

Accepted Manuscript

Amphiphilic nebramine-based hybrids Rescue legacy antibiotics from intrinsic resistance in multidrug-resistant *Gram-negative bacilli*

Xuan Yang, Derek Ammeter, Temilolu Idowu, Ronald Domalaon, Marc Brizuela, Oreofe Okunnu, Liting Bi, Yanelis Acebo Guerrero, George G. Zhanel, Ayush Kumar, Frank Schweizer

PII: S0223-5234(19)30406-4

DOI: <https://doi.org/10.1016/j.ejmech.2019.05.003>

Reference: EJMECH 11313

To appear in: *European Journal of Medicinal Chemistry*

Received Date: 12 November 2018

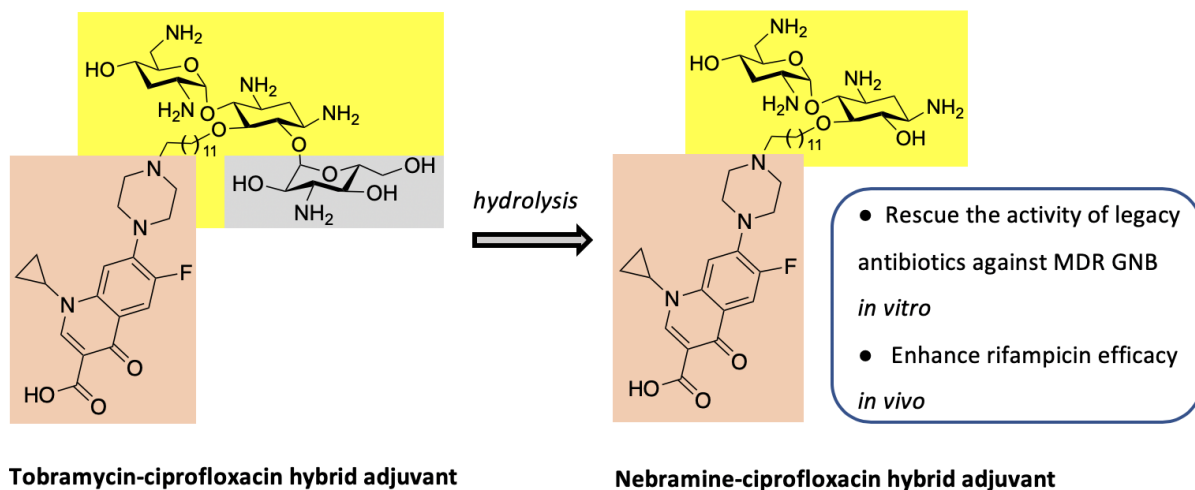
Revised Date: 24 April 2019

Accepted Date: 1 May 2019



Please cite this article as: X. Yang, D. Ammeter, T. Idowu, R. Domalaon, M. Brizuela, O. Okunnu, L. Bi, Y.A. Guerrero, G.G. Zhanel, A. Kumar, F. Schweizer, Amphiphilic nebramine-based hybrids Rescue legacy antibiotics from intrinsic resistance in multidrug-resistant *Gram-negative bacilli*, *European Journal of Medicinal Chemistry* (2019), doi: <https://doi.org/10.1016/j.ejmech.2019.05.003>.

This is a PDF file of an unedited manuscript that has been accepted for publication. As a service to our customers we are providing this early version of the manuscript. The manuscript will undergo copyediting, typesetting, and review of the resulting proof before it is published in its final form. Please note that during the production process errors may be discovered which could affect the content, and all legal disclaimers that apply to the journal pertain.



**Amphiphilic Nebramine-based Hybrids Rescue Legacy Antibiotics
from Intrinsic Resistance in Multidrug-resistant *Gram-negative*
*Bacilli***

Xuan Yang ^a, Derek Ammeter ^a, Temilolu Idowu ^a, Ronald Domalaon ^a, Marc Brizuela ^a, Oreofe Okunnu ^a, Liting Bi ^a, Yanelis Acebo Guerrero ^b, George G. Zhanel ^c, Ayush Kumar ^b, Frank Schweizer ^{a, b, *}

^a Department of Chemistry, University of Manitoba, Winnipeg, MB, R3T 2N2, Canada.

^b Department of Microbiology, University of Manitoba, Winnipeg, MB R3T 2N2, Canada.

^c Department of Medical Microbiology, University of Manitoba, Winnipeg, MB R3T 1R9, Canada.

Abstract

The inability to discover novel class of antibacterial agents, especially against Gram-negative bacteria (GNB), compel us to consider a broader non-conventional approach to treat infections caused by multidrug-resistant (MDR) bacteria. One such approach is the use of adjuvants capable of revitalizing the activity of current existing antibiotics from resistant pathogens. Recently, our group reported a series of tobramycin (TOB)-based hybrid adjuvants that were able to potentiate multiple classes of legacy antibiotics against various MDR GNB. Herein, we report the modification of TOB-based hybrid adjuvants by replacing TOB domain by the pseudo-disaccharide nebramine (NEB) through selective cleavage of the α -D-glucopyranosyl linkage of TOB. Potent synergism was found for combinations of NEB-based hybrid adjuvants with multiple classes of legacy antibiotics including fluoroquinolones (moxifloxacin and ciprofloxacin), tetracyclines (minocycline), or rifamycin (rifampicin) against both wild-type and MDR *P. aeruginosa* clinical isolates. We also demonstrated that a combination of the optimized NEB-CIP hybrid **1b** and rifampicin protects *Galleria mellonella* larvae from the lethal effects of extensively drug-resistant (XDR) *P. aeruginosa*. Mechanistic evaluation of NEB-based hybrid adjuvants revealed that the hybrids affect the outer- and inner membranes of wild-type *P. aeruginosa* PAO1. This study describes an approach to optimize aminoglycoside-based hybrids to yield lead adjuvant candidates that are able to resuscitate the activity of partner antibiotics against MDR GNB.

Keywords: Nebramine; Hybrids; Adjuvants; Synergy; Antibacterial; Multi-drug resistant Gram-negative bacilli

1. Introduction

Starting from Fleming's discovery of penicillin in 1929 [1], a large number of antibiotics have been discovered, developed, and marketed. Antibiotics have saved countless lives and played a key role in the advancement of medical science for the past 70 years [2,3]. However, rampant and indiscriminate use of antibiotics has escalated the prevalence of multidrug-resistant (MDR) bacterial infections, especially those that are caused by Gram-negative pathogens. Worse still, there is a steady decline in the discovery of novel drug classes able to eradicate MDR Gram-negative pathogens which is largely due to the lack of understanding of the physicochemical properties necessary for antibacterial agents to efficiently traverse and accumulate inside Gram-negative bacterial cell [4,5]. There is an urgent need to find novel and perhaps unconventional approaches to address bacterial infection. Co-administration of helper molecules called adjuvants capable of enhancing the activity of currently used antibiotics and extend the life of legacy antibiotics is a viable strategy to overcome antimicrobial resistance [6,7].

Our group recently has demonstrated that amphiphilic TOB-based conjugates were able to revive the antibacterial activity of multiple classes of antibiotics against MDR Gram-negative bacilli (GNB), especially against *P. aeruginosa* [7–14]. For example, we first reported TOB-ciprofloxacin hybrids with poor intrinsic antibacterial activity were able to restore the activity of fluoroquinolone antibiotics against ciprofloxacin-resistant MDR or XDR (extensively drug-resistant) *Pseudomonas aeruginosa* in combination therapy [8]. Structure-activity studies revealed that the presence of both TOB and ciprofloxacin pharmacophores tethered by a 12-carbon-long (C_{12}) aliphatic linker is critical to the potentiation of fluoroquinolone antibiotics [8]. Encouraged by these results, an unconventional structure-activity relationship study was pursued by replacing the ciprofloxacin fragment of TOB-ciprofloxacin hybrid by other pharmacophores.

Since then, we have developed a series of TOB-moxifloxacin hybrids [9], TOB-efflux pump inhibitors conjugates [10,11], TOB-lysine peptoid conjugates [12,13], as well as TOB-polymyxin B₃ hybrids [14]. Biological evaluations revealed that these TOB-based conjugates retained the adjuvant properties of TOB-ciprofloxacin hybrids to a variable extent. These results suggest that the TOB fragment linked to C₁₂ tether is the core scaffold that is responsible for the adjuvant properties. Mechanistic studies revealed that these TOB-based conjugates permeabilize the outer membrane and dissipate the proton motive force (PMF) located in the cytoplasmic membrane of *P. aeruginosa* [9,10,12].

TOB is known to eradicate Gram-negative bacteria by disruption of the outer membrane at higher concentrations ($\geq 8 \mu\text{g/mL}$) [15]. However, at lower concentrations ($< 4 \mu\text{g/mL}$), TOB, selectively interacts with the 16S rRNA, thereby causing inhibition of bacterial protein translation [15,16]. The TOB's pseudo-disaccharide segment (ring I and ring II), namely NEB (NEB), is the essential pharmacophore responsible for most of the specificity of the interactions with the ribosome [17–21]. In addition, it was recently reported that an amphiphilic NEB derivative displayed potent activity against certain TOB-resistant Gram-negative bacteria suggesting that amphiphilic NEB analogs possess a different mode of action than TOB [22]. In addition, neamine-based and neosamine-based amphiphiles have been reported to possess potent antipseudomonal properties by interacting with the outer membrane of *P. aeruginosa* [23–25].

To understand the effect of TOB on the overall adjuvant activity of previously reported TOB-based conjugates, we decided to replace TOB by NEB and evaluate its microbiological activity. We questioned whether the modification of the TOB domain would retain the adjuvant properties of our reported conjugates. To accomplish this aim, we selected TOB-moxifloxacin and TOB-ciprofloxacin as lead compounds and replaced TOB by NEB, while keeping the

moxifloxacin (MOX) and ciprofloxacin (CIP) fragments and the C_{12} hydrocarbon tether as shown in hybrid NEB-MOX (**1a**) and NEB-CIP (**1b**) (Fig. 1). In addition, we also prepared a NEB-NMP (1-(1-naphthylmethyl)-piperazine) hybrid **2** containing a slightly reduced C_{10} hydrocarbon tether to potentially reduce non-specific protein binding and investigated its adjuvant properties. NMP is a well-known efflux pump inhibitor (EPI) of various efflux pumps in Gram-negative bacteria except *P. aeruginosa* [26].

2. Results and Discussion

2.1 Chemistry

The preparation of NEB-based hybrids (**1a**, **1b**, and **2**) were done by selective degradation of TOB-based hybrids as outlined in Scheme 1. Commercially available tobramycin was transformed into the *N*-Boc-, and *O*-TBDMS-protected tobramycin **3** with the exception of the sterically hindered C-5 alcohol, following previously reported procedures (Scheme 1) [9,10,12,27]. Alkylation of **3** with 1,12-dibromododecane or 1,10-dibromodecane in the presence of a phase transfer catalyst, tetrabutylammonium hydrogen sulfate (TBAHS), afforded bromoalkylated tobramycin (**4a** and **4b**). This bromide (**4a**) was then converted to primary alcohol **5** followed by oxidation reaction using pyridinium chlorochromate (PCC) to generate aldehyde **6** in good yield. Protected hybrid **7a** and **7b** were synthesized via reductive amination between moxifloxacin methyl ester or ciprofloxacin methyl ester and aldehyde **6**. Heating hybrids **7a** and **7b** in aqueous HCl solution resulted in regioselective hydrolysis of the α -D-glucopyranosyl bond [21,22] along with the simultaneous removal of Boc and TBDMS protecting groups. To avoid a laborious separation and purification of the obtained pseudo-

disaccharides, NEB-MOX and NEB-CIP hybrids, the four free amino groups of NEB were protected by (Boc)₂O to afford the corresponding *N*-Boc-protected NEB-MOX hybrid **8a** and *N*-Boc-protected NEB-CIP hybrid **8b** that could easily be purified by flash chromatography. De-esterification and subsequent global deprotection of the amino groups finally resulted in desired the NEB-MOX (**1a**) and NEB-CIP (**1b**) compounds (Scheme 1). A related strategy was used to synthesize NEB-NMP (**2**) (Scheme 1).

2.2 Combination Study of Hybrids with Antibiotics

To determine whether the NEB-MOX hybrid **1a** retain the adjuvant properties of previously reported TOB-moxifloxacin hybrids, checkerboard studies were performed. Initially, we assessed the combination of hybrid **1a** with three different classes of clinically-used antibiotics including the fluoroquinolone antibiotic moxifloxacin, the tetracycline antibiotic minocycline, and the rifamycin antibiotic rifampicin against wild-type *P. aeruginosa* PAO1 (Table 1) by using the fractional inhibitory concentration index (FICI) as a measure of the interaction between two agents. FICI of ≤ 0.5 , > 0.5 to ≤ 4 , and > 4 indicate synergy, no interaction, and antagonism, respectively [28]. In accordance with previous findings against wild-type *P. aeruginosa* PAO1 [8,10,12], NEB-MOX hybrid **1a** displayed weak antibacterial activity (MIC = 32 $\mu\text{g/mL}$) as a stand-alone agent. However, it was found to be synergistic (FICI of 0.25) with the fluoroquinolone moxifloxacin (Table 1). Synergism was also observed with minocycline (FICI of 0.38) as well as the outer membrane-impermeable antibiotic rifampicin (FICI of 0.07) (Table 1). The absolute MICs [the MIC of antibiotics in the presence of 8 $\mu\text{g/mL}$ (7.5 μM) hybrid **1a**] of three tested antibiotics, moxifloxacin, minocycline, or rifampicin, in combination therapy with hybrid **1a** were significantly reduced compared to monotherapy,

especially for rifampicin (≥ 256 -fold potentiation). It should be noted that the clinically-approved β -lactamase inhibitor avibactam is typically administered at 15 μ M concentration to potentiate the cephalosporin ceftazidime in *in vitro* studies [29,30].

