Pharmacological Characterization of the Spectrum of Antiviral Activity and Genetic Barrier to Drug Resistance of M2-S31N Channel Blockers

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ABSTRACT

Adamantanes (amantadine and rimantadine) are one of the two classes of Food and Drug Administration–approved antiviral drugs used for the prevention and treatment of influenza A virus infections. They inhibit viral replication by blocking the wild-type (WT) M2 proton channel, thus preventing viral uncoating. However, their use was discontinued due to widespread drug resistance. Among a handful of drug-resistant mutants, M2-S31N is the predominant mutation and persists in more than 95% of currently circulating influenza A strains. We recently designed two classes of M2-S31N inhibitors, S31N-specific inhibitors and S31N/WT dual inhibitors, which are represented by N-[(5-cyclopropyl-1,2-oxazol-3-yl)methyl]adamantan-1-amine (WJ379) and N-[(5-bromothiophen-2-yl)methyl]adamantan-1-amine (BC035), respectively. However, their antiviral activities against currently circulating influenza A viruses and their genetic barrier to drug resistance are unknown. In this report, we evaluated the therapeutic potential of these two classes of M2-S31N inhibitors (WJ379 and BC035) by profiling their antiviral efficacy against multidrug-resistant influenza A viruses, in vitro drug resistance barrier, and synergistic effect with oseltamivir. We found that M2-S31N inhibitors were active against several influenza A viruses that are resistant to one or both classes of Food and Drug Administration–approved anti-influenza drugs. In addition, M2-S31N inhibitors display a higher in vitro genetic barrier to drug resistance than amantadine. The antiviral effect of WJ379 was also synergistic with oseltamivir carboxylate. Overall, these results reaffirm that M2-S31N inhibitors are promising antiviral drug candidates that warrant further development.

Introduction

Influenza viruses are the causative agents that lead to annual seasonal influenza epidemics as well as sporadic, more devastating influenza pandemics (Rappuoli and Dormitzer, 2012; Monto and Webster, 2013). On average, influenza virus infection leads to 36,000 deaths in the United States and approximately 250,000–500,000 deaths globally each year (Thompson et al., 2003, 2004). However, current countermeasures against influenza infection are curtailed by the emergence of drug-resistant strains. Resistance to the only orally bioavailable neuraminidase inhibitor, oseltamivir, has been continuously reported and was prevalent in the 2008–2009 influenza season (Cheng et al., 2009; Samson et al., 2013). The use of M2 channel blockers (amantadine and rimantadine) is no longer recommended by the Centers for Disease Control and Prevention due to prevalent drug resistance (Bright et al., 2006; Fiore et al., 2008). Thus, novel antivirals are clearly needed. Toward this goal, we chose M2-S31N as the drug target to develop the next generation of antiviral drugs. The M2-S31N mutant is an ideal antiviral drug target because: 1) M2-S31N persists in more than 95% of currently circulating influenza A viruses among humans, including oseltamivir-sensitive and oseltamivir-resistant strains (Dong et al., 2015), thus targeting M2-S31N is likely to yield broad-spectrum antiviral drugs; and 2) M2 is a validated antiviral drug target, and there is no such homolog proton channel encoded by the human genome, thus M2 inhibitors are expected to have high selectivity. As a homotetrameric proton-selective channel, one mutation in M2 actually results in four changes at the same time, which leads to a profound impact on the structure and function of this very constricted channel. As a result, only a very limited number of M2 mutants confer both drug resistance and transmissibility among humans, of which M2-S31N is the predominant mutant. This small set of transmissible mutants suggests that M2 is a highly conserved drug target compared with other viral proteins, rendering it an ideal drug target for the development of anti-influenza drugs (Wang et al., 2015).

M2-S31N mutant was traditionally tagged as an “undruggable” target, and decades of traditional medicinal chemistry campaign failed to yield a single hit compound (Wanka et al., 2013; Wang et al., 2015). Nevertheless, guided by information

ABBREVIATIONS: BC035, N-[(5-bromothiophen-2-yl)methyl]adamantan-1-amine; CPE, cytopathic effect; DMEM, Dulbecco’s modified Eagle’s medium; FBS, fetal bovine serum; MDCK, Madin-Darby canine kidney; MOI, multiplicity of infection; MTT, 3-(4,5-dimethylthiazol-2-yl)-2,5-diphenyltetrazolium bromide; PBS, phosphate-buffered saline; PCR, polymerase chain reaction; ST6Gal I, β-galactoside α-2,6-sialytransferase I; TEVC, two-electrode voltage clamp; WJ379, N-[(5-cyclopropyl-1,2-oxazol-3-yl)methyl]adamantan-1-amine; WT, wild-type.
gathers from previous structure-activity relationship studies of amantadine (Wang et al., 2015) and breakthroughs in M2 structural biology and mechanistic studies (Hong and DeGrado, 2012), steady progress has been made toward the design of M2-S31N inhibitors (Wang et al., 2013a; Wu et al., 2014; Li et al., 2016). They are broadly classified as S31N-specific inhibitors and S31N/wild-type (WT) dual inhibitors. S31N-specific inhibitors target the S31N channel only, not the WT, and one representative example is N-[(5-cyclopentyl-1,2-oxazol-3-yl)methyl]adamantan-1-amine (WJ379) (Wang et al., 2013b). S31N/WT dual inhibitors target both S31N and WT M2 channels, and one representative example is N-[(5-bromothiophen-2-yl)methyl]adamantan-1-amine (BC035) (Wu et al., 2014). Their channel blockage and antiviral effects have been confirmed in electrophysiological two-electrode voltage clamp (TEVC) assays and antiviral plaque assays, respectively. Their modes of binding were revealed by both solution and solid-state NMR studies (Cady et al., 2010, 2011; Wang et al., 2013b; Williams et al., 2013; Wu et al., 2014).

