Crystal Structure of the Middle East Respiratory Syndrome Coronavirus (MERS-CoV) Papain-like Protease Bound to Ubiquitin Facilitates Targeted Disruption of Deubiquitinating Activity to Demonstrate Its Role in Innate Immune Suppression

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Background: MERS-CoV papain-like protease (PL(pro)) processes viral polyproteins and has deubiquitinating activity.

Results: A crystal structure of MERS-CoV PL(pro) bound to ubiquitin guided mutagenesis to disrupt PL(pro) deubiquitinating activity without affecting polyprotein cleavage. Our strategy to selectively disable PL(pro) deubiquitinating activity enables the study of its specific functions in infection.

Conclusion: The deubiquitinating activity of MERS-CoV PL(pro) suppresses the induction of interferon-beta (IFN-beta) expression.

Significance: Our strategy to selectively disable PL(pro) deubiquitinating activity enables the study of its specific functions in infection.

Middle East respiratory syndrome coronavirus (MERS-CoV) is a newly emerging human pathogen that was first isolated in 2012. MERS-CoV replication depends in part on a virus-encoded papain-like protease (PL(pro)) that cleaves the viral replicase polyproteins at three sites releasing non-structural protein 1 (nsp1), nsp2, and nsp3. In addition to this replicative function, MERS-CoV PL(pro) was recently shown to be a deubiquitinating enzyme (DUB) and to possess deISGylating activity, as previously reported for other coronaviral PL(pro) domains, including that of severe acute respiratory syndrome coronavirus (SARS-CoV). These activities have been suggested to suppress host antiviral responses during infection. To understand the molecular basis for ubiquitin (Ub) recognition and deconjugation by MERS-CoV PL(pro), we determined its crystal structure in complex with Ub. Guided by this structure, mutations were introduced into PL(pro) to specifically disrupt Ub binding without affecting viral polyprotein cleavage, as determined using an in trans nsp3 Δ 4 cleavage assay. Having developed a strategy to selectively disable PL(pro) DUB activity, we were able to specifically examine the effects of this activity on the innate immune response. Whereas the wild-type PL(pro) domain was found to suppress IFN-beta promoter activation, PL(pro) variants specifically lacking DUB activity were no longer able to do so. These findings directly implicate the DUB function of PL(pro), and not its proteolytic activity per se, in the inhibition of IFN-beta promoter activity. The ability to decouple the DUB activity of PL(pro) from its role in viral polyprotein processing now provides an approach to further dissect the role(s) of PL(pro) as a viral DUB during MERS-CoV infection.

The Middle East respiratory syndrome coronavirus (MERS-CoV) was first isolated in June 2012 from a patient in Saudi Arabia who had died from progressive respiratory and renal failure. Since then, over 800 cases have been reported, with a case fatality rate surpassing 30% (2). The progression and severity of the symptoms observed in MERS patients resemble the severe acute respiratory syndrome (SARS) observed in patients infected with SARS-CoV, which caused a global pandemic in 2003, resulting in over 8000 cases, with a case fatality rate of ~10% (3). Whereas the SARS-CoV outbreak was contained within months, MERS cases continue to occur 2 years after the emergence of MERS-CoV in the human population. Currently, dromedary camels are suspected to be one of the direct reservoirs for the zoonotic transmission of MERS-CoV, although the exact chain of transmission remains to be explored in more detail (4, 5). MERS-CoV and SARS-CoV are enveloped, positive-sense single-stranded RNA (+RNA) viruses that belong to the Betacoronavirus genus in the family Coronaviridae of the Nidovirales order (6). The CoV non-structural proteins (nsps), which...
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drive viral genome replication and subgenomic RNA synthesis, are encoded within a large replicase gene that encompasses the 5'-proximal three-quarters of the CoV genome. The replicase gene contains two open reading frames, ORF1a and ORF1b. Translation of ORF1a yields polyprotein 1a (pp1a), and -1 ribosomal frameshifting facilitates translation of ORF1b to yield pp1ab (7). The pp1a and pp1ab precursors are co- and post-translationally processed into functional nsps by multiple ORF1a-encoded protease domains. CoVs employ either one or two papain-like proteases (PL\textsuperscript{pro}s), depending on the virus species, to release nsp1, nsp2, and nsp3 and a chymotrypsin-like protease (3CL\textsubscript{pro}) that cleaves all junctions downstream of nsp4 (reviewed in Ref. 8). Comparative sequence analysis of the MERS-CoV genome and proteome allowed for the prediction and annotation of 16 nsps, along with the location of the probable proteolytic cleavage sites (6). The MERS-CoV PL\textsuperscript{pro} domain, which resides in nsp3, has recently been confirmed to recognize and cleave after the sequence LXGG at the nsp1 ↓ 2 and nsp2 ↓ 3 junctions, as defined previously for other CoV PL\textsuperscript{pro}s, as well as an LXGG sequence, which constitutes the nsp3 ↓ 4 cleavage site (9, 10).

These recognition sequences within pp1a/pp1ab resemble the C-terminal LRGG motif of ubiquitin (Ub), an 8.5-kDa protein that can be conjugated to lysine residues or the N terminus of target proteins as a form of post-translational modification through the action of the cellular E1/2/3 ligase system (reviewed in Ref. 11). Additional Ub molecules can be linked to any of the 7 lysine residues in Ub itself or to its N terminus to generate polyubiquitin (poly-Ub) chains of various linkage types (11). The best-studied linkages are the ones occurring at Lys\textsuperscript{48} of Ub, which results in the targeting of the tagged substrate to the 26 S proteasome for degradation, and at Lys\textsuperscript{63}, which generates a scaffold for the recruitment of cellular proteins to activate numerous signaling cascades, including critical antiviral and proinflammatory pathways (11). The C terminus of Ub can be recognized by deubiquitinating enzymes (DUBs), which catalyze the deconjugation of Ub, thus reversing the effects of ubiquitination (12). Interestingly, CoV PL\textsuperscript{pro}s, including those of MERS- and SARS-CoV, have been suggested to act as multifunctional proteases that not only cleave the viral polyproteins at internal LXGG cleavage sites but also remove Ub and the antiviral Ub-like molecule interferon-stimulated gene 15 (ISG15) from cellular proteins, presumably to suppress host antiviral pathways (9, 13–19).

Activation of antiviral and proinflammatory pathways is a critical first line of defense against virus infections, including those caused by nidoviruses. Viral RNA molecules are recognized by pattern recognition receptors, such as the cytoplasmic RIG-I-like receptors (RLRs) RIG-I and MDA5, which are activated by intracellular viral RNA transcripts bearing 5’-tri- and diphosphates and double-stranded RNA (dsRNA) replication intermediates, respectively (20, 21). Upon their stimulation, RLRs signal through the mitochondrial antiviral signaling protein (MAVS), leading to the formation of a signaling complex at the mitochondrial membrane and ultimately to the activation of transcription factors IRF-3 and NF-κB. These transcription factors in turn regulate the expression of antiviral type I interferons (IFN), including IFN-β, which acts through autocrine and paracrine receptor-mediated signaling pathways to induce the transcription of numerous interferon-stimulated genes (ISGs) that will interfere with virus replication as well as proinflammatory cytokines, such as IL-6, IL-8, and TNF-α. Regulation of the antiviral and proinflammatory pathways is largely Ub-dependent, because multiple factors in the innate immune cascade are ubiquitinated, including RIG-I, which is critical for downstream signaling. Cellular DUBs function to prevent excessive inflammation and immune responses during infection by removal of Ub from innate immune factors (reviewed in Ref. 22).

