Mass spectrometry reveals potential of β-lactams as SARS-CoV-2 Mpro inhibitors
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**Mass spectrometry reveals potential of β-lactams as SARS-CoV-2 M\textsuperscript{pro} inhibitors**

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The main viral protease (M\textsuperscript{pro}) of SARS-CoV-2 is a nucleophilic cysteine hydrolase and a current target for anti-viral chemotherapy. We describe a high-throughput solid phase extraction coupled to mass spectrometry M\textsuperscript{pro} assay. The results reveal some β-lactams, including penicillin esters, are active site reacting M\textsuperscript{pro} inhibitors, thus highlighting the potential of acylating agents for M\textsuperscript{pro} inhibition.

The main viral protease (M\textsuperscript{pro}) of severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2)\textsuperscript{2} is a COVID-19 treatment target.\textsuperscript{2} M\textsuperscript{pro} along with the papain-like protease (PL\textsuperscript{pro}), processes initially translated viral polyproteins to give cleaved proteins with biological functions essential for viral replication in cells.\textsuperscript{3} Following formation of a non-covalent enzyme-substrate complex, M\textsuperscript{pro} catalysis proceeds via His-41 enabled reaction of Cys-145 with a scissile peptide bond forming a hydrolytically labile thioester. M\textsuperscript{pro} cleaves after glutamine residues with a preference for small-residues on the C-terminal side of the cleaved amide (Fig. 1A and B).\textsuperscript{4}

Most reported M\textsuperscript{pro} assays measure fluorescence, as precedent for other protease assays.\textsuperscript{1,5} Whilst efficient, such methods do not simultaneously monitor substrate depletion/product formation and some compounds interfere with fluorescence.\textsuperscript{8} We were thus interested in establishing an alternative mass spectrometry (MS)-based high-throughput M\textsuperscript{pro} assay for identifying new inhibitors and testing known drugs.

Solid phase extraction coupled with MS (SPE-MS) has been applied to high-throughput screens of enzymes.\textsuperscript{7} We envisaged it could simultaneously monitor both M\textsuperscript{pro} substrate depletion/product formation and covalent modification. The latter is of interest because many reported inhibitors of nucleophilic cysteine enzymes work by covalent reaction.\textsuperscript{8} Here we report how such an assay enabled identification of new M\textsuperscript{pro} inhibitors, including β-lactams, the most important antibacterial class.\textsuperscript{9}

We developed conditions for an SPE-MS based SARS-CoV-2 M\textsuperscript{pro} assay (0.15 μM M\textsuperscript{pro}, 2.0 μM TSAVLQ/SGFRK-NH\textsubscript{2}, 20 mM HEPEs, pH 7.5, 50 mM NaCl) using protein prepared as reported.\textsuperscript{1,10} Isolated M\textsuperscript{pro} was found to be active when monitoring turnover of peptide substrates, including TSAVLQ/SGFRK-NH\textsubscript{2} which was cleaved to give TSAVLQ and SGFRK-NH\textsubscript{2} fragments (Fig. 1C and D). Kinetic parameters were determined for the 11-mer substrate (K\textsubscript{m} = 14.4 μM; k\textsubscript{cat} = 2.7 min\textsuperscript{−1}), both by monitoring substrate depletion and N-terminal product formation (Fig. S1, ESI†). The efficiency (k\textsubscript{cat}/K\textsubscript{m}) of M\textsuperscript{pro} determined by SPE-MS (28 500 M\textsuperscript{−1} s\textsuperscript{−1}) is comparable to that observed for a similar substrate Mca-AVLQ/SGFRK(Dnp)K using a fluorescence resonance energy transfer (FRET) assay (27 000 M\textsuperscript{−1} s\textsuperscript{−1}, as reported and in our hands).\textsuperscript{7} Steady state kinetics for a 37-mer substrate were also investigated; a 2-fold increase in k\textsubscript{cat}/K\textsubscript{m} (60 026 M\textsuperscript{−1} s\textsuperscript{−1}) was observed (Fig. S2, ESI†). Comparison of kinetic parameters for the SARS-CoV-2 M\textsuperscript{pro} and related SARS-CoV M\textsuperscript{pro} reveal similar k\textsubscript{cat}/K\textsubscript{m} values (though the values for SARS-CoV were somewhat lower when using shorter substrates in an HPLC assay) (Table S1, ESI†). Note, the interconversion between monomeric/dimeric forms of M\textsuperscript{pro} has the potential to introduce complexity in kinetic analyses.\textsuperscript{11}