In this study, we further evaluated the therapeutic potential of both classes of M2 inhibitors, S31N-specific inhibitors and S31N/WT dual inhibitors. Specifically, from the standpoint of developing therapeutics, we are interested in testing whether the potent antiviral effect of these compounds on the model virus, A/WSN/33 (H1N1), can be extended to the currently circulating influenza A strains among humans. Furthermore, with these tools compounds in hand, we would like to address the issue of drug resistance. For example, will the S31N mutant virus become resistant to the newly developed S31N inhibitors under drug selection pressure? If yes, which mutations will be selected? How many passages does it take for the S31N mutant virus to evolve drug resistance? In addition, as we already learned the lessons of antibiotics and antivirals, resistance is unfortunately inevitable. It is not a question of yes or no but rather a question of when (Clavel and Hance, 2004; Hayden and de Jong, 2011; McKimm-Breschkin, 2013; Walsh and Wencewicz, 2014; Blair et al., 2015). With this in mind, what one can do is to slow down the resistance evolution rather than eradicate it. Toward this goal, we would like to test the combination therapy potential of M2-S31N inhibitors with oseltamivir, as this offers a means to delay resistance evolution against both oseltamivir and M2-S31N inhibitors.

Materials and Methods

Cell Lines, Viruses, and Viral Infection. Madin-Darby canine kidney (MDCK) cells were grown at 37°C in 5% CO2 atmosphere in Dulbecco’s modified Eagle’s medium (DMEM; high glucose, with L-glutamine) supplemented with 10% fetal bovine serum (FBS), 100 IU/ml penicillin, and 100 μg/ml streptomycin. MDCK cells overexpressing α-2,6-sialytransferase I (ST6Gal I) were obtained from Dr. Yoshihiro Kawaoka at the University of Wisconsin (Madison, WI) under material transfer agreement and were maintained in the culture media were harvested, and cell debris was removed by centrifugation at 9000 rpm for 30 minutes. Virus titers were determined by plaque assay using MDCK cells expressing ST6Gal I.

Compounds. WJ379 and BC035 were synthesized in house as previously described (Wang et al., 2013b; Wu et al., 2014). Amantadine hydrochloride was purchased from Sigma-Aldrich (St. Louis, MO).

Plaque Assay. Plaque assays were carried out as previously described (Jing et al., 2008; Bahnunik et al., 2009), except MDCK cells expressing ST6Gal I were used instead of regular MDCK cells. In brief, a confluent monolayer of ST6Gal I MDCK cells was incubated with ~100-pfu virus samples in DMEM with 0.5% bovine serum albumin for 1 hour at 4°C, then 37°C for 1 hour. The inoculums were removed, and the cells were washed with phosphate-buffered saline (PBS). The cells were then overlaid with DMEM containing 1% Avicel microcrystalline cellulose (FMC BioPolymer, Philadelphia, PA) and N-acetyl trypsin (2.0 μg/ml). To examine the effect of the compounds on plaque formation, the overlay media were supplemented with compounds at testing concentrations. At day 2 after infection, the monolayers were fixed and stained with crystal violet dye solution (0.2% crystal violet, 20% methanol).

Cytotoxicity Assay and Cytopathic Effect Assay. The cytotoxicity of compounds was determined in MDCK cells. Cells were treated with different concentrations of WJ379 or BC035 and stained with 3-(4,5-dimethylthiazol-2-yl)-2,5-diphenyltetrazolium bromide (MTT) for 4 hours. A virus-induced cytopathic effect (CPE) assay was performed as previously described (Atkins et al., 2012; Beyleveld et al., 2013). In brief, MDCK cells were grown in DMEM supplemented with 5% FBS in 96-well plates. When 90% confluence was reached, cells were washed once with 100 μl of PBS buffer and infected with virus at multiplicity of infection (MOI) of 0.002. Then DMEM (without FBS) with indicated concentrations of compounds was added. After incubating at 37°C for 72 hours, 20 μl of 5 μg/ml MTT reagent was added to each well, and the plates were incubated at 37°C for 4 hours. Then the cells were washed once with PBS, and 100 μl of 0.1 N HCl in isopropanol was added. The absorbance was read at 560 nm with a plate reader. The assays were repeated in quadruplicate.