The DUB activities of MERS- and SARS-CoV PL\textsuperscript{pro}s have been implicated in the suppression of host antiviral pathways because these proteases can suppress IFN-β induction upon their ectopic expression (9, 13, 15, 16, 19, 23). Previous work has shown that during infection, SARS-CoV indeed suppresses the host’s antiviral responses by preventing the induction of IFN-β expression in cell culture (24–26). Similarly, MERS-CoV infection has been found to elicit a poor type-1 IFN response in cultured monocyte-derived dendritic cells (27) and alveolar epithelial A549 cells (28) as well as ex vivo in bronchial and lung tissue samples (28). Furthermore, delayed induction of proinflammatory cytokines in human airway epithelial cells infected with MERS-CoV has been reported (29).

Although the above observations suggest that MERS- and SARS-CoV actively suppress antiviral responses, such as IFN-β production and inflammation, they do not directly implicate the DUB activity of PL\textsuperscript{pro} as being responsible for (part of) this suppression. Due to the dependence of MERS-CoV replication on the ability of PL\textsuperscript{pro} to cleave the nsp1–nsp3 region of the replicase polyproteins, studying the role of PL\textsuperscript{pro} DUB activity, specifically in the suppression of the cellular innate immune response, is difficult because both activities depend on the same enzyme active site. Selective inactivation of only the DUB activity of PL\textsuperscript{pro} would enable the study of how this activity alone affects cellular signaling; however, achieving this requires detailed information on the structural basis of Ub recognition and deconjugation by PL\textsuperscript{pro}. To this end, we determined the crystal structure of MERS-CoV PL\textsuperscript{pro} bound to Ub to elucidate the molecular determinants of Ub recognition. Based on the structure of this complex, mutations were introduced that selectively disrupted Ub recognition by targeting regions of the Ub-binding site on PL\textsuperscript{pro} that were sufficiently distant from the active site of the protease. Using this approach, we were able to remove the DUB activity from PL\textsuperscript{pro} without affecting its ability to cleave the nsp3 ↓ 4 cleavage site in trans. This enabled us, for the first time, to demonstrate that the DUB activity of MERS-CoV PL\textsuperscript{pro} can suppress the MAVS-mediated induction of IFN-β expression.

EXPERIMENTAL PROCEDURES

Cells, Antibodies, and Plasmids—HEK293T cells were cultured in Dulbecco’s modified Eagle’s medium (DMEM) supplemented with 10% fetal calf serum (FCS; Bodinco BV), 100 units/ml penicillin, 100 units/ml streptomycin, and 2 mM L-glutamine (cell culture medium and supplements were obtained from Lonza).

Primary antibodies used were mouse anti-HA (ab18181; Abcam), mouse anti-V5 (37-7500; Invitrogen), mouse anti-β-actin (A5316; Sigma-Aldrich), mouse anti-FLAG (F3165;
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Sigma-Aldrich), and rabbit anti-GFP (30). As secondary antibodies, horseradish peroxidase (HRP)-conjugated antibodies were used (P0447 and P0217; Dako).

The following plasmids were described elsewhere: pASK3 (31), pcDNA-eGFP (30), pCMV-FLAG-UB (32), pLuc-IFN-β (33), pEG-F-RIG-I (34), pcDNA-FLAG-MAVS (35), and pEGFP-C1-IRF3 (36).

Construction of MERS-CoV PLpro Expression Plasmids—A cDNA fragment encoding the PLpro domain (amino acids 1479–1803 of the MERS-CoV pp1a/pp1ab) was amplified from cDNA using standard methodologies. The following expression constructs were generated: pCAGGS-HA-nsp3-4-V5 (amino acids 854–3246), pCAGGS-HA-nsp3C-4-V5 (amino acids 1480–1803), and pCAGGS-HA-nsp3C-4-V5 (amino acids 1480–1803). Expression and Purification of MERS-CoV PLpro for Crystallization—E. coli BL21(DE3) GOLD cells harboring pE-SUMO-PLpro were grown at 37 °C with aeration in 500 ml of lysogeny broth containing kanamycin (35 μg/ml) to an A600 of 0.6–0.8. Expression of the His6-SUMO-PLpro fusion protein was then induced by the addition of 1 mM isopropyl β-D-1-thiogalactopyranoside for 18 h at 16 °C with aeration. Cells were pelleted by centrifugation and stored at −80 °C.

Cell pellets were resuspended in ice-cold lysis buffer (150 mM Tris, pH 8.5, 1 mM NaCl, 0.1 mM phenylmethylsulfonyl fluoride (PMSF), 2 mM DTT) and lysed using a French pressure cell (AMINCO). Cell lysis was clarified by centrifugation (17,211 × g for 4 °C), and the supernatant containing the His6SUMO-PLpro fusion was applied to a column containing nickel-nitriolotriacetic acid affinity resin (Qiagen). The column was washed with 10 column volumes of lysis buffer supplemented with 25 mM imidazole, followed by elution of the fusion protein with lysis buffer containing 250 mM imidazole. The His6SUMO tag was then removed from PLpro by adding His6-tagged Ulp1 SUMO protease to the eluted SUMO-PLpro fusion, followed by dialysis of the protein mixture overnight against 2 liters of cleavage buffer (150 mM NaCl, 50 mM Tris, pH 8.0, 1 mM DTT) at 4 °C. Tag-free PLpro was then separated from His6SUMO and the His6-Ulp1 SUMO protease by passing the dialyzed protein mix through a nickel-nitriolotriacetic acid gravity column. The flow-through contained purified PLpro that was subsequently dialyzed against 20 mM HEPES, pH 7.0, 200 mM NaCl, 10% (v/v) glycerol, and 0.1 mg/ml lysozyme, and lyzed for 1 h at 4 °C, followed by sonication. The lysate was clarified by centrifugation at 20,000 × g for 20 min at 4 °C, and the soluble fraction was applied to Talon resin (GE Healthcare) pre-equilibrated with lysis buffer. After a 2-h rolling incubation at 4 °C, the beads were washed four times with wash buffer (20 mM HEPES, pH 7.0, 200 mM NaCl, 10% (v/v) glycerol, and 20 mM imidazole), followed by the elution of the protein with elution buffer (20 mM HEPES, pH 7.0, 200 mM NaCl, 10% (v/v) glycerol, and 250 mM imidazole). Eluted protein was dialyzed against storage buffer (20 mM HEPES, pH 7.0, 100 mM NaCl, 50% (v/v) glycerol, 2 mM dithiothreitol (DTT)) and stored at −80 °C. N-terminal Ub is cleaved from the Ub-PLpro-His6 fusion protein by the PLpro domain itself during expression. To achieve removal of the Ub from mutated and/or inactive PLpro, E. coli strain C2523 containing pCG1, expressing the ubiquitin-specific processing protease 1 (Ubp1), was used (37).

