



# Vancomycin and Clarithromycin Show Synergy against *Mycobacterium abscessus* In Vitro

Devika Mukherjee,<sup>a</sup> Mu-Lu Wu,<sup>b</sup>  Jeanette W. P. Teo,<sup>c</sup>  Thomas Dick<sup>a,d</sup>

Department of Microbiology and Immunology, Yong Loo Lin School of Medicine, National University of Singapore, Singapore<sup>a</sup>; Department of Medicine, Yong Loo Lin School of Medicine, National University of Singapore, Singapore<sup>b</sup>; Department of Laboratory Medicine, National University Hospital, Singapore<sup>c</sup>; Public Health Research Institute, New Jersey Medical School, Rutgers, The State University of New Jersey, Newark, New Jersey, USA<sup>d</sup>

**ABSTRACT** Lung disease caused by *Mycobacterium abscessus* is increasing, and current clarithromycin-based treatment regimens are only moderately effective. Here, we determined the effect of clarithromycin-vancomycin combination against *M. abscessus* complex isolates *in vitro*. Synergy was found with a fractional inhibitory concentration index (FICI) score of  $\leq 0.5$  and a 4- to 10-fold decrease in MIC.

**KEYWORDS** *Mycobacterium abscessus*, clarithromycin, synergy, vancomycin

The rapidly growing *Mycobacterium abscessus* gained importance as a pathogen in the early 1990s (1). *M. abscessus* mostly causes lung infections in vulnerable populations, including patients with cystic fibrosis, but also causes skin, soft tissue, and ocular infections (2). Patterns of drug resistance differ among the three currently recognized subspecies of the complex *M. abscessus* subsp. *abscessus*, *M. abscessus* subsp. *bolletii*, and *M. abscessus* subsp. *massiliense* (3, 4). Hence distinguishing between the subspecies is important clinically because they respond differently to antibiotic therapy (5, 6). Treatment regimens are combination based and rely on a macrolide (usually clarithromycin) and an aminoglycoside (such as amikacin) along with another active antimicrobial, such as a  $\beta$ -lactam (imipenem, ceftazidime) (7). Therapy is lengthy, requiring negative sputum cultures for 1 year (8), and often unsuccessful. Treatment failure is often attributed to clarithromycin resistance that is prevalent in the *M. abscessus* complex (1). Constitutive resistance to macrolides occurs due to point mutations at position 2058 or 2059 of the 23S rRNA (*rrl*) gene (9, 10). Inducible macrolide resistance in *M. abscessus* subsp. *abscessus* and *M. abscessus* subsp. *bolletii* is conferred by the ribosomal methylase gene *erm(41)* (11). However, the functionality of the *erm(41)* gene in these two subspecies is complicated by sequevars that carry a T→C substitution at position 28 of its coding sequence. A C28 *erm(41)* sequevar is nonfunctional and hence susceptible to clarithromycin (11). On the other hand, *M. abscessus* subsp. *massiliense* usually possesses a truncated, nonfunctional *erm(41)* gene copy and thus does not display inducible macrolide resistance (9, 11).

Previously, we screened a library of U.S. Food and Drug Administration-approved drugs for activity against *M. abscessus* and found that the glycopeptide vancomycin showed weak growth inhibitory activity against the clinical isolate *M. abscessus* Bamboo (12). Vancomycin is a tricyclic glycopeptide antibiotic from *Amycolatopsis orientalis* and is commonly used against Gram-positive bacteria. It prevents the cross-linking of *N*-acetylglucosamine/*N*-acetylmuramic acid peptides, thus inhibiting peptidoglycan synthesis of the cell wall (13). This results in bacterial cell wall weakening and thus may facilitate increased penetration of other antimicrobials and enhance their potency. Here, we asked whether vancomycin can be used to enhance clarithromycin potency

Received 22 June 2017 Returned for modification 14 July 2017 Accepted 8 September 2017

Accepted manuscript posted online 18 September 2017

**Citation** Mukherjee D, Wu M-L, Teo JWP, Dick T. 2017. Vancomycin and clarithromycin show synergy against *Mycobacterium abscessus* *in vitro*. Antimicrob Agents Chemother 61:e01298-17. <https://doi.org/10.1128/AAC.01298-17>.