Serial Passage Experiments and Resistance Mutation Identification. MDCK cells were infected with A/WSN/33 (H1N1) virus or A/WSN/33 N31S (H1N1) at an MOI of 0.001 for 1 hour. Then the inoculum was removed, and MDCK cells were incubated with compounds at concentrations shown in Table 2 or in the absence of compounds to evaluate cell culture–adapted mutations. In the first passage, the applied compound concentrations were slightly below their corresponding EC50 values. In the following passages, the compound concentrations were gradually increased, as shown in Table 2. In each passage, the viruses were harvested when significant cytopathic effect was observed, which usually takes 2–3 days after virus infection. The titers of harvested viruses were determined by plaque assay. At selected passages, as shown in Table 2, influenza M segments were subjected to sequencing. Influenza viral RNA was isolated using QIAamp viral RNA Mini Kit (Qiagen, Hilden, Germany). The M segment cDNA was generated with reverse-transcription polymerase chain reaction (PCR) using M-specific primers (5’-AGCAAAAGCAGGTAGATATTGAAAG-3’ and 5’-TAGTTTTTTACTC-CAGCTCTATGTTG-3’). Reverse-transcription PCR products were analyzed with agarose gel electrophoresis and purified with Wizard SV Gel and PCR Clean-up System (Promega, Madison, WI). Purified PCR products were sequenced by Genewiz, Inc. (South Plainfield, NJ).

Electrophysiological TEVC Assay. The corresponding drug-resistant mutations identified from serial drug-passage experiments were introduced to M2 sequences in pGEM3 vector with the QuikChange Site-Directed Mutagenesis Kit (Agilent, Santa Clara, CA) as described previously (Khurana et al., 2009). mRNA preparation and microinjection and electrophysiological TEVC recordings were carried out as previously described (Jing et al., 2008). The inhibition kinetics time constant was determined by fitting the period of recording trace when the compounds are present to a one-phase exponential decay equation (t) = A*exp(-t/T) + C in Clampfit 10.3 (Molecular Devices, Sunnyvale, CA).

Combinational Therapy. Combination evaluations were performed in quintuplicate using the CPE assay described earlier except that neutral red was used for staining instead of MTT. In brief, MDCK cells were seeded in 96-well plates for 24 hours. Seven serial
half-logarithmic dilutions of WJ379 and oseltamivir carboxylate were prepared and added to MDCK cells infected with influenza A virus A/WSN/33 (H1N1) (MOI 0.001) in the 96-well plate. After incubation at 37°C in a humidified incubator with 5% CO2 for 72 hours, the medium was removed, and cells were stained with 100 μl of neutral red in DMEM (40 mg/ml) for 4 hours. After washing once with 150 μl of PBS, the neutral red was extracted from cells with 150 μl of neutral red destain solution [ethanol/water/glacial acetic acid: 50/49/1 (v/v/v)] to form a homogenous solution (Repetto et al., 2008). The absorbance at 540 nm was measured using a Multiskan FC Microplate Photometer (Fisher Scientific, Houston, TX). Drug-drug interaction was evaluated using the MacSynergy II software program, which automatically calculates volumes of synergy or antagonism for each three-dimensional plot of data (Prichard and Shipman, 1990; Tarbet et al., 2012). The value ranges 0–25, 25–50, 50–100, or over 100 μm% (*μm × μm × %) are considered as insignificant, minor but significant, moderate, or strong synergy or antagonism, respectively. Synergy plots were made at the 95% confidence limit.

**M2 Sequence Analysis.** All M2 protein full-length sequences of influenza virus A isolated from humans were obtained from the Influenza Research Database (http://www.fludb.org, accessed on January 18, 2016). A total of 18,393 M2 sequences were aligned by MEGA6 (www.megasoftware.net) using the ClustalW method. The frequencies of the appearance of substitutions of L26I and I32T were identified.

### Results

**WJ379 and BC035 Are Potent M2-S31N Channel Blockers and Antivirals against S31N Containing the A/WSN/33 (H1N1) Virus.** We previously reported on two classes of S31N inhibitors, S31N-specific inhibitors (Wang et al., 2013b; Li et al., 2016) and S31N/WT dual inhibitors (Wang et al., 2013a; Wu et al., 2014), which are represented by WJ379 and BC035, respectively. To select nontoxic drug concentrations for the following serial viral passage experiments, the cytotoxicity and selectivity indexes of these two compounds were determined. The CC50 values of WJ379 and BC035 were 125 and 123 μM, respectively (Table 1). Their antiviral activities were further quantified in both plaque assays and cytopathic effect assays using the influenza A virus strain A/WSN/33 (H1N1) (Table 1). Both the plaque assay and CPE assay were standard antiviral assays used to determine the efficacy of antiviral drugs. The difference is that the plaque assay quantifies the change of viral titer upon drug treatment, whereas the CPE assay quantifies the change of cell survival upon viral infection and drug treatment (Atkins et al., 2012; Beyleveld et al., 2013). In general, there is a positive correlation between these two assays. In the plaque assays, the EC50 values of WJ379 and BC035 against the A/WSN/33 (H1N1) virus were 0.49 and 2.2 μM, respectively, which were consistent with those of WJ379 and BC035 in the CPE assays (0.36 and 6.20 μM, respectively) (Table 1). The selective indexes of WJ379 and BC035 were 255 and 56, respectively. On the basis of these results, the highest drug concentrations used for the following serial viral passage experiments were set to 5 and 16 μM for WJ379 and BC035, respectively, which conferred minimal cytotoxicity.