To validate our findings in wild-type *P. aeruginosa* strain, we performed the same checkerboard study using a panel of eight MDR or XDR *P. aeruginosa* clinical isolates (Supplementary Information Table S1) as previously studied for TOB-based hybrids [8,10–12]. Notably, among this panel of clinical isolates, two strains (*P. aeruginosa* 91433 and 101243) are non-susceptible or resistant to colistin that is considered to be the antibiotic of last resort for the treatment of carbapenem-resistant Gram-negative bacterial infections [31]. We determined the FIC index of hybrid **1a** in combination with moxifloxacin, ciprofloxacin, minocycline, or rifampicin across the eight clinical isolates panel. Strong potentiation was seen with moxifloxacin, ciprofloxacin, minocycline, or rifampicin (FIC indices of 0.004 to 0.28) against these pathogens, with the exception of ciprofloxacin against *P. aeruginosa* 100036 and 101885 strains (FICI > 0.5) (Table 2, Table 3, Table 4).

Next, we evaluated the adjuvant potencies of hybrid **1a** by comparing the absolute MICs [in the presence of 8 μ g/mL (7.5 μ M) hybrid **1a**] of the four antibiotics to their established susceptibility breakpoints. According to the Clinical and Laboratory Standards Institute (CLSI), the susceptible breakpoint, a chosen concentration (μ g/mL) of an antibiotic which defines a strain of bacteria whether it is susceptible to this antibiotic, of ciprofloxacin for *P. aeruginosa* is 1 μ g/mL [32]. However, the established susceptibility breakpoints for the other three tested antibiotics against *P. aeruginosa* are not available since they are unconventional antibiotics for the treatment of *P. aeruginosa* infections. Therefore, the susceptibility breakpoints of minocycline for *Acinetobacter* spp. (≤ 4 μ g/mL) and rifampicin for *Enterococcus* spp. (≤ 1

$\mu\text{g/mL}$) reported by CLSI were used as interpretative guidelines [32]. It is noteworthy that the French Society for Microbiology has established a rifampicin breakpoint for *Acinetobacter baumannii* based on MIC distributions (susceptible, $\leq 4 \mu\text{g/mL}$; intermediate, $8\text{--}16 \mu\text{g/mL}$; and resistant, $\geq 16 \mu\text{g/mL}$) [33]. In addition, we conservatively considered the susceptibility breakpoint of moxifloxacin for *P. aeruginosa* to be similar to that of ciprofloxacin, as both belong to the fluoroquinolone class of antibiotics.

For the two fluoroquinolones, combinations of NEB-MOX hybrid **1a** with moxifloxacin yielded stronger potentiation than ciprofloxacin against the panel of MDR/XDR *P. aeruginosa* clinical isolates (Table 2). The adjuvant potency of hybrid **1a** in combination with moxifloxacin is comparable to previously reported TOB-ciprofloxacin hybrid [8]. In 37.5% of cases, both hybrid **1a** and TOB-ciprofloxacin hybrid **1b**, at concentrations of $\leq 8 \mu\text{g/mL}$ ($6.8\text{--}7.5 \mu\text{M}$), were able to bring down the MIC of moxifloxacin below its interpretative susceptibility breakpoint ($\leq 1 \mu\text{g/mL}$) against moxifloxacin-resistant MDR/XDR *P. aeruginosa* isolates (Table 2) [8]. However, the same susceptibility breakpoint was not reached for ciprofloxacin in combination with hybrid **1a** at concentration of $8 \mu\text{g/mL}$ ($7.5 \mu\text{M}$) against all the tested ciprofloxacin-resistant MDR/XDR *P. aeruginosa* isolates (Table 2). In contrast, the MICs of minocycline (8/8 minocycline-resistant MDR/XDR *P. aeruginosa* isolates) and rifampicin (7/8 rifampicin-resistant MDR/XDR *P. aeruginosa* isolates) were strongly reduced below their susceptibility breakpoints in the presence of $8 \mu\text{g/mL}$ ($7.5 \mu\text{M}$) hybrid **1a**, an effect that is consistent with previously reported TOB-efflux pump inhibitor conjugates and TOB-lysine peptoid conjugates (Table 3, Table 4) [10,12].

A summarized result of antibacterial activity of minocycline (MIN) and rifampicin (RIF) alone or in combination with a fixed concentration of $8 \mu\text{g/mL}$ ($7.5 \mu\text{M}$) hybrid **1a** against the

panel of eight MDR/XDR *P. aeruginosa* clinical isolates is shown in Table 5. The MIC₈₀ of minocycline and rifampicin in combination with 8 µg/mL (7.5 µM) hybrid **1a** were significantly lower in comparison to the MIC₈₀ of the antibiotic alone. Moreover, the absolute MIC₈₀ of minocycline (1 µg/mL) and rifampicin (0.13 µg/mL) were found to be less than their respective CLSI susceptibility breakpoints. Similarly, we demonstrated strong synergy of NEB-CIP (**1b**) with minocycline or rifampicin against wild-type and MDR *P. aeruginosa* strains (Table 6). For instance, in presence of only 4 µg/mL (4.1 µM) of hybrid **1b**, minocycline showed a 32-fold potentiation while rifampicin resulted in a 128 – ≥256-fold potentiation in wild-type and MDR *P. aeruginosa* strains (Table 6).

The observed potentiation of rifampicin by hybrid **1a** and **1b** may be explained by our previous findings that demonstrated that amphiphilic TOB-based hybrid adjuvants perturb the outer membrane of *P. aeruginosa* in a dose-dependent manner, thus facilitating the entry of antibiotics that are unable to cross the outer membrane of Gram-negative bacteria, such as rifampicin [8–10,12]. NEB-based hybrids seem to have a similar membrane effect as that of TOB-based hybrids. Since rifampicin is a poor substrate for *P. aeruginosa* RND efflux pumps [10,12], outer membrane perturbation is most likely to be the reason to explain the observed strong synergistic effects of hybrid **1a** and **1b** in combination with rifampicin against *P. aeruginosa*.

We also investigated synergy of NEB-NMP hybrid **2** with various antibiotic classes including fluoroquinolones (moxifloxacin, ciprofloxacin), tetracyclines (minocycline), or rifamycin (rifampicin) against wild-type and MDR *P. aeruginosa* strains (Table 7). More importantly, NEB-NMP (**2**) reduced the MIC of minocycline below its CLSI susceptibility

breakpoint ($\leq 4 \mu\text{g/mL}$) against all tested *P. aeruginosa* strains. The observed adjuvant property of NEB-NMP (**2**) is consistent with that of reported TOB-NMP conjugate [10].

Besides *P. aeruginosa*, we also explored the synergistic effects of NEB-based hybrids (**1a** and **1b**) with minocycline or rifampicin against other MDR GNBs such as *Acinetobacter baumannii*, *Escherichia coli*, *Klebsiella pneumoniae*, and *Enterobacter cloacae* (Tables 8 and 9). Again, both NEB-MOX **1a** and NEB-CIP **1b** displayed poor antibacterial activity by themselves against these pathogens (MICs of $\geq 8 \mu\text{g/mL}$). In the case of *A. baumannii*, minocycline was not potentiated against the four tested isolates while NEB-MOX **1a** was able to synergize rifampicin, leading to 32- to 64-fold reductions in MICs at a concentration of $8 \mu\text{g/mL}$ ($7.5 \mu\text{M}$) of the adjuvant. Similarly, against *A. baumannii*, we observed an additive relationship of NEB-CIP (**1b**) with minocycline while the combination of NEB-CIP (**1b**) with rifampicin remained synergistic (Table 9). With respect to *K. pneumoniae*, *E. cloacae*, or *E. coli*, NEB-MOX (**1a**) and NEB-CIP (**1b**) displayed strong synergism with rifampicin against all isolates tested while synergism of NEB-MOX (**1a**) and NEB-CIP (**1b**) with minocycline was only observed in few isolates (Tables 8 and 9).

2.3 Time-kill Curve

To confirm the synergistic activity between NEB-based hybrids and minocycline or rifampicin, time-kill assays were performed. We first studied the time killing kinetics of minocycline at $4 \mu\text{g/mL}$ ($\frac{1}{2} \times \text{MIC}$) in combination with NEB-MOX **1a** at sub-inhibitory concentration ($\frac{1}{2} \times \text{MIC} = 16 \mu\text{g/mL}$ or $\frac{1}{4} \times \text{MIC} = 8 \mu\text{g/mL}$) against *P. aeruginosa* wild-type PAO1 (Fig. 2A). We set a fixed concentration of $4 \mu\text{g/mL}$ minocycline for the kinetic study since the CLSI susceptibility breakpoint of minocycline is $\leq 4 \mu\text{g/mL}$. It was demonstrated that

combination of bacteriostatic minocycline ($4\ \mu\text{g/mL}$) with $\frac{1}{2} \times \text{MIC}$ of hybrid **1a** became bactericidal and resulted in complete eradication of *P. aeruginosa* PAO1 over a 24 h time period. This enhanced killing efficiency of minocycline in combination with hybrid **1a** is consistent with our previous findings for TOB-based hybrids [10,12] and are likely the results of the membrane effects induced by hybrid **1a**. Furthermore, we also studied the killing kinetics of NEB-CIP **1b** in combination with rifampicin against XDR *P. aeruginosa* PA259. A combination of sub-MIC of **1b** ($1\ \mu\text{g/mL}$, MIC of **1b** is $>128\ \mu\text{g/mL}$) and rifampicin ($1/16 \times \text{MIC} = 1\ \mu\text{g/mL}$) yielded a 3-order magnitude decrease in viable bacterial counts over 8 h time period (Fig. 2B). Complete eradications were observed at a higher concentration of **1b** ($4\ \mu\text{g/mL}$) in combination with rifampicin at $1\ \mu\text{g/mL}$ or $4\ \mu\text{g/mL}$ for only 4 h of antimicrobial exposure (Fig. 2B).

2.4 Hemolytic Activity and *In Vivo* Efficacy Study

To investigate whether the adjuvant properties of the NEB-based hybrids translates into a measurable *in vivo* effect, we selected the established *in vivo* *Galleria mellonella* larvae infection model to study the efficacy of hybrid **1b**-rifampicin combination therapies against *P. aeruginosa* [34,35]. Initially, we demonstrated that NEB-CIP **1b** was non-hemolytic to pig erythrocytes ($<10\%$ at $512\ \mu\text{g/mL}$) (Fig. 3). We also examined the tolerability of **1b** on *G. mellonella* and found that the larvae survived beyond 96 h when administered with 100 mg/kg dosage of **1b** (Fig. 4). However, colistin resulted in 70% and 90% larvae deaths at the dosage of 75 mg/kg and 100 mg/kg, respectively, after 96 h, consistent with known toxicity of colistin to eukaryotic cells. We also established that 5 CFU of XDR *P. aeruginosa* PA264 alone resulted in 100% lethality of the larvae after 18 h. To assess the ability of combination therapy of **1b** and rifampicin to protect against XDR *P. aeruginosa* PA264-challenge larvae, single treatment doses of rifampicin +

compound **1b** (25 + 25 mg/kg, 50 + 50 mg/kg, and 75+75 mg/kg) were administered 2 h post inoculation with 5 CFU XDR *P. aeruginosa* PA264 (bacterial isolate was only susceptible to colistin). The results showed that monotherapy with a single dose of rifampicin (75 mg/kg) or **1b** (100 mg/kg) resulted in 10% and 0% survival of the larvae after 18 h, respectively (Fig. 5). In contrast, combination of rifampicin and **1b** improved the survival of the wax moth larvae in a dose-dependent manner (Fig. 5). For instance, a single dose combination of rifampicin with **1b** (75 + 75 mg/kg) resulted in 87% and 53% survival after 18 h and 24 h respectively. A 50 + 50 mg/kg single dose combination of rifampicin and **1b** resulted in 60% and 33% survival after 18 h and 24 h, respectively, while a 25 + 25 mg/kg single dose combination of rifampicin and **1b** resulted in a 33% and 13% survival after 18 h and 24 h, respectively. This clearly demonstrates a dose-dependent survivability of the infected larvae when treated with a combination of rifampicin and compound **1b**. It is interesting to note that a 25 + 25 mg/kg rifampicin + **1b** was more effective (13% survival) than 25 mg/kg of colistin (0% survival) after 24 h, although it is unclear whether the inability of colistin to protect the larvae is due to lack of effectiveness or a colistin-induced toxicity. Overall, these results demonstrate the therapeutic potential of NEB-based hybrid **1b** + rifampicin to treat MDR/XDR infections *in vivo*. We also assessed the toxicity of adjuvants **1a** or **1b** against the HepG2 and HEK293 cell lines alone and in combination with rifampicin. These results confirmed that adjuvants **1a** and **1b** do not possess elevated toxicity at their synergistic concentration alone and in combination with Rifampicin. (Figure S1).

