The following full text is a publisher's version.

For additional information about this publication click this link.
http://hdl.handle.net/2066/33363

Please be advised that this information was generated on 2019-10-17 and may be subject to change.
A Proline-Rich Region in the Coxsackievirus 3A Protein Is Required for the Protein To Inhibit Endoplasmic Reticulum-to-Golgi Transport

Els Wessels, Daniël Duijsings, Richard A. Notebaart, Willem J. G. Melchers and Frank J. M. van Kuppeveld


Updated information and services can be found at:
http://jvi.asm.org/content/79/8/5163

These include:

**REFERENCES**

This article cites 35 articles, 24 of which can be accessed free at: http://jvi.asm.org/content/79/8/5163#ref-list-1

**CONTENT ALERTS**

Receive: RSS Feeds, eTOCs, free email alerts (when new articles cite this article), more»
A Proline-Rich Region in the Coxsackievirus 3A Protein Is Required for the Protein To Inhibit Endoplasmic Reticulum-to-Golgi Transport

Els Wessels, Daniël Duijsings, Richard A. Notebaart, Willem J. G. Melchers, and Frank J. M. van Kuppeveld

Department of Medical Microbiology, Nijmegen Center for Molecular Life Sciences, University Medical Center Nijmegen, and Center for Molecular and Biomolecular Informatics, University of Nijmegen, Nijmegen, The Netherlands

Received 13 July 2004/Accepted 17 November 2004

The ability of the 3A protein of coxsackievirus B (CVB) to inhibit protein secretion was investigated for this study. Here we show that the ectopic expression of CVB 3A blocked the transport of both the glycoprotein of vesicular stomatitis virus, a membrane-bound secretory marker, and the alpha-1 protease inhibitor, a luminal secretory protein, at a step between the endoplasmic reticulum (ER) and the Golgi complex. CVB 3A contains a conserved proline-rich region in its N terminus. The importance of this proline-rich region was investigated by introducing Pro-to-Ala substitutions. The mutation of Pro19 completely abolished the ability of 3A to inhibit ER-to-Golgi transport. The mutation of Pro14, Pro17, or Pro20 also impaired this ability, but to a lesser extent. The mutation of Pro14 had no effect. We also investigated the possible importance of this proline-rich region for the function of 3A in viral RNA replication. To this end, we introduced the Pro-to-Ala mutations into an infectious cDNA clone of CVB3. The transfection of cells with in vitro-transcribed RNAs of these clones gave rise to mutant viruses that replicated with wild-type characteristics. We concluded that the proline-rich region in CVB 3A is required for its ability to inhibit ER-to-Golgi transport, but not for its function in viral RNA replication. The functional relevance of the proline-rich region is discussed in light of the proposed structural model of 3A.

Enteroviruses (poliovirus, coxsackievirus, echovirus, and several unnamed viruses) are small viruses that contain a 7.5-kb single-stranded RNA genome with positive polarity. The genomic RNA harbors one large open reading frame that encodes the viral polyprotein. This polyprotein is proteolytically cleaved into several polyproteins through the secretory pathway (8). The step blocked by the 2B protein resulted in the accumulation in the ER of both the glycoprotein and the alpha-1 protease inhibitor. The mechanism by which the 3A protein inhibits ER-to-Golgi transport is as yet unknown.

In addition to its function in manipulating intracellular protein transport, the enterovirus 3A protein is involved in multiple steps in the process of vRNA replication. The 3A protein is a small hydrophobic protein (87 to 89 amino acids [aa]) that contains a C-terminal hydrophobic anchor which is responsible for its membrane association (29). Several studies have shown that mutations in 3A give rise to defects in vRNA synthesis (1, 10, 12, 35). The membrane-bound precursor 3AB is most likely a small hydrophobic protein (85 to 87 amino acids [aa]) that contains a C-terminal hydrophobic anchor which is responsible for its membrane association (29). Several studies have shown that mutations in 3A give rise to defects in vRNA synthesis (1, 10, 12, 35). The membrane-bound precursor 3AB is most likely a small hydrophobic protein (85 to 87 amino acids [aa]) that contains a C-terminal hydrophobic anchor which is responsible for its membrane association (29). Several studies have shown that mutations in 3A give rise to defects in vRNA synthesis (1, 10, 12, 35).
All enterovirus 3A proteins contain a proline-rich region in their N termini. The biological significance of this proline-rich region, which may be involved in protein-protein interactions, was investigated by the individual expression of CVB3 3A mutants and the introduction of these mutations into an infectious cDNA clone of CVB3. Our results indicate that the integrity of this proline-rich region is required for the inhibition of ER-to-Golgi transport by the CVB3 3A protein, but not for its functions in RNA replication.