In vitro DUB activity assays were performed as described by van Kasteren et al. (30). Briefly, the indicated amounts of purified MERS-CoV PLpro wild type or active site mutant (C1592A) were incubated with 2.5 μg of either Lys48-linked poly-Ub chains or Lys63-linked poly-Ub chains (Boston Biochem) in a final volume of 10 μl. Isopeptidase T (Boston Biochem) served as a positive control. After a 2-h incubation at 37 °C, the reaction was stopped by the addition of 4X Laemmli sample buffer (4X Laemmli, 500 mM Tris, 4% SDS, 40% glycerol, 0.02% bromphenol blue, 2 mM DTT, pH 6.8). SDS-polyacrylamide gels were stained with Coomassie Brilliant Blue (Sigma-Aldrich) and scanned using a GS-800 calibrated densitometer (Bio-Rad).

Expression and Purification of MERS-CoV PLpro for Crystallization—E. coli BL21(DE3) GOLD cells harboring pE-SUMO-PLpro were grown at 37 °C with aeration in 500 ml of lysogeny broth containing kanamycin (35 μg/ml) to an A600 of 60.6–0.8. Expression of the His6-SUMO-PLpro fusion protein was then induced by the addition of 1 mM isopropyl β-D-1-thiogalactopyranoside for 18 h at 16 °C with aeration. Cells were pelleted by centrifugation and stored at −80 °C.

Covalent Coupling of Ub to PLpro—Ub(1–75)-3-bromopropylamine (Ub-3Br) is a modified form of Ub with a reactive C

MERS-CoV PLpro and pcDNA3.1-MERS-CoV-PLpro sequence encoding a His6-SUMO purification tag, which facil-

ated purification of the product by immobilized metal (nickel) affinity chromatography as described below.

To obtain high expression in eukaryotic cells, the sequence of MERS-CoV nsp3–4 (amino acids 854–3246) was PCR-amplified, cloned downstream of the T7 promoter of expression vector pE-SUMO (LifeSensors), and used to transform Escherichia coli BL21 (DE3) GOLD cells (Stratagene) grown under kanamycin selection (35 μg/ml). Recombinant expression plasmid (pE-SUMO-PLpro) was isolated from a single colony, and DNA sequencing confirmed the expected sequence of the PLpro domain and the in-frame fusion of the 5'-end to a C-terminal His6 purification tag to produce pASK-MERS-CoV-PLpro.

Using standard methodologies, the sequence encoding amino acids 1480–1803 of MERS-CoV pp1a/pp1ab was PCR-amplified, cloned downstream of the T7 promoter of expression vector pE-SUMO (LifeSensors), and used to transform Escherichia coli BL21 (DE3) GOLD cells (Stratagene) grown under kanamycin selection (35 μg/ml). Recombinant expression plasmid (pE-SUMO-PLpro) was isolated from a single colony, and DNA sequencing confirmed the expected sequence of the PLpro domain and the in-frame fusion of the 5'-end to a C-terminal His6 purification tag, which facilitated purification of the product by immobilized metal (nickel) affinity chromatography as described below.

To obtain high expression in eukaryotic cells, the sequence of MERS-CoV nsp3–4 (amino acids 854–3246) was flanked by an N-terminal HA tag and a C-terminal V5 tag was optimized based on the human codon usage frequency, and potential splice sites and polyadenylation signals were removed. This sequence was synthesized (Invitrogen) and subsequently amplified, cloned downstream of the T7 promoter of expression vector pE-SUMO (LifeSensors), and used to transform Escherichia coli BL21 (DE3) GOLD cells (Stratagene) grown under kanamycin selection (35 μg/ml). Recombinant expression plasmid (pE-SUMO-PLpro) was isolated from a single colony, and DNA sequencing confirmed the expected sequence of the PLpro domain and the in-frame fusion of the 5'-end to a C-terminal His6 purification tag, which facilitated purification of the product by immobilized metal (nickel) affinity chromatography as described below.

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Table 1
Crystallographic statistics for MERS-CoV PLpro and PLpro-Ub structures

<table>
<thead>
<tr>
<th>Crystal geometry</th>
<th>PLpro</th>
<th>Open PLpro-Ub</th>
<th>Closed PLpro-Ub</th>
</tr>
</thead>
<tbody>
<tr>
<td>Space group</td>
<td>P6₁</td>
<td>P6₁</td>
<td>P6₁</td>
</tr>
<tr>
<td>Unit cell (Å)</td>
<td>a = b = 137.94 c = 57.70; α = β = γ = 90°</td>
<td>a = b = 136.77 c = 57.99; α = β = γ = 90°</td>
<td>a = b = 176.92 c = 84.55; α = β = γ = 90°</td>
</tr>
<tr>
<td>Resolution range (Å)</td>
<td>4.55–2.60 (2.20–2.80)</td>
<td>4.23–2.15 (2.22–2.15)</td>
<td>4.24–2.60 (2.90–2.80)</td>
</tr>
<tr>
<td>Wavelength (Å)</td>
<td>1.28294</td>
<td>1.28280</td>
<td>1.2819</td>
</tr>
<tr>
<td>Multiplicity</td>
<td>8.7 (8.8)</td>
<td>3.7 (3.7)</td>
<td>14.4 (14.7)</td>
</tr>
<tr>
<td>Completeness (%)</td>
<td>100.00 (100.00)</td>
<td>98.73 (98.12)</td>
<td>99.97 (100)</td>
</tr>
<tr>
<td>Anomalous completeness</td>
<td>99.8 (98.5)</td>
<td>92.4 (92.6)</td>
<td>100 (100)</td>
</tr>
<tr>
<td>Kmin</td>
<td>0.085 (0.76)</td>
<td>0.041 (0.79)</td>
<td>0.061 (0.78)</td>
</tr>
<tr>
<td>CC1/2</td>
<td>0.99 (0.54)</td>
<td>1 (0.93)</td>
<td>1 (0.98)</td>
</tr>
<tr>
<td>I/σl</td>
<td>17.13 (3.42)</td>
<td>20.52 (1.97)</td>
<td>34.01 (3.69)</td>
</tr>
<tr>
<td>Wilson B-factor (Å²)</td>
<td>75.15</td>
<td>46.79</td>
<td>74.96</td>
</tr>
<tr>
<td>Figure of merit</td>
<td>0.12</td>
<td>0.18</td>
<td>0.23</td>
</tr>
<tr>
<td>Figure of merit after RESOLVE</td>
<td>0.64</td>
<td>0.63</td>
<td>0.67</td>
</tr>
</tbody>
</table>

Phasing statistics

| Reflections in test set | 1570 | 1996 | 1609 |
| Protein atoms | 2384 | 3020 | 3020 |
| Zn atoms | 1 | 1 | 1 |
| Solvent molecules | 26 | 205 | 65 |
| Rmerge | 0.23 (0.27) | 0.20 (0.23) | 0.24 (0.28) |
| Rfree | 0.002/0.60 | 0.002/0.52 | 0.002/0.54 |
| Average B-factor (Å²) | 95/5 | 95/5 | 93/7 |
| R-factor for macromolecules | 76.70 | 66.80 | 86.50 |
| R-factor for solvent | 76.70 | 69.20 | 86.60 |

Ramachandran plot

- Favorable/allowed (%) | 95/5 | 95/5 | 93/7 |
- Average B-factor (Å²) | 76.70 | 66.80 | 86.50 |
- B-Factor for macromolecules | 76.70 | 69.20 | 86.60 |
- B-Factor for solvent | 76.65 | 65.40 | 84.20 |

*Values in parentheses refer to the highest resolution shell.

terminus that forms an irreversible covalent linkage to the active site cysteine of DUBs and was prepared according to Messick et al. (38) and Borodovsky et al. (39). Purified PLpro was incubated with a 2-fold molar excess of Ub-3Br and incubated for 1 h at room temperature with end-over-end mixing. The resulting PLpro-Ub complex was dialyzed into 20 mM Tris, pH 8.5, 150 mM NaCl, 2 mM DTT, and excess Ub-3Br was removed by gel filtration using a Superdex 75 column.

