). Given our observation that PSaV VPg was required for viral translation and infectivity, this also suggested that PSaV VPg was associated with the cellular translation machinery. To investigate if the PSaV

VPg protein interacted with the translation initiation factor complex (eIF4F), we purified the eIF4F complex from mock and infected cells using m7-GTP sepharose resin, which binds to eIF4E, and therefore can be used to enrich eIF4F-interacting proteins. The eIF4E containing complex isolated from infected cells also contained PSaV VPq, both as precursor and mature forms (Fig. 3A). As expected, the eIF4E protein was isolated by m7-GTP sepharose whereas GAPDH was not, confirming the specificity of the assay (Fig. 3A). To examine the interaction of PSaV VPg and eIF4F complex from the cell lysates, recombinant His-tagged VPg protein was incubated with nuclease-treated cell lysates and purified using cobalt resin. Western blot analysis showed that the components of eIF4F were pulled down with His-tagged VPg, but not with BSA (Fig. 3B). No interaction between VPg and GAPDH was observed, verifying the specificity of the pull down assay. To further confirm the association of VPg with components of the eIF4F complex, a capture ELISA-based binding assay was performed whereby wells were coated with recombinant PSaV VPg or BSA and then incubated with lysates from a permissive cell. The retention of the eIF4F complex was then examined by ELISA using anti-initiation factor antibodies. VPg retained the eIF4E, 4A and 4G components of the eIF4F complex confirming the association of PSaV VPg with these cellular translation initiation factors (Fig. 3C). As expected, control wells coated with BSA did not show any interaction with the eIF4F components (Fig. 3C).

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Porcine sapovirus VPg binds to recombinant elF4E directly. To determine if VPg interacted directly with elF4E, as observed for other caliciviruses, an ELISA-based capture assay was performed. Plates coated with PSaV VPg, but not BSA, showed a direct binding with purified recombinant elF4E in dose dependent manner (Fig. 4A). To confirm this interaction, His-tagged PSaV VPg protein was immobilized on cobalt resin and incubated with recombinant elF4E in a pull down assay. Western blot analysis further demonstrated direct interaction between PSaV VPg and elF4E, but no interaction was found in resin treated with BSA as a control (Fig. 4B).

Porcine sapovirus translation is insensitive to cap analogue but requires an eIF4E-4G interaction. To further examine the functional requirements of PSaV RNA translation, RRL was used as an experimental system to probe the relative roles of eIF4E and the eIF4E-eIF4G interaction. To determine whether or not the interaction of eIF4E with cap analog inhibits PSaV translation, the effect of increasing concentrations of cap analogue on PSaV translation was examined. As expected, cap analogue inhibited cap-dependent translation, but had no effect on FMDV IRES-dependent translation (Fig. 5A). In contrast, PSaV translation was unaffected, suggesting that there are distinct sites for VPg and cap binding to eIF4E, fitting with our ability to co-purify VPg on m7-GTP sepharose (Fig. 3A). In addition, when eIF4E was sequestered by the addition of recombinant eIF4E binding protein (4E-BP1), translation of PSaV RNA was reduced, as was cap-

dependent translation (Fig. 5B). As expected, 4E-BP1 had no effect on PTV IRES-mediated translation (Fig. 5B). The 4E-BP1 mediated inhibition of PSaV and cap-dependent translation could be restored by the addition of recombinant eIF4E confirming the specificity of the inhibitory effect of 4E-BP1 on eIF4E (Fig. 5C).

Porcine sapovirus translation requires an intact elF4G. To examine the role

of the eIF4E-4G interaction and to examine if the N-terminal eIF4E binding

domain of eIF4G is required for PSaV translation, RRL was pretreated with

FMDV Lb protease, which cleaves eIF4G separating the eIF4E-binding domain

from eIF4A, PABP and eIF3 binding domains (Fig. 6A). Cleavage of eIF4G was

verified by western blot analysis, showing increasing eIF4G cleavage with higher

concentrations of Lb protease (Fig. 6B). Cleavage of eIF4G reduced translation

of PSaV RNA and cap-dependent translation, whereas PTV IRES-dependent

translation was slightly increased (Fig. 6C). A protein translated from PSaV RNA

preparations corresponding to a host mRNA (highlighted with an asterisk in Fig.

6C) was inhibited by eIF4G cleavage.