MATERIALS AND METHODS

Cells and viruses. Buffalo green monkey (BGM) kidney cells were grown in minimal essential medium (MEM) (Gibco) supplemented with 10% fetal bovine serum. COS-1 cells were grown in Dulbecco’s modified Eagle’s medium (Gibco) supplemented with 10% fetal bovine serum. Cells were grown at 37°C in a 5% CO2 incubator. All viruses used for this study were recombinant CVB3 viruses obtained by the transfection of T7 RNA polymerase-generated runoff RNA transcripts from the infectious cDNA clones described below. Virus yields were determined by end-point titration as described previously (30). Virus titers were calculated and expressed as 50% tissue culture infective dose (TCID50) values (23).

Plasmids. (i) p53CB3/T7. The CVB3 infectious cDNA clone used for this study was p5CB3/T7, which contains a full-length cDNA of CVB3 (strain Nancy) behind a T7 RNA polymerase promoter. This cDNA clone was constructed by removing the nonviral nucleotides between the T7 promoter and the 5' end of the CVB3 genome from plasmid pCB3/T7 (14). Furthermore, an MluI site was introduced downstream of the 3' end of the CVB3 genome to ensure that in vitro-transcribed RNAs did not contain nonviral nucleotides at their 3' ends, resulting in increased infectivity of the RNA transcripts (data not shown). (ii) p53CB3-LUC. Plasmid p53CB3-LUC, which contains the firefly luciferase gene in place of the P1 capsid coding region, was derived from pCB3-LUC (30) and contains the same deletion of nonviral nucleotides at the 5' and 3' termini as p5CB3/T7. (iii) pSVG-GFP. The plasmid pSVG-GFP (28), which encodes the 0.045 VSVG protein fused to enhanced green fluorescent protein (EGFP) at its C terminus, was kindly provided by P. Keller and K. Simons (Max Planck Institute of Molecular Biology and Genetics, Dresden, Germany). (iv) p3A. For construction of the p3A plasmid, the 3A coding sequence was amplified by use of a forward primer that introduced a SalI restriction site and a start codon preceded by a Kozak sequence (p3120-4, 5'-GGG GGG GGA TCC CTA TTG AAA ACC CGC AAA GAG-3'). Virus titer in the medium was collected and adjusted to 1.0% lysis buffer by the addition of 200 μl of 5% lysis buffer (250 mM Tris [pH 7.4], 750 mM NaCl, 5 mM EDTA, 5% Nonidet P-40, 0.25% sodium dodecyl sulfate [SDS]). The cells were washed twice with PBS and then boiled in 1 ml of lysis buffer (50 mM Tris [pH 7.4], 150 mM NaCl, 1 mM EDTA, 1% Nonidet P-40, 0.05% SDS). An anti-EGFP rabbit polyclonal antiserum (1:10,000) was added to the cell lysate and culture medium, and the mixtures were incubated at 4°C for 16 h. Antibody-protein complexes were collected by the use of protein A-Sepharose (Amersham Biosciences) for 1.5 h, washed twice with dilution buffer (0.01 M Tris [pH 8.0], 0.14 M NaCl, 0.01% bovine serum albumin, 0.1% Tween 20, 0.1% BSA in Tris-buffered saline [TBS]), once with TBS-X-100 (pH 8.0), once with TBS, and then precipitated. The samples were resuspended in 25 μl of Laemmli sample buffer, boiled for 5 min, and analyzed by SDS-polyacrylamide gel electrophoresis (SDS-PAGE). The amounts of radiolabeled A1PI-EYFP in the cell fraction and the medium fraction were quantified by phosphorimaging (Bio-Rad Multi-Analyzer, version 1.0.1).

Site-directed mutagenesis. In vitro mutagenesis was performed with single-stranded DNAs generated from a subgenomic pALTER phagemid construct containing the Xhol (nucleotide [nt] 2043) to SalI (nt 7438) fragment of CVB3 by the use of the Altered Sites in vitro mutagenesis system according to the manufacturer’s instructions. The following synthetic oligonucleotides were used to introduce site-specific mutations (as well as restriction sites, which are underlined): primer p390-1, 5'-AGG GGG TCG ACC ATG GCA CCA GTA TAC AAG-3' [the SalI site is underlined] and a reverse primer (p388-6, 5'-GGG GGG GGA TCC CTA TTG AAA ACC CGC AAA GAG-3') that anneals downstream of the 5' end of the CVB3 genome to introduce site-specific mutations (as well as restriction sites, which are underlined); primer p390-2, 5'-GGG GGG GGA TCC CTA TTG AAA ACC CGC AAA GAG-3' [the SalI site is underlined] and a reverse primer (p388-9, 5'-AAT GGC CGG TGT CTC TGG TGC AAC GCT AAT-3') that introduces the SalI restriction site and a stop codon (the BamH site is underlined) followed by a Kozak sequence (p3120-4, 5'-GGG GGG GGA TCC CTA TTG AAA ACC CGC AAA GAG-3'). The PCR products were cloned into pEGFP-C3 (Clontech) from which the EGFP coding region had been deleted.

