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Published in:
Journal of General Virology

Link to article, DOI:
10.1099/jgv.0.000664

Publication date:
2017

Document Version
Peer reviewed version

Journal of General Virology

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--Manuscript Draft--

Manuscript Number:	JGV-D-16-00608R1
Full Title:	Determinants of the VP1/2A junction cleavage by the 3C protease in foot-and-mouth disease virus infected cells
Article Type:	Standard
Section/Category:	Animal - Positive-strand RNA Viruses
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Abstract:	The foot-and-mouth disease virus (FMDV) capsid precursor, P1-2A, is cleaved by FMDV 3C protease to yield VP0, VP3, VP1 and 2A. Cleavage of the VP1/2A junction is the slowest. Serotype O FMDVs with uncleaved VP1-2A (having a K210E substitution in VP1; at position P2 in cleavage site) have been described previously and acquired a second site substitution (VP1 E83K) during virus rescue. Furthermore, introduction of the VP1 E83K substitution alone generated a second site change at the VP1/2A junction (2A L2P, position P2' in cleavage site). These virus adaptations have now been analysed using Next Generation Sequencing to determine sub-consensus level changes in the virus; this revealed other variants within the E83K mutant virus population that changed residue VP1 K210. The construction of serotype A viruses with a blocked VP1/2A cleavage site (containing K210E) has now been achieved. A collection of alternative amino acid substitutions were made at this site and the properties of the mutant viruses determined. Only the presence of a positively charged residue at position P2 in the cleavage site permitted efficient cleavage of the VP1/2A junction, consistent with analyses of diverse FMDV genome sequences. Interestingly, in contrast to the serotype O virus results, no second site mutations occurred within the VP1 coding region of serotype A viruses with the blocked VP1/2A cleavage site. However, some of these viruses acquired changes in the 2C protein that is involved in enterovirus morphogenesis. These results have implications for the testing of potential antiviral agents targeting the FMDV 3C protease.

Determinants of the VP1/2A junction cleavage by the 3C protease in foot-and-mouth disease virus infected cells

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Running title: VP1/2A cleavage within FMDV-infected cells.

Keywords: picornavirus; polyprotein processing; cleavage specificity; virus capsid assembly; proteolysis

Abstract word count: 250; Text word count: 4900 (excl. Abstract, references, Figure legends)

Figures 5; Tables 3; Supplementary Table: S1

Abstract

The foot-and-mouth disease virus (FMDV) capsid precursor, P1-2A, is cleaved by FMDV 3C protease to yield VP0, VP3, VP1 and 2A. Cleavage of the VP1/2A junction is the slowest. Serotype O FMDVs with uncleaved VP1-2A (having a K210E substitution in VP1; at position P2 in cleavage site) have been described previously and acquired a second site substitution (VP1 E83K) during virus rescue. Furthermore, introduction of the VP1 E83K substitution alone generated a second site change at the VP1/2A junction (2A L2P, position P2' in cleavage site). These virus adaptations have now been analysed using Next Generation Sequencing to determine sub-consensus level changes in the virus; this revealed other variants within the E83K mutant virus population that changed residue VP1 K210. The construction of serotype A viruses with a blocked VP1/2A cleavage site (containing K210E) has now been achieved. A collection of alternative amino acid substitutions were made at this site and the properties of the mutant viruses determined. Only the presence of a positively charged residue at position P2 in the cleavage site permitted efficient cleavage of the VP1/2A junction, consistent with analyses of diverse FMDV genome sequences. Interestingly, in contrast to the serotype O virus results, no second site mutations occurred within the VP1 coding region of serotype A viruses with the blocked VP1/2A cleavage site. However, some of these viruses acquired changes in the 2C protein that is involved in enterovirus morphogenesis. These results have implications for the testing of potential antiviral agents targeting the FMDV 3C protease.

Introduction

Foot-and-mouth disease virus (FMDV) is the prototypic member of the *Aphthovirus* genus within the family *Picornaviridae* and seven different serotypes (O, A, C, SAT 1-3 and Asia-1) have been identified. All FMDVs have a positive sense RNA genome (ca. 8400 nt) that includes a single large open reading frame (ca. 7000 nt) encoding a polyprotein (Belsham, 2005). The full-length polyprotein

is never observed since during, and after, synthesis it is processed, mainly by virus-encoded proteases, to generate 15 distinct mature products plus multiple precursors. The FMDV polyprotein includes two *trans*-acting proteases; these are the Leader (L) protease and the 3C protease ($3C^{pro}$). The L protease is only responsible for one cleavage within the polyprotein that occurs at its own C-terminus (i.e. the L/P1-2A junction, Strebel & Beck, 1986; Medina *et al*., 1993). However, this protease also induces cleavage of the translation initiation factor eIF4G, this results in the inhibition of host cell, cap-dependent, protein synthesis (reviewed in Belsham, 2005). The $3C^{pro}$ cleaves all the other junctions within the FMDV polyprotein except for the VP4/VP2 junction and the 2A/2B junction. Cleavage of VP0 to VP4 and VP2 occurs on encapsidation of the viral RNA and also within assembled empty capsid particles (Curry *et al*., 1995; Gullberg *et al*., 2013a; Gullberg *et al.*, 2013b). Separation of the 2A peptide from the 2B protein is dependent on the 2A coding sequence. However, this region only encodes 18 amino acids (without any protease motifs) but its presence results in a break in the polyprotein during its synthesis; this is described as "ribosomal skipping" (Donnelly *et al.*, 2001) or "StopGo" (Atkins *et al*., 2007).

The FMDV capsid protein precursor, P1-2A (Fig. 1), is processed by the $3C^{pro}$ to VP0, VP3, VP1 and 2A. The scission of the VP1-2A junction is the slowest of these cleavages within cell-free translation systems (Ryan *et al.*, 1989) and within mammalian cells (Gullberg *et al*., 2013a; Gullberg *et al*., 2013b) since the uncleaved VP1-2A can still be detected when all other junctions are fully cleaved (e.g. when P1-2A is expressed with a low-level of $3C^{pro}$). However, in peptide cleavage assays, using short synthetic substrates, it has been found that the peptide corresponding to the VP1/2A cleavage site was the most rapidly processed (Birtley *et al.*, 2005).

The FMDV $3C^{pro}$ cleaves a variety of different junction sequences (the amino acid residues at the cleavage junctions are indicated as: P4P3P2P1/P1'P2'P3'P4'). The cleavage sites recognized by the FMDV $3C^{pro}$ have either glutamine (Gln, Q) or glutamate (Glu, E) at the P1 position (Curry *et al*.,

2007). The consensus sequence (in single letter code) for the VP1/2A junction in serotype O and A FMDVs is PxKQ/xLNF. The Q residue at the P1 position together with the P4-Pro (P), P2-Lys (K) and P4´-Phe (F) residues, represent key determinants of $3C^{pro}$ specificity at this site (Birtley *et al*., 2005; Curry *et al.*, 2007; Zunszain *et al.*, 2010). Analysis of aligned FMDV $3C^{pro}$ cleavage sites from over 100 strains of the virus (including representatives of all serotypes) revealed that sites with P1-Q have a strong selectivity for P2-K, indicating that recognition of the P1 residue by $3C^{pro}$ is influenced by the P2 residue (Curry *et al.*, 2007). Recently, we have shown that changing the P2-K residue to E at the VP1/2A junction (i.e. K210E in VP1), in a serotype O virus, greatly inhibited cleavage at this junction and resulted in the formation of infectious virus particles containing the uncleaved VP1-2A (Gullberg *et al.*, 2013b). The "self-tagged" viruses containing this modification (K210E) also acquired, during the virus rescue procedure, a second amino acid substitution within VP1 (E83K). Interestingly, introduction of this E83K substitution alone into the virus, generated a second site mutant (L2P, in the 2A sequence; this is position P2' in the VP1/2A junction) that also blocked cleavage (Gullberg *et al.*, 2014). We have now expanded this analysis to identify the determinants of cleavage at the VP1/2A junction within the context of infectious serotype O and A FMD viruses using a variety of different approaches. Within the serotype A FMDVs, no second site changes in VP1 were observed in viruses where the VP1/2A cleavage was inhibited, but some evidence for changes in 2C was obtained. For certain picornaviruses, within the enterovirus genus, interactions between the virus capsid proteins and the 2C non-structural protein have been implicated in the process of virus morphogenesis (Liu *et al*., 2010; Wang *et al*., 2012; Wang *et al*., 2014).

Results

Modification of the VP1/2A cleavage site in a serotype A FMDV.