Porcine sapovirus translation is sensitive to eIF4E depletion. To further examine the role of the PSaV VPg-eIF4E interaction, the effect of eIF4E depletion on PSaV translation was investigated. RRL was depleted of eIF4E using m7-GTP sepharose after the addition of 4E-BP1 to prevent the concomitant

removal of eIF4G. Depletion of eIF4E was confirmed by western blot analysis. eIF4E was significantly depleted, whereas the levels of eIF4A and eIF4G remained largely similar to mock depleted lysate (Fig. 7A). Cap and PSaV-VPg dependent translation were inhibited by eIF4E depletion, however PTV IRES-mediated translation was slightly stimulated (Fig. 7B). The addition of recombinant eIF4E restored cap dependent and PSaV VPg-dependent translations to levels similar to those observed in mock depleted lysates (Fig. 7B).

Porcine sapovirus requires elF4E in the cell culture. RNA interference was used to deplete elF4E and the effect on PSaV replication was examined. The expression of elF4E was confirmed after double transfection of siRNA against elF4E (Fig. 8A), showing a significant reduction in elF4E expression. Subsequently, inoculation of PSaV showed an elF4E siRNA-mediated inhibition of virus replication. PSaV mRNA levels were significantly reduced in cells transfected with elF4E siRNA (Fig. 8B).

DISCUSSION

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In the current study, we have demonstrated that the PSaV VPg protein is associated with the eIF4F translation initiation complex facilitating viral protein synthesis. Our data fits with previous studies on other member of the Caliciviridae indicating that VPg functions as proteinaceous cap substitute (9, 10, 20). This novel mechanism of protein-primed translation initiation is also found in members of *Potyviridae* family of RNA viruses that infect plants (27, 28). Recent studies also indicate that members of *Astroviridae* possess a genome-linked VPg protein and the linkage of VPg to the viral RNA is essential for infectivity (29), although whether in this instance, VPg contributes to viral translation has yet to be determined. In the case of potyviruses, the interaction of VPg with eIF(iso)4E is a major determinant of a host susceptibility whereby mutations in eIF(iso)4E lead to resistance to infection (30). Our data indicates that the recruitment of eIF4F complex to the 5' end of PSAV RNA occurs via a direct VPg-eIF4E interaction and that this interaction occurs independently of the cap-binding site on eIF4E. In contrast, the interaction of potyvirus VPq with eIF4E competes for cap binding and can inhibit host cell translation (31). Within the *Caliciviridae* family, the interaction of VPg with eIF4E appears to be conserved, as similar VPq-eIF4E interactions have been described in FCV, a member of the *Vesivirus* genus, and MNV, a member of the *Norovirus* genus (9, 10). Importantly, whilst the interaction of the FCV VPg protein with eIF4E is essential for viral translation, the MNV VPg-eIF4E interaction does not appear to contribute to viral protein synthesis and may play a secondary role in the modulation of eIF4E activity. In the case of MNV, we have recently identified a direct VPg-eIF4G interaction that is essential for MNV translation initiation (32). Our data would indicate that PSaV VPg-dependent translation is functionally identical to that of FCV in that a VPg-eIF4E interaction is essential, as is the interaction of eIF4E with eIF4G. The functional requirements and possible interaction of VPg with other components of the eIF4F complex is the focus of on-going studies.

With the data presented in the current study, functional information on the relative requirements of some of the eIF4F components for three of the five genera of the Caliciviridae family, namely Vesivirus, Norovirus and Sapovirus, have now been described. However, further studies will be required to unravel the mechanism of translation used by members of Lagovirus and Nebovirus genera. In the case of lagoviruses, reverse genetics studies would indicate that uncapped in vitro transcribed RNA is infectious when transfected into immortalized cells, indicating that VPg is not essential for the initiation of infection (33). Therefore, whilst the interaction of translation initiation factors with the VPg proteins of caliciviruses is a conserved feature, subtle differences in the functional requirements of initiation factors apparent between genera. Similar observation have been made in the study of IRES-mediated translation of the Picornaviridae; for example, the hepatitis A virus IRES requires eIF4E and an intact eIF4G, whereas that of

poliovirus and FMDV does not require eIF4E and can function using a cleaved form of eIF4G (34, 35). The biological relevance of the subtle differences in initiation factor requirements for calicivirus translation has yet to be determined. but may in some way have occurred as a consequence of the variation in pathogenesis, i.e. FCV and PSaV typically cause acute self-limiting infection in the natural host, whereas MNV usually causes long-term persistent infection. These differences in the nature of the disease may be at least partially due to a consequence of differences in the translation efficiency of viral RNA in cells, although further comparative studies on the efficiency of translation area required. Fitting with this hypothesis, the PSaV VPg protein shares a higher degree of sequence similarity with FCV than MNV. In summary, our study provides additional insights into the novel mechanism of protein-primed VPg-dependent translation initiation used by members of the Caliciviridae family of small positive sense RNA viruses. This work also highlights how viruses have often evolved novel mechanisms to translate their mRNAs in the presence of high levels of competing cellular mRNAs.