**Copyright** © 2017 Mukherjee et al. This is an open-access article distributed under the terms of the [Creative Commons Attribution 4.0 International license](https://creativecommons.org/licenses/by/4.0/).

Address correspondence to Thomas Dick, [td367@njms.rutgers.edu](mailto:td367@njms.rutgers.edu).

D.M and M.-L.W. contributed equally to the work.

**TABLE 1** *In vitro* synergy of vancomycin and clarithromycin in *M. abscessus* complex isolates

Isolate code	<i>M. abscessus</i> subspecies <sup>a</sup>	<i>erm</i> (41) sequevar <sup>a</sup>	MIC ( $\mu$ M) of <sup>b</sup> :				FICI
			CLR alone	VAN alone	CLR in combination	VAN in combination	
ATCC 19977	<i>abscessus</i>	T28	6.25	25	0.39	3.12	0.19
CCUG 50184T	<i>bolletii</i>	T28	12.5	12.5	0.78	1.56	0.19
CCUG 48898T	<i>massiliense</i>	Deleted	1.56	50	0.39	3.12	0.31
Bamboo	<i>abscessus</i>	C28	1.56	25	0.20	3.12	0.25
M337	<i>abscessus</i>	T28	6.25	100	0.78	12.5	0.25
M199	<i>abscessus</i>	T28	12.5	100	1.56	12.5	0.24
M404	<i>abscessus</i>	C28	0.78	6.25	0.20	1.56	0.49
M9	<i>abscessus</i>	T28	6.25	100	1.56	6.25	0.31
M422	<i>abscessus</i>	T28	3.12	25	0.39	6.25	0.37
M111	<i>massiliense</i>	Deleted	0.39	6.25	0.10	1.56	0.49
M506	<i>bolletii</i>	C28	1.56	200	0.39	50	0.50
M232	<i>bolletii</i>	T28	12.5	50	3.12	12.5	0.49

<sup>a</sup>Subspecies were determined by sequencing *rpoB* and *hsp65*; *erm*(41) sequevar was determined by sequencing the gene.

<sup>b</sup>Experiments were repeated twice independently, and mean values are shown. Standard deviations were  $\pm 50\%$  of the shown values. VAN, vancomycin; CLR, clarithromycin.

and examined the *in vitro* synergistic potential of these two drugs against *M. abscessus* complex type strains and clinical isolates.

Type strains *M. abscessus* subsp. *abscessus* ATCC 19977, *M. abscessus* subsp. *bolletii* Culture Collection University of Gothenburg (CCUG) 50184T, and *M. abscessus* subsp. *massiliense* CCUG 48898T ( $n = 3$ ) and clinical isolates ( $n = 9$ ) were used for susceptibility and synergy testing (Table 1). Cultures were grown as described previously (12). Whole-genome sequencing of *M. abscessus* Bamboo showed that this strain represents a C28 sequevar, rendering the isolate sensitive to clarithromycin (14). The other eight clinical isolates were obtained from the strain collection of the clinical microbiology laboratory at the National University Hospital, Singapore. The isolates were speciated using *rpoB* and *hsp65* (15), as described previously (12). The *erm*(41) and *rml* genes were analyzed as previously described (12). The 28th nucleotide of *erm*(41) was examined for T/C polymorphisms. The presence of mutations at nucleotide positions 2058 to 2059 of *rml* encoding the 23S rRNA were also examined. Mutations at these positions are responsible for constitutive clarithromycin resistance. None of the isolates used in this study possessed *rml* mutations.

Vancomycin was dissolved in water and clarithromycin in acetone. The effect of acetone on growth of the bacteria was tested up to a concentration of 2% (equivalent to the highest concentration used) and was found to have no effect on the growth of the bacteria. MICs were determined using 2-fold serial dilutions of the drugs in 96-well microtiter plates that were incubated with the bacterial cultures at 37°C for 72 h. After this, optical density at 600 nm ( $OD_{600}$ ) was measured using the Tecan infinite Pro 200 plate reader.  $OD_{600}$  was used as a measure of growth, and growth inhibition was assessed in comparison to growth in drug-free wells. The concentration of each drug that inhibited 90% growth was defined as its MIC. The interaction between clarithromycin and vancomycin was assessed using a broth microdilution checkerboard assay. The concentrations of the drugs used were decided based on MICs and were within the range of 0.05 to 200  $\mu$ M for both vancomycin and clarithromycin. Fractional inhibitory concentration index (FICI) was calculated as (MIC of drug A in combination/MIC of drug A alone) + (MIC of drug B in combination/MIC of drug B alone), where A is clarithromycin and B is vancomycin. Synergy was defined as a FICI score of  $\leq 0.5$  (16).