DNA transfections. BGM cell monolayers were grown in 6-well plates (for A1PI secretion assays or Western blot analysis) or on coverslips in 24-well plates (for microscopic purposes) to subconfluence and then transfected with 2 μg of plasmid DNA per well of a 6-well plate or with 0.5 μg of plasmid DNA per well of a 24-well plate. COS cell monolayers were grown in 24-well plates to subconfluence and then transfected with 0.75 μg of plasmid DNA (see below). Transfections were performed by use of the FuGENE 6 reagent (Roche) according to the manufacturer’s instructions. Cells were grown at 37°C until further analysis, unless otherwise stated.

VSVG trafficking. The subcellular localization of VSVG-GFP was determined as described previously (5). Briefly, BGM cells expressing either VSVG-GFP alone or VSVG-GFP together with 3A were incubated at 40°C. After a temperature shift to 32°C, the cells were fixed, and analyzed by confocal laser scanning microscopy (CLSM) under a TCS NT microscope (Leica Lasertechnik GmbH, Heidelberg, Germany). Rabbit polyclonal anti-calreticulin was obtained from Sigma-Aldrich. Mouse monoclonal anti-GM130 was obtained from BD. Alexa fluoro 594 goat anti-rabbit immunoglobulin G and Alexa fluoro 594 goat anti-mouse immunoglobulin G were obtained from Molecular Probes. Primary antibodies were diluted 1:200, and conjugates were diluted 1:1,500.

A1PI secretion assay. BGM cells grown in six-well plates were transfected with plasmids DNA, and 20 h after transfection, were washed with phosphate-buffered saline (PBS) and incubated in MEM lacking methionine (Sigma) for 30 min at 37°C. Proteins were pulse labeled with [35S]methionine (50 μCi/well) for 30 min at 37°C and then washed twice with PBS, after which 800 μl of fresh serum-free MEM was added. After a 2-h chase, the medium was collected and adjusted to 1% lysis buffer by the addition of 200 μl of 5% lysis buffer (250 mM Tris [pH 7.4], 750 mM NaCl, 5 mM EDTA, 5% Nonidet P-40, 0.2% sodium dodecyl sulfate [SDS]). The cells were washed twice with PBS and then boiled in 1 ml of lysis buffer (50 mM Tris [pH 7.4], 150 mM NaCl, 1 mM EDTA, 1% Nonidet P-40, 0.05% SDS). An anti-EGFP rabbit polyclonal antiserum (1:1,000) was added to the cell lysate and culture medium, and the mixtures were incubated at 4°C for 16 h. Antibody-protein complexes were collected by the use of protein A-Sepharose (Amersham Biosciences) for 1.5 h, washed twice with dilution buffer (0.01 M Tris [pH 8.0], 0.14 M NaCl, 0.01% bovine serum albumin, 0.1% Tween 20, 0.1% BSA in Tris-buffered saline [TBS]), once with TBS-X-100 (pH 8.0), once with TBS, and then precipitated. The samples were resuspended in 25 μl of Laemmli sample buffer, boiled for 5 min, and analyzed by SDS-polyacrylamide gel electrophoresis (SDS-PAGE). The amounts of radiolabeled A1PI-EYFP in the cell fraction and the medium fraction were quantified by phosphorimaging (Bio-Rad Multi-Analyzer, version 1.0.1).

Transfection of cells with plasmids. Plasmids were linearized with MluI, purified, and transcribed in vitro by T7 RNA polymerase as described by the manufacturer’s instructions. Cells were grown at 37°C until further analysis, unless otherwise stated.
previously (30). The RNA transcripts were checked by agarose gel electrophoresis. BGM monolayer cells grown to subconfluence in 25-cm² flasks were transfected with 2.5 µg of RNA transcripts by the DEAE-dextran method as described previously (30). After transfection, the cells were grown at 37°C. When virus growth was observed, the cultures were incubated until the cytopathic effect (CPE) was complete. In cases in which no CPE was observed after 5 days, the cultures were subjected to three successive cycles of freezing and thawing, and 200 µl was passed onto fresh BGM monolayer cells, which were grown at 37°C for another 5 days.

**Sequence analysis of viral RNA.** RNAs were isolated from virus suspensions and reverse transcribed as described previously (30). The 3A coding region was amplified by PCRs with SuperTag DNA polymerase (HT Biotechnology), and the sequences were analyzed.

**Single-cycle growth analysis.** Confluent BGM monolayer cells were infected with virus at a multiplicity of infection (MOI) of 1 TCID₅₀ for 30 min at room temperature. The cells were washed three times with PBS, supplied with MEM, and grown at 37°C. At the indicated times, the cells were disrupted by three cycles of freezing and thawing, and the virus titers were determined by end-point titration.