**M2-S31N Inhibitors Are Potent Antivirals against Human Clinical Isolates of Multidrug-Resistant Influenza A Viruses.** To determine whether the potent antiviral activity of WJ379 and BC035 on A/WSN/33 (H1N1) can be extended to other S31N-containing influenza A viruses, WJ379 and BC035 were tested in plaque assays against human clinical isolates of multidrug-resistant influenza A viruses, including A/California/07/2009 (H1N1) (amantadine-resistant, oseltamivir-sensitive), A/Texas/04/2009 (H1N1) (amantadine-resistant, oseltamivir-resistant), A/Denmark/524/2009 (H1N1) (amantadine-resistant, oseltamivir-sensitive), and A/Denmark/528/2009 (H1N1) (amantadine-resistant, oseltamivir-resistant). As these human clinical isolates did not produce countable plaques using regular MDCK cells (data not shown), an engineered MDCK cell line overexpressing the human ST6Gal I was used for this purpose as it expresses N-acetyl sialic acid linked to galactose by an α-2,6-linkage on its cell surface (Hatakeyama et al., 2005). This cell line mimics human epithelial cells and is the only cell line that is suitable to perform plaque assays for human influenza viruses (Matrosovich et al., 2003; Hatakeyama et al., 2005). With this cell line and optimized conditions, we were able to get uniform and reproducible plaques with all four strains. Representative images of plaque assays with A/California/07/2009 (H1N1) and A/Texas/04/2009 (H1N1) are shown in Fig. 1. The antiviral EC50 values of compound WJ379 were in the submicromolar range, whereas for compound BC035, the EC50 values were in the low micromolar range (Fig. 1, D and E). Of note, oseltamivir carboxylate only reduced plaque size, but not plaque number, whereas M2-S31N inhibitors completely inhibited plaque formation.

<table>
<thead>
<tr>
<th>Structure</th>
<th>M2-S31N channel inhibitiona</th>
<th>Plaque assay</th>
<th>CPE EC50 (μM)b</th>
<th>Cellular toxicity</th>
<th>CC50 (μM)c</th>
<th>SPd</th>
</tr>
</thead>
<tbody>
<tr>
<td>WJ379</td>
<td>85%/65%/b</td>
<td>0.49</td>
<td>0.36</td>
<td>125</td>
<td>255</td>
<td>56</td>
</tr>
<tr>
<td>BC035</td>
<td>76%/N.T.</td>
<td>2.2</td>
<td>6.20</td>
<td>125</td>
<td>255</td>
<td>56</td>
</tr>
</tbody>
</table>

aReported in Wu et al. (2014).
bReported in Wang et al. (2013b).
cReported in Ma et al. (2013).
dReported in Wu et al. (2014).

**M2-S31N Inhibitors Have a Higher In Vitro Genetic Barrier to Drug Resistance than Amantadine.** To evaluate the in vitro genetic barrier to drug resistance of these two S31N inhibitors, serial viral passage experiments in MDCK cells were performed with the influenza A/WSN/33 (H1N1) virus. The drug concentrations of BC035 and WJ379 applied at passage 1 were slightly below their EC50 values and were gradually increased in subsequent passages (Table 2). In the first two passages, the progeny viruses maintained full sensitivity to their respective compounds, as indicated by the EC50 values (Table 2). At passage 3, the EC50 values of WJ379 and BC035 were moderately increased by 4.2- and 2.8-fold, respectively. Significant resistance was observed at passage 4 in which the EC50 values increased more than...
10-fold in both cases. To test the persistence of the resulting drug-resistant mutants, the viruses were continuously passaged for two more rounds in the presence of compounds, and then five rounds in the absence of compounds. We found that the viruses at passage 11 were resistant to both WJ379 and BC035.

To rule out the possibility that the observed resistance was due to cell culture–adapted mutations, the A/WSN/33 (H1N1) virus was also passed in the absence of compound, and the drug sensitivities of the resulting viruses against WJ379 and BC035 were tested in plaque assays. At passage 6, the EC50 values of WJ379 and BC035 were 0.65 and 2.9 μM, respectively, which were similar to their corresponding EC50 values at passage 0, indicating that the elevated EC50 values in serial passage experiments in the presence of WJ379 and BC035 were not due to the virus adaption in cell culture.