2.5 Tetracycline Uptake Assay

To gain insight to the synergistic mechanism of NEB-MOX hybrid **1a** with minocycline, fluorescence-based tetracycline uptake assay for Gram-negative bacteria [36] was performed to investigate the effect of hybrid **1a** on the uptake of tetracycline (Fig. 6). Our results indicate that, similar to TOB-based hybrids [10], hybrid **1a** enhances the uptake of tetracycline in *P. aeruginosa* PAO1 in a concentration-dependent manner. Comparable enhancements in tetracycline uptake were also observed with membrane-targeting antibiotic colistin (Fig. 6). We previously reported that TOB-based hybrids not only permeabilize the Gram-negative bacterial outer membrane but also depolarize the cytoplasmic membrane [8–10,12]. TOB-based hybrids specifically dissipate the electrical component ($\Delta\psi$) of the proton motive force (PMF) resulting in a compensatory increase in transmembrane chemical component (ΔpH) in order to counter this effect and maintain ATP synthesis level. The effect of TOB-based hybrids on $\Delta\psi$ is likely retained in NEB-MOX hybrid **1** which is consistent with the observed synergy of hybrid **1a** with minocycline, as tetracycline uptake is ΔpH -dependent [36]. Disruption of $\Delta\psi$ by hybrid **1a** is compensated by an increase in ΔpH that in turn enhances the uptake of tetracycline antibiotics. This was further corroborated by the observation that CCCP (carbonyl cyanide *m*-chlorophenyl hydrazone) inhibits tetracycline accumulation (Fig. 6). CCCP is an uncoupler of oxidative phosphorylation that disrupts the proton gradient (ΔpH) of bacterial membranes [37]. Moreover, minocycline is known to inhibit preferentially the biosynthesis of envelop proteins [38] which, perhaps, elicits further compromise of the intrinsic resistance barrier (the Gram-negative bacterial outer membrane), thereby augmenting the effects of NEB-based hybrid **1a**.

3 Conclusions

In this study, we demonstrated that NEB-based hybrids (**1a**, **1b**, and **2**) are capable of potentiating multiple classes of antibiotics including fluoroquinolones (moxifloxacin, ciprofloxacin), tetracycline (minocycline), and rifamycin (rifampicin) against wild-type and MDR/XDR GNBs including *P. aeruginosa*, *A. baumannii*, *K. pneumonia*, and *E. cloacae* strains. The adjuvant potencies of NEB-based hybrids (**1a**, **1b**, and **2**) are comparable to that of TOB-based hybrids as studied before [7–14], suggesting that cleavage of the 3-deoxy-3-amino α -D-glucosidic linkage in TOB to yield NEB did not significantly alter the adjuvant properties of this scaffold. Mechanistic study of NEB-MOX **1a** confirm that it also retains the membrane effects of TOB-based hybrid adjuvants including TOB-fluoroquinolone hybrids. Modification of the tobramycin domain of TOB-based hybrid suggests that the pseudo-disaccharide NEB linked to C_{12} tether is the essential membrane active core responsible for the adjuvant properties. This study provides further insight into structural optimization of previously investigated TOB-based hybrid adjuvants. Moreover, the reduced number of basic functions in NEB when compared to TOB may result in reduced aminoglycoside-induced cytotoxicity.

4 Experimental section

4.1 Synthetic Chemistry

4.1.1 General Comments

Reactions were monitored by thin-layer chromatography (TLC) on silica gel 60 F254 (0.25 mm, Merck) and the compounds were visualized using ultraviolet light and/or stain with

ninhydrin solution (ninhydrin and acetic acid in ethanol). 1D and 2D (^1H , ^{13}C , DEPT, COSY, HSQC, HMBC) nuclear magnetic resonance (NMR) characterization experiments were performed on either Bruker AMX-500 or Bruker AMX-300 spectrophotometer in the noted deuterated solvents. Chemical shifts (δ) are reported in parts per million with CHCl_3 (7.26 ppm), DHO (4.79 ppm), and CD_2HOH (3.31 ppm) used as internal standards. NMR spectra were analyzed using Mnova Software 8.0 version. Electrospray ionization (ESI) mass spectrometry (MS) experiments were carried out on a Varian 500 MS ion trap mass spectrometer. Matrix-assisted laser desorption ionization (MALDI) MS experiments were performed on a Bruker Daltonics Ultraflex MALDI TOF/TOF mass spectrometer. Analytical high-performance liquid chromatography (HPLC) was carried out on Breeze HPLC Waters with 2998 PDA detector (1.2 nm resolution) connected to a Synergi 4 μm Polar-RP 80 Å LC column (50 mm \times 4.6 mm, Phenomenex). Yields are given following purification, unless otherwise stated. All of the tested compounds are at least 95% pure as estimated by HPLC.

4.1.2 Synthetic Procedures and Characterizations

Detailed experimental procedures of compounds **3**, **4a**, **4b**, **5**, **6**, **9**, moxifloxacin methyl ester and ciprofloxacin methyl ester were described in the supporting information.

General synthetic procedure A: final deprotection of compounds 8a and 8b. Compound **8a** or **8b** (0.014 mmol) was dissolved in MeOH (2 mL). 2 N lithium hydroxide solution (1 mL) was then added to the solution while stirring. The reaction mixture was stirred at room temperature for 30 min. In an ice bath, careful acidification of the solution to pH = 6 was done by slow addition of 1 N HCl (a.q.). The solvent was removed *in vacuo*. The residue was purified by flash chromatography (elution with a gradient of DCM/MeOH from 9:1 to 1:1, v/v) to afford a

white solid which was dissolved in TFA (2 mL) and H₂O (1 mL) solution and stirred for 2 h at room temperature. The solvent was removed under reduced pressure to give a yellow residue. 20 mL of methanol and ether solution (1:20, v/v) was added to this residue in several portions and then the solvent was decanted to get a yellow solid as nebramine-based hybrid TFA salt. Stoichiometric amount of HCl aqueous solution was added into it before lyophilizing the solution to afford a yellow solid as the final product as the HCl salt.

*General synthetic procedure B: synthesis of **7a** and **7b** via reductive amination.*

Moxifloxacin methyl ester (0.49 mmol) or ciprofloxacin methyl ester was mixed with aldehyde **6** (0.41 mmol), followed by the addition of dry DCE (25 mL) and AcOH (2.3 μ L, 0.041 mmol) under N₂ gas. The reaction mixture was stirred at room temperature for 7 h before NaBH(OAc)₃ (1.64 mmol) was added at 0 °C. The solution was gradually warmed to room temperature while stirring overnight. The reaction mixture was cooled to 0 °C and quenched carefully by the drop-wise addition of saturated NaHCO₃ solution (10 mL). The solution was then extracted with DCM (3 \times 15 mL). The organic layer was washed with brine, dried over anhydrous sodium sulfate and concentrated in vacuo. The crude product was purified by flash chromatography (elution with a gradient of DCM/MeOH from 50:1 to 10:1, v/v) to afford the desired product as a white solid.

*General synthetic procedure C: synthesis of Boc-protected NEB-based hybrids **8a**, **8b** and **10** [21,22].* 40% HCl (3 mL) and MeOH (5 mL) were added to **7a**, **7b** or **9** (0.048 mmol) slowly. The reaction was heated to 70 °C and stirred 24 h. The solution was cooled down to room temperature and neutralized with solid sodium bicarbonate before concentrated to dryness. The residue was taken up in 30 mL of MeOH, filtered and concentrated to give a crude 5-*O*-(dodecyl-moxifloxacin methyl ester)-nebramine or 5-*O*-(dodecyl-ciprofloxacin methyl ester)-nebramine HCl salt. The above crude product was dissolved in MeOH (15 mL) at room temperature.

Triethylamine (69 μ L, 0.48 mmol) and (Boc)₂O (0.38 mmol) were added into the solution and stirred overnight at 55 °C. Upon completion, the reaction mixture was concentrated *in vacuo*. Purification by flash column chromatography (elution with a gradient of DCM/MeOH from 30:1 to 10:1 for **8a** and **8b**, elution with a gradient of DCM/MeOH from 100:1 to 40:1 for compound **10**) to afford a white solid as desired product.

5-O-(dodecyl-moxifloxacin)-nebramine 5·HCl (1a). Synthesized following general procedure A. Yield: 8 mg (53%). ¹H NMR (500 MHz, deuterium oxide) δ 8.96 (s, 1H, N-CH of aromatic ring), 7.58 (d, *J* = 69.9 Hz, 1H, F-C-CH of aromatic ring), 5.67 – 5.53 (m, 1H, CH of H-1'), 4.39 – 4.02 (m, 5H, CH of cyclopropyl, 2×N-CHH of moxifloxacin, CH of H-5', CH of H-4), 4.02 – 3.56 (m, 13H, OCH₂ of linker, CH of H-4', CH of moxifloxacin, N-CHH of moxifloxacin, CH of H-2', N-CHH of linker, OCH₃ of moxifloxacin, CH of H-5, CH of H-6, CH of H-1), 3.56 – 3.29 (m, 5H, 2×N-CHH of moxifloxacin, CH₂ of H-6', CH of H-3), 3.28 – 3.09 (m, 2H, N-CHH of moxifloxacin, N-CHH of linker), 3.09 – 2.95 (m, 1H, CH of moxifloxacin), 2.58 – 2.50 (m, 1H, CHH of H-2), 2.39 – 2.28 (m, 1H, CHH of H-3'), 2.23 – 2.14 (m, 1H, CHH of H-3'), 2.14 – 0.82 (m, 29H, CHH of H-2, 10×CH₂ of linker, 2×C-CH₂ of moxifloxacin, 2×CH₂ of cyclopropyl). ¹³C NMR (125 MHz, deuterium oxide, some carbons are doubling due to fluorine atom) δ 176.37 (CO of quinoline), 169.71 (CO of carboxylic acid), 153.23 (CF of quinoline), 152.25 (CF of quinoline), 151.04 (CH, C-2 of quinoline), 141.77 (C-8 of quinoline), 135.02 (C-7 of quinoline), 134.85 (C-8a of quinoline), 117.57 (C-4a of quinoline), 106.84 (CH, C-5 of quinoline), 106.67 (C-3 of quinoline), 92.08 (C-1'), 82.73 (C-6), 75.07 (C-4), 73.48 (O-CH₂ of linker), 73.22 (C-5'), 72.69 (C-5), 63.83 (C-4'), 62.24 (O-CH₃), 56.96 (N-CH₂ of linker), 54.21 (CH₂ of pyrrolidine), 52.41 (CH of pyrrolidine), 50.90 (CH₂ of pyrrolidine), 49.87 (C-1), 48.94 (C-3), 47.53 (C-2'), 41.36 (N-CH₂ of piperidine), 39.30 (C-6'), 36.00 (CH of cyclopropyl),

35.56 (CH of pyrrolidine), 29.64 (O-CH₂-CH₂ of linker), 29.27 (CH₂ of linker), 29.12 (CH₂ of linker), 28.99 (C-3'), 28.82 (CH₂ of linker), 28.70 (CH₂ of linker), 28.21 (CH₂ of linker), 28.06 (C-2), 27.92 (CH₂ of linker), 26.04 (CH₂ of linker), 25.30 (CH₂ of linker), 20.15 (CH₂ of piperidine), 17.95 (CH₂ of piperidine), 9.90 (CH₂ of cyclopropyl), 8.17 (CH₂ of cyclopropyl).

MALDI-TOF-MS *m/e* calcd for C₄₅H₇₂FN₇O₉Na [M+Na]⁺: 896.5273, found: 896.5290.

5-O-(dodecyl-ciprofloxacin)-nebramine 5·HCl (1b). Synthesized following general procedure A. Yield: 13.4 mg (32%). ¹H NMR (500 MHz, deuterium oxide) δ 8.67 (s, 1H, N-CH of aromatic ring), 7.62 – 7.44 (m, 2H, C-CH of aromatic ring), 5.58 (d, *J* = 3.2 Hz, 1H, anomeric H-1'), 4.14 – 4.06 (m, 2H, H of piperazine), 4.05 – 3.94 (m, 3H, NC-H of cyclopropyl, C-H of C-O of linker), 3.89 – 3.72 (m, 7H, H-6, H-2', H-4', 2C-H of C-O of linker, 2C-H of C-N of linker), 3.69 – 3.58 (m, 2H, H-1, H-5'), 3.48 – 3.26 (m, 9H, H-3, 2H of H-6', 4H of piperazine, 2C-H of linker), 2.53 (m, 1H, H-2), 2.32 (m, 1H, H-3'), 2.16 (m, 1H, H-3'), 1.96 (m, 1H, H-2), 1.88 – 1.78 (m, 2H, C-H of linker), 1.69 – 1.58 (m, 2H, C-H of linker), 1.50 – 1.28 (m, 18H, CH₂ of cyclopropyl and CH₂ of linker), 1.23 (m, 2H, CH₂ of cyclopropyl). ¹³C NMR (125 MHz, deuterium oxide) δ 176.11 (CO of quinoline), 169.10 (CO of carboxylic acid), 154.48 (CF of quinoline), 152.48 (CF of quinoline), 148.48 (CH, C-2 of quinoline), 144.32 (C-7 of quinoline), 144.24 (C-7 of quinoline), 139.10 (C-8a of quinoline), 118.99 (C-4a of quinoline), 110.97 (C-5 of quinoline), 110.78 (C-5 of quinoline), 106.85 (C-8 of quinoline), 105.83 (C-3 of quinoline), 92.05 (C-1'), 82.69 (C-5), 74.99 (C-4), 73.59 (O-CH₂ of linker), 73.19 (C-5'), 72.68 (C-6), 63.86 (C-4'), 57.17 (N-CH₂ of linker), 51.46 (N-CH₂ of piperazine), 49.87 (C-1), 48.96 (C-3), 47.54 (C-2'), 46.61 (N-CH₂ of piperazine), 39.33 (C-6'), 36.28 (CH of cyclopropyl), 29.55 (O-CH₂-CH₂ of linker), 28.93 (CH₂ of linker), 28.89 (CH₂ of linker), 28.82 (C-3'), 28.81 (CH₂ of linker), 28.68 (CH₂ of linker), 28.34 (CH₂ of linker), 27.90 (CH₂ of linker), 25.85 (CH₂ of linker), 25.33 (CH₂

of linker), 23.43 (CH₂ of linker), 7.60 (CH₂ of cyclopropyl). MALDI-TOF-MS *m/e* calcd for C₄₁H₆₆FN₇O₈Na [M+Na]⁺: 826.4851, found: 826.4820.

5-O-((10-(4-(naphthalen-1-ylmethyl)piperazin-1-yl)docyl)-nebramine 6·HCl (2).