**Analysis of viral RNA synthesis.** BGM cell monolayers were transfected with 1 µg of T7 RNA polymerase-generated RNA transcripts from MluI-linearized pS3CB1T7-LUC plasmids as described above. At the indicated times posttransfection, the cells were lysed and luciferase activities was assayed as described previously (30).

**Calculations.** Data are presented as mean values ± standard errors of the means (SEM). Differences were tested for significance by analysis of variance (least significant difference [LSD]).

**Western blot analysis.** BGM cells grown in six-well plates were transfected with pc-A1PI-EYFP-S-EGFP-3A plasmids (wild type or mutant). At 24 h posttransfection, the cells were lysed in 1× lysis buffer (50 mM Tris [pH 7.4], 150 mM NaCl, 1 mM EDTA, 1% Nonidet P-40, 0.05% SDS). Samples were run in an SDS–12.5% polyacrylamide gel and transferred to a nitrocellulose membrane (Bio-Rad). EGFP fusion proteins were stained with an anti-EGFP polyclonal antibody (Santa Cruz), and Renilla luciferase, an internal control, was visualized with the Lumi-Lightplus Western blotting substrate (Roche Molecular Biochemicals) according to the manufacturer’s instructions.

**Mammalian two-hybrid analysis.** COS cells grown in 24-well plates were transfected with a total of 0.75 µg of plasmid DNA (1:1:1 mix of the pACT, pBIND, and pG5lac plasmids). At 48 h posttransfection, the cells were lysed, and both the firefly luciferase and Renilla luciferase enzyme activities were measured from the same cell lysate by use of a dual-luciferase reporter assay system (Promega) as described previously (4). An analysis of the Renilla luciferase activities, encoded by the pBIND plasmid and allowing monitoring of the transfection efficiency, revealed no gross differences in efficiencies of transfection among the different samples.

**RESULTS**

**Inhibition of ER-to-Golgi transport by CVB3 and 3A expression.** To monitor secretory pathway trafficking, we made use of a GFP fusion of the temperature-sensitive ts045 mutant of VSVG, a well-known membrane-bound secretory marker (VSVG-GFP). Figure 1A shows that at the nonpermissive temperature (40°C), VSVG-GFP was efficiently secreted into the medium during a 2-h chase period. In order to quantify the inhibitory effects of CVB3 infection and 3A expression on protein secretion, we made use of the reporter protein A1PI, a secreted soluble glycoprotein. In pulse-chase experiments, the level of A1PI secretion can be determined by measuring the percentages of reporter protein in the cell and medium fractions. For this study, a fusion protein of A1PI and EYFP was used because the A1PI protein was found to migrate to the same position as a nonspecific protein band in BGM cell lysates (data not shown). Figure 2A shows that the A1PI-EYFP fusion protein, which was labeled for a 30-min pulse period and immunoprecipitated with anti-EYFP, was efficiently secreted into the medium during a 2-h chase period.

The inhibitory effect of CVB3 infection on protein secretion was determined at various times p.i. Because enterovirus infection shifts off cap-dependent translation (9), a plasmid was used that contained the A1PI coding sequence behind the PV 5’ noncoding region. Cells transfected with this construct were infected with CVB3 (MOI = 50), pulse labeled for 30 min with [³⁵S]methionine at 2, 4, or 6 h p.i., and subsequently chased for 2 h in the presence of unlabeled methionine. In cells labeled at 2 h p.i. (i.e., chased between 2.5 and 4.5 h p.i.), the majority of A1PI was secreted into the medium (Fig. 2A). In cells labeled at 4 or 6 h p.i. (i.e., chased between 4.5 and 6.5 h p.i. and between 6.5 and 8.5 h p.i., respectively), however, only a small amount of A1PI was observed in the medium fraction, whereas a large amount of A1PI was retained in the cell. The amount of A1PI in the medium fraction was determined as the percentage of the total amount of A1PI and compared to that of control cells (for which the value was normalized to 100% A1PI secretion). The average results of three independent experiments are shown in Fig. 2B. The results demonstrate that CVB3 infection inhibited reporter protein secretion to approximately 30% compared to control cells from about 4 h p.i.