In order to determine whether the key elements of the results obtained with the serotype O FMDV sequences (Gullberg *et al.*, 2014) also applied to serotype A FMDV, the effect of modifying the

VP1/2A cleavage site within a serotype A FMDV was examined. The VP1/2A cleavage site sequence in the A22 strain of FMDV (AP**A**KQ/LLNFD) differs at just 1 out of the 10 residues flanking the junction from the serotype O (strain O1 Manisa, abbreviated thoughout as O1M) sequence (AP**V**KQ/LLNFD) analysed previously (Gullberg *et al*., 2013b; Gullberg *et al*., 2014) (see Fig. 1). The K210E substitution (at the P2 position) was introduced into a full-length FMDV cDNA, based on the backbone of a chimeric O1 Kaufbeuren (O1K) virus containing the coding sequence for the VP2-VP3-VP1-2A region of the A22 capsid protein precursor (Fig.1). Virus was successfully rescued from this chimeric wt O1K/A22 plasmid and also from the O1K/A22 VP1 K210E mutant (this had changed the codon encoding VP1 residue 210 from AAA to GAA). However, when the capsid protein coding sequences within the rescued virus were determined, it was found that the K210E substitution in VP1 had reverted in the virus by passage 2 (Psg 2) to the wt sequence (this only requires a single nt change) (see Fig. 1).

Two further modifications were, therefore, introduced into the serotype A viruses, the 2A L2P modification was made in isolation (using 3 nt changes, TTG to CCA) and a double mutant containing both the K210E substitution (the single nt change) and the 2A L2P substitution. Viruses were rescued successfully from both of these mutant plasmids. Consensus sequencing indicated that the expected mutations were still present within these rescued viruses and that no other mutations were detected within the VP2-2A coding region (see Fig. 1).

Analysis of the FMDV capsid proteins within cells infected with the wt and mutant O1K/A22 viruses, as determined by immunoblotting using anti-VP2 and anti-2A antibodies, is shown in Fig. 2. As expected, the production of VP0 and VP2 was very similar in each of the infected cell extracts (Fig. 2(a), lanes 2-7). However, the presence of the uncleaved VP1-2A was only observed with the mutant viruses, either containing the 2A L2P substitution alone (Fig. 2(b), lanes 4 and 5) or with the double mutant (VP1 K210E and 2A L2P) (Fig. 2(b), lanes 6 and 7).

These results were confirmed using immunofluorescence (IF) studies (Fig. 3). Consistent with the immunoblotting data, the presence of FMDV 2A (still attached to VP1) was detected in cells infected with the O1K/A22 2A L2P mutant virus (Fig. 3(g)) and with the double mutant (O1K/A22 VP1 K210E and 2A L2P) virus (Fig. 3(h)). In contrast, no signal for the 2A peptide was observed in cells infected with the wt O1K/A22 virus (Fig. 3(f)) or in uninfected cells (Fig. 3(e)). The presence of the FMDV capsid proteins could be detected in cells infected with each of the viruses (Fig. 3(b-d)) but not in uninfected cells (Fig. 3(a)). These results are consistent with those obtained using the serotype O FMDVs previously (Gullberg *et al.*, 2014). It seems that the free 2A peptide is not efficiently detected within cells using the IF approach; it is assumed that either it breaks down very quickly or the conditions of the IF assay are not suitable for detection of this short peptide.

Use of NGS to determine sequence diversity within rescued FMDVs.

As described previously (Gullberg *et al.*, 2013b; Gullberg *et al*., 2014), consensus sequencing of the capsid coding region (P1-2A) of the serotype O FMDVs rescued from the K210E and E83K mutant forms of the O1K/O1M cDNAs identified the presence of additional amino acid substitutions in the rescued viruses. We wished to analyse these adaptations in more detail, in particular to examine the appearance of sub-consensus level changes throughout the near complete genome sequence including the complete polyprotein coding region. To achieve this, RNA was extracted from the rescued O1K/O1M VP1 E83K and O1K/O1M VP1 K210E viruses (as described by Gullberg *et al*., 2013b; Gullberg *et al*., 2014) at Psg 2 and/or Psg 3. Two separate, but overlapping, cDNA fragments including the near complete genome (ca. 8kb, downstream of the poly(C) tract) were produced by RT-PCR, mixed and then sequenced using NGS at a coverage of about 5,000 reads per nt (except near the extreme 5'- and 3'-termini).

This analysis showed that the rescued virus O1K/O1M VP1 E83K retained the expected substitution (encoding E83K) in 100% of the progeny at Psg 2 but there was some heterogeneity in the sequence near the VP1/2A junction (see Table 1). As described earlier, the consensus sequencing indicated that a substitution (L2P) within the 2A sequence occurred within this rescued virus (Gullberg et al., 2014). The analysis by NGS (see Table 1) demonstrated that at Psg 2 some 83% of the reads corresponded to this L2P substitution in 2A while two other variants were also present (albeit at relatively low levels, 4% and 9%) which each encoded the K210N substitution in VP1 (c.f. the K210E change described previously in O1M, (Gullberg *et al*., 2014)). No other coding changes were present anywhere in the genome at an abundance of more than 3%.

Consensus sequence analysis of the rescued O1K/O1M VP1 K210E virus has shown previously the generation of the E83K substitution (Gullberg *et al*., 2013b). Using NGS, it was found that the E83K substitution in VP1 was encoded in 78% of the reads generated at Psg 2 and in 99% of the reads at Psg 3 (Table 1), consistent with the earlier consensus sequencing (Gullberg *et al*., 2013b). The K210E substitution was maintained in this rescued virus in 100% of the reads at Psg 2 and Psg 3.

For the rescued serotype A viruses, consensus (Sanger) sequencing of the rescued O1K/A22 2A L2P virus demonstrated the maintenance of the introduced changes and did not reveal any additional modifications resulting in amino acid substitutions within the P1-2A coding region. This was confirmed by NGS but an A to G nucleotide change, resulting in a single amino acid substitution (T44 to A within the 2C protein), was found in 13% of the reads from the rescued virus (Table 2). Within the O1K/A22 VP1 K210E and 2A L2P virus, only the expected changes in the P1-2A coding region were observed but an additional change, resulting in the amino acid substitution A73V in the 2C protein, was detected in 100% of the sequence reads, see Table 2. The plasmid pO1K/A22 K210E L2P from which this virus was rescued has been confirmed as having the expected sequence in the 2C coding region (100% identity to O1K, data not shown) and thus this sequence change had occurred

during virus rescue. The significance of these changes in 2C is unknown; neither residue is completely conserved among FMDV strains (Carrillo *et al*., 2005). The A73V change in 2C was not present in the rescued O1K/A22 wt or the O1K/A22 2AL2P and there was no evidence for the T44A amino acid substitution in either the O1K/A22 wt or the O1K/A22 VP1 K210E and 2A L2P virus that was encoded in a minority of the O1K/A22 2A L2P virus reads.

Exploring potential sequence diversity at the VP1/2A cleavage site.

The results described previously (Gullberg *et al*., 2013b; Gullberg *et al*., 2014) indicated that modification of the VP1/2A junction sequence from PxKQ/xLNF at the P2 position (from K to E) or the P2' position (from L to P) was sufficient to strongly inhibit cleavage by $3C^{pro}$ at this protein junction but these changes did not affect virus viability. Furthermore, the NGS data (Table 1) indicated that the K to N substitution at residue 210 of VP1 was also probably viable since some 13% of the virus population acquired this change. To establish the range of amino acid substitutions that could be tolerated at this junction, mutagenesis of the codon for residue 210 within VP1 was undertaken within the context of the O1K/A22 full-length cDNA. The mutagenesis generated 9 different codon sequences that encoded 7 distinct amino acid substitutions, see Table 3. RNA transcripts were produced from the mutant cDNAs and electroporated into BHK cells and infectious viruses were rescued in each case. From the virus harvests, RNA was extracted and the sequence of VP1-2A coding region was determined, changes (if any) are shown in Table 3. Consistent with the studies described above, the O1K/A22 VP1 K210E mutant (with a single nt change, GAA) again reverted to the parental sequence, however when 2 nt changes were introduced (GAG) to produce the K210E substitution then viruses that retained these 2 nt changes were obtained. Thus the VP1 substitutions K210Q, K210R, K210A, K210V, K210M, K210N and K210E (as the GAG double mutant) were all viable without reversion or other adaptation within VP1 (Table 3). Using consensus