The MICs of the drugs alone and in combination are presented in Table 1. The MIC of vancomycin ranged from 6.25 to 200  $\mu$ M, and that of clarithromycin ranged from 0.39 to 12.5  $\mu$ M. The MICs of both drugs were reduced by 4- to 10-fold when tested in combination. Synergy was demonstrated for all of the laboratory strains and the clinical isolates. Synergy was also evaluated on induction of clarithromycin resistance, which

**TABLE 2** *In vitro* synergistic effect of clarithromycin and vancomycin against two *M. abscessus* type strains with inducible clarithromycin resistance under induced conditions

Strain	Day	MIC ( $\mu\text{M}$ ) of:				FICI <sup>a</sup>
		CLR alone	VAN alone	CLR in combination	VAN in combination	
Preincubation induction assay						
<i>M. abscessus</i> subsp. <i>abscessus</i> ATCC 19977	3	>200	12.5	0.39	3.12	<0.25
<i>M. abscessus</i> subsp. <i>bolletii</i> CCUG 50184T	3	>200	6.25	3.12	1.56	<0.25
Standard inducible resistance assay						
<i>M. abscessus</i> subsp. <i>abscessus</i> ATCC 19977	3	6.25	25	0.39	3.12	0.19
	7	25	100	0.39	12.5	0.14
	14	>200	100	12.5	6.25	<0.13
<i>M. abscessus</i> subsp. <i>bolletii</i> CCUG 50184T	3	12.5	12.5	0.78	1.56	0.19
	7	25	50	1.56	3.12	0.12
	14	>200	50	25	1.56	<0.16

<sup>a</sup>A less than symbol (<) preceding a FICI score indicates that an MIC of the drug alone was higher than the greatest concentration tested, which was used in FICI calculation.

was achieved by preincubating bacterial cultures with clarithromycin for 24 h at 0.1  $\mu\text{M}$  (a concentration that does not inhibit bacterial growth on its own) as previously described (12). This preincubation assay resulted in a shift in the clarithromycin MIC to >200  $\mu\text{M}$ . The two subspecies type strains with inducible clarithromycin resistance (ATCC 19977 and CCUG 50184T) were tested after preincubation with clarithromycin, and both showed a dramatic reduction in clarithromycin MIC, from >200 to 0.39  $\mu\text{M}$  for *M. abscessus* subsp. *abscessus* and 3.12  $\mu\text{M}$  for *M. abscessus* subsp. *bolletii*, when combined with vancomycin (Table 2). When combined with clarithromycin, the vancomycin concentration was 4-fold lower than with vancomycin alone. In addition, the standard inducible resistance assay for clarithromycin with prolonged incubation was carried out as described by Nash et al. (11) (Table 2). Similar to the results with the preincubation assay, at 14 days, the MIC for clarithromycin alone was >200  $\mu\text{M}$ . In combination with vancomycin, clarithromycin MIC shifted to 12.5 and 25  $\mu\text{M}$  for *M. abscessus* subsp. *abscessus* and *M. abscessus* subsp. *bolletii*, respectively.

Taken together, our results indicate that combinations of vancomycin and clarithromycin *in vitro* have synergistic effects and may thus be useful in treating *M. abscessus* infections. To our knowledge, this is the first report demonstrating vancomycin-clarithromycin synergy in *M. abscessus*. The reduced MICs may facilitate achievement of clinically useful *in vivo* drug concentrations and thus make therapy more effective. The observed synergy may also allow for lower doses of either antibiotic and hence reduce toxicity (17).