To quantify the inhibitory effect of 3A on protein secretion, we coexpressed the 3A protein (behind an SV40 promoter)
**Control cells**

- **A**
  - 40°C
  - Left: VSV-G
  - Middle: ER marker

- **B**
  - 40°C-32°C (45 min)
  - Left: VSV-G
  - Middle: Golgi marker

- **C**
  - 40°C-32°C (120 min)
  - Left: VSV-G

**CVB3 infected cells**

- **D**
  - 40°C
  - Left: VSV-G
  - Middle: ER marker

- **E**
  - 40°C-32°C (120 min)
  - Left: VSV-G
  - Middle: ER marker

- **F**
  - 40°C-32°C (120 min)
  - Left: VSV-G
  - Middle: Golgi marker

**3A-expressing cells**

- **G**
  - 40°C
  - Left: VSV-G
  - Middle: ER marker

- **H**
  - 40°C-32°C (120 min)
  - Left: VSV-G
  - Middle: ER marker

- **I**
  - 40°C-32°C (120 min)
  - Left: VSV-G
  - Middle: Golgi marker
and the A1PI secretion marker (behind a CMV promoter) from a single plasmid. The 3A protein was expressed as an EGFP-3A fusion protein (the fusion of EGFP to the N terminus of 3A did not affect its protein secretion inhibition function [data not shown]). As a control, a plasmid was constructed that contained the EGFP sequence behind the SV40 promoter. Western blot analysis showed that both proteins were efficiently expressed (Fig. 2C). Figure 2D shows that the expression of the 3A protein resulted in a severely reduced amount of labeled reporter protein in the medium fraction. A quantitative analysis of A1PI secretion in three independent experiments showed that 3A expression inhibited reporter protein secretion to approximately 25% of that of control cells (Fig. 2E) (the percentage of A1PI secretion was calculated as described above).

**Importance of proline-rich region in 3A for inhibition of ER-to-Golgi transport.** The enterovirus and rhinovirus 3A proteins are characterized by the presence of a proline-rich region in the N terminus (Fig. 3). This proline-rich region is located at aa 17 to 19 (numbering refers to the CVB3 3A protein). Pro17 and Pro19 are present in all 63 enterovirus and rhinovirus 3A proteins that have been sequenced to date (except for enterovirus [EV] type 71). Pro18 is present in nearly all enteroviruses and rhinoviruses (except for coxsackievirus A16 [CVA16], CVA24, EV70, and EV71). All human enterovirus group B (HEV-B) members (which include all CVB types, all echoviruses, and EV71) contain Pro17, Pro18, and Pro19.

![FIG. 1. CVB3 infection and expression of the 3A protein inhibit VSVG-GFP trafficking. BGM cells were transfected with a construct coding for the GFP-tagged ts045 temperature-sensitive mutant of the VSVG protein, either alone or together with 3A, and grown at 40 °C for 20 h. (A to C) Control cells. In control cells, VSVG was improperly folded at 40 °C, and as a consequence, was retained in the ER, as shown by its colocalization with calreticulin (merged picture on the right in panel A). Upon shifting to the permissive temperature (32 °C), the VSVG-GFP protein was correctly folded and transported out of the ER. VSVG could be observed in the Golgi complex after 45 min, as shown by its colocalization with GM130, a cis-Golgi marker (B), and at the plasma membrane after 120 min (C). (D to F) Cells infected with CVB3 (MOI of 50) for 5 h at 40 °C. At 40 °C, VSVG was retained in the ER (D). Upon shifting to 32 °C for 120 min, VSVG could be found in the ER (E) and a post-ER compartment that also contained the cis-Golgi marker (F). (G to H) 3A-expressing cells. VSVG was retained in the ER at 40 °C (G), whereas it was observed in the ER (H) and a post-ER compartment that also contained the cis-Golgi marker (I) when shifted to 32 °C for 120 min. Bar = 10 μm.

![FIG. 2. CVB3 infection (MOI of 50) and expression of the 3A protein inhibit A1PI secretion. BGM cells were transfected with A1PI expression constructs. Twenty hours after transfection, the cells were starved of methionine for 30 min, labeled with [35S]methionine for 30 min, and then chased for 2 h. Cell (C) and medium (M) fractions were collected and analyzed for the amount of labeled reporter protein by immunoprecipitation with an anti-EGFP antiserum, SDS-PAGE, and phosphorimaging. (A) Cells transfected with a plasmid containing A1PI behind the PV noncoding region were infected and subjected to pulse-chase analysis at 2, 4, and 6 h p.i. The differences in migration between A1PI in the medium and cell fractions were due to differences in the glycosylation state (endoglycosidase F treatment resulted in faster migration of A1PI in both the medium and cell fractions [data not shown]). (B) Average secretion (means ± standard errors of the means [SEM]) of three independent experiments. A1PI secretion was calculated as the percentage of A1PI secretion in uninfected control cells, which was normalized to 100%. (C to E) BGM cells were transfected with constructs expressing either EGFP or EGFP-3A from an SV40 promoter and the A1PI-EYFP protein from a cytomegalovirus promoter. (C) Western blot analysis of EGFP and EGFP-3A expression. (D) Analysis of A1PI secretion. (E) Average secretion (means ± SEM) of three independent experiments. A1PI secretion was calculated as the percentage of A1PI secretion in EGFP-expressing control cells, which was normalized to 100%.
ruses, some CVA types, and several unassigned EVs) contain additional Pro residues at positions 14 and 20.