Crystallographic data

Crystal PLpro (P6₁), open PLpro (P6₁), and closed PLpro (P6₁) were cryoprotected in 1.85 M AmSO₄, 15% glycerol and 22% PEG 4000, 0.1 M trisodium citrate, pH 5.6, 10% 1,2-propanediol respectively, before flash cooling in liquid nitrogen.

Data Collection and Structure Determination—X-ray diffraction data were collected from all crystals at the Zn-K absorption edge at beamline 08B1-1 of the Canadian Light Source and integrated using XDS (40). Integrated data were then scaled using Scala (41). Initial phase estimates for reflections collected from unliganded and Ub-bound PLpro were determined via a single wavelength anomalous dispersion experiment. The position of the zinc anomalous scatterer was identified using HySS (42), and density modification was performed with RESOLVE (43) within the phenix.autosol pipeline (44). Initial models were constructed using phenix.autobuild, and further model building and refinement were carried out using Coot (45) and phenix.refine (46). Crystallographic statistics for all structures are found in Table 1.

Protease Activity Assays in Cell Culture—HEK293T cells, grown to 80% confluence in 12-well plates, were transfected using the calcium phosphate transfection method (47). To determine the DUB activity of MERS-CoV PLpro, plasmids encoding FLAG-tagged Ub (0.25 µg), GFP (0.25 µg), and MERS-CoV-PLpro-V5 (0.15 µg) were co-transfected. A combination of plasmids encoding GFP (0.25 µg), HA-nsp3C-4-V5 (0.2 µg), and MERS-CoV-PLpro-V5 (0.15 µg) were assayed to assess the in trans cleavage activity of MERS-CoV-PLpro. Total amounts of transfected DNA were equalized to 2 µg by the addition of empty pcDNA vector. At 18 h post-transfection, cells were lysed in 2X LSB. Proteins were separated in an SDS-PAGE using Coo electrophoresis.
polyacrylamide gel and blotted onto Hybond-P (GE Healthcare) using the Trans-blot turbo transfer system (Bio-Rad). Aspecific binding to the membrane was blocked with dried milk powder solution, and after antibody incubation, protein bands were visualized using Pierce ECL 2 Western blotting substrate (Thermo Scientific).

Luciferase-based IFN-β Reporter Assay—Using the calcium phosphate method, 80% confluent HEK293T cells in 24-well plates were transfected with 5 ng of plasmid pRL-TK (Promega) encoding Renilla luciferase; IFN-β-Luc firefly reporter plasmid (25 ng); innate immune response inducer plasmids encoding RIG-I(2CARD), MAVS, or IRF3(5D) (25 ng); and the indicated quantities of MERS-CoV PLpro or MERS-CoV nsp3-encoding expression plasmids. Total amounts of transfected DNA were equalized to 1 μg by the addition of empty pcDNA vector. At 16 h post-transfection, cells were lysed in 1× passive lysis buffer (Promega). Firefly and Renilla luciferase activity was measured using the Dual-Luciferase reporter assay system (Promega) on a Mithras LB 940 multimode reader (Berthold Technologies). Experiments were performed in triplicate and independently repeated at least four times. Firefly luciferase activity was normalized to Renilla luciferase, and statistical significance was determined using an unpaired two-tailed Student’s t test. Values of <0.05 were considered statistically significant. 4× LSB was added to the remaining lysates, and these samples were analyzed by Western blotting as described above.

RESULTS

DUB Activity of Recombinant MERS-CoV PLpro

It was recently shown in cell culture experiments that ectopic expression of MERS-CoV PLpro resulted in deconjugation of poly-Ub and ISG15 from cellular targets (9, 16). DUB activity of purified recombinant MERS-CoV PLpro was also demonstrated using Ub-7-amino-4-trifluoromethylcoumarin (48) or Ub-7-amino-4-methylcoumarin (49) as a substrate. To characterize the direct activity of recombinant MERS-CoV PLpro toward poly-Ub, we purified the enzyme from E. coli and incubated it with either Lys48-linked or Lys63-linked poly-Ub chains. Wild-type PLpro degraded both Lys48-linked and Lys63-linked poly-Ub chains in a concentration-dependent manner, whereas mutating the active site nucleophile (C1592A) severely reduced the activity of the enzyme toward both Ub linkage types (Fig. 1). No clear preference of the enzyme for cleaving either the Lys63 or the Lys48 Ub linkage was observed under the conditions used in this in vitro DUB assay (Fig. 1, compare A and B). This assay clearly demonstrated that the protease domain used throughout this study for ectopic expression and crystallization experiments possesses DUB activity toward Lys48- and Lys63-linked Ub chains and that this activity does not require other viral or cellular proteins. During the preparation of this manuscript, an article by Báez-Santos et al. (50) was published in which similar results were presented.

Crystal Structures of MERS-CoV PLpro and PLpro-Ub Complexes

MERS-CoV PLpro—The crystal structure of PLpro was determined both on its own and as a covalent complex with Ub (PLpro-Ub). The PLpro domain crystallized in space group P63, and consistent with another recently determined crystal structure of MERS-CoV PLpro (49), we found the protease to adopt a fold consistent with DUBs of the ubiquitin-specific protease (USP) family. The structure includes a C-terminal catalytic domain containing a right-handed fingers, palm, and thumb domain organization as well as an N-terminal Ub-like (Ubl) domain found in many USPs, including that of SARS-CoV (51, 52) (Fig. 2A). The packing of the palm and thumb domains forms a cleft leading into the active site in a manner consistent with the domain organization prototyped by the Clan CA group of cysteine proteases (53). The Ubl domain packs against the thumb domain composed of helices α2–7, which in turn packs against the palm domain composed of strands β6, β7, and β14–19. Extending from the palm, the fingers domain is composed of strands β10, β11, β13, β14, and β19 and contains a C9 zinc ribbon motif (54) coordinating a zinc atom via residues Cys1675, Cys1677, Cys1707, and Cys1709 in tetrahedral geometry, similar to that of SARS PLpro, transmissible gastroenteritis coronavirus (PLpro), and cellular USP2 and USP21 (51, 55–57).