194 level sequencing, no changes in the 2C coding region were detected in any of these rescued viruses
195 either (data not shown).
196 The cleavage of the VP1/2A junction in cells infected with the rescued mutant viruses was assessed
197 using the IF assay, as described above. The presence of the FMDV capsid proteins (using anti-FMDV
198 antisera) and of the VP1-2A (using anti-2A antibodies) was determined in BHK cells infected with
199 the different viruses. FMDV infection, but with no staining for VP1-2A, was observed in cells
200 infected with the viruses containing the VP1 residue K210 (wt) and R210 (Fig. 4). In contrast, cells
201 infected with the rescued viruses having the substitutions in VP1 K210Q, K210A, K210V, K210M,
202 K210N and K210E (double mutant) each showed staining both for the FMDV capsid proteins and for
203 2A (using the anti-2A antisera), indicative of blocked VP1/2A cleavage (see Fig. 4 and Table 3). No
204 staining with either antiserum was observed in uninfected cells, as expected (Fig. 4).
205 To confirm these results, immunoblotting was performed using anti-2A antibodies to determine the
206 presence of the uncleaved VP1-2A within infected cells. The results are shown in Fig. 5(a). Consistent
207 with the IF results, no VP1-2A product was detected in uninfected cells or in wt (K210) or mutant
208 K210R FMDV-infected cells. In contrast, the presence of VP1-2A was readily apparent within cells
209 infected with mutant FMDVs having the K210Q, K210A, K210V, K210M, K210N and K210E
210 substitutions. The presence of FMDV capsid proteins in the lysates from cells infected with each of
211 the different FMDV variants was verified using anti-VP2 antibodies that recognizes both VP0 and
212 VP2 (Fig. 5(b)). These results support the IF data and indicate that the VP1/2A junction is only
213 cleaved when residue 210 in VP1 is either K or R (these are both basic residues).
214

215 **Discussion**

216 In our earlier studies, it was shown that the K210E substitution in VP1 within the FMDV O1M capsid
217 inhibited cleavage of the VP1/2A junction and resulted in generation of a second site substitution

(E83K in VP1) in the mutant virus (Gullberg *et al*., 2013b). Furthermore, introduction of the E83K substitution alone in VP1 resulted in the production of another second site change (with a substitution of L2P in 2A) that also blocked VP1/2A junction processing in cells infected with the rescued virus (Gullberg *et al*., 2014). In contrast, this study, has shown that when the K210E substitution (GAA mutant) was introduced into the VP1 of a serotype A virus (O1K/A22), the virus reverted to wt (AAA) very rapidly (single nt change). However, introduction of 2 nt changes (GAG codon) enabled the K210E substitution to be maintained. Consistent with the serotype O virus results (Gullberg *et al*., 2013b; Gullberg *et al*., 2014), this amino acid substitution alone was sufficient to block VP1/2A cleavage (see Figs. 4 and 5). In addition, introduction of the 2A L2P change alone (employing 3 nt changes) or also with the K210E substitution resulted in the generation of viruses which maintained each of these changes. Furthermore, the presence of the uncleaved VP1-2A protein was observed within cells infected with these serotype A viruses (Figs. 2 and 3). Thus, consistent with results using the O1K/O1M FMDV (Gullberg *et al*., 2013b; Gullberg *et al*., 2014), it is possible to obtain infectious serotype A FMDVs, containing the uncleaved VP1-2A. However, in contrast to the results using the serotype O virus, there was no apparent selection for a substitution at residue E83 in VP1 (or elsewhere within the VP1) within the serotype A background. The basis for this difference is not known but it is noteworthy that the serotype A capsid proteins assemble into FMDV empty capsids much more efficiently than the serotype O proteins (Abrams *et al*., 1995; Porta *et al*., 2013). It is also apparent that some of the rescued serotype A viruses, with the VP1/2A junction rendered non-cleavable, acquired second site mutations within the non-structural protein 2C (see Table 2). In particular, the A73V variant within 2C was encoded by 100% of the sequence reads at Psg 3 of the rescued O1K/A22 VP1-K210E and 2A-L2P virus. This suggests a strong selective pressure for this amino acid substitution. The significance of this is currently unknown but there is some evidence for

241 interactions between the capsid proteins and the 2C protein of enteroviruses (e.g. poliovirus) during
242 virus morphogenesis (Liu *et al*., 2010; Wang *et al*., 2012; Wang *et al.*, 2014).
243 Interestingly, it was also observed, using NGS, that during the rescue of the O1K/O1M VP1 E83K
244 virus a minority of the virus population encoded a K210N substitution in VP1 (c.f. the K210E
245 substitution observed in a laboratory grown O1M virus, Gullberg *et al*., 2013b). It should be noted
246 that the majority of the serotype O VP1 E83K mutant virus RNA acquired the 2A L2P substitution
247 during the virus rescue procedure (see Table 1). This encouraged analysis of the range of substitutions
248 that can be accommodated at residue 210 in VP1; this is at position P2 relative to the VP1/2A cleavage
249 site. Within the serotype A background, there appears to be significant selection pressure against the
250 K210E substitution, since following independent transfections of a mutant RNA containing a single
251 nt change (GAA) reversion to the wt (AAA) sequence occurred. However, when 2 nt changes were
252 used (GAG) to make this amino acid substitution then the K210E substitution was maintained. The
253 single nt substitution to make the K210E substitution was also maintained in the O1K/A22 K210E
254 and L2P double mutant; presumably the presence of the two substitutions that blocked VP1/2A
255 cleavage overcame the selective pressure for reversion. In addition, a range of other amino acid
256 substitutions were tolerated, most of these substitutions (e.g. K210A, K210V, K210M, K210N)
257 blocked cleavage of the VP1/2A junction, thus the VP1-2A product was stable (see Figs. 4 and 5). In
258 contrast, the 2A peptide was released from the VP1 in the K210R mutant. Therefore, it appears that
259 the presence of a positively charged residue (K or R) at residue 210 in VP1 is essential for VP1/2A
260 cleavage and a negative charge (as in K210E) is less well tolerated by itself and was selected against.
261 These results are consistent with the strong predominance of the K and R residues at this position in
262 the "logos plot" generated by Curry *et al*., (2007) for $3C^{pro}$ cleavage sites, with Q at the P1 position,
263 based on the known sequences of over 100 strains of FMDV.

Using peptide cleavage assays, the VP1/2A peptide was the most efficiently cleaved substrate for FMDV $3C^{pro}$ (Birtley *et al.*, 2005). However, making the K210A substitution abrogated cleavage of this peptide, in accordance with the results presented here. Zunszain *et al.*, (2010), have described additional modifications to the peptide substrate, which corresponds to the VP1/2A junction. Changing the P2 residue in the cleavage site (corresponding to K210 in VP1) from K to R or to ornithine (also positively charged) had relatively modest effects on the cleavage rate. However, substitution to the neutral T residue abrogated cleavage as observed here with the K210 changed to Q, A, V, M or N (see Table 3, Figs. 4 and 5).

It has been proposed that the FMDV $3C^{pro}$ may be a good target for the development of an antiviral agent (Roqué Rosell *et al*., 2014). Furthermore, it was shown that compounds that resemble the peptide substrate can act as an efficient inhibitor of this protease. The presence of a positively charged residue at the P2 position generated the most effective inhibitors while compounds containing neutral residues (e.g. G and Q) or a negatively charged residue (E) at this position were much less effective, consistent with the poor cleavage of the VP1/2A junction seen here in viruses containing equivalent substitutions.

It is important to note that viable FMDVs with the VP1/2A junction uncleaved can be obtained (as here, and as described previously for serotype O viruses, Gullberg *et al.*, 2013b; Gullberg *et al.*, 2014). Thus, it may be wise to focus screens for such antiviral agents on other $3C^{pro}$ cleavage sites so that the block on polyprotein processing is most effective at inhibiting virus replication.

The results presented here demonstrate that the combination of reverse genetics and NGS provides powerful tools to direct and identify virus adaptation thus permitting novel aspects of the virus biology to be identified.