Proline-rich regions are often involved in protein-protein interactions (reviewed in reference 13). To investigate the functional importance of the proline-rich region in the CVB3 3A protein, we constructed mutant 3A expression plasmids. Since Pro17, Pro18, and Pro19 are the most conserved proline residues, we first replaced these three residues simultaneously with Ala residues (P17A/P18A/P19A). Figures 4A and B show that this 3A mutant was no longer able to inhibit protein secretion. This was not due to reduced expression of the mutant protein, as it was expressed at a similar level as wild-type 3A (Fig. 4E). Moreover, in cells that coexpressed this mutant 3A protein and VSVG-GFP, we observed that VSVG accumulated at the plasma membrane (data not shown). Thus, the proline-rich region is required for the ability of 3A to inhibit protein secretion.

To investigate the importance of the Pro residues individually, we constructed mutant 3A proteins in which single Pro residues at positions 14, 17, 18, 19, and 20 were replaced with Ala residues (mutations P14A, P17A, P18A, P19A, and P20A, respectively). The P19A mutation completely abolished the ability of 3A to inhibit A1PI secretion (to a similar extent as the P17A/P18A/P19A mutant) (Fig. 4C and D). The P14A, P17A, and P20A mutations also impaired the ability of 3A to inhibit protein secretion, although to a lesser extent. The P18A mutation had no effect on the secretion inhibition activity of 3A. Western blot analysis showed that all mutant 3A proteins were efficiently expressed (Fig. 4E). Thus, the Pro residues at positions 14, 17, 19, and 20, but not that at position 18, are important for the ability of 3A to inhibit protein secretion.

Importance of proline-rich region in 3A for its function in viral replication. To study the effect of 3A mutations on viral RNA replication and virus growth, we introduced mutations into an infectious cDNA clone of CVB3. For each mutation, two p53CB3/T7 clones were tested, derived from two independently generated site-directed mutagenesis clones. The effects of the P17A/P18A/P19A, P14A, P17A, P18A, P19A, and P20A mutations on virus viability were studied by the transfection of BGM cells with RNA transcripts. The results obtained for the P17A/P18A/P19A mutant are described below. Cells transfected with RNA transcripts carrying single Pro mutations exhibited complete CPE in all transfections (Fig. 5A). vRNAs were isolated from these cell cultures, and the 3A coding region was amplified by reverse transcription-PCR and then sequenced. In all cases, the original mutations were retained in the vRNAs, and no secondary amino acid replacements had occurred. The mutant viruses were further characterized by single-cycle growth analysis (Fig. 5B). Viruses carrying mutations exhibited wild-type growth characteristics. This indicated that the mutant 3A proteins were correctly folded. In conclusion, mutation of the individual Pro residues had no effect on viral replication.

Identification of a second-site suppressor mutation. Cells transfected with RNA transcripts containing the P17A/P18A/P19A mutations exhibited complete CPE in all transfections (Fig. 5A). vRNAs were isolated from these cell cultures, and the 3A coding region was amplified by reverse transcription-PCR and then sequenced. In all cases, the original mutations were retained in the vRNAs, and no secondary amino acid replacements had occurred. The mutant viruses were further characterized by single-cycle growth analysis (Fig. 5B). Viruses carrying mutations exhibited wild-type growth characteristics. This indicated that the mutant 3A proteins were correctly folded. In conclusion, mutation of the individual Pro residues had no effect on viral replication.