PLpro Covalently Bound to Ub—The MERS-CoV PLpro-Ub complex crystallized in two different space groups (P63 and P6522), which revealed a considerable level of conformational flexibility in the protein. Electron density maps calculated using diffraction data collected from PLpro-Ub complex that crystal-
lized in space group P6₃ revealed weak density for the covalently bound Ub molecule. Although the entire bound Ub molecule could be modeled within its binding site on PLₚro in this crystal form, high temperature factors for atoms comprising the modeled Ub molecule suggested that it was not rigidly bound to the protease despite being covalently linked to the active site cysteine. Further analysis of the crystal packing revealed that the Ub molecule was fully exposed to solvent and not involved in crystal contacts, which provided a degree of mobility to Ub when bound to PLₚro (Fig. 3A). This result

FIGURE 2. MERS-CoV PLₚro and PLₚro-Ub structures. A, structure of the MERS-CoV PLₚro domain (2.15 Å resolution). The palm, thumb, fingers, and N-terminal ubiquitin-like (Ubl) domains are indicated by colored panels, and arrows indicate the active site and C₄ zinc ribbon motif. The active site residues are depicted as sticks. B, structure of the MERS-CoV PLₚro bound to Ub (2.8 Å resolution). PLₚro-Ub is shown in green, and the covalently bound Ub molecule is orange and shown as tubes. Active site residues are shown as sticks with Gly⁷⁵ and the 3CN linker of Ub covalently linked to Cys¹⁵⁹² of PLₚro. C, superposition showing a ~6.8-Å movement of the zinc ribbon motif between the open (yellow) and closed (green) PLₚro-Ub structures and a previously reported PLₚro structure (gray) (Protein Data Bank entry 4P16 (49)). Our PLₚro structure is not shown because it is highly similar to the open PLₚro-Ub structure. Movement of the zinc ribbon motif was determined by measuring the distance between the zinc atom of the respective structures. Superpositions were performed in Coot (45). Ub was removed from the closed and open PLₚro-Ub structures for clarity. Figures were created using PyMOL (70).

FIGURE 3. Crystal packing arrangement of the open and closed MERS-CoV PLₚro-Ub structures. The contents of four unit cells are shown, with PLₚro and Ub depicted in gray and orange, respectively. A, the open PLₚro-Ub structure crystallized in space group P6₃, where Ub was found to face the solvent, uninformed in crystal contacts. B, the closed PLₚro-Ub structure crystallized in space group P6₃,22, where Ub no longer faces the solvent, and is involved in crystal contacts. Images were created using PyMOL (70).
encouraged us to pursue additional crystallization conditions, which yielded crystals of PL\textsuperscript{pro}-Ub in space group P6\textsubscript{3}22 (Figs. 2B and 3B). The crystal packing in this space group allowed for multiple crystal contacts between the bound Ub monomer and surrounding symmetry mates and resulted in clear, well-defined density for the Ub molecule (Fig. 3B). Interestingly, relative to the P6\textsubscript{3} crystal forms of PL\textsuperscript{pro}, the fingers domain in this crystal form was moved toward Ub (Fig. 2C). In light of these movements, the PL\textsuperscript{pro}-Ub structure with the fingers domain positioned away from Ub (space group P6\textsubscript{3}) will hereafter be referred to as “open” PL\textsuperscript{pro}-Ub, whereas the structure with the fingers domain shifted toward Ub (space group P6\textsubscript{3}22) will be referred to as “closed” PL\textsuperscript{pro}-Ub. An overlay of the different PL\textsuperscript{pro} crystal structures that have been determined reveals that these structures vary in the position of the zinc ribbon motif, further suggesting a high degree of mobility for this region (Fig. 2C). In line with this observation, movement of the fingers domain toward bound Ub was also reported for the SARS-CoV PL\textsuperscript{pro} domain, which displayed a 3.8-Å movement of the zinc atom when comparing the Ub-bound and unbound structures (58). Further comparison of the closed MERS-CoV PL\textsuperscript{pro}-Ub structure with the recently determined SARS-CoV PL\textsuperscript{pro}-Ub structure (58) revealed differences in the relative orientation of the fingers domain of the two proteases. The MERS-CoV PL\textsuperscript{pro} fingers domain was found to be shifted ~26° away from the palm domain compared with that of SARS-CoV PL\textsuperscript{pro}, resulting in a slight difference in the Ub binding orientation, with the MERS-CoV PL\textsuperscript{pro}-bound Ub being positioned closer toward helix α7 of the palm domain (Fig. 4).

**PL\textsuperscript{pro} Active Site Organization and Interaction with the C-terminal RLRGG Motif of Ub**

The cleft formed between the palm and thumb domains of PL\textsuperscript{pro} guides the C-terminal \textsuperscript{272}RLRGGE\textsuperscript{346} motif of Ub toward the protease active site, and the interactions between the C-terminal motif of Ub and the active site cleft are depicted in Fig. 5 (A and B). The PL\textsuperscript{pro} active site is composed of a Cys\textsuperscript{1592}-His\textsuperscript{1759}-Asp\textsuperscript{1774} catalytic triad, which adopts a catalytically competent arrangement in both the unliganded and Ub-bound structures of PL\textsuperscript{pro} (Fig. 5C). The oxyanion hole of the PL\textsuperscript{pro} active site appears to be composed of backbone amides from residues Asn\textsuperscript{1590}, Asn\textsuperscript{1591}, and Cys\textsuperscript{1592}, which appear suitably arranged to stabilize the negative charge that develops on the carbonyl oxygen of the scissile bond during catalysis (Fig. 5C). Interestingly, as noted by Lei et al. (49), the MERS-CoV PL\textsuperscript{pro} active site appears incomplete. In SARS-CoV PL\textsuperscript{pro}, Trp\textsuperscript{107} (amino acid numbering according to the structure of Protein Data Bank entry 2FE8) is positioned within the enzyme’s active site with the indole nitrogen of its side chain oriented such that it is probably involved in forming part of the oxyanion hole (51). In the case of MERS-CoV PL\textsuperscript{pro}, we and others (48, 49) have found the structurally equivalent residue in MERS-CoV PL\textsuperscript{pro} to be Leu\textsuperscript{1587}; which would be unable to participate in stabilizing the oxyanion during catalysis. Furthermore, it was recently shown that MERS-CoV PL\textsuperscript{pro} L1587W mutants show greater catalytic efficiency than wild-type PL\textsuperscript{pro} (48, 49). Given the effect this residue has on the catalytic rate of PL\textsuperscript{pro}, it will be very interesting to understand how this residue influences MERS-CoV replication kinetics. It has been proposed that the decreased catalytic efficiency may influence maturation of the MERS-CoV polyprotein (48) and could be involved in the recognition of residues downstream of the scissile bond of the polyprotein cleavage sites or in the modulation of PL\textsuperscript{pro} DUB activity.