As a comparison, we carried out a serial viral passage experiment with the A/WSN/33 N31S (H1N1) virus against amantadine. The A/WSN/33 N31S (H1N1) virus is amantadine-sensitive. The EC50 value of amantadine against the A/WSN/33 N31S virus (H1N1) was 0.26 μM. Amantadine was applied at 0.2 μM in passage 1 (Table 2), which was close to its EC50 value. This condition was chosen to make a side-by-side comparison with the passage experiments of WJ379 and BC035. In contrast to the emergence of complete resistance to WJ379 and BC035 by the A/WSN/33 (H1N1) virus at passage 4, complete amantadine resistance against the WSN N31S (H1N1) virus was observed as early as passage 1 (30% plaque remaining even when treated with 30 μM amantadine). These results indicate that M2-S31N inhibitors, such as WJ379 and BC035, have a higher genetic barrier to resistance than amantadine.

Sequencing M2 Genes Reveals Mutations that Confer Resistance to M2-S31N Inhibitors. To identify how M2-S31N evolved to become resistant to WJ379 and BC035, the M2 genes from viruses at passages 0, 3, 4, 5, 6, and 9 were reverse-transcribed and sequenced. The sequencing traces are shown in Fig. 2, and the resulting M2 mutations at each passage are shown in Table 2. For WJ379, no M2 mutation was identified up to passage 3. At passage 4, a substantial population of L26I mutation emerged, and its percentage continued to rise throughout passages 5 and 6 and completely
Channel blockage is expressed as percentage of current (et al., 1992; Wang et al., 1993; Pinto and Lamb, 2006). The TEVC assay is one of the gold-standard assays to study the proton conductance property of M2 channels as well as their drug inhibition (Pinto and Lamb, 2006). To test this hypothesis, we repeated the serial passage experiments with BC035, one of the S31N/WT dual inhibitors. Similar to the results of WJ379, no mutation was identified up to passage 3. At passage 4, a small but obvious population of N31D mutants emerged, and its percentage continued to rise throughout passages 5 and 6. Similarly, the N31D mutation also completely reverted back to N31 at passage 9 when the drug selection pressure was removed, whereas another mutation, I32T, which emerged at passage 5, continued to increase throughout passages 6–9 and became the predominant mutation at passage 9 by complete replacement of I32.

**M2 Mutants Selected from Serial Passage Experiments Have Reduced Drug Sensitivity to M2-S31N Inhibitors in TEVC Assays.** In the aforementioned serial passage experiments, we identified two amino acid substitutions, L26I and N31S, for WJ379 and two amino acid substitutions, N31D and I32T, for BC035. As we cannot distinguish whether these two substitutions occur in the same M2 protein or at two different M2 proteins, we therefore generated all possible M2 constructs and tested their drug sensitivity in TEVC assays. Specifically, in the case of WJ379, we recorded the channel blockage of WJ379 against M2-N31S/L26I (single mutation), M2-N31S (single mutation), and M2-N31S/L26I (double mutations) in TEVC assays. In the case of BC035, we recorded its channel blockage against M2-N31S/L26I (single mutation), M2-N31S (single mutation), and M2-N31S/L26I (double mutations). The TEVC assay is one of the gold-standard assays to study the proton conductance property of M2 channels as well as their drug inhibition (Pinto et al., 1992; Wang et al., 1993; Pinto and Lamb, 2006).

Channel blockage is expressed as percentage of current inhibition at a 2-minute time point after compound treatment. Figure 3 shows the percentage of current inhibition of the M2 mutants by 100 μM WJ379 or 100 μM BC035. For the M2 mutants selected by WJ379, M2-N31S was nearly completely resistant to WJ379, as its conductance was inhibited less than 10% by 100 μM WJ379 (Dong et al., 2015). Another single mutant, M2-S31N/L26I, remained sensitive to WJ379, although it was less sensitive than the original M2-S31N. The percentage of current inhibitions for M2-S31N/L26I and M2-S31N were 64% and 82%, respectively, in the presence of 100 μM WJ379. Dose-response experiments revealed that the IC\(_{50}\) of WJ379 against the M2-S31N/L26I mutant was 72.9 μM, in contrast to 27.9 μM against M2-S31N (Fig. 4A). Similar to the results of the single mutant M2-N31S, the double mutant M2-N31S/L26I was nearly completely resistant to WJ379, showing 11% inhibition by 100 μM WJ379 (Fig. 3A). For the mutants selected by BC035, 100 μM BC035 had minimal inhibition against the M2-N31D single mutant and the M2-N31D/I32T double mutant (Fig. 3B). However, the M2-S31N/I32T single mutant remained sensitive to BC035 (Fig. 3B). The IC\(_{50}\) of BC035 against M2-S31N/I32T was 50.5 μM, only a 2.5-fold increase compared with the IC\(_{50}\) value of BC035 against M2-S31N (Fig. 4B).