Material and Methods

288 *Plasmid construction*

289 The structures of plasmids containing full-length FMDV cDNAs used in this study are indicated in
290 Fig.1. The chimeric pO1K/A22 plasmids (containing the A22 Iraq capsid coding sequences, as used
291 in Porta *et al.*, 2013; Polacek *et al.*, 2013) in the FMDV O1 Kaufbeuren (O1K) backbone were
292 generated using the same procedures as used previously for the production of the pO1K/O1M VP1
293 K210E (Gullberg *et al.*, 2013b). Briefly, the cDNAs corresponding to the A22 VP2-2A coding region
294 were amplified from pGEM-3Z-A-P1-2A-mIRES-3C (Gullberg *et al.*, 2013a) and pGEM-3Z-A-P1-
295 2A-mIRES-3C VP1K210E (Gullberg *et al.*, 2013b) with primers FMDVA_*NheI*VP4VP2_Fw and
296 FMDVA_*ApaI*2A2B_Re (see Supplementary Table S1) and used to generate the full-length cDNAs
297 termed pO1K/A22 wt and pO1K/A22 VP1 K210E, respectively (Fig.1). In order to produce
298 pO1K/A22 2A L2P and the double mutant pO1K/A22 VP1 K210E and 2A L2P, intermediate
299 plasmids (using pO1K/A22 wt and pO1K/A22 VP1K210E, as described above, as templates) were
300 generated. This was achieved using the QuikChange site-directed mutagenesis method (with
301 *Pfu*Turbo DNA polymerase; Stratagene), according to the manufacturer´s instructions, with primers
302 containing the desired modifications (see Supplementary Table S1, namely FMDVA_2AL2P_Fw
303 together with FMDVA_2AL2P_Re or FMDVA_VP1K210E_2AL2P_Re). The subsequent steps to
304 produce the four pO1K/A22 variants were performed essentially as described for the serotype O
305 plasmid pO1K/O1M VP1 E83K (Gullberg *et al.*, 2014). Plasmids were amplified in *E. coli* Top10
306 cells (Invitrogen), purified (Midiprep kit; Thermo Scientific) and verified by sequencing of the capsid
307 coding region (and for pO1K/A22 VP1 K210E the 2C coding region as well) with a BigDye
308 Terminator v. 3.1 Cycle Sequencing Kit and a 3500 Genetic Analyzer (Applied Biosystems).
309 Additional mutations, encoding changes at the VP1/2A junction, were introduced into the pO1K/A22
310 full-length FMDV cDNA (Fig.1) by site-directed mutagenesis using a megaprimer (146 bp) that was
311 prepared by PCR using primer O1PN20 and primer 13LPN21, (see Supplementary Table S1), that

had NNN at the position corresponding to the codon for the VP1 residue 210. This degenerate megaprimer was used, with the pO1K/A22 full-length cDNA template and *Pfu*Turbo DNA polymerase (as above) to generate a collection of 9 plasmids encoding a variety of different amino acids, with diverse properties, in place of VP1 residue K210; this is at position P2 relative to the VP1/2A cleavage site. The details of each modification made are indicated in Table 3.

Rescue of modified viruses from cDNA.

Plasmids pO1K/A22 (wt), pO1K/A22 VP1 210E, pO1K/A22 2A L2P and pO1K/A22 VP1 K210E 2A L2P, (as shown in Fig.1) containing the full-length FMDV cDNA sequences were linearized by digestion with *HpaI*, purified (using a QIAquick PCR purification kit; Qiagen) and transcribed *in vitro* using T7 RNA polymerase (Megascript kit; Ambion). The transcripts were analyzed using agarose gel electrophoresis and then introduced into baby hamster kidney (BHK) cells by electroporation as described previously (Nayak *et al.*, 2006; Bøtner *et al.*, 2011). At 2 days post electroporation, the rescued viruses were harvested and amplified in one, or two, subsequent passages (Psg 2 and Psg3) in BHK cells. After these passages, viral RNA was extracted (QIAamp RNA blood mini kit; Qiagen), reverse transcribed using ready-to-go you-prime first-strand beads (GE Healthcare Life Sciences), and the FMDV cDNA corresponding to the VP2-2A coding region was amplified in a PCR (Expand high-fidelity PCR system; Roche). Control reactions, lacking reverse transcriptase, were used to show that the PCR products obtained were derived from the viral RNA and not from residual DNA template. The amplicons (~2,000 bp) including the entire VP2-2A coding region were visualized in agarose gels, purified (GeneJET gel extraction kit, Thermo Scientific) and sequenced, on both strands, as above. Sequences were analysed using Vector NTI software (Invitrogen).

For the library of VP1 K210 mutants, mutant viruses were rescued essentially as described above. The sequencing covered the VP1-2A coding region (from a PCR product of ca. 700bp) both before

and after virus rescue. The sequence of the 2C coding region was also determined in selected cases. The rescued viruses were titrated (and were in most cases ca. 10^6 to 10^7 $TCID_{50}$/ml), in some cases a 4^{th} passage in BHK cells was required to reach this titre.

The rescued serotype O viruses O1K/O1M VP1 E83K and O1K/O1M VP1 K210E viruses have been described previously (Gullberg *et al*., 2013b; Gullberg *et al*., 2014).

RT-PCR and Next Generation Sequencing (NGS).

For the purpose of NGS, extracted RNA (isolated as described above from virus harvests) was converted to cDNA using SuperScript III (Invitrogen) with a T_{27} reverse primer according to the manufacturer's protocol. Two cDNA amplicons were prepared by PCR using Phusion DNA polymerase (Thermo Fisher) with the primers 13-N PN 2 + 10-P PN 30 (Supplementary Table S1) and separately 8-A PN 200 + 13-N PN 3 (Supplementary Table S1). These overlapping fragments (ca. 4kb and 4.2kb respectively) correspond to the most of the FMDV genome (downstream of the poly(C) tract, see Belsham (2005)), including the complete polyprotein coding region (ca. 7kb) but excluding the S-fragment at the 5'-terminus of the viral genome. The fragments were gel purified, mixed and then analysed by NGS essentially as described previously (Fahnøe *et al*., 2014; Hadsbjerg *et al*., 2016). The parental sequences of the FMDV chimeric O1K/O1M cDNA (as described by Gullberg *et al*., 2013b) was assembled from the O1K sequence (Acc. No. X00871) and the coding sequence for the O1M capsid proteins (from Acc. No. AY593823) with known differences (see Gullberg *et al.*, 2013b), while the chimeric O1K/A22 sequence was generated using the O1K sequence and the A22 Iraq sequence (Carrillo *et al*., 2005, Acc. No. AY593764.1). The derived sequences were used as the reference for mapping of sequence reads using Samtools (Li *et al*., 2009), VarScan 2 (Koboldt *et al*., 2012) and VCFtools (Danecek *et al.*, 2011), in succession, in order to generate consensus sequences from the mapped reads. Subsequently, consensus sequences were

aligned using MAFFT in Geneious (Biomatters, Auckland, New Zealand). Finally, a combination of Samtools (Li *et al.*, 2009), Lo-Freq (Wilm *et al*., 2012) and SnpEff (Cingolani *et al.*, 2012) was used for downstream single nucleotide variant (SNV) analysis.

Virus infection of BHK cells.

Virus titers were determined, as tissue culture infectious doses ($TCID_{50}$), by titration in BHK cells according to standard procedures (Reed & Muench, 1938).

Monolayers of BHK cells, grown in 35-mm wells, were inoculated with the rescued viruses at a multiplicity of infection (MOI) of 0.1 $TCID_{50}$/cell. At the indicated times post infection, cell lysates were prepared using 20 mM Tris-HCl (pH 8.0), 125 mM NaCl and 0.5% NP-40, and clarified by centrifugation at 18,000 × g for 10 min at 4°C.

Immunoblot analysis.

Immunoblotting was performed, using cell lysates, according to standard methods as described previously (Polacek *et al*., 2013). Briefly, aliquots of cell lysate were mixed with Laemmli sample buffer (with 25mM dithiothreitol), the proteins were separated by SDS-PAGE (12.5% or 4-15% polyacrylamide) and transferred to polyvinylidene difluoride membranes (PVDF, Millipore). Specific proteins were detected with primary antibodies recognizing: FMDV VP2 (monoclonal antibody 4B2, a gift from L. Yu, as described by Yu *et al.*, 2011) and FMDV 2A (ABS31; Millipore). Bound proteins were visualized using appropriate horseradish peroxidase-conjugated secondary antibodies (Dako) and a chemiluminescence detection kit (ECL Prime, Amersham) with a Chemi-Doc XRS system (Bio-Rad).

Immunofluorescence assays.

Monolayers of BHK cells, grown on glass coverslips in 35-mm well plates, were infected with the rescued O1K/A22 viruses (MOI 0.1). At 6-8 hrs post infection, the cells were fixed, stained and mounted as previously described (Gullberg *et al*., 2013b) using rabbit anti-FMDV A-Iraq serum and anti-FMDV 2A (ABS31, as above) followed by a donkey Alexa-fluor 568-labelled anti-rabbit IgG (A10042, Life Technologies). The slides were mounted with Vectashield (VECTOR laboratories) containing 4′,6-diamidino-2-phenylindole (DAPI) and images were captured using an epifluorescence microscope.

Acknowledgements

We wish to thank Li Yu (Chinese Academy of Agricultural Sciences, China) for the anti-VP2 antibody. This work was supported by the Danish Council for Independent Research-Technology and Production Sciences (FTP grant 09-070549) to CP and GJB.