FIG. 3. Alignment of aa 14 to 20 of the enterovirus and rhinovirus 3A proteins. The genome organization of CVB3 is depicted. CVB3 contains a single open reading frame flanked by a 5′ and 3′ nontranslated region (NTR) and a poly(A) tail. The four capsid proteins (VP1 to VP4) and seven nonstructural proteins (2A, 2B, 2C, 3A, 3B, 3C, and 3D) are shown. The 3A protein of CVB3 is an 89-aa protein which contains a C-terminal hydrophobic domain (aa 61 to 82). 3A contains several Pro residues (at positions 14 and 17 to 20) in its N terminus. An alignment of these residues for all enteroviruses and rhinoviruses that have been sequenced to date is shown. The species names are shown in bold. HEV-B, human enterovirus B; HEV-A, human enterovirus A; HEV-C, human enterovirus C; HEV-D, human enterovirus D; PV, poliovirus; HRV-A, human rhinovirus A; HRV-B, human rhinovirus B; CVB, coxsackievirus B; ECHO(*), all echoviruses sequenced to date (i.e., echoviruses 1 to 7, 9, 11 to 21, 24 to 27, and 29 to 33); CVA, coxsackievirus A; EV, enterovirus.
FIG. 4. Proline-rich region is required for secretion inhibition by CVB3 3A. Cells were transfected with plasmids expressing the indicated 3A mutant proteins from an SV40 promoter and the A1PI reporter protein from a cytomegalovirus promoter. Twenty hours after transfection, the cells were labeled with [35S]methionine for 30 min and chased in the presence of unlabeled methionine for 2 h. Cell (C) and medium (M) fractions were collected, immunoprecipitated with an anti-EGFP serum, analyzed by SDS-PAGE (A and C), and quantified by phosphorimaging (B and D). The amount of secreted A1PI in the absence of 3A was normalized to 100%, and the ability of 3A and 3A mutants to secrete A1PI was calculated as a percentage of the A1PI secretion in control cells without 3A. Values represent means ± SEM of three independent experiments. a, significantly different from A1PI secretion in control cells without 3A; b, significantly different from A1PI secretion in the presence of wild-type 3A (calculated by analysis of variance with LSD; P < 0.05). (E) Western blot of EGFP-3A wild-type and mutant proteins.
<table>
<thead>
<tr>
<th>Mutation</th>
<th>Virus growth</th>
</tr>
</thead>
<tbody>
<tr>
<td>P17A/P18A/P19A</td>
<td>q.i.</td>
</tr>
<tr>
<td>P14A</td>
<td>+</td>
</tr>
<tr>
<td>P17A</td>
<td>+</td>
</tr>
<tr>
<td>P18A</td>
<td>+</td>
</tr>
<tr>
<td>P19A</td>
<td>+</td>
</tr>
<tr>
<td>P20A</td>
<td>+</td>
</tr>
</tbody>
</table>

**A** Mutation of the indicated 3A residues was assayed for virus growth. Mutations were introduced into the infectious cDNA clone p53CB3/T7. Copy RNA transcripts were transfected into BGM cells and examined for the ability to yield viruses. Mutations of the P17A/P18A/P19A residues, which caused a quasi-infectious (q.i.) phenotype, were also obtained by yeast two-hybrid analysis (34). The possibility was considered that the second-site suppressor mutation S31C did not rescue the defect in protein secretion inhibition caused by the P17A/P18A/P19A mutations.

It has been suggested that the enterovirus 3A protein forms a homodimer. Cross-linking and analytical ultracentrifugation studies showed that the first 60 aa of the PV 3A protein form a homodimer (26). Evidence for PV 3A homomultimerization was also obtained by yeast two-hybrid analysis (34). The possibility was considered that the second-site suppressor mutation S31C might restore 3A-3A interactions that were disrupted by the P17A/P18A/P19A mutations. We investigated homomultimerization reactions of CVB3 wild-type 3A and 3A proteins carrying the P17A/P18A/P19A or P17A/P18A/P19A/S31C mutations by use of a mammalian two-hybrid system (4). This way, we cloned the 3A sequences in the correct reading frame into the expression plasmids pACT (which provides the yeast Gal4 DNA binding domain). COS cells were cotransfected with these two plasmids and with the yeast GAL4 binding sites upstream of a minimal TATA box that precedes the firefly luciferase gene. An analysis of the luciferase activity showed that the wild-type CVB3 3A protein did indeed form homomultimers (Fig. 6E). No multimerization was observed with 3A carrying the P17A/P18A/P19A/S31C mutation. No obvious increase in multimerization was observed with 3A carrying mutation P17A/P18A/P19A/S31C.

**DISCUSSION**

In this study, we showed that CVB3 infection and expression of the 3A protein alone interfere with protein secretion by blocking ER-to-Golgi transport. Moreover, we demonstrated that the proline-rich region in the N terminus of 3A is required for this ability. Pro17, Pro18, and Pro19 are evolutionarily conserved in nearly all enteroviruses and rhinoviruses. Of these residues, Pro17 was found to be the most important for 3A to inhibit protein secretion. Mutation of this residue almost completely abolished this activity. The mutation of Pro17, on the other hand, was far less disruptive for the inhibitory activity of 3A. Mutation of this residue was even less disruptive than mutations of the less-conserved Pro14 and Pro20 residues, which are conserved in all HEV-B members (i.e., all CVB3s and echoviruses, some CVAs, and some unnamed enteroviruses) but not in other enteroviruses and rhinoviruses. Remarkably, the mutation of Pro18 had no notable effect.

The mechanism by which 3A inhibits protein secretion is still unknown. Therefore, we can only speculate about a role of the proline-rich region in the inhibition of protein secretion. Pro residues can play an important role in protein-protein interactions (reviewed in reference 32). We propose that the 3A protein exerts its activity by tethering a cellular protein through an interaction with its proline-rich region.