Compound **10** (9 mg, 0.008 mmol) was dissolved in TFA (0.5 mL) and H₂O (0.25 mL) solution and then stirred for 2 h at room temperature. The solvent was removed under reduced pressure to give a white residue. Amount of 5 mL of methanol and ether solution (1:20, v/v) was added to this residue in several portions and then the solvent was decanted to get the final product **2** as TFA salt. Stoichiometric amount of HCl aqueous solution was added into it before lyophilizing the solution to afford a white solid as the final product **2** as HCl salt. Yield: 5.4 mg (72%). ¹H NMR (500 MHz, deuterium oxide) δ 8.27 – 8.21 (m, 1H), 8.07 – 7.97 (m, 2H), 7.72 – 7.61 (m, 2H), 7.61 – 7.54 (m, 2H), 5.56 (d, *J* = 3.1 Hz, 1H, anomeric CH of H-1'), 4.22 (s, 2H, CH₂ of naphthylmethyl), 4.08 – 3.93 (m, 3H), 3.88 – 3.48 (m, 8H), 3.43 – 3.29 (m, 4H), 3.28 – 2.78 (m, 7H), 2.56 – 2.45 (m, 1H, CHH of H-2), 2.34 – 2.27 (m, 1H, CHH of H-3'), 2.18 – 2.10 (m, 1H, CHH of H-3'), 1.92 – 1.82 (m, 1H, CHH of H-2), 1.74 – 1.66 (m, 2H, N-CH₂-CH₂ of linker), 1.66 – 1.58 (m, 2H, O-CH₂-CH₂ of linker), 1.41 – 1.24 (m, 12H, 6×CH₂ of linker). ¹³C NMR (125 MHz, deuterium oxide) δ 133.69 (C of naphthyl), 131.88 (C of naphthyl), 129.30 (CH of naphthyl), 129.13 (CH of naphthyl), 128.82 (CH of naphthyl), 126.77 (CH of naphthyl), 126.33 (CH of naphthyl), 125.53 (CH of naphthyl), 123.90 (CH of naphthyl), 92.10 (C-1'), 82.70 (C-6), 75.26 (C-4), 73.47 (O-CH₂ of linker), 73.11 (C-5'), 72.67 (C-5), 63.73 (C-4'), 58.24 (CH₂ of naphthylmethyl), 56.82 (4×CH₂ of piperazine, N-CH₂ of linker), 49.82 (C-1), 48.85 (C-3), 47.47 (C-2'), 39.18 (C-6'), 29.48 (O-CH₂-CH₂ of linker), 28.80 (C-3'), 28.70 (2×CH₂ of linker), 28.55 (CH₂ of linker), 28.23 (CH₂ of linker), 28.03 (C-2), 25.77 (CH₂ of linker), 25.26 (CH₂ of linker),

23.46 (N-CH₂-CH₂ of linker). MALDI-TOF-MS *m/e* calcd for C₃₇H₆₂N₆O₅Na [M+Na]⁺: 693.468, found: 693.469.

5-O-(dodecyl-moxifloxacin methyl ester)-1,3,2',6',3''-penta-N-(tert-butoxycarbonyl)-4',2'',4'',6''-tetra-O-TBDMS-tobramycin (**7a**). Synthesized following general procedure B. Yield: 764 mg (93%). ¹H NMR (500 MHz, methanol-d₄) δ 8.71 (s, 1H), 7.68 (d, J = 14.1 Hz, 1H), 5.51 – 5.39 (m, 2H, anomeric H), 4.26 – 4.17 (m, 1H), 4.16 – 4.08 (m, 1H), 4.07 – 3.89 (m, 3H), 3.87 (s, 3H), 3.82 – 3.52 (m, 16H), 3.53 – 3.35 (m, 5H), 3.31 – 3.25 (m, 1H), 2.87 – 2.78 (m, 1H), 2.66 – 2.55 (m, 1H), 2.52 – 2.35 (m, 3H), 2.15 – 2.00 (m, 1H), 1.99 – 1.90 (m, 1H), 1.90 – 1.81 (m, 1H), 1.80 – 1.72 (m, 1H), 1.72 – 1.16 (m, 72H), 1.03 – 0.90 (m, 37H), 0.26 – 0.06 (m, 24H). ¹³C NMR (125 MHz, methanol-d₄, some carbons are doubling due to fluorine atom) δ 174.88, 174.86, 166.74, 158.19, 158.03, 157.49, 157.44, 157.00, 155.93, 153.95, 152.25, 142.63, 142.57, 137.98, 137.89, 135.13, 121.96, 121.90, 109.81, 108.78, 108.59, 96.80 (2C, anomeric C), 86.59, 80.66, 80.57, 80.32, 80.16, 79.52, 78.28, 75.22, 74.83, 73.57, 72.62, 68.81, 65.12, 62.90, 61.65, 57.67, 56.98, 55.53, 55.48, 52.95, 52.08, 51.78, 50.17, 49.93, 42.14, 41.20, 38.54, 36.69, 31.90, 31.24, 30.84, 30.76, 30.73, 30.70, 29.29, 29.24, 29.12, 28.96, 28.91, 28.90, 28.71, 28.10, 27.69, 27.02, 26.93, 26.73, 26.68, 26.64, 26.54, 26.21, 25.18, 23.85, 19.52, 19.11, 18.97, 18.93, 10.00, 9.96, -3.26, -3.82, -3.93, -4.16, -4.21, -4.42, -4.62, -4.87. MALDI-TOF-MS *m/e* calcd for C₁₀₁H₁₈₁FN₈O₂₃Si₄Na [M+Na]⁺: 2028.2198, found: 2028.2174.

5-O-(dodecyl-ciprofloxacin methyl ester)-1,3,2',6',3''-penta-N-(tert-butoxycarbonyl)-4',2'',4'',6''-tetra-O-TBDMS-tobramycin (**7b**). Synthesized following general procedure B. Yield: 724 mg (69%). ¹H NMR (300 MHz, CDCl₃) δ 8.52 (s, 1H), 8.00 (d, J = 13.2 Hz, 1H), 7.26 (d, J = 7.1 Hz, 1H), 5.29 – 5.00 (m, 4H), 4.88 – 4.70 (m, 1H), 4.64 – 4.50 (m, 1H), 4.34 – 4.00 (m, 3H), 3.90 (s, 3H), 3.84 – 3.11 (m, 22H), 2.75 – 2.65 (m, 3H), 2.50 – 2.39 (m, 2H), 2.06

– 1.94 (m, 1H), 1.60 – 1.08 (m, 76H), 0.97 – 0.81 (m, 36H), 0.19 – -0.01 (m, 24H). ^{13}C NMR (75 MHz, CDCl_3 , some carbons are doubling due to fluorine atom) δ 173.11, 166.49, 155.08, 148.38, 144.56, 138.00, 123.02, 113.39, 113.08, 109.98, 104.79, 79.44, 79.25, 58.67, 52.89, 52.09, 49.83, 49.77, 48.33, 34.53, 30.08, 29.74, 29.67, 28.65, 28.52, 28.42, 27.59, 26.72, 26.16, 26.02, 25.80, 18.53, 18.36, 18.12, 17.93, 8.15, -3.77, -4.17, -4.87, -4.95, -5.05, -5.20. MALDI-TOF-MS m/e calcd for $\text{C}_{97}\text{H}_{175}\text{FN}_8\text{O}_{22}\text{Si}_4\text{Na}$ $[\text{M}+\text{Na}]^+$: 1958.178, found: 1958.125.

5-O-(dodecyl-moxifloxacin methyl ester)-1,3,2',6'-tetra-N-(tert-butoxycarbonyl)-nebramine (8a). Synthesized following general procedure C. Yield: 40 mg (65%, two steps). ^1H NMR (300 MHz, methanol- d_4) δ 8.71 (s, 1H), 7.68 (d, $J = 14.5$ Hz, 1H), 5.31 – 5.25 (m, 1H, anomeric H-1'), 4.16 – 4.06 (m, 1H), 3.99 – 3.88 (m, 1H), 3.87 (s, 3H), 3.76 – 3.51 (m, 12H), 3.50 – 3.36 (m, 4H), 3.31 – 3.23 (m, 3H), 2.92 – 2.81 (m, 1H), 2.68 – 2.58 (m, 1H), 2.50 – 2.37 (m, 3H), 2.07 – 1.90 (m, 2H), 1.89 – 1.40 (m, 46H), 1.39 – 1.14 (m, 19H), 0.99 (dd, $J = 4.7, 2.4$ Hz, 1H). ^{13}C NMR (75 MHz, methanol- d_4 , some carbons are doubling due to fluorine atom) δ 174.97, 166.77, 158.24, 157.95, 157.49, 156.56, 153.28, 152.30, 142.59, 142.49, 138.06, 137.91, 135.19, 121.93, 121.83, 109.81, 108.84, 108.52, 97.46 (anomeric C), 87.23, 80.81, 80.42, 80.25, 78.93, 77.23, 74.00, 73.26, 67.14, 63.05, 61.65, 56.74, 55.35, 52.29, 52.12, 49.00, 41.20, 38.59, 35.93, 34.84, 31.55, 30.80, 30.69, 30.51, 28.90, 28.88, 28.81, 28.76, 28.49, 27.85, 27.31, 24.98, 23.59, 21.01, 13.95, 10.01, 9.91. MS (ESI) m/e calcd for $\text{C}_{66}\text{H}_{107}\text{FN}_7\text{O}_{17}$ $[\text{M}+\text{H}]^+$: 1289.6, found: 1289.4.

5-O-(dodecyl-ciprofloxacin methyl ester)-1,3,2',6'-tetra-N-(tert-butoxycarbonyl)-nebramine (8b). Synthesized following general procedure C. Yield: 52 mg (31%, two steps). ^1H NMR (300 MHz, CDCl_3) δ 8.54 (s, 1H), 7.99 (d, $J = 13.2$ Hz, 1H), 7.28 (d, $J = 7.3$ Hz, 1H), 5.36 – 5.12 (m, 2H), 5.09 – 4.88 (m, 3H), 3.96 – 3.21 (m, 25H), 3.18 – 3.08 (m, 2H), 2.78 – 2.68 (m,

4H), 2.52 – 2.43 (m, 2H), 2.37 – 2.25 (m, 1H), 2.21 – 2.08 (m, 1H), 1.72 – 1.03 (m, 76H). ^{13}C NMR (75 MHz, CDCl_3) δ 173.28, 166.28, 157.97, 155.12, 148.41, 144.56, 138.06, 122.91, 113.37, 113.07, 109.80, 104.90, 80.26, 79.40, 58.62, 52.85, 52.09, 49.65, 46.06, 34.66, 30.16, 29.60, 29.54, 29.50, 28.45, 28.42, 28.35, 28.33, 27.46, 26.52, 26.09, 8.18. MALDI-TOF-MS m/e calcd for $\text{C}_{62}\text{H}_{100}\text{FN}_7\text{O}_{16}\text{Na}$ $[\text{M}+\text{Na}]^+$: 1240.711, found: 1240.658.

*5-O-((10-(4-(naphthalen-1-ylmethyl)piperazin-1-yl)docyl)-1,3,2',6'-tetra-*N*-(tert-butoxycarbonyl)-nebramine (10)*. Synthesized following general procedure C. Yield: 27 mg (53%, two steps). ^1H NMR (500 MHz, methanol- d_4) δ 8.29 – 8.25 (m, 1H), 7.87 – 7.83 (m, 1H), 7.81 – 7.77 (m, 1H), 7.52 – 7.44 (m, 2H), 7.44 – 7.37 (m, 2H), 5.25 (d, $J = 3.8$ Hz, 1H, anomeric CH of H-1'), 3.94 (s, 2H, CH_2 of naphthylmethyl), 3.93 – 3.88 (m, 1H), 3.70 – 3.47 (m, 5H), 3.47 – 3.31 (m, 5H), 3.28 – 3.19 (m, 3H), 2.83 – 2.44 (m, 8H), 2.44 – 2.37 (m, 1H), 2.01 – 1.92 (m, 1H), 1.92 – 1.85 (m, 1H), 1.65 – 1.58 (m, 1H), 1.55 – 1.48 (m, 4H), 1.48 – 1.38 (m, 36H, 4 \times *t*-Bu of Boc), 1.33 – 1.22 (m, 12H, 6 \times CH_2 of linker). ^{13}C NMR (125 MHz, methanol- d_4) δ 159.35, 158.27, 157.98, 157.49, 135.47, 134.63, 133.92, 129.42, 129.29, 128.92, 126.80, 126.70, 126.08, 125.78, 97.43, 87.27, 80.83, 80.43, 80.29, 78.92, 77.28, 74.04, 73.25, 67.14, 67.13, 61.63, 59.62, 54.06, 53.50, 52.85, 50.84, 50.29, 42.28, 35.95, 34.82, 31.54, 30.77, 30.61, 30.59, 30.56, 28.89, 28.86, 28.80, 28.75, 28.57, 27.30, 27.14. MALDI-TOF-MS m/e calcd for $\text{C}_{57}\text{H}_{95}\text{N}_6\text{O}_{13}$ $[\text{M}+\text{H}]^+$: 1071.696, found: 1071.716.

4.2 Microbiology

4.2.1 Clinical Isolates

Clinically-relevant bacterial strains were collected from the Canadian National Intensive Care Unit (CAN-ICU) study [39] and Canadian Ward Surveillance (CANWARD) studies [40,41]. All pathogens obtained from CAN-ICU and CANWARD studies have received ethics approval from the University of Manitoba Ethics Committee. In addition, participating Canadian health centers have obtained appropriate ethics approval to submit clinical specimens.