Next, the SPE-MS assay was validated for inhibition studies with ebselen,\textsuperscript{1} N\textsubscript{3},\textsuperscript{3} disulfiram,\textsuperscript{1} and boceprevir\textsuperscript{12} using the 11-mer TSAVLQ/SGFRK-NH\textsubscript{2} substrate (Table 1 and Fig. S3, ESI†). The ebselen IC\textsubscript{50} was ~0.09 μM under standard conditions (0.15 μM M\textsuperscript{pro}, 2.0 μM TSAVLQ/SGFRK-NH\textsubscript{2} i.e. [S] < K\textsubscript{m}, 20 mM HEPEs, pH 7.5, 50 mM NaCl at ambient temperature) compared to an IC\textsubscript{50} of ~0.67 μM using a FRET assay (0.2 μM M\textsuperscript{pro}, 20 μM Mca-AVLQ/SGFRK(Dnp)K i.e. [S] ≈ K\textsubscript{m} 50 mM Tris–HCl, pH 7.3, 1 mM EDTA, 30 °C) (Table 1, entry 1; Fig. S3D, ESI†).

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We optimized the assay for studying covalent modifications with a higher M<sup>pro</sup> concentration being used to enable robust analyses (1 μM M<sup>pro</sup>), though IC<sub>50</sub> and preliminary covalent modification data can be accumulated from the same experiment. SPE purification is denaturing, so monomer modification was observed. Assay validation used N3;<sup>1</sup> predominantly (but not exclusively) a single N3 adduct was observed (Fig. 2A, B and Fig. S4, ESIT), consistent with structural work revealing Cys-145 reaction<sup>†</sup> (Fig. 1B and Fig. S5, Table S2, ESIT). We exploited selective reaction of N3 to test selectivity of other nucleophilic serine enzymes including proteases and serine enzymes; they inhibit other nucleophilic serine enzymes; antibodies form stable acyl–enzyme complexes with bacterial L-lysine chloromethyl ketone, substantial covalent modification was noted, some (related to) known inhibitors, 1,14 including auranofin, cisplatin, IPA-3, bismuth subsalicylate, thioguanine, carmustine, and disulfiram (Tables S3 and S4, ESIT). IC<sub>50</sub>S were determined for compounds with ≥80% inhibition at 20 μM, excluding known interference compounds.<sup>15</sup> Auranofin (IC<sub>50</sub> ~ 1.5 μM; reported IC<sub>50</sub> ~ 0.5 μM<sup>14</sup>), an α-chloroketone (TPCK) (IC<sub>50</sub> ~ 0.8 μM), IPA-3 (IC<sub>50</sub> ~ 0.1 μM), and 5-thioguanine (IC<sub>50</sub> ~ 13.5 μM) are some of the more potent inhibitors (Fig. S8, ESIT). Some of these covalently modified M<sup>pro</sup>, sometimes with more than one reaction being observed (Fig. S9–S15, ESIT). Active site selectivity was investigated using N3 treated and untreated M<sup>pro</sup>. Following N3 treatment, in some cases, e.g. TPCK and N<sub>2</sub>-p-toluenesulfonyl-l-lysine chloromethyl ketone, substantial covalent modification was no longer observed, implying selective Cys-145 reaction (Fig. 2D, F and Fig. S12, S13, ESIT). Although further validation is required, with BAY 11-7082 and IPA-3 the multiple adds observed with unmodified M<sup>pro</sup> were diminished when the active site was N3 blocked, suggesting reaction with Cys-145 might alter the M<sup>pro</sup> conformation (Fig. S9 and S11, ESIT).