Two well-known protein interaction domains that interact with Pro residues are Src homology 3 (SH3) and WW domains. SH3 domains recognize proline-rich sequences containing the core PXXP, where “X” denotes any amino acid. WW domains bind ligands containing PPXY or PPLP core motifs, usually flanked by additional Pro residues (13, 17). It seems unlikely, however, that 3A interacts with proteins containing an SH3 or a WW domain. When considering putative interaction domains, one should take into account the fact that the Pro17 and Pro20 residues are not conserved among all enteroviruses and rhinoviruses. The 3A proteins of CVB3 and PV (which lacks Pro14 and Pro20) most likely use identical mechanisms to inhibit protein secretion. Given the observation that a mutation of Pro18 had little effect on this ability, these proteins most likely only share Pro17 and Pro19 for their secretion inhibition function. Therefore, alternative interaction domains or mechanisms should be considered.

Recently, the structure of the first 60 aa of the PV 3A protein was determined by nuclear magnetic resonance spectroscopy (26). The PV 3A protein was found to form a classic homodimer. Dimerization occurs through ionic interactions, hydrogen bonds, and hydrophobic interactions between two helices formed by aa 23 to 29 and aa 32 to 41. Figure 7 shows the putative structure of the first 60 aa of CVB3, obtained by molecular modeling of the published PV 3A structure. The structure suggests that the proline-rich regions of two interacting 3A proteins are oriented in such a way that they are contiguous and thereby form a Pro platform. We suggest that this Pro platform, rather than specific SH3 or WW binding domains, may be the interaction domain responsible for the binding of a (still unknown) cellular protein.

The CVB3 3A protein inhibited protein secretion to an
extent similar to that previously described for the 3A protein of the closely related PV (7). A PV mutant (mutant 3A-2) containing a Ser insertion between 3A residues 14 and 15 (corresponding to aa 15 and 16 in CVB3) was strongly impaired in inhibiting A1PI secretion (7). The PV carrying this insertion mutation showed a reduced ability to inhibit the presentation of MHC I-antigen complexes (3) and to block the secretion of cytokines and interleukins (6). The introduction of this mutation into CVB 3A (i.e., a Ser insertion between residues 15 and 16) also interfered with the ability of 3A to inhibit A1PI secretion (data not shown). The mutation disrupted this 3A function to a similar extent as the P19A mutation. It is therefore reasonable to assume that CVB3 carrying Pro-to-Ala mutations (in particular P19A) is also impaired in the ability to suppress MHC I-antigen presentation and to block the secretion of cytokines and interleukins.

Enterovirus genome replication takes place at secretory pathway-derived membrane vesicles that accumulate in the cytosol of the infected cell. The 2BC protein has been identified as playing a major role in the accumulation of these vesicles (2, 24, 25). It has been speculated that the 3A-induced inhibition of ER-to-Golgi transport might also contribute to the accumulation of the vesicles with which the viral replication complexes are associated (27). However, in the present study, we showed that viruses carrying mutations in 3A that interfered with its ability to inhibit ER-to-Golgi transport replicated with wild-type growth characteristics, arguing against a possible role of 3A in the accumulation of replication vesicles. It
cannot be excluded that the 3A protein contributes to an accumulation of vesicles, but this activity does not seem to be essential for viral RNA replication, at least not in vitro.

In contrast to the wild-type phenotype of viruses carrying the single Pro-to-Ala mutations, the P17A/P18A/P19A mutant yielded a quasi-infectious phenotype. Upon multiple RNA transfections, only on one occasion was virus obtained. A sequence analysis of the viral RNA showed that a second-site suppressor mutation at position 31 of 3A (S31C) had occurred. This second-site suppressor mutation rescued a defect in 3A in viral RNA replication, but not its ability to inhibit protein secretion. Since the single Pro-to-Ala mutations did not affect viral RNA replication, it can be hypothesized that the P17A/P18A/P19A mutations interfere with the conformation of 3A or its precursor 3AB and thereby with its function in vRNA replication. Indeed, we found that the P17A/P18A/P19A mutation interfered with 3A homomultimerization in a mammalian two-hybrid system. This finding is remarkable because the structural model predicts no important role for the proline-rich region in dimerization. Together, these data are consistent with the idea that the P17A/P18A/P19A mutation causes a general disruption of the 3A structure. How the S31C suppressor mutation, which is present in the loop between the two α-helices implicated in dimerization (Fig. 7), can (partially) rescue the defect in vRNA replication imposed by the P17A/P18A/P19A mutation remains to be established. Further research is needed to establish the requirement of 3A dimerization for its function in vRNA replication and its ability to inhibit ER-to-Golgi trafficking.

ACKNOWLEDGMENTS

We thank Jeroen van Kieldonk, Vladimir van Hock, and Sander Jannink for technical assistance, Henri Dijkman for assistance with the VSVG-GFP plasmid. This work was partly supported by grants from The Netherlands Organization for Scientific Research (NWO-VIDI-917.46.305), the M. W. Beijerinck Virology Fund from the Royal Netherlands Academy of Sciences, and the European Communities (INTAS 2012).

REFERENCES