Interestingly, differences were observed in the position of a loop on PL\textsuperscript{pro} connecting strands β15 and β16, which is structurally analogous to the blocking loop (BL2) first described in the structure of USP14 (59). This loop is disordered in our unliganded PL\textsuperscript{pro} structure and that previously determined by others (49); however, in both of our PL\textsuperscript{pro}-Ub structures, we found this loop to be fully resolved, supported by the main-chain hydrogen-bonding interactions between Arg\textsuperscript{74} of Ub and Gly\textsuperscript{1750} of PL\textsuperscript{pro}, as well as a hydrophobic interaction between Val\textsuperscript{1757} and Pro\textsuperscript{1643}, two PL\textsuperscript{pro} residues present on opposite sides of the active site cleft (Fig. 5A). The side-chain η-amino group of the Ub residue Arg\textsuperscript{74} is also hydrogen-bonded to the main-chain carbonyl group of PL\textsuperscript{pro} residue Thr\textsuperscript{1755}; however, this interaction is only seen in the open PL\textsuperscript{pro}-Ub structure. The
Structure-guided Design of PLpro Mutants Defective in DUB Activity

We previously demonstrated that the DUB activity of the papain-like protease 2 (PLP2) from equine arteritis virus (another member of the nidovirus order), which resembles the ovarian tumor (OTU) domain-containing family of DUBs (60), could be selectively removed without affecting its ability to process the equine arteritis virus replicase polyprotein. This allowed us to establish that the DUB activity of PLP2 is directly responsible for suppressing Ub-dependent antiviral pathways during infection of primary host cells (61). Subsequently, Ratia et al. (62) applied a similar strategy to the SARS-CoV PLpro domain in order to partially remove the DUB activity of PLpro while maintaining the nsp2-3-processing function. We now used the crystal structure of the USP-like MERS PLpro-Ub complex to guide the design of mutations targeting the Ub-binding site on PLpro that would completely disrupt Ub binding without affecting the structural integrity of the active site. PLpro residues interacting directly with Ub were replaced with larger, bulkier residues that would prevent Ub binding by altering both shape and surface electrostatics of the Ub-binding site. Individual mutation of eight different PLpro residues (Arg1649, Thr1653, Ala1656, Asn1673, Val1674, Val1691, Val1706, and Gln1708) and combinations thereof were generated (Fig. 6, A–D). Importantly, these residues are located at a distance from the PLpro active site, and thus we hypothesized that they would only participate in DUB activity and not polyprotein processing.

Despite significant movement within the fingers domain of PLpro, most interactions between the protease and Ub are consistent between the open and closed Ub-bound complexes. Residue Ile44 of Ub, which forms part of the hydrophobic patch that is commonly recognized by Ub-binding proteins (63), interacts with the hydrophobic side chain of Val1691 of PLpro (Fig. 6B). Residues Gln9 and Glu53 of Ub form hydrophobic-bonding interactions with Thr1653 that is present on helix a7, which runs through the center of PLpro. Two arginine residues, Arg1649 of PLpro and Arg72 of Ub (the latter of which forms part of the C-terminal tail of Ub that is bound in the PLpro active site cleft) are oriented such that the guanidinium groups of these residues are arranged in a stacked conformation (Fig. 6C). In addition, due to the inward movement toward Ub of the closed PLpro-Ub fingers domain, a unique hydrophobic-bonding interaction between Gln62 of Ub and Gln1708 of PLpro and a hydrophobic interaction between Phe4 of Ub and Val1706 of PLpro...
were found to occur in this complex (Fig. 6D). Residue Ala^{1656} is positioned near the C terminus of PL^{pro} helix α7, and although it is not directly involved in Ub binding, we believed that it was positioned such that the introduction of larger residues (e.g. arginine or phenylalanine) could disrupt Ub recognition, and thus this residue was targeted for mutation (Fig. 6C). Two residues on the solvent-facing region of the PL^{pro} zinc ribbon motif, Asn^{1673} and Val^{1674}, were also targeted for mutagenesis. Although they do not bind Ub at the S1 binding site (the sub-strate binding site on PL^{pro} responsible for binding mono(Ub) in our structure; see Ref. 64 for nomenclature), we hypothesized that it may inhibit association with the distal Ub on Lys^{63} poly-Ub chains based on a superposition of a Lys^{63}-linked di-Ub model onto the PL^{pro}-bound Ub molecule of the closed PL^{pro}-Ub complex structure determined here (not shown). In addition, the crystal structure of USP21 bound to linear di-Ub was recently determined and revealed that the tip of the fingers domain of this DUB acts as an S2 recognition site, binding to the distal Ub of a linear di-Ub molecule (57). Given the structural similarity between Lys^{63} di-Ub and linear di-Ub and the clear activity we observed for MERS-CoV PL^{pro} toward Lys^{63}, we hypothesized that mutating residues Asn^{1673} and Val^{1674} near the zinc ribbon may also disrupt Ub processing.

**Targeted Mutations within the PL^{pro}-Ub Binding Site Disrupt Ub Processing but Not Proteolytic Cleavage of the nsp3 \( \downarrow \) 4 Site**

Using a previously described ectopic expression assay (61), we monitored the effects of amino acid substitutions in PL^{pro}, as described above, on overall levels of Ub-conjugated proteins in HEK293T cells as well as the ability of these PL^{pro} variants to process the MERS-CoV nsp3 \( \downarrow \) 4 polypeptide cleavage site in trans. V5-tagged PL^{pro} (wild type and mutants) was co-expressed with N-terminally HA-tagged and C-terminally V5-tagged MERS-CoV nsp3C-4 excluding the PL^{pro} domain, hereafter referred to as HA-nsp3C-4-V5. We assume that the successful processing of the nsp3 \( \downarrow \) 4 site in HA-nsp3C-4-V5 is indicative of unaltered proteolytic cleavage capability of PL^{pro}, which during infection facilitates the release of nsp1, -2, and -3 from the viral polyproteins. Processing of HA-nsp3C-4-V5 in trans by wild-type PL^{pro} and our panel of mutants was visualized via Western blotting (Fig. 7A). Whereas wild-type PL^{pro} was able to cleave HA-nsp3C-4-V5 substrate in trans, the PL^{pro} active site mutant C1592A was unable to cleave the nsp3 \( \downarrow \) 4 site (Fig. 7A, compare lanes 5 and 6 and lanes 19 and 20). As expected, each of the substitutions in the Ub-binding site of PL^{pro} only minimally affected nsp3 \( \downarrow \) 4 cleavage, with the exception of the A1656R mutant that displayed a clearly reduced ability to cleave HA-nsp3C-4-V5 compared with wild-type PL^{pro} (Fig. 7A, compare lanes 5 and 10). This suggests that Ala^{1656} of PL^{pro} may be involved in recognizing and binding sequences in the vicinity of the nsp3 \( \downarrow \) 4 cleavage site. Most double and triple substitutions tested were also slightly less efficient in cleaving HA-nsp3C-4-V5 compared with the wild-type control.