The screen identified β-lactam drugs as potential M<sup>pro</sup> inhibitors, including penicillins and cephalosporins (Table S5, ESIT). This was of interest, as in preliminary work we observed some β-lactams react covalently (data not shown). β-Lactam antibiotics form stable acyl–enzyme complexes with bacterial nucleophilic serine enzymes; they inhibit other nucleophilic serine enzymes including proteases and β-lactamases<sup>16</sup> and nucleophilic cysteine enzymes.<sup>17</sup>

Studies on cephalosporins identified as potential inhibitors from the screen revealed no substantial covalent M<sup>pro</sup> modification,

Table 1  IC<sub>50</sub>S of selected M<sup>pro</sup> inhibitors determined using SPE-MS assays compared to those obtained using FRET assays

<table>
<thead>
<tr>
<th>Inhibitor</th>
<th>IC&lt;sub&gt;50&lt;/sub&gt; (SPE-MS) [μM]&lt;sup&gt;&lt;i&gt;a&lt;/i&gt;&lt;/sup&gt;</th>
<th>IC&lt;sub&gt;50&lt;/sub&gt; (SPE-MS)&lt;sup&gt;&lt;i&gt;b&lt;/i&gt;&lt;/sup&gt; [μM]</th>
<th>IC&lt;sub&gt;50&lt;/sub&gt; (FRET) [μM]</th>
</tr>
</thead>
<tbody>
<tr>
<td>Ebselen</td>
<td>0.09 ± 0.07</td>
<td>0.09 ± 0.07</td>
<td>0.67 ± 0.09&lt;sup&gt;&lt;i&gt;c&lt;/i&gt;&lt;/sup&gt;</td>
</tr>
<tr>
<td>N3</td>
<td>0.04 ± 0.01</td>
<td>0.03 ± 0.01</td>
<td>n.d.</td>
</tr>
<tr>
<td>Disulfiram</td>
<td>0.60 ± 0.02</td>
<td>0.46 ± 0.02</td>
<td>9.35 ± 0.18&lt;sup&gt;&lt;i&gt;c&lt;/i&gt;&lt;/sup&gt;</td>
</tr>
<tr>
<td>Boceprevir</td>
<td>11.0 ± 4.8</td>
<td>9.2 ± 5.5</td>
<td>2.70 ± 0.05&lt;sup&gt;&lt;i&gt;c&lt;/i&gt;&lt;/sup&gt;</td>
</tr>
</tbody>
</table>

<sup>a</sup> Mean of two independent replicates each performed in technical duplicate (n = 2 ± standard deviation, SD). Conditions: 0.15 μM M<sup>pro</sup> and 2.0 μM TSAVLQ/SGFRK-NH<sub>2</sub> substrate in 20 mM HEPES, pH 7.5, 50 mM NaCl. 8 30 min inhibitor preincubation. 6 60 min inhibitor preincubation.

<sup>c</sup> Excellent Z'-factors and signal to noise ratios reveal the assay robustness (Fig. S7, ESIT). In addition to ebselen (identification of which validates the method), diverse inhibitors (≥80% at a fixed 20 μM inhibitor concentration) were identified, some (related to) known inhibitors,<sup>1,14</sup> including auranofin, cisplatin, IPA-3, bismuth subsalicylate, thioguanine, carmustine, and disulfiram (Tables S3 and S4, ESIT).
though cephalosporin C Zn(II) salt and cephalosporin C Na(I) salt inhibited. However, the IC_{50}s for cephalosporin C Zn(II) salt and ZnCl_2 were similar, indicating much of the inhibition is due to Zn(II) ions (Fig. S16, ESI †), as observed for cephalosporin C Zn(II) salt inhibition of other enzymes.  