### Table 2

<table>
<thead>
<tr>
<th>Passage No.</th>
<th>WJ379</th>
<th>BC035</th>
<th>Ama</th>
<th>EC(_{50})</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>μM</td>
<td>μM</td>
<td>μM</td>
<td>μM</td>
</tr>
<tr>
<td>0</td>
<td>0.49</td>
<td>N31</td>
<td>2.2</td>
<td>N31</td>
</tr>
<tr>
<td>1</td>
<td>0.30</td>
<td>N.T.</td>
<td>2.0</td>
<td>N.T.</td>
</tr>
<tr>
<td>2</td>
<td>0.60</td>
<td>N.T.</td>
<td>4.0</td>
<td>N.T.</td>
</tr>
<tr>
<td>3</td>
<td>1.20</td>
<td>N.T.</td>
<td>8.0</td>
<td>N.T.</td>
</tr>
<tr>
<td>4</td>
<td>2.50</td>
<td>L26I</td>
<td>16.0</td>
<td>N31D/I32T</td>
</tr>
<tr>
<td>5</td>
<td>5.0</td>
<td>L26I</td>
<td>16.0</td>
<td>N31D/I32T</td>
</tr>
<tr>
<td>6</td>
<td>5.0</td>
<td>N31S/L26I</td>
<td>16.0</td>
<td>N31D/I32T</td>
</tr>
<tr>
<td>7</td>
<td>0</td>
<td>N.T.</td>
<td>0</td>
<td>N.T.</td>
</tr>
<tr>
<td>8</td>
<td>0</td>
<td>N.T.</td>
<td>2.0</td>
<td>N.T.</td>
</tr>
<tr>
<td>9</td>
<td>0</td>
<td>L26I</td>
<td>0</td>
<td>I32T</td>
</tr>
<tr>
<td>10</td>
<td>0</td>
<td>N.T.</td>
<td>0</td>
<td>N.T.</td>
</tr>
<tr>
<td>11</td>
<td>0</td>
<td>N.T.</td>
<td>0</td>
<td>N.T.</td>
</tr>
</tbody>
</table>

Ama, amantadine; Res, rimantadine; N.T., not tested.

Complete resistant viruses were selected as shown by the plaque-reduction assays. No complete plaque inhibition was observed even when amantadine was added at 30 μM (30% of plaque remained compared with no drug control).

**Correlation between Electrophysiological TEVC IC\(_{50}\) Values with Antiviral EC\(_{50}\) Values Reveals the Importance of Drug Inhibition Kinetics.** In general, there is a positive correlation between an M2 channel blocker’s electrophysiological IC\(_{50}\) value and its antiviral EC\(_{50}\) value. A more potent channel blocker normally has higher antiviral activity (Wang et al., 2013b; Li et al., 2016). However, when correlating the IC\(_{50}\) and EC\(_{50}\) values of WJ379 and BC035 against M2 mutants, we found different results (Table 3). The single mutant (S31N/L26I) selected by WJ379 only conferred a 2.7-fold increase in TEVC IC\(_{50}\) values (calculated based on 2-minute time points); however, it led to more than a 60-fold increase in antiviral EC\(_{50}\) value. This discrepancy led us to further investigate the kinetics of drug binding in both S31N and S31N/L26I channels. It is of note that the percentage of channel blockage was recorded 2 minutes after compound treatment at pH 5.5. An examination of the current-inhibition traces revealed that, for S31N channel inhibition, equilibrium
Fig. 2. M2 gene sequencing traces. M2 genes at passages 0, 3, 4, 5, 6, and 9 were sequenced by Sanger sequencing. The regions (residues 18–37) that cover detected mutations are shown. Mutations are indicated by arrows. Sequencings from WJ379 serial passage experiments are shown in (A–F): WJ379, passage 0 (A); WJ379, passage 3 (B); WJ379, passage 4 (C); WJ379, passage 5 (D); WJ379, passage 6 (E); WJ379, passage 9 (F). Sequencings from BC035 serial passage experiments are shown in (G–L): BC035, passage 0 (G); BC035, passage 3 (H); BC035, passage 4 (I); BC035, passage 5 (J); BC035, passage 6 (K); BC035, passage 9 (L).
was not reached at the 2-minute time point (Fig. 5A) when tested at 100 μM, which means the true IC50 is actually lower than the recorded IC50 if enough time is given to achieve equilibrium. In contrast, for M2-S31N/L26I inhibition by WJ379 and M2-S31N/I32T inhibition by BC035, the TEVC IC50 values at 2-minute time points were true IC50 values, as equilibriums were reached before the 2-minute time point (Fig. 5, A and B). Fitting the current-conductance trace of WJ379 in inhibiting M2-S31N/L26I using a one-phase exponential decay equation gave a time constant of 8.5 seconds, which is much faster than the 45.3-second time constant in the case of M2-S31N inhibition by WJ379. Similar results were observed for BC035 in inhibiting M2-S31N and M2-S31N/I32T were 29.5 and 5.5 seconds, respectively. Another example of slow drug inhibition kinetics is amantadine and amantadine in inhibiting the WT-M2 channel was treated with amantadine, the IC50 values