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582	FIGURE LEGENDS		
583	FIG 1 The porcine sapovirus genome is linked to mature viral protein-genome		
584	(VPg) at its 5' terminal. (A) A schematic presentation of the porcine sapovirus		
585	genome showing the non-structural (NS1-NS6-7) and structural (VP1 and VP2)		
586	proteins. (B) Monolayers of LLC-PK1 cells were either mock infected or infected		
587	with PSaV at a m.o.i. of 10 TCID50/cell. After adsorption, the media was replaced		
588	with EMEM containing GCDCA and FBS. Infection proceeded for 30 h, then cell		
589	lysates and purified RNA were prepared. Purified RNAs were subjected to		
590	ribonuclease treatment then cell lysates and treated RNA were subsequently		

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FIG 2 Porcine sapovirus requires VPg linkage to confer virus infectivity and viral RNA translation. (A) Monolayers of LLC-PK1 cells were infected by either mock or PSaV at m.o.i. of 10 TCID50/cell. Cells were harvested at 12, 24 and 36 h.p.i., lysed, and the total RNA extracted. RNA isolated from infected cells during the time course were used to program in vitro translation reaction using rabbit reticulocyte lysates (RRL). The translation products were analysed by SDS-PAGE and the translation profiles were then evaluated by autoradiography. Asterisk refers to the translated background proteins from RRL. (B) Proteins produced by in vitro translation were immunoprecipitated using antibodies against the murine norovirus NS7 protein, PSaV VPg and capsid proteins overnight. Immonoprecipitates were washed 3 times with RIPA buffer and then resolved by 12.5 % SDS-PAGE. Protein precipitates were analysed by autoradiography. (C) RNA samples prepared from in vitro transcribed and capped Cap-Rluc:FMDV IRES:Fluc dicistronic RNA, mock and PSaV-infected cells and capped in vitro transcripts from the PSaV full length cDNA clone pCV4A were pretreated with and without proteinase K at 37°C for 30 min. Following RNA purification, the purified RNA samples were analyzed by agarose gel electrophoresis to confirm their integrity. (D) RNA samples were then used to program RRLs and were subjected to an in vitro translation reaction. (E) RNA extracted from PSaV infected cells, mock or proteinase K treated was transfected into LLC-PK1 cells expressing BVDV Npro. Serial 10-fold dilutions of RNA preparations were transfected and 4 d post transfection the cells were washed and incubated in 1.3 % avicel-based overlay media containing 2.5 % FBS, 0.225% sodium bicarbonate and supplemented with 200 µm GCDCA. Cells were immediately fixed and stained.

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FIG 3 The porcine sapovirus VPq binds to the cellular translation initiation factors during virus infection. (A) Monolayers of LLC-PK1 cells transduced with BVDV Npro were either mock infected or infected with PSaV at an m.o.i. of 10 TCID50/cells. 36 h post infection, cells were collected and lysed in capsepharose buffer. Lysates were centrifuged and further treated with RNAse. One thousand micrograms of lysates were incubated with cap-sepharose beads overnight. After washing the bound proteins were analysed by SDS-PAGE and western blot. (B) His-tag pull down assay was performed using 10 ug of Histagged VPg or BSA immobilized on HisPur cobalt resin. Increasing amounts (0-50 ug) of nuclease-treated cell lysates were then incubated overnight with the bait VPg protein. Protein complexes were extensively washed, eluted and analyzed by western blot. (C) A capture ELISA was performed using 1 μ g of purified recombinant PSaV VPg or BSA as a control. Ten micrograms of nuclease-treated cytoplasmic extracts were incubated with either target, extensively washed prior to detection with rabbit antibodies to eIF4E, eIF4A or eIF4G. Antibody binding was detected using a secondary anti-rabbit HRP

conjugated antibody followed by incubation with ELISA substrate. Samples were analysed in triplicate and in at least three independent experiments. One representative dataset is shown. Error bars represent standard deviation between the triplicated samples.