4.2.2 Antimicrobial Susceptibility Testing

The antimicrobial activity of the compounds against a panel of bacteria was evaluated by broth microdilution assay in accordance with the Clinical and Laboratory Standards Institute (CLSI) guidelines [32]. was performed to assess the *in vitro* antibacterial activity. Bacterial cultures grown overnight were diluted in saline to achieve a 0.5 McFarland turbidity, followed by 1:50 dilution in Mueller-Hinton broth (MHB) for inoculation to a final concentration of 5×10^5 CFU/mL. The minimum inhibitory concentrations (MICs) of the antimicrobial agents were determined using 96-well plates containing 2-fold serial dilutions with MHB and incubated with equal volumes of inoculum for 18 h at 37 °C. MIC was determined as the lowest concentration to inhibit visible bacterial growth in the form of turbidity, which was confirmed using an EMax Plus microplate reader (Molecular Devices, San Jose, CA, USA) at a wavelength of 590 nm. The wells containing MHB broth with or without bacterial cells were used as positive or negative controls, respectively.

4.2.3 Checkerboard Assay

The checkerboard method [42] was used to assess synergism in all tested combinations. Fractional inhibitory concentrations (FICs) were calculated as follows: $FIC_{\text{antibiotic}} = MIC_{\text{combo}}/MIC_{\text{antibiotic alone}}$; $FIC_{\text{adjuvant}} = MIC_{\text{combo}}/MIC_{\text{adjuvant alone}}$, where MIC_{combo} is the lowest inhibitory concentration of drug in the presence of the adjuvant. The FIC index was calculated by adding the FIC values. FIC indices (FICI) were interpreted as follows: ≤ 0.5 , synergy, $0.5 < FICI \leq 4.0$, no interaction, and ≥ 4.0 , antagonism [28].

4.2.4 Time-kill Curve Assay

The kinetics of bacterial killing was measured using *P. aeruginosa* PAO1 and PA259 as previously described [12]. Overnight bacterial culture was diluted in saline to 0.5 McFarland turbidity and then 1:50 diluted in Luria-Bertani broth (LB). The cell suspension (*P. aeruginosa* PAO1) was incubated with the combination of $\frac{1}{4} \times MIC$ (8 $\mu\text{g/mL}$) or $\frac{1}{2} \times MIC$ (16 $\mu\text{g/mL}$) of hybrid **1a** with 4 $\mu\text{g/mL}$ of minocycline. Untreated cells in media and cells treated with $4 \times MIC$ (4 $\mu\text{g/mL}$) of colistin were used as negative and positive controls respectively (Fig. 2A). Respect to the time-kill curve of **1b** (Fig. 2B), the cell suspension (*P. aeruginosa* PA259) was incubated with rifampicin (4 $\mu\text{g/mL}$) and **1b** (4 $\mu\text{g/mL}$) alone or the combination of **1b** with rifampicin at various concentrations as shown in Fig 2B. Samples were incubated at 37 °C for 24 h. At specific intervals (Fig. 2), aliquots (100 μL) were removed from the samples, serially diluted in PBS, and plated on LB agar plates. Bacterial colonies were formed and counted after 20 h of incubation at 37 °C.

4.2.5 Hemolytic Assay

The hemolytic activities of the newly synthesized compounds were determined and quantified as the amount of hemoglobin released by lysing porcine erythrocytes. Fresh blood drawn from the antecubital vein of a pig (Animal Care and Use Program, University of Manitoba) was centrifuged at 1000 g at 4 °C for 10 mins, washed with PBS thrice and resuspended in the same buffer. The final cell concentration used was 3×10^8 cells/mL. Compounds were serially diluted with PBS and added to wells in a 96-well plate at twice the desired concentrations. Equal volumes of erythrocyte solution were then added to each well and incubated at 37 °C for 1 h. Intact erythrocytes were subsequently pelleted by centrifuging at 1000 g at 4 °C for 10 mins, and the supernatants were transferred to a new 96-well plate. Hemoglobin release was determined by measuring the absorbance on EMax[®] Plus microplate reader (Molecular Devices, Sunnyvale, CA, USA) at 570 nm. Blood cells in PBS (0% hemolysis) and 0.1 % Triton X-100 (100% hemolysis) were used as negative and positive controls, respectively. Percent hemolysis was calculated as $[\% \text{ hemolysis} = (X - 0\%) / (100\% - 0\%)]$, where X is the optical density values of the compounds at different concentrations.

4.2.6 *Galleria mellonella* Model of *P. aeruginosa* Infection

In vivo synergistic effects were determined using *Galleria mellonella* infection model, as previously described [8]. Briefly, worms were purchased from The Worm Lady[®] Live Feeder (ON, Canada), stored in their natural habitat at 16 °C, and used within 10 days of delivery. The worms (average weight of 250 mg) were used for tolerability and efficacy studies. Tolerability study was performed by injecting 10 μ L of antimicrobial agents only at concentrations

equivalent to 100 mg/kg or 200 mg/kg. The worms (ten in each group) were incubated at 37 °C and monitored for 96 h. For efficacy studies, the virulence and bacterial load required to kill 100 % of the worms within 12 – 18 h was first determined, which is approximately 5 CFU. Overnight grown culture of MDR *P. aeruginosa* PA264 isolate was standardized to 0.5 McFarland standard and diluted in PBS to a final concentration of 5×10^2 CFU/mL. 10 μ L of this solution (~ 5 CFU) was injected into each worm and incubated for 2 h at 37 °C. After the 2 h challenge, worms in monotherapy experimental groups (fifteen worms per group) were treated with 10 μ L injection of rifampicin, compound **1b**, or PBS alone. The worms in combination therapy groups were treated with rifampicin + compound **1b** (25 + 25 mg/kg, 50 + 50 mg/kg, or 75 + 75 mg/kg). Worms treated with 10 μ L PBS negative control. The worms were incubated at 37 °C in Petri dishes lined with filter paper and scored for survivability every 6 h for up to 24 h. This experiment was repeated to give a total of thirty worms ($n = 30$) in each case. Survival data curves were plotted using Kaplan-Meier survival analysis. Worms were considered dead if they do not respond to touch.

4.2.7 Tetracycline Uptake Assay

Fluorescence-based tetracycline uptake assay in bacterial cells was performed following previously reported method [36]. Culture of *P. aeruginosa* PAO1 was grown to $OD_{600} = 0.6$ followed by washing and re-suspending it in $\frac{1}{4}$ volume of 10 mM HEPES, pH 7.2, 100 μ L/well cell suspension was treated with varying concentrations of test compounds in the presence of 128 μ g/mL of tetracycline. Fluorescence was recorded at a continuous interval of 1 min for 30 min at room temperature on a FlexStation 3 (Molecular Devices, Sunnyvale, USA) microplate reader at

the excitation wavelength of 405 nm and emission wavelength of 535 nm. Experiments were performed in triplicates. Averages of triplicate experiments are shown in Fig. 6.

Conflicts of Interest

There are no conflicts of interest to declare.

Acknowledgments

The work was supported by NSERC-DG 321252 and MHRC.

References

- [1] American Chemical Society International Historic Chemical Landmarks. Discovery and Development of Penicillin.
<http://www.acs.org/content/acs/en/education/whatischemistry/landmarks/flemingpenicillin.html> (accessed on October 11, 2018), (n.d.).
- [2] A. Coates, Y. Hu, R. Bax, C. Page, The future challenges facing the development of new antimicrobial drugs, *Nat. Rev. Drug Discov.* 1 (2002) 895–910. doi:10.1038/nrd940.
- [3] J.H. Powers, Antimicrobial drug development – the past, the present, and the future, *Clin. Microbiol. Infect.* 10 (2004) 23–31. doi:10.1111/j.1465-0691.2004.1007.x.
- [4] D.J. Payne, M.N. Gwynn, D.J. Holmes, D.L. Pompliano, Drugs for bad bugs: confronting the challenges of antibacterial discovery, *Nat. Rev. Drug Discov.* 6 (2006) 29.
<http://dx.doi.org/10.1038/nrd2201>.
- [5] L.L. Silver, Are natural products still the best source for antibacterial discovery? The bacterial entry factor, *Expert Opin. Drug Discov.* 3 (2008) 487–500.

doi:10.1517/17460441.3.5.487.

- [6] G.D. Wright, Antibiotic Adjuvants: Rescuing Antibiotics from Resistance, Trends Microbiol. 24 (2016) 862–871. doi:10.1016/j.tim.2016.06.009.
- [7] R. Domalaon, T. Idowu, G.G. Zhanel, F. Schweizer, Antibiotic Hybrids: the Next Generation of Agents and Adjuvants against Gram-Negative Pathogens? Clin. Microbiol. Rev. 31 (2018) e00077-17. doi:10.1128/CMR.00077-17.
- [8] B.K. Gorityala, G. Guchhait, D.M. Fernando, S. Deo, S.A. McKenna, G.G. Zhanel, A. Kumar, F. Schweizer, Adjuvants based on hybrid antibiotics overcome resistance in *Pseudomonas aeruginosa* and enhance fluoroquinolone efficacy, Angew. Chem., Int. Ed. Engl. 55 (2016) 555–559. doi:10.1002/anie.201508330.
- [9] B.K. Gorityala, G. Guchhait, S. Goswami, D.M. Fernando, A. Kumar, G.G. Zhanel, F. Schweizer, Hybrid antibiotic overcomes resistance in *P. aeruginosa* by enhancing outer membrane penetration and reducing efflux, J. Med. Chem. 59 (2016) 8441–8455. doi:10.1021/acs.jmedchem.6b00867.
- [10] X. Yang, S. Goswami, B.K. Gorityala, R. Domalaon, Y. Lyu, A. Kumar, G.G. Zhanel, F. Schweizer, A tobramycin vector enhances synergy and efficacy of efflux pump inhibitors against multidrug-resistant Gram-negative bacteria, J. Med. Chem. 60 (2017) 3913–3932. doi:10.1021/acs.jmedchem.7b00156.
- [11] X. Yang, R. Domalaon, Y. Lyu, G. Zhanel, F. Schweizer, Tobramycin-Linked Efflux Pump Inhibitor Conjugates Synergize Fluoroquinolones, Rifampicin and Fosfomycin against Multidrug-Resistant *Pseudomonas aeruginosa*, J. Clin. Med. 7 (2018) 158. doi:10.3390/jcm7070158.
- [12] Y. Lyu, X. Yang, S. Goswami, B.K. Gorityala, T. Idowu, R. Domalaon, G.G. Zhanel, A.

- Shan, F. Schweizer, Amphiphilic tobramycin–lysine conjugates sensitize multidrug resistant Gram-negative bacteria to rifampicin and minocycline, *J. Med. Chem.* 60 (2017) 3684–3702. doi:10.1021/acs.jmedchem.6b01742.
- [13] Y. Lyu, R. Domalaon, X. Yang, F. Schweizer, Amphiphilic lysine conjugated to tobramycin synergizes legacy antibiotics against wild-type and multidrug-resistant *Pseudomonas aeruginosa*, *Biopolymers*. (2017) e23091. doi:10.1002/bip.23091.
- [14] R. Domalaon, X. Yang, Y. Lyu, G.G. Zhanel, F. Schweizer, Polymyxin B 3 –Tobramycin Hybrids with *Pseudomonas aeruginosa* -Selective Antibacterial Activity and Strong Potentiation of Rifampicin, Minocycline, and Vancomycin, *ACS Infect. Dis.* 3 (2017) 941–954. doi:10.1021/acsinfecdis.7b00145.
- [15] J.B. Bulitta, N.S. Ly, C.B. Landersdorfer, N.A. Wanigaratne, T. Velkov, R. Yadav, A. Oliver, L. Martin, B.S. Shin, A. Forrest, B.T. Tsuji, Two mechanisms of killing of *Pseudomonas aeruginosa* by tobramycin assessed at multiple inocula via mechanism-based modeling, *Antimicrob. Agents Chemother.* 59 (2015) 2315–2327. doi:10.1128/AAC.04099-14.
- [16] B.D. Davies, J. Davis, Misreading of Ribonucleic Acid Code Words Induced by Aminoglycoside Antibiotics, *J. Biol. Chem.* 243 (1968) 3312–3316.
- [17] D. Fourmy, M.I. Recht, S.C. Blanchard, J.D. Puglisi, Structure of the A site of *Escherichia coli* 16S ribosomal RNA complexed with an aminoglycoside antibiotic, *Science*. 274 (1996) 1367–1371. <http://www.ncbi.nlm.nih.gov/pubmed/8910275>.
- [18] D. Fourmy, M.I. Recht, J.D. Puglisi, Binding of neomycin-class aminoglycoside antibiotics to the A-site of 16 s rRNA, *J. Mol. Biol.* 277 (1998) 347–362. doi:10.1006/jmbi.1997.1552.

- [19] Q. Vicens, E. Westhof, Crystal Structure of a Complex between the Aminoglycoside Tobramycin and an Oligonucleotide Containing the Ribosomal Decoding A Site, *Chem. Biol.* 9 (2002) 747–755. doi:10.1016/S1074-5521(02)00153-9.
- [20] S.R. Lynch, R.L. Gonzalez, J.D. Puglisi, Comparison of X-ray crystal structure of the 30S subunit-antibiotic complex with NMR structure of decoding site oligonucleotide-paromomycin complex, *Structure*. 11 (2003) 43–53. doi:10.1016/S0969-2126(02)00934-6.
- [21] F. Agnelli, S.J. Sucheck, K.A. Marby, D. Rabuka, S.-L. Yao, P.S. Sears, F.-S. Liang, C.-H. Wong, Dimeric aminoglycosides as antibiotics, *Angew. Chem., Int. Ed. Engl.* 43 (2004) 1562–1566. doi:10.1002/anie.200353225.
- [22] Y. Berkov-Zrihen, I.M. Herzog, R.I. Benhamou, M. Feldman, K.B. Steinbuch, P. Shaul, S. Lerer, A. Eldar, M. Fridman, Tobramycin and nebramine as pseudo-oligosaccharide scaffolds for the development of antimicrobial cationic amphiphiles, *Chem. Eur. J.* 21 (2015) 4340–4349. doi:10.1002/chem.201406404.
- [23] L. Zimmermann, I. Das, J. Désiré, G. Sautrey, V. Barros R. S., M. El Khoury, M.-P. Mingeot-Leclercq, J.-L. Decout, New Broad-Spectrum Antibacterial Amphiphilic Aminoglycosides Active against Resistant Bacteria: From Neamine Derivatives to Smaller Neosamine Analogues, *J. Med. Chem.* 59 (2016) 9350–9369. doi:10.1021/acs.jmedchem.6b00818.
- [24] M. Ouberaï, F. El Garch, A. Bussiere, M. Riou, D. Alsteens, L. Lins, I. Baussanne, Y.F. Dufrêne, R. Brasseur, J.-L. Decout, M.-P. Mingeot-Leclercq, The *Pseudomonas aeruginosa* membranes: A target for a new amphiphilic aminoglycoside derivative? *Biochim. Biophys. Acta - Biomembr.* 1808 (2011) 1716–1727. doi:10.1016/j.bbamem.2011.01.014.