To test this hypothesis, we combined WJ379 and oseltamivir carboxylate using the two-drug combination protocol (Hayden, 2013; Dunning et al., 2014). The efficacy of oseltamivir carboxylate alone was first determined by CPE assay. The EC50 of oseltamivir carboxylate against A/WSN/33 (H1N1) in MDCK cell culture was 18.4 nM in the CPE assay. In the combination therapy, a matrix was created to combine 10–10,000 nM WJ379 with 1–1000 nM oseltamivir carboxylate. Compounds were added to confluent MDCK cells that were infected with the A/WSN/33 (H1N1) virus at MOI 0.01. Cell viability was evaluated at 72 hours after infection by neutral red staining. The synergistic effect was calculated with MacSynergy II software (Prichard and Shipman, 1990; Prichard et al., 1993; Smee et al., 2010). As shown in Fig. 7, a region of significant synergy (29.0–42.4 μM2%) was observed for WJ379 and oseltamivir carboxylate at concentrations of 320–1000 and 32–100 nM, respectively. The calculated net
effect across the entire surface was a volume of synergy of 166, indicating a strong synergy.

Discussion

Despite the existence of influenza vaccines and antivirals, influenza virus infection is still one of the leading causes of death in the United States (Thompson et al., 2003, 2004). Among the two classes of Food and Drug Administration–approved anti-influenza drugs, adamantanes are no longer recommended, which leaves oseltamivir as the only orally bioavailable drug on the market. With the continuous prescription of oseltamivir, it will only be a matter of time before predominant flu strains become resistant to it. The alarming fact is that oseltamivir-resistant strains have been continuously reported, and certain strains appear to adapt to the fitness of transmission among humans, which could lead to the next influenza pandemic (Hurt et al., 2009; Kelso and Hurt, 2012; Hurt, 2014). In addressing this unmet medical need, we revisited the M2 proton channel and aim to develop the next generation of antivirals by targeting the M2-S31N mutant. M2-S31N is the predominant mutant among currently circulating influenza A viruses, including those that are resistant to oseltamivir (Dong et al., 2015). Thus, targeting M2-S31N is expected to yield broad-spectrum antivirals that are active against both oseltamivir-sensitive and oseltamivir-resistant strains (Wang, 2015). To test this hypothesis, we chose two M2-S31N inhibitors, WJ379 and BC035, which represent S31N-specific inhibitors and S31N/WT dual inhibitors, respectively, and tested their antiviral efficacy in plaque assays. It was found that WJ379 had potent antiviral activity against all four human clinical isolates with submicromolar efficacy, including two 2009 pandemic strains that are resistant to both amantadine and rimantadine (A/Texas/04/2009 and A/Denmark/528/2009). BC035 similarly inhibited both oseltamivir-sensitive and oseltamivir-resistant influenza A strains with low micromolar EC50 values. These results highlight the great therapeutic potential of the first-in-class M2-S31N inhibitors: they can serve as the second line of defense should oseltamivir fail to confine the next influenza outbreak caused by influenza A strains.

With these tool compounds in hand, we began to investigate the potential issue of drug resistance. This is critical, as addressing the efficacy is only the first step in developing antiviral drugs. Ideal antiviral drugs should also bear a high genetic barrier to drug resistance such that they can be used for a longer period of time. The genetic barrier is defined in this study as the ease of resistance generation, although it is also defined in other reports as the number of mutations needed for resistance (Vingerhoets et al., 2005; Fofana et al., 2013). The first-generation M2 channel blockers amantadine and rimantadine were rendered ineffective due to the emerging M2-S31N mutant. Related to the second generation of M2 channel blockers, which are the M2-S31N inhibitors, the concern is whether the M2-S31N channel will similarly develop resistance to S31N inhibitors. To address this, two S31N inhibitors, WJ379 and BC035, were subjected to serial passage experiments in an attempt to select resistant viruses. Not surprisingly, resistant strains were selected for both compounds at passage 4. In comparison with the genetic