References

Abrams, C.C., King, A.M. & Belsham, G.J. **(1995).** Assembly of foot-and-mouth disease virus empty capsids synthesized by a vaccinia virus expression system. *J Gen Viro*l **76**, 3089-3098.

Atkins, J.F., Wills, N.M. Loughran, G., Wu, C.Y., Parsawar, K., Ryan, M.D., Wang, C.H. & Nelson, C.C. (2007). A case for "StopGo": reprogramming translation to augment codon meaning of GGN by promoting unconventional termination (Stop) after addition of glycine and then allowing continued translation (Go). *RNA* **13**, 803-810.

Belsham, G.J. (2005). Translation and replication of FMDV RNA. *Curr Top Microbiol Immunol* **288,** 43-70.

Birtley, J.R., Knox, S.R., Jaulent, A.M., Brick, P., Leatherbarrow, R.J. & Curry S. (2005). Crystal structure of foot-and-mouth disease virus 3C protease. New insights into catalytic mechanism and cleavage specificity. *J Biol Chem* **280,** 11520-11527.

Bøtner, A., Kakker, N.K., Barbezange, C., Berryman, S., Jackson, T. & Belsham, G.J. (2011). Capsid proteins from field strains of foot-and-mouth disease virus confer a pathogenic phenotype in cattle on an attenuated, cell-culture-adapted virus, O1 Kaufbeuren virus. *J Gen Virol* **92,** 1141-1151.

Carrillo, C., Tulman, E.R., Delhon, G., Lu, Z., Carreno, A., Vagnozzi, A., Kutish, G.F. & Rock, D.L. (2005). Comparative genomics of foot-and-mouth disease virus. *J Virol* **79,** 6487-6504.

Cingolani, P., Platts, A., Wang, L.L., Coon, M., Nguyen, T., Wang, L., Land, S.J., Lu, X. & Ruden, D.M. (2012). A program for annotating and predicting the effects of single nucleotide

polymorphisms, SnpEff: SNPs in the genome of Drosophila melanogaster strain w1118; iso-2; iso-3. *Fly (Austin)*. **6,** 80-92.

Curry, S., Abrams, C.C., Fry, E., Crowther, J.C., Belsham, G.J., Stuart, D.I. & King, A.M. (1995). Viral RNA modulates the acid sensitivity of foot-and-mouth disease virus capsids. *J Virol* **69,** 430-438.

Curry, S., Roque-Rosell, N., Zunszain, P.A. & Leatherbarrow, R.J. (2007). Foot-and-mouth disease virus 3C protease: recent structural and functional insights into an antiviral target. *Int J Biochem Cell Biol* **39,** 1-6.

Danecek, P., Auton, A., Abecasis, G., Albers, C.A., Banks, E., DePristo, M.A., Handsaker, R.E., Lunter, G., Marth, G.T., Sherry, S.T., McVean, G. & Durbin, R. (2011). The variant call format and VCFtools. *Bioinformatics.* **27,** 2156–2158.

Donnelly, M.L., Luke, G., Mehrotra, A., Li, X., Hughes, L.E., Gani, D. & Ryan MD. (2001). Analysis of the aphthovirus 2A/2B polyprotein 'cleavage' mechanism indicates not a proteolytic reaction, but a novel translational effect: a putative ribosomal 'skip'. *J Gen Virol* **82,** 1013-1025.

Ellard, F.M., Drew, J., Blakemore, W.E., Stuart, D.I. & King, A.M. (1999). Evidence for the role of His-142 of protein 1C in the acid-induced disassembly of foot-and-mouth disease virus capsids. *J Gen Virol* **80,** 1911-1918.

Fahnøe, U., Pedersen, A.G., Risager, P.C., Nielsen, J., Belsham, G.J., Höper, D., Beer, M. & Rasmussen, T.B. (2014). Rescue of the highly virulent classical swine fever virus strain "Koslov" from cloned cDNA and first insights into genome variations relevant for virulence. *Virology* **468-470**, 379-387.

Gullberg, M., Muszynski, B., Organtini, L.J., Ashley, R.E., Hafenstein, S.L., Belsham, G.J. & Polacek C. (2013a). Assembly and characterization of foot-and-mouth disease virus empty capsid particles expressed within mammalian cells. *J Gen Virol* **94,** 1769-1779.

Gullberg, M., Polacek, C., Bøtner, A. & Belsham, G.J. (2013b). Processing of the VP1/2A junction is not necessary for production of foot-and-mouth disease virus empty capsids and infectious viruses: characterization of "self-tagged" particles. *J Virol* **87,** 11591-11603.

Gullberg, M., Polacek, C. & Belsham, G.J. (2014). Sequence adaptations affecting cleavage of the VP1/2A junction by the 3C protease in foot-and-mouth disease virus-infected cells. *J Gen Virol* **95,** 2402-2410.

Hadsbjerg, J., Friis, M.B., Fahnøe, U., Nielsen, J., Belsham, G.J. & Rasmussen, T.B. (2016). Sequence adaptations during growth of rescued classical swine fever viruses in cell culture and within infected pigs. *Vet Micro* **192**, 123-134.

Koboldt, D., Zhang, Q., Larson, D., Shen, D., McLellan, M., Lin, L., Miller, C., Mardis, E., Ding, L. & Wilson, R. (2012). VarScan 2: Somatic mutation and copy number alteration discovery in cancer by exome sequencing. *Genome Research* **22,** 568-576. URL:http://varscan.sourceforge.net

Li, H., Handsaker, B., Wysoker, A., Fennell, T., Ruan, J., Homer, N., Marth, G., Abecasis, G., Durbin, R. & 1000 Genome Project Data Processing Subgroup. (2009). The Sequence Alignment/Map format and SAMtools. *Bioinformatics* **25,** 2078-2079.

Liu, Y., Wang, C., Mueller, S., Paul, A.V., Wimmer, E. & Jiang, P. (2010) Direct interaction between two viral proteins, the nonstructural protein 2C and the capsid protein VP3, is required for enterovirus morphogenesis. *PLoS Pathog.* **6(8),** e1001066.

Medina, M., Domingo, E., Brangwyn, J.K. & Belsham, G.J. (1993). The two species of the foot-and-mouth disease virus leader protein, expressed individually, exhibit the same activities. *Virology* **194,** 355-359.

Nayak, A., Goodfellow, I.G., Woolaway, K.E., Birtley, J., Curry, S. & Belsham, G.J. (2006). Role of RNA structure and RNA binding activity of foot-and-mouth disease virus 3C protein in VPg uridylylation and virus replication. *J Virol* **80,** 9865-9875.

Polacek, C., Gullberg, M., Li, J. & Belsham, G.J. (2013). Low levels of foot-and-mouth disease virus 3C protease expression are required to achieve optimal capsid protein expression and processing in mammalian cells. *J Gen Virol* **94,** 1249-1258.

Porta, C., Xu, X., Loureiro, S., Paramasivam, S., Ren, J., Al-Khalil, T., Burman, A., Jackson, T., Belsham, G.J., Curry, S., Lomonossoff, G.P., Parida, S., Paton, D., Li, Y., Wilsden, G., Ferris, N., Owens, R., Kotecha, A., Fry, E., Stuart, D.I., Charleston, B. & Jones, I.M. (2013).

493 Efficient production of foot-and-mouth disease virus empty capsids in insect cells following down
494 regulation of 3C protease activity. *J Virol Methods*. **187**, 406-412.
495
496 **Reed, L.J. & Muench, H. (1938).** A simple method of estimating fifty percent endpoints. *Am J Hyg*
497 **27,** 493-497.
498
499 **Roqué Rosell, N.R., Mokhlesi, L., Milton, N.E., Sweeney, T.R., Zunszain, P.A., Curry, S. &**
500 **Leatherbarrow, R.J. (2014).** Design and synthesis of irreversible inhibitors of foot-and-mouth
501 disease virus 3C protease. *Bioorg Med Chem Lett*. **24**, 490-494.
502
503 **Ryan, M.D., Belsham, G.J. & King, A.M. (1989).** Specificity of enzyme-substrate interactions in
504 foot-and-mouth disease virus polyprotein processing. *Virology* **173,** 35-45.
505
506 **Strebel, K. & Beck E. (1986).** A second protease of foot-and-mouth disease virus. *J Virol* **58,** 893-
507 899.
508
509 **Wang, C., Jiang, P., Sand, C., Paul, A.V. & Wimmer, E. (2012)** Alanine scanning of poliovirus
510 2CATPase reveals new genetic evidence that capsid protein/2CATPase interactions are essential for
511 morphogenesis. *J Virol.* **86,** 9964-9975.
512
513 **Wang C, Ma HC, Wimmer E, Jiang P & Paul AV. (2014)** A C-terminal, cysteine-rich site in
514 poliovirus 2C(ATPase) is required for morphogenesis. *J Gen Virol.* **95,** 1255-1265.
515

Wilm, A., Aw, P.P., Bertrand, D., Yeo, G.H., Ong, S.H., Wong, C.H., Khor, C.C., Petric, R., Hibberd, M.L. & Nagarajan, N. (2012). LoFreq: a sequence-quality aware, ultra-sensitive variant caller for uncovering cell-population heterogeneity from high-throughput sequencing datasets. *Nucl. Acids Res.* **40,** 11189-11201.