- [25] L. Zimmermann, J. Kempf, F. Briée, J. Swain, M.-P. Mingeot-Leclercq, J.-L. Décout, Broad-spectrum antibacterial amphiphilic aminoglycosides: A new focus on the structure of the lipophilic groups extends the series of active dialkyl neamines, *Eur. J. Med. Chem.* 157 (2018) 1512–1525. doi:10.1016/j.ejmech.2018.08.022.
- [26] J.A. Bohnert, W. V Kern, Selected Arylpiperazines Are Capable of Reversing Multidrug Resistance in *Escherichia coli* Overexpressing RND Efflux Pumps Selected Arylpiperazines Are Capable of Reversing Multidrug Resistance in *Escherichia coli* Overexpressing RND Efflux Pumps, *Antimicrob. Agents Chemother.* 49 (2005) 849–852. doi:10.1128/AAC.49.2.849.
- [27] G. Guchhait, A. Altieri, B. Gorityala, X. Yang, B. Findlay, G.G. Zhanel, N. Mookherjee, F. Schweizer, Amphiphilic tobramycins with immunomodulatory properties, *Angew. Chem., Int. Ed. Engl.* 54 (2015) 6278–6282. doi:10.1002/anie.201500598.
- [28] F.C. Odds, Synergy, antagonism, and what the checkerboard puts between them, *J. Antimicrob. Chemother.* 52 (2003) 1. doi:10.1093/jac/dkg301.
- [29] J. Berkhout, M.J. Melchers, A.C. Van Mil, W.W. Nichols, J.W. Mouton, In vitro activity of ceftazidime-avibactam combination in in vitro checkerboard assays, *Antimicrob. Agents Chemother.* 59 (2015) 1138–1144. doi:10.1128/AAC.04146-14.
- [30] H.S. Sader, M. Castanheira, R.E. Mendes, R.K. Flamm, D.J. Farrell, R.N. Jones, Ceftazidime-avibactam activity against multidrug-resistant *Pseudomonas aeruginosa* isolated in U.S. Medical Centers in 2012 and 2013, *Antimicrob. Agents Chemother.* 59 (2015) 3656–3659. doi:10.1128/AAC.05024-14.
- [31] K.S. Kaye, J.M. Pogue, T.B. Tran, R.L. Nation, J. Li, Agents of Last Resort: Polymyxin Resistance, *Infect. Dis. Clin. North Am.* 30 (2016) 391–414.

doi:10.1016/J.IDC.2016.02.005.

- [32] Clinical and Laboratory Standards Institute (CLSI), Performance Standards for Antimicrobial Susceptibility Testing, 26th ed., Clinical and Laboratory Standards Institute, Wayne, Pennsylvania, USA, 2016.
- [33] P. Bonnet, R., Caron, F., Cavallo, J.D.; Chardon, H., Chidiac, C., Courvalin, P., Drugeon, H., Dubreuil, L., Jarlier, V.; Jehl, F., Lambert, T., Leclercq, R., Nicolas-Chanoine, M.H., Plesiat, P.; Ploy, M.C., Quentin, C., Soussy, C.J., Varon, E., Weber, Comité de L'Antibiogramme de la Société Française de Microbiologie-Recommandations 2012. January Edition, (2012).
- [34] D.H. Adamson, V. Krikstopaityte, P.J. Coote, Enhanced efficacy of putative efflux pump inhibitor/antibiotic combination treatments versus MDR strains of *Pseudomonas aeruginosa* in a *Galleria mellonella* *in vivo* infection model, J. Antimicrob. Chemother. 70 (2015) 2271–2278. doi:10.1093/jac/dkv111.
- [35] J. Krezdorn, S. Adams, P.J. Coote, A *Galleria mellonella* infection model reveals double and triple antibiotic combination therapies with enhanced efficacy versus a multidrug-resistant strain of *Pseudomonas aeruginosa*, J. Med. Microbiol. 63 (2014) 945–955. doi:10.1099/jmm.0.074245-0.
- [36] L. Ejim, M.A. Farha, S.B. Falconer, J. Wildenhain, B.K. Coombes, M. Tyers, E.D. Brown, G.D. Wright, Combinations of antibiotics and nonantibiotic drugs enhance antimicrobial efficacy, Nat. Chem. Biol. 7 (2011) 348–350. doi:10.1038/nchembio.559.
- [37] P. Mitchell, Chemiosmotic coupling in oxidative and photosynthetic phosphorylation, Biochim. Biophys. Acta. 1807 (2011) 1507–1538. doi:10.1016/j.bbabbio.2011.09.018.
- [38] I. Chopra, K. Hacker, Effects of tetracyclines on the production of extracellular proteins

- by members of the propionibacteriaceae, *FEMS Microbiol. Lett.* 60 (1989) 21–24.
doi:<http://dx.doi.org/>.
- [39] G.G. Zhanel, M. DeCorby, N. Laing, B. Weshnoweski, R. Vashisht, F. Tailor, K.A. Nichol, A. Wierzbowski, P.J. Baudry, J.A. Karlowsky, P. Lagace-Wiens, A. Walkty, M. McCracken, M.R. Mulvey, J. Johnson, D.J. Hoban, Antimicrobial-resistant pathogens in intensive care units in Canada: results of the Canadian National Intensive Care Unit (CAN-ICU) Study, 2005-2006, *Antimicrob. Agents Chemother.* 52 (2008) 1430–1437.
doi:10.1128/AAC.01538-07.
- [40] G.G. Zhanel, H.J. Adam, M.R. Baxter, J. Fuller, K.A. Nichol, A.J. Denisuik, P.R.S. Lagace-Wiens, A. Walkty, J.A. Karlowsky, F. Schweizer, D.J. Hoban, Antimicrobial susceptibility of 22746 pathogens from Canadian hospitals: results of the CANWARD 2007-11 study, *J. Antimicrob. Chemother.* 68 Suppl 1 (2013) i7-22.
doi:10.1093/jac/dkt022.
- [41] G.G. Zhanel, M. DeCorby, H. Adam, M.R. Mulvey, M. McCracken, P. Lagace-Wiens, K.A. Nichol, A. Wierzbowski, P.J. Baudry, F. Tailor, J.A. Karlowsky, A. Walkty, F. Schweizer, J. Johnson, D.J. Hoban, Prevalence of antimicrobial-resistant pathogens in Canadian hospitals: results of the Canadian Ward Surveillance Study (CANWARD 2008), *Antimicrob. Agents Chemother.* 54 (2010) 4684–4693. doi:10.1128/AAC.00469-10.
- [42] G. Orhan, A. Bayram, Y. Zer, I. Balci, Synergy tests by E test and checkerboard methods of antimicrobial combinations against *Brucella melitensis*, *J. Clin. Microbiol.* 43 (2005) 140–143. doi:10.1128/JCM.43.1.140-143.2005.

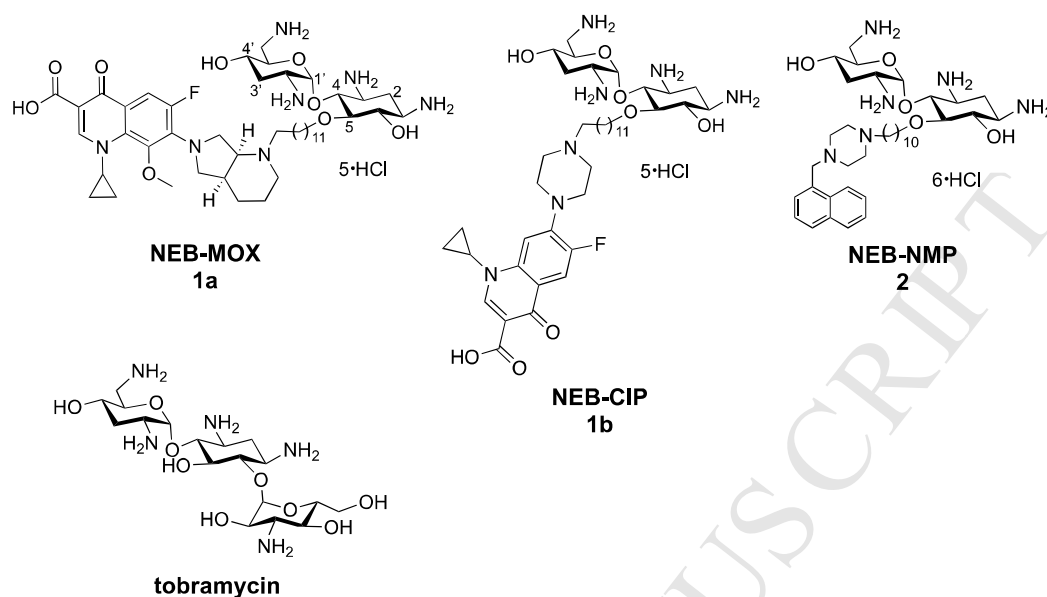


Fig. 1. Structures of the nebramine-moxifloxacin (NEB-MOX) hybrid **1a**, nebramine-ciprofloxacin (NEB-CIP) hybrid **1b**, nebramine-NMP (NEB-NMP) hybrid **2**, and tobramycin.

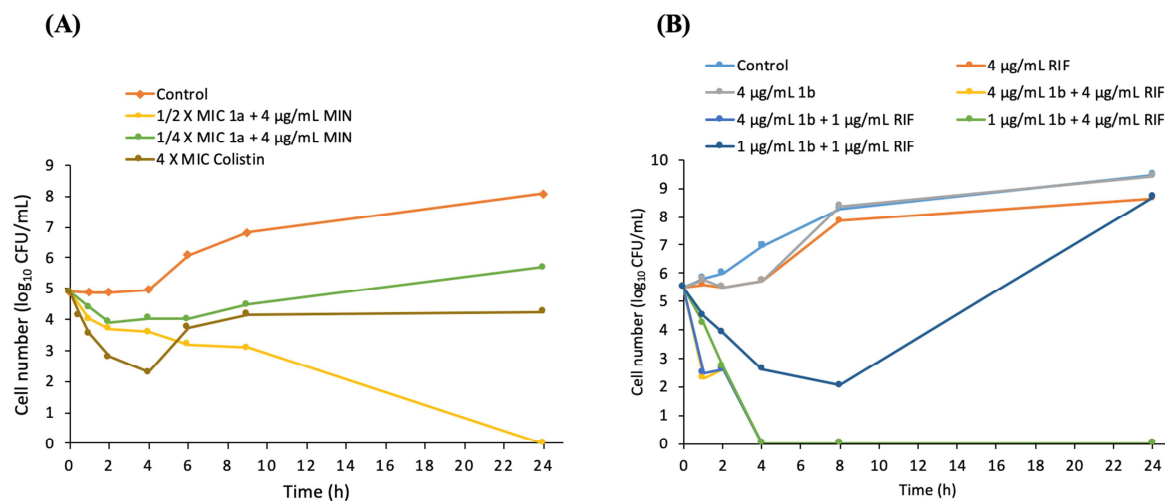


Fig. 2. (A) Time killing kinetics of minocycline (MIN) (4 µg/mL) in combination with NEB-MOX (**1a**) at 1/2 × MIC (16 µg/mL) or 1/4 × MIC (8 µg/mL) against *P. aeruginosa* PAO1.

Untreated cells in media and cells treated with $4 \times \text{MIC}$ ($4 \mu\text{g/mL}$) of colistin were used as negative and positive controls respectively. (B) Time killing kinetics of rifampicin in combination with NEB-CIP (**1b**) at various concentrations against XDR *P. aeruginosa* PA259. Untreated cells in media was used as a negative control. MIC of **1b** is $>128 \mu\text{g/mL}$ and MIC of RIF is $16 \mu\text{g/mL}$ against *P. aeruginosa* PA259 strain.

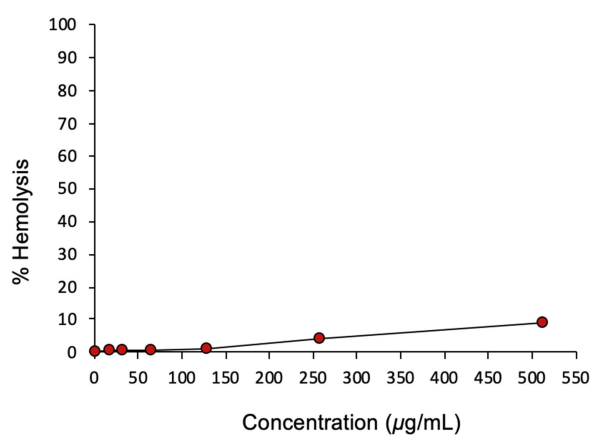


Fig. 3. Hemolytic activity of NEB-CIP (**1b**). Triton X-100 (0.1%) was employed as positive control to calculate the percentage of hemolysis.