In order to analyze the effect of the mutations on overall DUB activity, PL^{pro}-V5 was co-expressed with FLAG-Ub, and the levels of FLAG-Ub-conjugated cellular proteins were visualized via Western blotting (Fig. 7B). Expression of wild-type PL^{pro} resulted in a strong decrease of the accumulation of FLAG-Ub conjugates, whereas a negligable effect was observed upon expression of active site mutant C1592A (Fig. 7B, compare lanes 3 and 4 and lanes 16 and 17). Substitutions of residue Val^{1691}, positioned on strand β12 of PL^{pro}, and Thr^{1653} and Ala^{1656}, residues located on helix α7 (Fig. 6, B and C), displayed the clearest reduction of PL^{pro} DUB activity (Fig. 7B, lanes 5–8). The V1691R mutation had the most pronounced effect, and a PL^{pro} T1653R/V1691R double mutant also displayed severely reduced DUB activity, comparable with that seen for the active site mutant (Fig. 7B, compare lanes 4 and 5 and lanes 17 and 22). Notably, a more conservative substitution at the...
same position, V1691L, had a much less pronounced effect on DUB activity (Fig. 7B, lane 6). Substitution of Val1674 with either Ser or Arg impaired DUB activity but to a much lesser extent than substitutions targeting Val1691, Thr1653, and Ala1656 (Fig. 7B, compare lanes 5–8, 10, and 11). The N1673R substitution did not negatively affect DUB activity of PLpro at all, whereas the N1673R/V1674S double substitution resulted in slightly greater DUB activity (Fig. 7B, lanes 9 and 20). These results do not support our hypothesis based on modeling that Asn1673 and Val1674 might form part of an S2 binding site that recognizes an additional distal Ub within a Lys63-linked chain. Further structural studies are needed to validate the role of these residues in binding Ub chains. It should be noted, however, that these mutants may still be able to process Lys63-linked poly-Ub chains by recognizing a single Ub monomer at the end of a poly-Ub substrate, which may explain the ineffectiveness of these mutations in disrupting DUB activity.

Mutations at residues Val1706 and Gln1708 did not influence DUB activity of PLpro (Fig. 7B, lanes 18 and 19). Given that these residues were only found to interact with Ub in our closed PLpro structure (Fig. 6A), their failure to inhibit DUB activity in this cellular DUB assay is not surprising and indicates that these residues are not essential for Ub recognition. Interestingly and repeatedly observed, the R1649Y mutant was found to have even greater DUB activity than wild-type PLpro (Fig. 7B, compare lanes 3 and 12). This residue was found to interact with residue Arg72 of Ub, and although this result was unexpected, it is possible that the R1649Y mutant retains the ability to interact with Arg72 of Ub via a cation–π interaction between the aromatic tyrosine inserted into PLpro and the positively charged arginine of Ub. Together, the findings from our mutagenesis study demonstrate that it is possible to selectively decouple the DUB and polyprotein processing activities of MERS-CoV PLpro through structure-guided site-directed mutagenesis.

**PLpro DUB Activity Suppresses the Innate Immune Response**

Conjugation and deconjugation of Ub plays an important role in the regulation of the innate immune response, and not surprisingly, pathogens have evolved mechanisms to subvert these Ub
dependent pathways (reviewed in Ref. 22). For arteriviruses, which are distant relatives of CoVs within the nidovirus order, it has been shown that the DUB activity of their PL2 is involved in antagonizing IFN-β activation upon ectopic expression, and for equine arteritis virus, this was confirmed during infection in host cells (61, 65). Coronavirus papain-like proteases have been suggested to act as IFN-β and NF-κB antagonists as well (15, 23, 66, 67). MERS-CoV PLpro is thought to possess these properties based on its capability to inhibit RIG-I-, MDA5-, and MAVS-induced IFN-β promoter stimulation and to reduce TNF-α-induced NF-κB reporter gene activity (9, 16). We therefore designed luciferase-based reporter gene assays to establish whether the DUB activity of MERS-CoV PLpro alone suffices to antagonize the IFN-β pathway. To this end, we first assessed at which level of this innate immune signal transduction pathway MERS-CoV PLpro is most active as a suppressor.

Innate immune signaling was induced in HEK293T cells by expression of one of three signaling factors, RIG-I, MAVS, or IRF3, which stimulate the pathway leading to IFN-β production at different levels. Because RIG-I and IRF3 normally need to be activated through post-translational modification (ubiquitination and phosphorylation, respectively), constitutively active variants were used (RIG-I(2CARD) and IRF3(5D)), which efficiently induce downstream signaling independent of these activation steps. Cells were co-transfected with plasmids encoding one of these innate immune signaling proteins and wild-type PLpro, the PLpro active site mutant C1592A, or full-length MERS-CoV nsp3 containing the PLpro domain. The inhibitory effect of the PLpro variants on the activation of the IFN-β promoter by the different stimuli was measured via co-expression of a firefly luciferase reporter gene under control of the IFN-β promoter. Another co-transfected plasmid encoding Renilla luciferase was included as an internal control in order to be able to correct for variability in transfection efficiency. At 16 h post-transfection, luciferase activities were measured, and activation of the IFN-β promoter induced by expression of RIG-I(2CARD), MAVS, or IRF3(5D) was set at 100% (Fig. 8). In accordance with Mielech et al. (16), we observed that MERS-CoV PLpro significantly reduced the IFN-β promoter activation that could be induced by expression of either RIG-I(2CARD) or MAVS. This effect was concentration-dependent, whereas the PLpro active site mutant was unable to block IFN-β promoter activation (Fig. 8, A and C). MERS-CoV nsp3 expression also inhibited RIG-I- and MAVS-mediated IFN-β promoter induction (Fig. 8, B and D), and together this suggested that PLpro inhibits innate immune signaling at least downstream of the MAVS adaptor and possibly also in the signaling between RIG-I and MAVS. MERS-CoV PLpro also inhibited activation of the IFN-β promoter after stimulation with IRF3(5D) in a concentration-dependent manner, whereas the C1592A mutant did not reduce IFN-β promoter activation (Fig. 8E). However, expression of full-length MERS-CoV nsp3 did not significantly inhibit IFN-β promoter activation after stimulation with IRF3(5D) (Fig. 8F). This suggests that the subcellular localization of the protease, which in the case of full-length nsp3 is membrane-anchored and in the case of the PLpro domain is presumably cytosolic, may be important in determining its substrate specificity. Taken together, our results suggest that MERS-CoV PLpro primarily interferes with the IFN-β signaling pathway at the level between MAVS and IRF3.

We therefore chose to use MAVS-mediated induction of IFN-β promoter activation in subsequent experiments. This also resulted in the strongest inhibition by PLpro, providing a maximum window to assess the effects on IFN-β promoter inhibition by the PLpro mutants with specifically inactivated DUB activity. Inhibition of IFN-β promoter activation by wild-type and mutant PLpro was determined by calculating the relative luciferase activity (Fig. 9). Expression of wild-type PLpro reduced MAVS-induced IFN-β promoter activity to ~20% of the control, whereas active site mutant C1592A reduced it by only a few percent compared with the untreated control (Fig. 9). Substitutions T1653R and A1656R resulted in greatly impaired DUB activity (Fig. 7B, lanes 7 and 8), and compared with wild-type PLpro, expression of these mutants resulted in higher IFN-β promoter activity, with relative luciferase values of ~54 and 58% respectively (Fig. 9). It should, however, be noted that the A1656R mutant was also impaired in cleaving the nsp3 4 site, and therefore this mutation nonspecifically disrupted the two proteolytic functions of PLpro. Strikingly, each mutant containing the V1691R substitution was completely unable to inhibit IFN-β promoter activation, resulting in relative luciferase activity levels similar to those seen with the active site mutant (Fig. 9, lanes 4, 16, and 17). This strongly suggested that the DUB activity of PLpro, which we found to be severely impaired in V1691R mutants (Fig. 7B), is responsible for suppressing MAVS-induced IFN-β promoter activity in this assay. The level of reduction in DUB activity corresponded to the degree of inhibition of IFN-β promoter activation for all PLpro mutants tested, which strengthens this conclusion. In accordance with its increased DUB activity, mutant R1649Y suppressed MAVS-induced IFN-β promoter activity more effectively than wild-type PLpro.