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<th>TABLE 3</th>
<th>Correlations of antiviral EC50 and TEVC IC50 values.</th>
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<td></td>
<td>Passage 0</td>
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<td>WJ379</td>
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<td>TEVC IC50 (µM)</td>
<td>27.1 (2 minutes) (S31N)</td>
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<td>Antiviral EC50 (µM)</td>
<td>0.49 (S31N)</td>
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<td>BC035</td>
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<tr>
<td>TEVC IC50 (µM)</td>
<td>20.5 (S31N)</td>
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<td>Antiviral EC50 (µM)</td>
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Fig. 5. Representative TEVC recording traces showing different inhibition kinetics. (A) WJ379 in inhibiting M2-S31N and M2-S31N/L26I channels. WJ379 inhibited the M2-S31N channel much slower than the M2-S31N/L26I channel. (B) BC035 in inhibiting M2-S31N and M2-S31N/I32T channels. BC035 inhibited the M2-S31N channel much slower than the M2-S31N/I32T channel. The inhibition kinetics time constant was determined by fitting the period of recording trace when the compounds are present to the one-phase exponential decay equation [f(t) = A*exp(-t/T) + C] in Clampfit 10.3. (C) Amantadine (Ama) in inhibiting the M2-WT channel.
barriers to drug resistance for the two classes of Food and Drug Administration–approved anti-influenza drugs, M2-S31N inhibitors outperformed amantadine and are only slightly less effective than oseltamivir. In general, complete resistance to oseltamivir was generated around passage 5 (Triana-Baltzer et al., 2011; Renzette et al., 2014). Sequencing the resulting resistant viruses revealed interesting findings. For the S31N-specific inhibitor WJ379, M2-S31N simply reverted back to N31S to become resistant to WJ379. This mutation is a dominant positive mutation, as the M2-N31S/L26I double mutant was also completely resistant to WJ379. The single mutant M2-S31N/L26I alone was only partially resistant to WJ379. For the M2-S31N/WT dual inhibitor BC035, we observed similar phenomena. As BC035 is a potent inhibitor of both the S31N and the S31 (WT) channels, M2-S31N could not revert back to S31 to become resistant to it; instead, it changed to N31D. N31D is also a dominant positive mutation, and the M2-N31D/I32T was completely resistant to BC035. The single mutation M2-S31N/I32T remained sensitive to BC035, and this mutation only caused a 2-fold EC50 increase. Interestingly, both of these highly resistant mutants, N31S and N31D, appeared to be less fit than the N31 mutant in cell culture; both N31S and N31D reverted back to N31 after releasing drug selection pressure.

Fast drug-binding kinetics were observed for both WJ379 in inhibiting M2-S31N/L26I and BC035 in inhibiting M2-S31N/I32T. It is possible that M2-S31N/L26I and M2-S31N/I32T might either adapt different structures or have different dynamics than M2-S31N, which allows drugs to easily escape from the channel cavity. For example, M2-S31N/L26I and M2-S31N/I32T might have an enlarged N-termini channel entrance such that drug can easily escape from the channel. Alternatively, M2-S31N/L26I and M2-S31N/I32T might be more dynamic than M2-S31N; thus, drugs have a higher probability to escape the channels when they adapt the Openout-Closedin conformation (Khurana et al., 2009).

Although resistant mutants (L26I and I32T) were selected from serial passage experiments in cell culture under the drug selection pressure of WJ379 and BC035, respectively, both mutants appear to be rare among human influenza A viruses. We retrieved and analyzed all of the human influenza A virus M2 sequences from the Influenza Research Database (http://www.fludb.org, accessed on January 18th, 2016). L26I occurred 70 times, and I32T only occurred twice out of 18,393 M2 sequences. These results indicate that viruses carrying either of these two mutants might have a reduced fitness of transmission among humans, although more stringent experiments need to be followed to test their fitness and transmissibility.

As resistance development is, unfortunately, inevitable, one standard approach to delay resistance evolution under drug...
selection pressure is combination therapy. Combination therapy has a proven track record of reducing resistance evolution and side effects, and it is highly recommended for people with compromised immune systems who might need extended antiviral treatment to clear the viruses (Ison, 2013). As an example, the triple-drug combination therapy, commonly known as highly active antiretroviral therapy, was shown to be more effective over single- or double-drug combination therapy in suppressing human immunodeficiency virus drug resistance (Gulick et al., 1997, 1998; De Clercq, 2007).

Therefore, exploring a double-drug combination of M2-S31N inhibitors with oseltamivir in the prevention and treatment of influenza infection is a rational approach to mitigate drug resistance. The need for combination therapy is further justified because monotherapy with oseltamivir was suboptimal in the treatment of H5N1-infected patients, with a mortality rate as high as 60% (Abdel-Ghafar et al., 2008; Kundan et al., 2008). It has been shown in a number of studies that a combination of 2 inhibitors (amantadine or rimantadine) with neuraminidase inhibitors (oseltamivir carboxylate or peramivir), ribavirin, or a combination of all three was in general more synergistic in in vitro cell culture assays and in vivo mouse studies (Govorkova et al., 2004; Ilyushina et al., 2006, 2007; Simeonova et al., 2007, 2008, 2009; Smeee et al., 2009; Bantia et al., 2010). Gratifyingly, our rationally designed M2-S31N inhibitor WJ379 displayed strong synergy with oseltamivir carboxylate, with a synergy volume of 166, suggesting that combination therapy of WJ379 with oseltamivir carboxylate might be an option for controlling influenza viruses in the future.

In summary, the potent, broad-spectrum antiviral activities of M2-S31N inhibitors against currently circulating influenza A viruses, coupled with the strong synergistic effect of M2-S31N inhibitors with oseltamivir, provide compelling evidence for further development of these second-generation M2 channel blockers.

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Authorship Contributions

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Conducted experiments: Ma, Zhang.

Performed data analysis: Ma, Zhang, Wang.

Wrote or contributed to the writing of the manuscript: Ma, Zhang, Wang.

References