Patients infected with strains possessing an intact *erm*(41) gene have a lower rate of successful treatment outcomes (18, 19). Here, using our preincubation assay and the standard inducible resistance assay with prolonged incubation, we were able to demonstrate synergy with this combination in the presence of the intact *erm*(41) gene. These results suggest that the clarithromycin-vancomycin combination may be useful in improving the treatment outcomes of infections involving organisms that harbor inducible clarithromycin resistance.

A limitation of using this combination is that there are no established breakpoints for *M. abscessus* infection. Another factor to consider is that vancomycin is administered intravenously (20), which makes adherence an issue due to the long treatment duration of *M. abscessus* infections. Whether this combination can be applied clinically is debatable, as it remains to be determined whether vancomycin MICs in combination are achievable in human serum and whether the toxicity will be reduced by the use of combination therapy. However, the synergistic effect seen between vancomycin and clarithromycin establishes the grounds for further investigation into the use of vancomycin-like antibiotics, such as teicoplanin and telavancin.

We made all of our potency determinations under standard mycobacterium culture

conditions, i.e., Middlebrook 7H9 broth with incubation at 37°C. Because the CLSI guidelines suggest the use of cation-adjusted Mueller-Hinton broth and incubation at 30°C for clinical drug susceptibility testing of rapidly growing mycobacteria (21), we also tested our antibiotic combination under additional conditions (see Tables S1 to S4 in the supplemental material). The drugs showed synergy under many of the conditions tested. However, we observed that assay conditions, including media composition, absence of detergent, and incubation temperature, can strongly affect the MICs (Tables S1 to S4).

In conclusion, vancomycin and clarithromycin exhibited a strong synergistic effect *in vitro* against all *M. abscessus* strains tested, suggesting potential clinical application. Studies in animals and clinical evaluation of efficacy are required to assess the usefulness of this novel combination *in vivo*. Furthermore, we identified effects of assay conditions on antibiotic potency, highlighting a need for further investigations to improve the predictive value of the *in vitro* growth inhibition assay for clinical outcome.

## SUPPLEMENTAL MATERIAL

Supplemental material for this article may be found at <https://doi.org/10.1128/AAC.01298-17>.

**SUPPLEMENTAL FILE 1**, PDF file, 0.3 MB.

## ACKNOWLEDGMENTS

This work was supported by the Singapore Ministry of Health's National Medical Research Council under its Translational Clinical Research Flagship Grant (NMRC/TCR/011-NUHS/2014) to T.D. and is part of the Singapore Programme of Research Investigating New Approaches to Treatment of Tuberculosis (SPRINT-TB; [www.sprinttb.org](http://www.sprinttb.org)) led by Nick Paton. D.M. received a research scholarship from Yong Loo Lin School of Medicine.

We thank Wei Chang Huang (Taichung Veterans General Hospital, Taichung, Taiwan) for providing the *M. abscessus* Bamboo strain and Dinah Binte Aziz, National University of Singapore, for discussion and comments on the manuscript.

D.M. and M.-L.W. carried out the experiments. J.W.P.T. provided and characterized the clinical strains. D.M., M.-L.W., and T.D. wrote the manuscript.

We declare that we have no conflicts of interest.