Taken together, our data show that the DUB activity of MERS-CoV PLpro suffices to efficiently suppress MAVS-induced IFN-β promoter activation and that this activity can be selectively disabled, without disrupting protease activity toward the nsp3 4 cleavage site, by targeting the Ub-binding site of the enzyme. This demonstrates for the first time that the DUB activity of MERS-CoV PLpro is specifically responsible for suppressing the innate immune response.

DISCUSSION

Guided by the MERS PLpro-Ub crystal structures, we here describe how the DUB activity of PLpro can be selectively disabled by introducing mutations into the S1 binding pocket of the protease (Fig. 6). Particularly, the substitution of Val1691 with the bulky and charged arginine residue severely impaired DUB activity in our cell culture-based assays. In addition, our results demonstrate that the majority of the mutations within the S1 Ub-binding site of PLpro that were tested do not affect trans cleavage of the nsp3 4 junction, with the exception of an A1656R mutant that did disrupt cleavage of the nsp3 4 site. The latter result indicates that Ala1656 resides in a region of PLpro that recognizes both Ub and a region of the nsp3C-4 construct that was used to test cleavage efficiency.
PLpro wild type and mutants (75 ng). At 16 h post-transfection, cells were lysed, and luciferase activity was measured. All experiments were repeated independently at least four times. Significance was evaluated using an unpaired two-tailed Student’s t test; significant values were indicated as follows: *, p < 0.05; **, p < 0.01. Bars, mean; error bars, S.D. Western blotting was used to verify expression of MERS-CoV PLpro.

Our results demonstrate that the DUB activity of MERS-CoV PLpro inhibits IFN-β promoter activation when innate immune signaling is induced by co-expression of either RIG-I or MAVS. The fact that suppression of IFN-β promoter activation was completely eliminated for several of our mutants (Fig. 9) strongly suggests that the proteolytic activity still present in those mutant enzymes has no additional role in the suppression of this particular branch of the innate immune response (e.g. by directly cleaving RIG-I or MAVS). A number of other CoV papain-like proteases with DUB activity have also been implicated in antagonizing the host innate immune response (15, 23, 66). In agreement with our data, recent studies have demonstrated the ability of MERS-CoV PLpro to inhibit RIG-I-, MDA5-, and MAVS-dependent IFN-β promoter activation as well as to down-regulate the level of IFN-β mRNA transcripts in MDA5-stimulated cells (16). The current data support the hypothesis that all of these activities solely depend on the de-ubiquitinating capacities of these coronavirus enzymes. Reports regarding the dependence of MERS-CoV PLpro-mediated IFN-β antagonism on the enzyme’s protease activity have, however, varied thus far. Mielech et al. (16) recently demonstrated that a MERS-CoV nsp3 fragment containing PLpro but excluding the transmembrane domain can inhibit MAVS-, RIG-I-, and MDA5-dependent IFN-β promoter activation, and MDA5 mediated IFN-β mRNA transcription only with a functional PLpro active site. Yang et al. (9) on the other hand used a MERS-CoV PLpro expression product extending into the nsp3 transmembrane region to demonstrate that down-regulation of RIG-I-stimulated IFN-β promoter activity is seen even with an active site knock-out mutant. Here we show that inhibition of RIG-I-, MAVS-, and IRF3-induced IFN-β promoter activity by the MERS-CoV PLpro domain is clearly dependent on a functional active site and that it is specifically the DUB activity of the protease that mediates this inhibition. However, the possibility cannot be ruled out that other parts of nsp3 contain additional innate immune suppressing activities, which may be responsible for the protease-independent effects reported with longer expression products.

Ubiquitination plays an important role in the regulation of pathways involved in detecting and counteracting viral infections, and, not surprisingly, a number of viruses of substantial diversity have been found to deploy DUBs that manipulate these signaling processes by reversing the post-translational modification of cellular proteins by Ub conjugation (19, 68). Some of these DUBs, specifically those found in (+)RNA viruses, are also critical for viral replication by catalyzing the proteolytic cleavage of specific sites in viral polyproteins, thus complicating our ability to study the direct effects of the additional DUB activity of these viral proteases. Ultimately, these effects need to be studied in the context of a viral infection; however, a simple inactivation of the protease/DUB would not only fail to prove the specific involvement of the DUB activity, it would also prevent viral replication. The method described here selectively removed the DUB activity of the MERS-CoV PLpro domain while leaving polyprotein processing activity at the nsp3 J 4 site unhindered, thus paving the way for the application of these mutations to recombinant MERS-CoV and the direct study of the role of DUB activity during infection.

We were able to show that Lys48- and Lys63-linked poly-Ub chains are processed in vitro by MERS-CoV PLpro at similar rates, which is in accordance with a recent report by Báez-Santos et al. (50). In contrast, SARS-CoV PLpro rapidly cleaves Lys48-linked poly-Ub and displays only moderate activity for Lys63 linkages in similar assays (62). It has been suggested that SARS-CoV PLpro may recognize Lys48-linked di-Ub via its S1 and S2 sites (62), although to date, no crystal structures have been reported of SARS-CoV PLpro in complex with a di-Ub substrate. Similarly, no such structural data have been obtained.
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for MERS-CoV PLpro, and thus future structural studies are necessary to determine precisely how MERS-CoV PLpro recognizes poly-Ub substrates and whether the preferences observed in expression systems can be confirmed in situations representative of an infection.

In addition to deconjugating Ub, MERS- and SARS-CoV PLpro also recognize the antiviral Ub molecule ISG15 (16, 17). In the absence of a crystal structure of a DUB from the USP family in complex with ISG15, it is difficult to predict which regions of PLpro may be specifically responsible for ISG15 binding. However, it is interesting to note that both the palm and fingers domains of the SARS-CoV PLpro domain (62) and the cellular USP21 (57), respectively, have been implicated in ISG15 recognition, probably through additional interactions between PLpro and the N-terminal Ubl fold of ISG15. Future structural work is necessary to identify the specific determinants of ISG15 recognition by MERS-CoV PLpro. Structure-guided mutagenesis of MERS-CoV PLpro to selectively disrupt deISGylation without affecting polyprotein cleavage would further expand our insights into the role of this additional activity in coronaviral immune evasion. The specific removal of DUB and potentially deISGylating activity from viral proteases that suppress the host innate immune response may open new avenues to engineer attenuated viruses for use as modified-live virus vaccines.

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REFERENCES

Crystal Structure of the Middle East Respiratory Syndrome Coronavirus (MERS-CoV) Papain-like Protease Bound to Ubiquitin Facilitates Targeted Disruption of Deubiquitinating Activity to Demonstrate Its Role in Innate Immune Suppression

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