FIG 4 Porcine sapovirus VPg binds to recombinant eIF4E. (A) A capture ELISA was performed using 1μ g of purified recombinant PSaV VPg or BSA as a control. Increasing concentrations of recombinant eIF4E were then incubated with both coated proteins and extensively washed prior to detection with rabbit antibodies to eIF4E. Antibody binding was detected using a secondary anti-rabbit HRP conjugated antibody followed by incubation with ELISA substrate. Samples were analysed in triplicate in at least three independent experiments. One representative dataset is shown. (B) A pull down assay was performed using 1 μ g of recombinant His-tagged VPg immobilized on HisPur cobalt resin or resin alone. Resin with and without VPg were washed, blocked with BSA and incubated with similar concentration of either BSA or recombinant eIF4E. Binding to eIF4E was detected by immunoblot with anti-eIF4E antibody. Samples were analysed in duplicate and in at least three independent experiments and one representative dataset is shown.

FIG 5 Porcine sapovirus translation is independent on cap analogue but requires the eIF4E-4G interaction. (A) In vitro translation was performed as illustrated by the experimental time line using either VPg-linked PSaV RNA or dicistronic RNA containing a cap-dependent CAT and PTV IRES-dependent Rluc. Translation reactions were preincubated with increasing concentrations of CAP analogue, and then the RNAs were added to initiate the protein synthesis. Profiles for VPg-, cap- and IRES-dependent translations were resolved by SDS-PAGE page. The gels were fixed, dried and exposed to X-ray film. The intensity of each band was quantitated with reference to the value obtained in the absence of cap analogue. (B) In vitro translation was performed following the experimental scheme with increasing amounts of recombinant 4E-BP1, before addition of PSaV RNA and dicistronic RNA. RNAs were then added to initiate the protein synthesis. Profiles for VPg-, cap- and IRES-dependent translations were separated by SDS-PAGE. The gels were fixed, dried and exposed to X-ray film. The intensity of each bands were quantitated with reference samples incubated with 4E-BP1 buffer only. The asterisks represent the background signals from the host mRNA translation profile. (C) Experimental scheme of in vitro translation was performed as previously described with addition of recombinant eIF4E after sequestration by 4E-BP1. Effects of separation by 4E-BP1 buffer or 4E-BP1 and subsequent complementation of eIF4E in the cap-, VPg-, and IRES-dependent translation were evaluated by SDS-PAGE and autoradiograph.

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FIG 6 Porcine sapovirus translation requires full-length eIF4G. (A) *In vitro* translation was performed following the experimental time-line using increasing amounts of FMDV Lb protease to cleave eIF4G. Subsequently elastatinal was added to quench the protease activity before the addition of PSaV RNA or *in vitro* transcribed dicistronic RNA. (B) The effect of Lb protease was confirmed by western blot using antibody against eIF4G. (C) Translation profiles for VPg-, capand IRES-dependent expressing proteins were resolved by SDS-PAGE. The gels were fixed, dried and exposed to X-ray film. The intensity of each bands were quantitated with reference samples incubated without Lb protease. The asterisk refers to the protein translated from PSaV RNA preparations corresponding to a host mRNA which is also inhibited by eIF4G cleavage.

FIG 7 Porcine sapovirus translation is sensitive to elF4E depletion. Mock-depleted or elF4E-depleted RRL were used for *in vitro* translation reaction with replenishment of recombinant elF4E or buffer alone. (A) Depletion of elF4E was verified by western blot using 0.25, 0.5 and 1.0 μ l of the RRL. (B) Translation of VPg-, cap-, and IRES dependent proteins were observed in mock and elF4E depleted lysates, with and without addition of recombinant elF4E.

FIG 8 eIF4E is required for PSaV replication in the cell culture. (A) LLC-PK1 cells were transfected with either control or eIF4E siRNAs as described in the

materials and methods. Reduced eIF4E expression was verified by western blot using antibody against eIF4E. (B) PSaV was then infected at m.o.i. of 0.2 TCID50/cell. Cells were harvested 24 h post infection. and RNA were extracted for qRT-PCR analysis targeting specifically to PSaV protease region. Samples were analysed in triplicate and in at least three independent experiments. Error bars represent standard error of the mean between the triplicated samples.





