We further investigated β-lactam reactions with M_{pro} using a diverse set of β-lactams (Fig. S17, ESI †). Though most β-lactams were inactive (IC_{50} > 100 μM), two penicillin esters manifested IC_{50}s < 5 μM, *i.e.* 1: a penicillin V sulfone C3 benzyl ester (IC_{50} ~ 1.5 μM), and 2: a derivative of penicillin G sulfoxide C3.

![Fig. 2](image1)

**Fig. 2**  N3 dependent reaction monitoring the active site selectivity of inhibitors. (A) Reaction of N3 with the M_{pro} active site Cys-145.  

![Fig. 3](image2)

**Fig. 3**  β-Lactams inhibit M_{pro}. IC_{50}s for (A) 1 (penicillin V sulfone C3 benzyl ester) and (B) 2 (C6-methoxy penicillin G sulfoxide C3 p-nitrobenzyl ester) determined using SPE-MS; data are a mean of technical duplicates with (a) 30 min and (b) 60 min preincubation. IC_{50}s are means of two independent repeats each composed of technical duplicates (n = 2 ± SD). Proposed reaction of 1 (C) and 2 (D) with M_{pro}. (E) A single molecule 1 covalently modifies M_{pro} through covalent reaction. Conditions: 1 μM M_{pro}, 20 μM β-lactam, 20 mM HEPES, pH 7.5, 50 mM NaCl. (F) 1 does not covalently modify M_{pro} preincubated with N3, suggesting 1 reacts with Cys-145. (H) 2 does not efficiently react with M_{pro} preincubated N3. Conditions: 1 μM M_{pro} preincubated with 3 μM N3, 20 μM 1 or 2, 20 mM HEPES, pH 7.5, 50 mM NaCl. Black spectra: wild-type M_{pro} (33796 Da).
p-nitrobenzyl ester (IC$_{50}$ ~ 3.5 µM), both with similar potency with either 30 or 60 min preincubation (Fig. 3A and B). Other β-lactams inhibited, though more weakly (Fig. S17, ESI†). The inhibition by the penicillin benzyl esters may, in part, reflect binding of the N3 benzyl ester, likely binding in the P1’ or P2 pocket (Fig. 1B). Structures of Mpro complexed with a β-lactam sub-families (Fig. S19–S21, ESI†). In some cases, e.g. clavulanate (Fig. S19H, ESI†) and moxalactam (Fig. S21F, ESI†), (partial) inhibitor fragmentation was observed. There was no clear correlation between a propensity to react covalently and Mpro inhibition; in some cases evidence for partial covalent modification, but no inhibition was observed (Fig. S17, ESI†). Covalent modification was observed with 1, but only to a small (<10%) extent with 2, suggesting the latter likely inhibits principally by a non-covalent interaction (Fig. 3C–H). After Cys-145 blocking with N3, no reaction with 1 was observed (Fig. 3G). Minor further modification of Cys-145 reacted Mpro was observed with 2 (Fig. 3H), suggesting the low levels of covalent modification by 2 do not solely involve Cys-145.

In summary, SPE-MS is a useful method for Mpro assays enabling analysis of inhibition by both substrate depletion/product formation. The method complements reported in vitro Mpro assays and compares favourably to those in terms of its robustness and ability to enable efficient high-throughput screening/repurposing efforts. The SPE-MS assay also enables ready analysis of covalent Mpro modification and use of Mpro reacted with a selective inhibitor such as N3/TPCK informs on whether covalent reaction of a test inhibitor occur at the active site or not.

Although the available evidence implies that β-lactams can inhibit Mpro non-covalently, the observation that some react with and inhibit Mpro by covalent active site modification should promote interest in the development of inhibitors for Mpro and other thiol proteases working via cysteinyl S-acylation. By contrast with S-alkylating inhibitors, which can have toxicity issues, S-acylation has not been widely explored for nucleophilic cysteine proteases.

The identification of β-lactam containing Mpro inhibitors with structures closely related to drugs should promote work on the development of related compounds for progression towards clinical use for treatment of COVID-19 and viral diseases.

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Conflicts of interest

There are no conflicts to declare.

Notes and references