Yu, Y., Wang, H., Zhao, L., Zhang, C., Jiang, Z. & Yu, L. (2011). Fine mapping of a foot-and-mouth disease virus epitope recognized by serotype-independent monoclonal antibody 4B2. *J Microbiol* **49,** 94-101.

Zunszain, P.A., Knox, S.R., Sweeney, T.R., Yang, J., Roque-Rosell, N., Belsham, G.J., Leatherbarrow, R.J. & Curry, S. (2010). Insights into cleavage specificity from the crystal structure of foot-and-mouth disease virus 3C protease complexed with a peptide substrate. *J Mol Biol* **395,** 375-389.

TABLES

Table 1. Analysis of SNVs within rescued O1K/O1M viruses as determined by NGS.

Nt position	wt	Variant	O1K/O1M VP1 E83K (Psg 2) (%)[1]	O1K/O1M VP1 K210E (Psg 2) (%)[1]	O1K/O1M VP1 K210E (Psg 3) (%)[1]	SNV effect (whole polyprotein)	SNV effect (individual protein)
762	T	C	6	-	-	(in 5' UTR)	-
948	T	G	-	1	3	(in 5' UTR)	-
1811	T	C	6	-	-	-	-
1875	A	G	3	-	-	T253A	VP4 (T52A)
2102	C	T	3	-	-	-	-
2357	A	G	-	3	3	-	-
3537	G	A	100	78	99	E807K	VP1 (E83K)
3918	A	G	-	100	100	K934E	VP1 (K210E)
3920	A	C	4	-	-	K934N	VP1 (K210N)
3920	A	T	9	-	-	K934N	VP1 (K210N)
3928	T	C	83	-	-	L937P	2A (L2P)
5166	A	G	3	-	-	S1350G	2C (S243G)
7392	T	C	-	5	7	F2092L	3D (F228L)
7765	A	G	2	-	-	K2216R	3D (K353R)

1: The percentage of each variant (≥ 1%) is given to the nearest integer.

535 **Table 2. Analysis of SNVs within rescued O1K/A22 viruses as determined by NGS.**

Nt position	wt	Variant	O1K/A22 (wt) (Psg 2) (%)[1]	O1K/A22 2A L2P (Psg 3) (%)[1]	O1K/A22 VP1 K210E 2A L2P (Psg 3) (%)[1]	SNV effect (whole polyprotein)	SNV effect (individual protein)
932	A	C	-	2	-	(in 5'-UTR)	-
1060	T	G	2	-	-	(in 5'-UTR)	-
1124	T	A	-	7	-	N2K	L (N2K)
1341	C	T	-	-	4	P75S	L (P75S)
1400	G	T	-	-	2	-	-
1865	C	T	-	2	-	-	-
2175	T	C	-	2	-	F353L	VP2 (F67L)
2342	A	G	-	-	2	-	-
2684	C	T	-	3	-	-	-
3154	T	C		1	-	V679A	VP3 (V174A)
3824	G	C	2	-	-	-	-
3884	T	C	-	8	-	-	-
3921	A	G	-	-	100	K935E	VP1 (K210E)
3930	T	C	-	90	100		
3931	T	C	-	98	100	L938P[2]	2A (L2P)[2]
3932	G	A	-	99	100		
4572	A	G	-	13	-	T1152A	2C (T44A)
4660	C	T	-	-	100	A1181V	2C (A73V)
4821	A	C	-	1	-	I1235L	2C (I127L)
4843	G	T	-	1	-	R1242I	2C (R134I)
5080	C	T	-	5	-	T1321I	2C (T213I)
6924	C	T	-	11	-	-	-
7170	T	C	3	-	-	Y2018H	3D (Y155H)
7358	C	T	-	-	4	-	-

536

537 1: The percentage of each variant (≥ 1%) is given to the nearest integer.

538 2: Change of the TTG to CCA codon was introduced by site-directed mutagenesis and the 3

539 changes together result in the 2A (L2P) substitution.

540

541

542 **Table 3. Influence of residue K210 in VP1 on VP1/2A junction cleavage in FMDV-infected**

543 **cells.**

Virus	VP1 210 codon	Viability	Rescued virus sequence	Rescued virus amino acid	Comment	VP1/2A cleavage[1]
pO1K/A22 K210	AAA	+	AAA	K	wt	+
pO1K/A22 K210Q	**C**AA[2]	+	CAA	Q		-
pO1K/A22 K210R	A**G**A[2]	+	AGA	R		+
pO1K/A22 K210A(v1)[3]	**GC**A[2]	+	GCA	A		-
pO1K/A22 K210A(v2)[3]	**G**C**G**[2]	+	GCG	A		-
pO1K/A22 K210V	**GTT**[2]	+	GTT	V		-
pO1K/A22 K210M	A**TG**[2]	+	ATG	M		-
pO1K/A22 K210N	AA**C**[2]	+	AAC	N		-
pO1K/A22 K210E(v1)[3]	**G**AA[2]	+	AAA	K	Reversion	+
pO1K/A22 K210E(v2)[3]	**G**A**G**[2]	+	GAG	E		-

544

545 1: VP1/2A cleavage was assessed from IF staining using anti-2A antibodies (as in Fig. 4) and by

546 immunoblotting (Fig. 5(a)).

547 2: nt changes in this codon are indicated in bold font.

548 3: (v1 or v2 to distinguish different codons)

549

Figure legends

Figure 1. Schematic structure of the plasmid containing the FMDV O1K/A22 cDNA and derivatives. The *NheI* and *ApaI* restriction enzyme sites (as indicated) were used as described in Materials and Methods to introduce cDNA fragments encoding the serotype A FMDV capsid proteins VP2-VP3-VP1-2A (from A22 Iraq, white fill) into the plasmid pT7S3 (Ellard *et al.*, 1999), containing a full-length cDNA corresponding to the O1Kaufbeuren B64 strain of FMDV (coding sequences marked in grey). The plasmid encoded amino acid sequences at the VP1/2A junction are shown. The FMDV O1K/A22 wild-type, single mutants (VP1 K210E or 2A L2P) and double mutant (VP1 K210E and 2A L2P) were produced as described in Materials and Methods. The full-length plasmids were linearized using *HpaI* prior to *in vitro* transcription and virus rescue. The locations of restriction sites used are marked: *NheI, ApaI* and *HpaI*. Sequence changes in the capsid coding region of the rescued viruses are indicated.

Figure 2. Detection of FMDV capsid proteins in BHK cells infected with O1K/A22 wild-type and mutant viruses. BHK cells were infected with O1K/A22 wild-type or mutant viruses (single mutant 2A L2P or double mutant VP1 K210E and 2A L2P) (MOI of 0.1) and whole cell lysates were prepared at the indicated times post infection. The presence of FMDV VP2 (and its precursor VP0) were detected by immunoblotting using anti-VP2 antibodies (panel (a)) and FMDV 2A (attached to VP1 as VP1-2A) was detected using anti-2A antibodies (panel (b)). Uninfected BHK cells were used as a negative control. Molecular mass markers (kDa) are indicated on the left.

Figure 3. Immunofluorescence staining of FMDV proteins within serotype A FMD virus-infected cells. FMDV proteins within uninfected or FMDV-infected cells (using MOI of 0.1) were detected (at 8 h p.i.) using an anti-FMDV A-Iraq polyclonal antibody (panels (a) - (d)) or an anti-2A

antibody (panels (e) - (h)) and a secondary antibody labeled with Alexa Fluor 568 (red). Uninfected cells are shown in panels (a) and (e). Cells were infected with the viruses O1K/A22 (wild-type) (panels (b) and (f)), O1K/A22 2A L2P (panels (c) and (g)) or O1K/A22 VP1 K210E and 2A L2P (panels (d) and (h)) as indicated. The cellular nuclei were visualized with DAPI (blue). Bar, 50 μm.