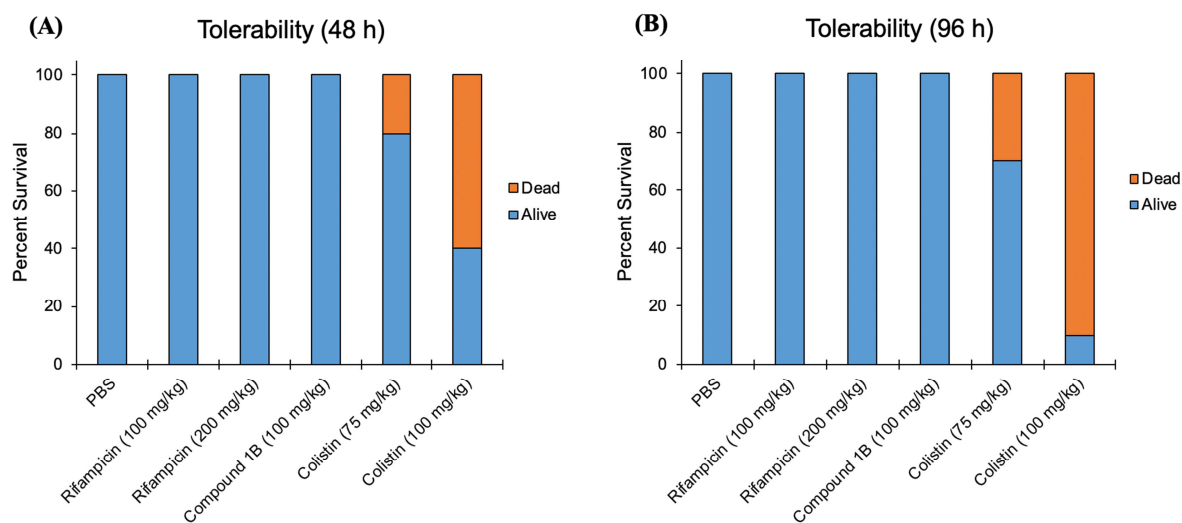


Fig. 4. Tolerability dosages of NEB-CIP (**1b**), rifampicin, and colistin on *G. mellonella* larvae ($n = 10$). Larvae survived up to 96 h when administered with 100 mg/kg dosage of **1b**.

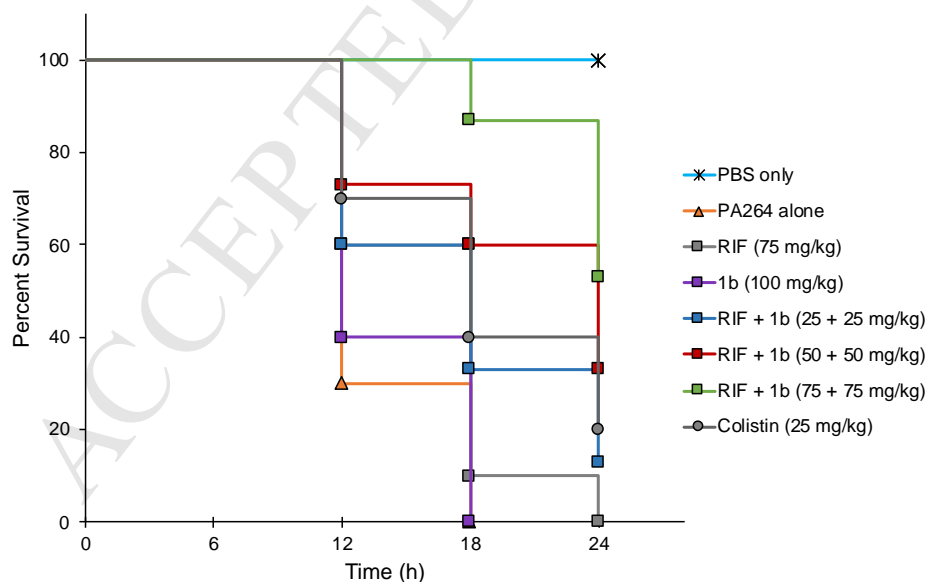


Fig. 5. Effect of treatment of *G. mellonella* larvae (inoculated with ~ 5 CFU of XDR *P. aeruginosa* PA264, $n = 30$ for each drug and dose combination) with rifampicin (75 mg/kg) and **1b** (100 mg/kg) alone, or rifampicin in combination with **1b** (25 + 25 mg/kg, 50 + 50 mg/kg, and 75+75 mg/kg) on survival. Single dose treatment administered at 0 h (2 h after inoculation).

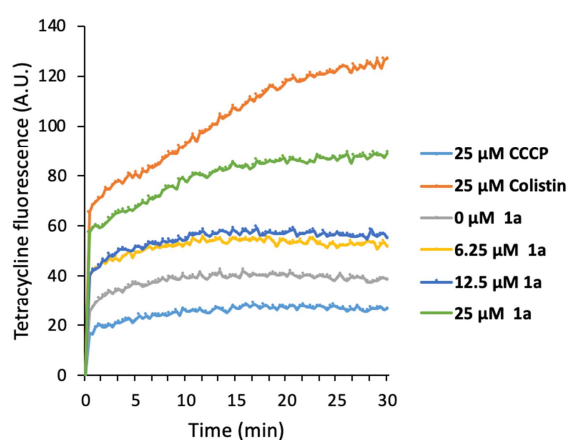
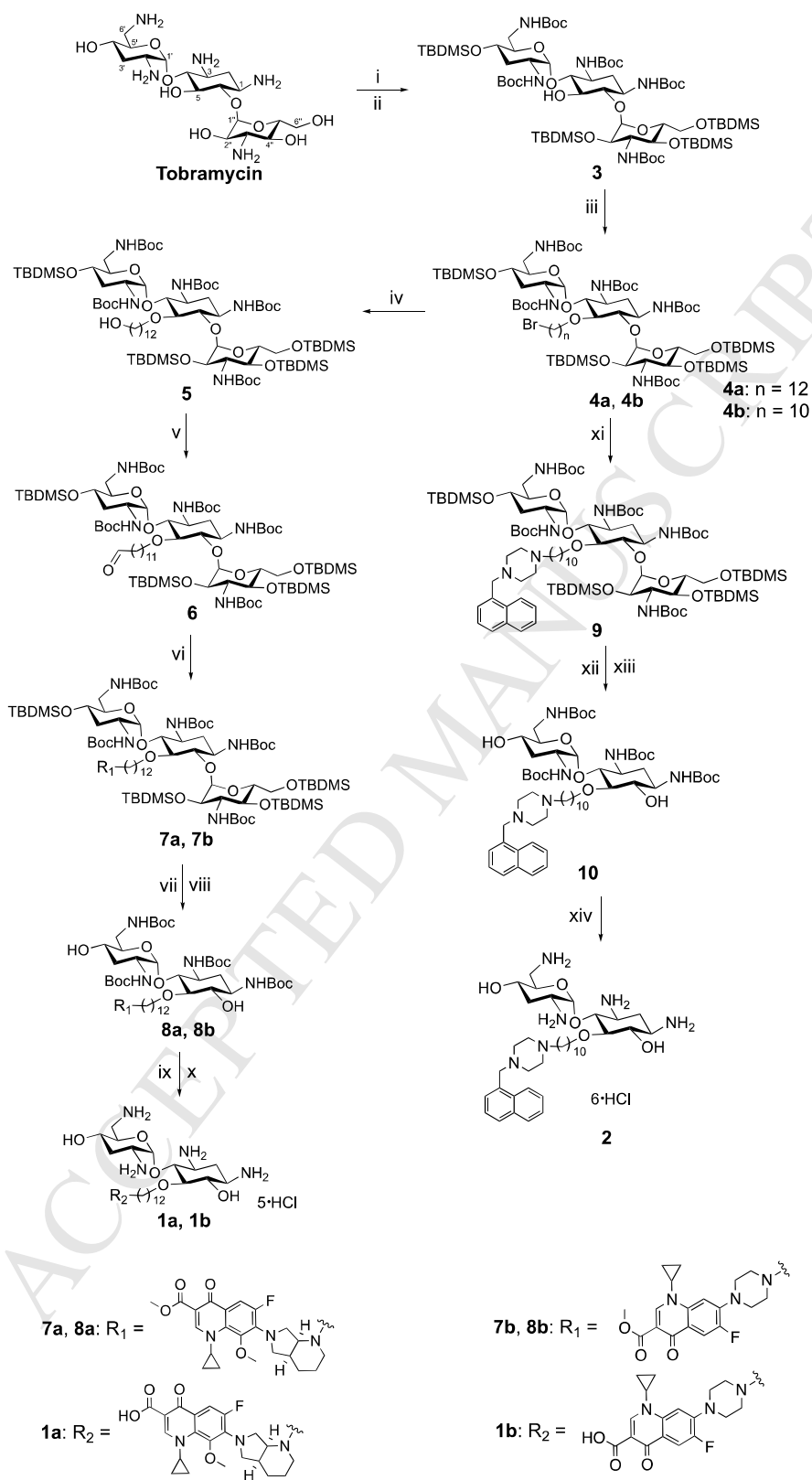


Fig. 6. Tetracycline uptake in *P. aeruginosa* PAO1 in the presence of increasing concentrations of NEB-MOX **1a**. Concentration of tetracycline was 128 $\mu\text{g/mL}$. Averages of triplicate experiments are shown.



Scheme 1. Synthesis of NEB-MOX (**1a**), NEB-CIP (**1b**), and NEB-NMP (**2**). Reagents and conditions: (i) (Boc)₂O, Et₃N, MeOH/H₂O (2:1), rt to 55 °C, overnight, 97%. (ii) TBDMS-Cl, 1-methylimidazole, DMF, N₂, rt, 4 days, 90%. (iii) 1,12-dibromododecane or 1,10-dibromodecane, KOH, TBAHS, toluene, rt, overnight, 78–81%. (iv) Cs₂CO₃, H₂O, DMF, 75 °C, 8 h, 67%. (v) PCC, NaOAc, DCM, rt, 2 h, 90%. (vi) moxifloxacin methyl ester, NaBH(OAc)₃, AcOH, DCE, rt, 93% for **7a**, 69% for **7b**; (vii) 40% HCl, MeOH, 70 °C, 48 h. (viii) (Boc)₂O, Et₃N, MeOH, 55 °C, overnight, 65% for **8a**, 31% for **8b** (two steps). (ix) 2 N LiOH, MeOH, rt, 30 min. (x) TFA/H₂O 2:1 (v/v), rt, 2 h, 52% for **1a**, 32% for **1b**. (xi) NMP (1-(1-naphthylmethyl)piperazine), K₂CO₃, DMF, 75 °C, 50%. (xii) 40% HCl, MeOH, 65 °C, 48 h. (xiii) (Boc)₂O, Et₃N, MeOH/H₂O (2/1, v/v), rt to 55 °C, overnight, 53% (two steps). (xiv) TFA/H₂O (2/1, v/v), rt, 30 min, 72%.

Table 1 Combination studies of NEB-MOX **1a** with moxifloxacin (MOX), minocycline (MIN) or rifampicin (RIF) against wild-type *P. aeruginosa* PAO1 strain.

Antibiotic (MIC ^a)	Hybrid (MIC ^a)	FICI	Absolute MIC ^b	Potential (fold) ^c
MOX (1)	1a (32)	0.25	0.13	8
MIN (8)	1a (32)	0.38	1	8
RIF (8)	1a (32)	0.07	≤0.03	≥256

^a All MIC data presented in µg/mL.

^b Absolute MIC (µg/mL) of antibiotic was determined in the presence of 8 µg/mL (7.5 µM) of hybrid **1a**.

^c Antibiotic activity potentiation at 8 µg/mL (7.5 µM) of hybrid **1a**.

Table 2 Combination studies of NEB-MOX **1a** with moxifloxacin (MOX) or ciprofloxacin (CIP) against MDR/XDR *P. aeruginosa* clinical isolates.

<i>P. aeruginosa</i>	Antibiotic (MIC ^a)	Hybrid (MIC ^a)	FICI	Absolute MIC ^b	Potential (fold) ^c
PA262-101856 ^d	MOX (64)	1a (>256)	0.13<x<0.16	8	8
PA262-101856 ^d	CIP (32)	1a (>256)	0.25<x<0.28	8	4
PA260-97103 ^d	MOX (64)	1a (32)	0.13	1	64
PA260-97103 ^d	CIP (32)	1a (32)	0.25	4	8
100036 ^d	MOX (128)	1a (128)	0.08	8	16
100036 ^d	CIP (32)	1a (128)	0.56	16	2
101885 ^d	MOX (64)	1a (128)	0.25	16	4
101885 ^d	CIP (16)	1a (128)	>1	NA	NA
PA259-96918 ^d	MOX (256)	1a (>256)	0.06<x<0.07	16	16
PA259-96918 ^d	CIP (128)	1a (>256)	0.25<x<0.27	32	4

PA264-104354 ^d	MOX (128)	1a (256)	0.09	8	16
PA264-104354 ^d	CIP (32)	1a (256)	0.16	4	8
91433 ^e	MOX (8)	1a (32)	0.31	0.5	16
91433 ^e	CIP (1)	1a (32)	0.25	0.06	16
101243 ^e	MOX (8)	1a (64)	0.16	0.25	32
101243 ^e	CIP (1)	1a (64)	0.25	0.13	8

^a All MIC data presented in $\mu\text{g/mL}$.

^b Absolute MIC ($\mu\text{g/mL}$) of antibiotic was determined in the presence of $8 \mu\text{g/mL}$ ($7.5 \mu\text{M}$) of hybrid **1a**.

^c Antibiotic activity potentiation at $8 \mu\text{g/mL}$ ($7.5 \mu\text{M}$) of hybrid **1a**.

^d with ⁸³Thr to ⁸³Ile mutation in gyr A [8].

^e without ⁸³Thr to ⁸³Ile mutation in gyr A [8].

Table 3 Combination studies of NEB-MOX **1a** with minocycline (MIN) against MDR/XDR *P. aeruginosa* clinical isolates.

<i>P. aeruginosa</i>	Antibiotic (MIC ^a)	Hybrid (MIC ^a)	FICI	Absolute MIC ^b	Potential (fold) ^c
PA262-101856	MIN (64)	1a (>256)	0.03<x<0.05	2	32
PA260-97103	MIN (8)	1a (32)	0.09	0.25	32
100036	MIN (16)	1a (128)	0.06	0.5	32
101885	MIN (16)	1a (128)	0.07	1	16
PA259-96918	MIN (16)	1a (>256)	0.03<x<0.04	0.5	32
PA264-104354	MIN (32)	1a (256)	0.05	0.5	64
91433	MIN (16)	1a (32)	0.19	0.5	32
101243	MIN (4)	1a (64)	0.13	0.25	16

^a All MIC data presented in $\mu\text{g/mL}$.

^b Absolute MIC ($\mu\text{g/mL}$) of antibiotic was determined in the presence of 8 $\mu\text{g/mL}$ (7.5 μM) of hybrid **1a**.

^c Antibiotic activity potentiation at 8 $\mu\text{g/mL}$ (7.5 μM) of hybrid **1a**.

Table 4 Combination studies of NEB-MOX **1a** with rifampicin (RIF) against MDR/XDR *P. aeruginosa* clinical isolates.

<i>P. aeruginosa</i>	Antibiotic (MIC ^a)	Hybrid (MIC ^a)	FICI	Absolute MIC ^b	Potential (fold) ^c
PA262-101856	RIF (1024)	1a (>256)	0.008<x<0.02	4	512
PA260-97103	RIF (4)	1a (32)	0.06	≤0.03	≥128
100036	RIF (8)	1a (128)	0.01	0.03	256
101885	RIF (8)	1a (128)	0.05	0.06	128
PA259-96918	RIF (8)	1a (>256)	0.004<x<0.01	≤0.03	≥256
PA264-104354	RIF (16)	1a (256)	0.02	≤0.06	≥256
91433	RIF (16)	1a (32)	0.16	0.13	128
101243	RIF (4)	1a (64)	0.13	0.13	32

^a All MIC data presented in µg/mL.

^b Absolute MIC (µg/mL) of antibiotic was determined in the presence of 8 µg/mL (7.5 µM) of hybrid **1a**.

^c Antibiotic activity potentiation at 8 µg/mL (7.5 µM) of hybrid **1a**.

Table 5 *In vitro* antibacterial activity of minocycline (MIN) and rifampicin (RIF) alone or in combination with a fixed concentration of 8 $\mu\text{g/mL}$ (7.5 μM) NEB-MOX **1a** against MDR/XDR *P. aeruginosa* clinical isolates ($n = 8$).

Antimicrobial/Hybrid	MIC ₅₀ ^a ($\mu\text{g/mL}$)	MIC ₈₀ ^a ($\mu\text{g/mL}$)	MIC Range ($\mu\text{g/mL}$)
MIN	16 \perp	32 \perp	4–64
MIN+ 1	0.5 \dagger	1 \dagger	0.25–2
RIF	8 \perp	16 \perp	4–1024
RIF+ 1	0.06 \dagger	0.13 \dagger	≤ 0.03 –4

\dagger , susceptible; \perp , resistant;

^a MIC₅₀ and MIC₈₀ are the MIC that inhibit the growth of 50% or 80% of all ($n = 8$) tested isolates.

Table 6 Combination studies of NEB-CIP **1b** with antibiotics against wild-type *P. aeruginosa* PAO1 and XDR *P. aeruginosa* strains.

<i>P. aeruginosa</i>	Antibiotic (MIC ^a)	Hybrid (MIC ^a)	FIC index	Absolute MIC ^b	Potential (fold)
PAO1	MIN (16)	1b (64)	0.047	0.5	32
PAO1	RIF (16)	1b (64)	0.047	≤ 0.06	≥ 256
PA259-96918	MIN (16)	1b (>128)	$0.031 < x < 0.063$	0.5	32
PA259-96918	RIF (16)	1b (>128)	$0.008 < x < 0.016$	≤ 0.06	≥ 256
PA264-104354	MIN (32)	1b (128)	0.039	1	32
PA264-104354	RIF (16)	1b (128)	0.039	0.13	128

^a All MIC data presented in $\mu\text{g/mL}$.

^b Absolute MIC ($\mu\text{g/mL}$) of antibiotic was determined in the presence of 4 $\mu\text{g/mL}$ (4.1 μM) of hybrid **1b**.

^c Antibiotic activity potentiation at 4 $\mu\text{g/mL}$ (4.1 μM) of hybrid **1b**.

Table 7 Combination studies of NEB-NMP **2** with antibiotics against wild-type *P. aeruginosa* PAO1 and MDR/XDR *P. aeruginosa* strains.

<i>P. aeruginosa</i>	Antibiotic (MIC ^a)	Hybrid (MIC ^a)	FICI	Absolute MIC ^b	Potential (fold) ^c
PAO1	MOX (1)	2 (256)	0.05	0.03	32
PAO1	MIN (8)	2 (256)	0.09	0.5	16
PAO1	RIF (16)	2 (256)	0.02	0.06	256
PA262-101856 ^d	MOX (64)	2 (512)	0.09	4	16
PA262-101856 ^d	CIP (32)	2 (512)	0.13	4	8
PA262-101856 ^d	MIN (128)	2 (512)	0.04	4	32
PA262-101856 ^d	RIF (1024)	2 (512)	0.02	4	256
PA260-97103 ^d	MOX (64)	2 (32)	0.08	0.5	128
PA260-97103 ^d	CIP (16)	2 (32)	0.38	2	8
PA260-97103 ^d	MIN (16)	2 (32)	0.09	0.25	64
PA260-97103 ^d	RIF (4)	2 (32)	0.05	0.06	64
100036 ^d	MOX (128)	2 (>512)	0.063<x<0.07	8	16
100036 ^d	CIP (64)	2 (>512)	0.125<x<0.133	8	8
100036 ^d	MIN (64)	2 (>512)	0.031<x<0.033	2	32
100036 ^d	RIF (16)	2 (>512)	0.004<x<0.012	0.06	256
101885 ^d	MOX (64)	2 (512)	0.07	4	16
101885 ^d	CIP (32)	2 (512)	0.13	4	8
101885 ^d	MIN (32)	2 (512)	0.04	0.5	64
101885 ^d	RIF (16)	2 (512)	0.02	0.13	128
PA259-96918 ^d	MOX (512)	2 (>512)	0.016<x<0.023	8	64
PA259-96918 ^d	CIP (256)	2 (>512)	0.063<x<0.078	16	16

PA259-96918 ^d	MIN (32)	2 (>512)	0.016<x<0.031	0.5	64
PA259-96918 ^d	RIF (16)	2 (>512)	0.004<x<0.006	≤0.06	≥256
91433 ^e	MOX (8)	2 (32)	0.25	1	8
91433 ^e	CIP (2)	2 (32)	0.38	0.25	8
91433 ^e	MIN (64)	2 (32)	0.19	2	32
91433 ^e	RIF (16)	2 (32)	0.50	4	4
101243 ^e	MOX (4)	2 (512)	0.13	0.5	8
101243 ^e	CIP (2)	2 (512)	0.16	0.5	4
101243 ^e	MIN (4)	2 (512)	0.09	0.5	8
101243 ^e	RIF (8)	2 (512)	0.05	0.25	32

^a All MIC data presented in $\mu\text{g/mL}$.

^b Absolute MIC ($\mu\text{g/mL}$) of antibiotic was determined in the presence of 8 $\mu\text{g/mL}$ (9.0 μM) of hybrid **2**.

^c Antibiotic activity potentiation at 8 $\mu\text{g/mL}$ (9.0 μM) of hybrid **2**.

^d with ⁸³Thr to ⁸³Ile mutation in gyr A. [8]

^e without ⁸³Thr to ⁸³Ile mutation in gyr A. [8]

Table 8 Combination studies of NEB-MOX **1** with minocycline (MIN) or rifampicin (RIF) against MDR *Acinetobacter baumannii*, *Klebsiella pneumoniae*, and *Enterobacter cloacae*.

Organisms	Antibiotic (MIC ^a)	Hybrid (MIC ^a)	FICI	Absolute MIC ^b	Potential (fold) ^c
<i>A. baumannii</i> AB027	MIN (1)	1a (>256)	>1	NA	NA
<i>A. baumannii</i> AB027	RIF (1)	1a (>256)	0.031<x<0.047	0.03	32
<i>A. baumannii</i> AB030	MIN (2)	1a (>16)	>1	NA	NA
<i>A. baumannii</i> AB030	RIF (1024)	1a (>16)	0.031<x<0.281	32	32
<i>A. baumannii</i> AB031	MIN (1)	1a (128)	>1	NA	NA
<i>A. baumannii</i> AB031	RIF (1)	1a (128)	0.04	0.02	64
<i>A. baumannii</i> 110193	MIN (1)	1a (>256)	>1	NA	NA
<i>A. baumannii</i> 110193	RIF (1)	1a (>256)	0.031<x<0.047	0.03	32
<i>K. pneumoniae</i> 116381	MIN (64)	1a (>256)	0.063<x<0.078	4	16
<i>K. pneumoniae</i> 116381	RIF (1024)	1a (>256)	0.002<x<0.006	≤1	≥1024
<i>E. cloacae</i> 117029	MIN (64)	1a (32)	0.19	4	16
<i>E. cloacae</i> 117029	RIF (4)	1a (32)	0.06	≤0.03	≥128

^aAll MIC data presented in µg/mL.

^bAbsolute MIC (µg/mL) of antibiotic was determined in the presence of 8 µg/mL (7.5 µM) of hybrid **1a**.

^cAntibiotic activity potentiation at 8 µg/mL (7.5 µM) of hybrid **1a**.

NA, not available (no synergy was observed).

Table 9 Combination studies of NEB-CIP **1b** with minocycline (MIN) or rifampicin (RIF) against wild-type or MDR *Acinetobacter baumannii*, *Escherichia coli*, *Klebsiella pneumoniae*, and *Enterobacter cloacae*.

Organisms	Antibiotic (MIC ^a)	Hybrid (MIC ^a)	FICI	Absolute MIC	Potentiation (fold) ^d
<i>A. baumannii</i> ATCC 17978	MIN (0.25)	1b (128)	0.520	0.13 ^b	2
<i>A. baumannii</i> ATCC 17978	RIF (2)	1b (128)	0.016	0.008 ^b	256
<i>A. baumannii</i> AB92247	MIN (0.125)	1b (128)	0.531	0.06 ^b	2
<i>A. baumannii</i> AB92247	RIF (2)	1b (128)	0.039	0.02 ^b	128
<i>A. baumannii</i> AB110193	MIN (1)	1b (>128)	>1	NA	NA
<i>A. baumannii</i> AB110193	RIF (1)	1b (>128)	0.016<x<0.031	0.02 ^b	64
<i>E. coli</i> ATCC 25922	MIN (1)	1b (8)	0.504	NA	NA
<i>E. coli</i> ATCC 25922	RIF (4)	1b (8)	0.133	0.03 ^c	128
<i>E. coli</i> 94474	MIN (64)	1b (>128)	0.063<x<0.078	4 ^b	16
<i>E. coli</i> 94474	RIF (8)	1b (>128)	0.004<x<0.035	0.03 ^b	256
<i>E. coli</i> 107115	MIN (32)	1b (32)	0.133	2 ^b	16
<i>E. coli</i> 107115	RIF (32)	1b (32)	0.015<x≤0.020	≤0.13 ^b	≥256
<i>K. pneumoniae</i> 113250	MIN (2)	1b (128)	0.504	1 ^b	2
<i>K. pneumoniae</i> 113250	RIF (32)	1b (128)	0.039	0.25 ^b	128
<i>K. pneumoniae</i> 113254	MIN (2)	1b (128)	0.504	1 ^b	2
<i>K. pneumoniae</i> 113254	RIF (16)	1b (128)	0.047	0.25 ^b	64
<i>K. pneumoniae</i> 116381	MIN (64)	1b (>128)	0.063<x<0.070	4 ^b	16
<i>K. pneumoniae</i> 116381	RIF (>128)	1b (>128)	≤0.039	1 ^b	≥128
<i>E. cloacae</i> 117029	MIN (32)	1b (32)	0.125	2 ^b	16
<i>E. cloacae</i> 117029	RIF (8)	1b (32)	0.023	≤0.03 ^b	≥256

^aAll MIC data presented in µg/mL.

^bAbsolute MIC ($\mu\text{g/mL}$) of antibiotic was determined in the presence of 4 $\mu\text{g/mL}$ (4.1 μM) of hybrid **1b**.

^cAbsolute MIC ($\mu\text{g/mL}$) of antibiotic was determined in the presence of 2 $\mu\text{g/mL}$ (2.0 μM) of hybrid **1b**.

^dAntibiotic activity potentiation at 8 $\mu\text{g/mL}$ (4.1 μM) or 2 $\mu\text{g/mL}$ (2.0 μM) of hybrid **1b**.

NA, not available (no synergy was observed).

Highlights:

- New amphiphilic nebramine (NEB)-based hybrids were prepared from tobramycin-based (TOB)-based hybrids.
- Potent synergism was found for combinations of NEB-based hybrid adjuvants with multiple classes of antibiotics against multi-drug resistant (MDR) Gram-negative bacilli.
- Combination of NEB-CIP hybrid **1b** with rifampicin protects *Galleria mellonella* larvae from the lethal effects of extensively drug-resistant (XDR) *P. aeruginosa*.