Figure 4. Determination of VP1/2A cleavage by immunofluorescence staining for FMDV proteins within cells. FMDV proteins within uninfected or FMDV-infected cells (using MOI of 0.1) were detected (at 6 h p.i.) using an anti-FMDV A-Iraq polyclonal antibody or an anti-2A antibody (as indicated) and a secondary antibody labeled with Alexa Fluor 568 (red) as in Fig. 3. The codon for residue 210 within VP1 (in parentheses) and the resulting individual amino acid residue within the different rescued viruses are indicated. Uninfected cells were used as a negative control. The cellular nuclei were visualized with DAPI (blue). Bar, 200 μm.

Figure 5. Assessment of FMDV VP1/2A cleavage in FMDV-infected BHK cells by immunoblotting. Uninfected or FMDV-infected BHK cell lysates were analysed by SDS-PAGE and immunoblotting (as in Fig. 2). Where applicable, the cells were infected with the indicated viruses (at an MOI of 0.1) and the presence of FMDV 2A (attached to VP1 as VP1-2A) was detected using anti-2A antibodies (panel (a)) while FMDV VP2 (and its precursor VP0) were detected by immunoblotting using anti-VP2 antibodies (panel (b)). Uninfected cells were used as a negative control. Molecular mass markers (kDa) are indicated on the left.

Figure 1

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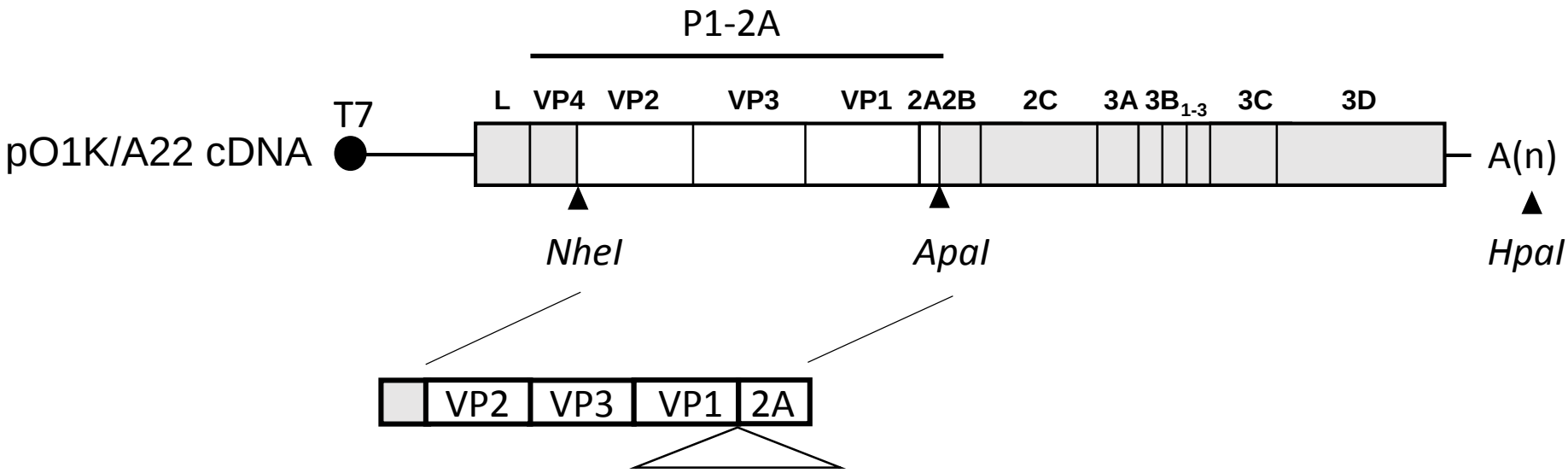

pO1K/A22 wild-type (wt)	APAKQ/LLNFD	APAKQ/LLNFD
pO1K/A22 VP1 K210E	APA**E**Q/LLNFD	APAKQ/LLNFD (reversion)
pO1K/A22 2A L2P	APAKQ/L**P**NFD	APAKQ/L**P**NFD
pO1K/A22 VP1 K210E 2A L2P	APA**E**Q/L**P**NFD	APA**E**Q/L**P**NFD
	Encoded sequence	*Rescued virus*

Figure 2

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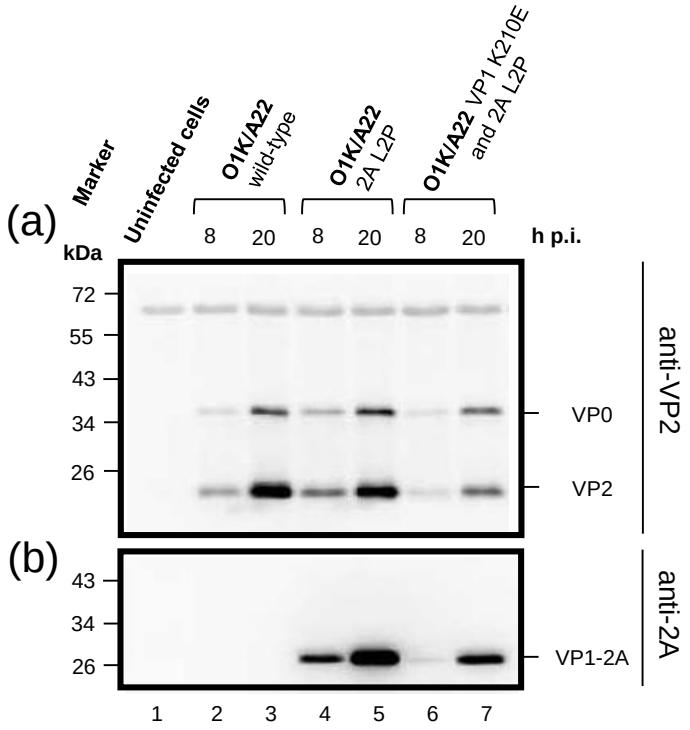

Figure 3

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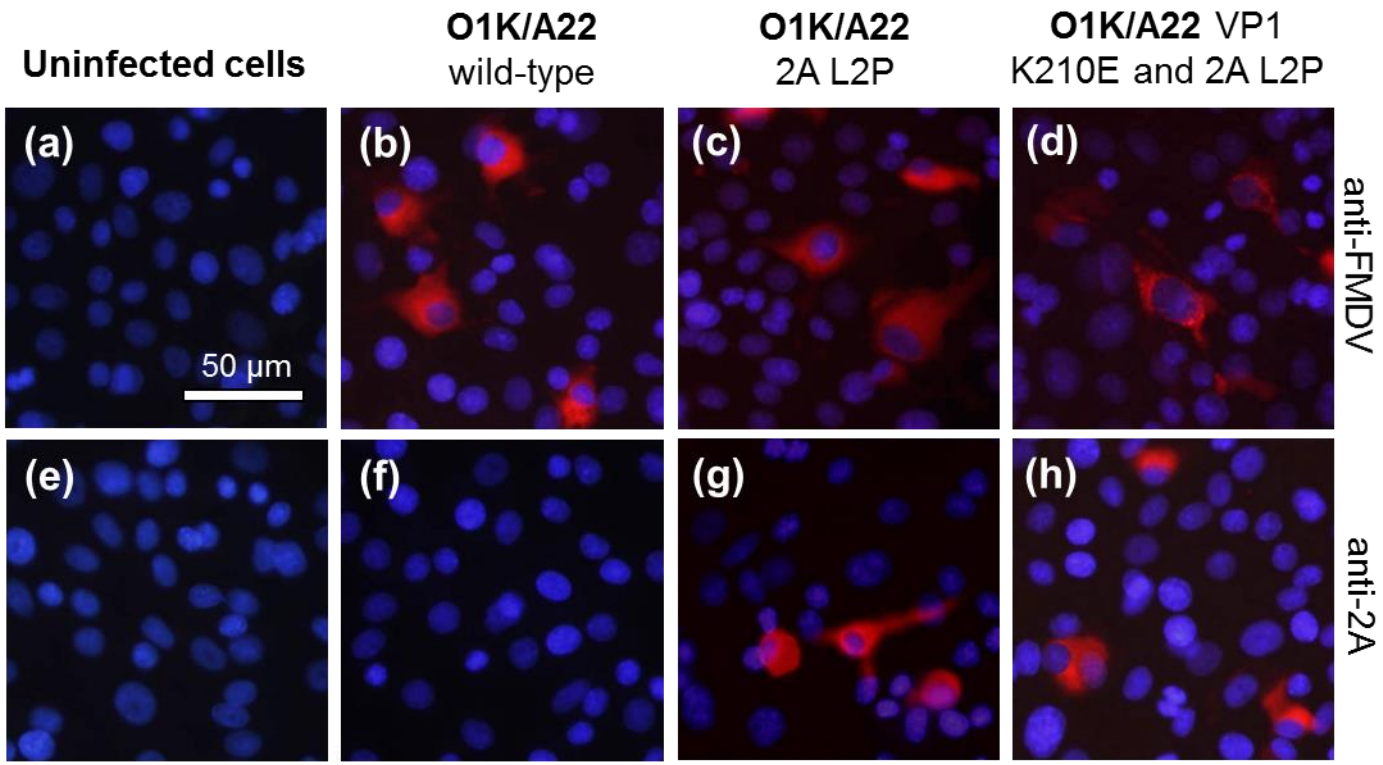

Fig. 3

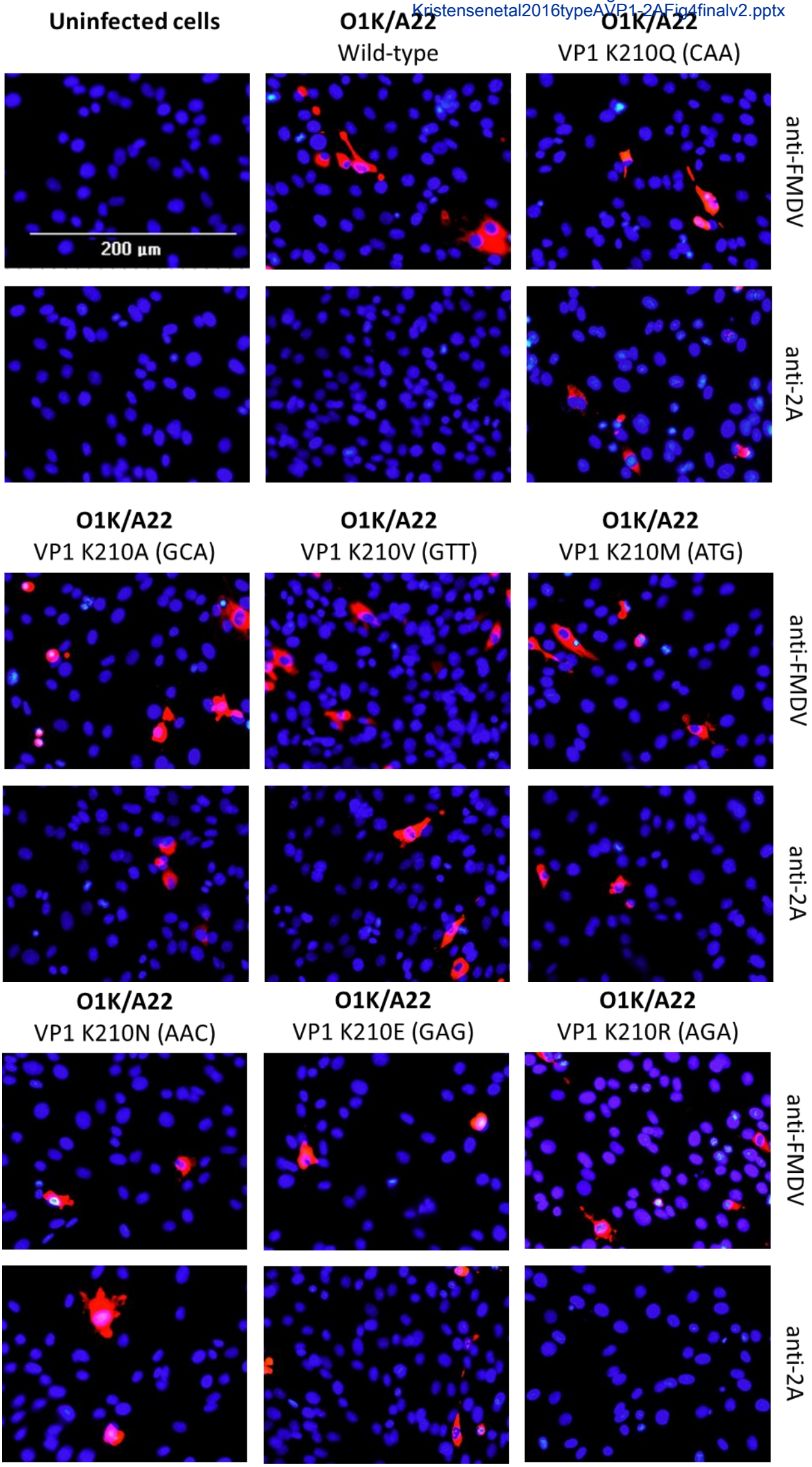

Figure 4

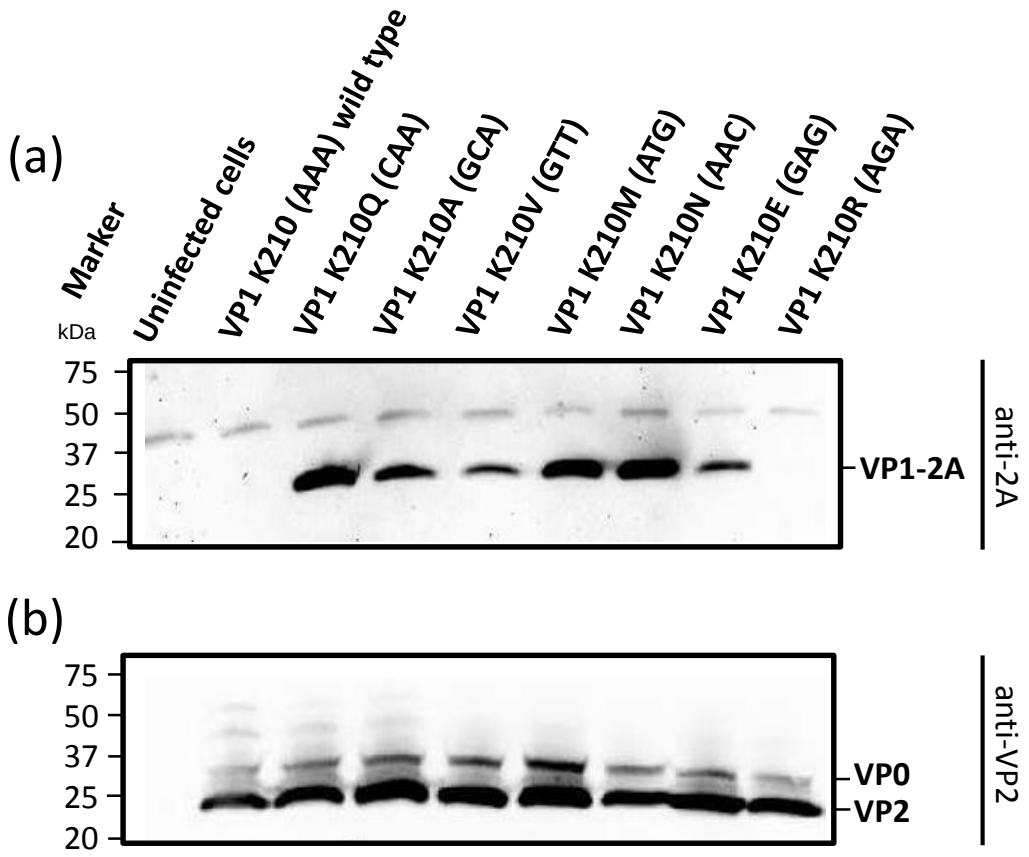

Fig. 5

Supplementary Table S1. Primers used for plasmid construction and cDNA synthesis

Primer name	Sequence (5´-3´)
FMDVA_*Nhe*IVP4VP2_Fw	CGCTCTGCTAGCCGATAAGAAGACCGAGGAGACCA
FMDVA_*Apa*I2A2B_Re	CTACTAGGGCCCGGGGTTGGACTCAACGTCTCCTG
FMDVA_2AL2P_Fw	CAACTT***CCA***AACTTCGATTTGCTCAAGTTGGCAGGAGAC
FMDVA_2AL2P_Re	GAAGTT***TGG***AAGTTGTTTTGCAGGTGCAATGATCTTCTG
FMDVA_VP1K210E_2AL2P_Re	GAAGTT***TGG***AAGTTGTT**C**TGCAGGTGCAATGATCTTCTG
13-N PN2	AAGTTTTACCGTCGTTCCCGACGTAAAAGGGAGGTAACCAC AAGCTTGAA
10-P PN 30	TCTGGACAGCACCTTTGTCG
8-A PN 200	GAGACGTTGAGTCCAACCC
13-N PN 3	CCGTAGGAGTGAAAATCCCGAAAGGGTTTTTCCCGCTTCCTT AATCCAAA
O1PN20	GACATGTCCTCCTGCATCTG
13LPN21	GCACCTGCA***NNN***CAACTTTTGAAC

[a] Underlined sequences represent restriction enzyme sites *NheI* and *ApaI*. Nucleotide changes producing amino acids substitutions are shown in boldface italics.