## REFERENCES

- Nessar R, Cambau E, Reyat JM, Murray A, Gicquel B. 2012. *Mycobacterium abscessus*: a new antibiotic nightmare. *J Antimicrob Chemother* 67:810–818. <https://doi.org/10.1093/jac/dkr578>.
- Rubio M, March F, Garrigo M, Moreno C, Espanol M, Coll P. 2015. Inducible and acquired clarithromycin resistance in the *Mycobacterium abscessus* complex. *PLoS One* 10:e0140166. <https://doi.org/10.1371/journal.pone.0140166>.
- Choi GE, Chang CL, Whang J, Kim HJ, Kwon OJ, Koh WJ, Shin SJ. 2011. Efficient differentiation of *Mycobacterium abscessus* complex isolates to the species level by a novel PCR-based variable-number tandem-repeat assay. *J Clin Microbiol* 49:1107–1109. <https://doi.org/10.1128/JCM.02318-10>.
- Kim HY, Kim BJ, Kook Y, Yun YJ, Shin JH, Kim BJ, Kook YH. 2010. *Mycobacterium massiliense* is differentiated from *Mycobacterium abscessus* and *Mycobacterium bolletii* by erythromycin ribosome methyltransferase gene (*erm*) and clarithromycin susceptibility patterns. *Microbiol Immunol* 54:347–353. <https://doi.org/10.1111/j.1348-0421.2010.00221.x>.
- Singh S, Bouzinbi N, Chaturvedi V, Godreuil S, Kremer L. 2014. *In vitro* evaluation of a new drug combination against clinical isolates belonging to the *Mycobacterium abscessus* complex. *Clin Microbiol Infect* 20:O1124–O1127. <https://doi.org/10.1111/1469-0691.12780>.
- Zhang Z, Lu J, Liu M, Wang Y, Zhao Y, Pang Y. 2017. *In vitro* activity of clarithromycin in combination with other antimicrobial agents against *Mycobacterium abscessus* and *Mycobacterium massiliense*. *Int J Antimicrob Agents* 49:383–386. <https://doi.org/10.1016/j.ijantimicag.2016.12.003>.
- Brown-Elliott BA, Nash KA, Wallace RJ, Jr. 2012. Antimicrobial susceptibility testing, drug resistance mechanisms, and therapy of infections with nontuberculous mycobacteria. *Clin Microbiol Rev* 25:545–582. <https://doi.org/10.1128/CMR.05030-11>.
- Griffith DE, Aksamit T, Brown-Elliott BA, Catanzaro A, Daley C, Gordin F, Holland SM, Horsburgh R, Huitt G, Iademarco MF, Iseman M, Olivier K, Ruoss S, von Reyn CF, Wallace RJ, Jr, Winthrop K. 2007. An official ATS/IDSA statement: diagnosis, treatment, and prevention of nontuberculous mycobacterial diseases. *Am J Respir Crit Care Med* 175:367–416. <https://doi.org/10.1164/rccm.200604-571ST>.
- Bastian S, Veziris N, Roux AL, Brossier F, Gaillard JL, Jarlier V, Cambau E. 2011. Assessment of clarithromycin susceptibility in strains belonging to the *Mycobacterium abscessus* group by *erm*(41) and *rhl* sequencing. *Antimicrob Agents Chemother* 55:775–781. <https://doi.org/10.1128/AAC.00861-10>.
- Wallace RJ, Jr, Meier A, Brown BA, Zhang Y, Sander P, Onyi GO, Bottger EC. 1996. Genetic basis for clarithromycin resistance among isolates of *Mycobacterium chelonae* and *Mycobacterium abscessus*. *Antimicrob Agents Chemother* 40:1676–1681.
- Nash KA, Brown-Elliott BA, Wallace RJ, Jr. 2009. A novel gene, *erm*(41), confers inducible macrolide resistance to clinical isolates of *Mycobacterium abscessus* but is absent from *Mycobacterium chelonae*. *Antimicrob Agents Chemother* 53:1367–1376. <https://doi.org/10.1128/AAC.01275-08>.
- Aziz DB, Low JL, Wu ML, Gengenbacher M, Teo JWP, Dartois V, Dick T. 2017. Rifabutin is active against *Mycobacterium abscessus* complex. *Antimicrob Agents Chemother* 61:e00155-17. <https://doi.org/10.1128/AAC.00155-17>.

13. Reynolds PE. 1989. Structure, biochemistry and mechanism of action of glycopeptide antibiotics. *Eur J Clin Microbiol Infect Dis* 8:943–950. <https://doi.org/10.1007/BF01967563>.
14. Yee M, Klinzing D, Wei JR, Gengenbacher M, Rubin EJ, Dick T. 2017. Draft genome sequence of *Mycobacterium abscessus* Bamboo. *Genome Announc* 5:e00388-17. <https://doi.org/10.1128/genomeA.00388-17>.
15. Adekambi T, Berger P, Raoult D, Drancourt M. 2006. *rpoB* gene sequence-based characterization of emerging non-tuberculous mycobacteria with descriptions of *Mycobacterium bolletii* sp. nov., *Mycobacterium phocaicum* sp. nov. and *Mycobacterium aubagnense* sp. nov. *Int J Syst Evol Microbiol* 56: 133–143. <https://doi.org/10.1099/ijs.0.63969-0>.
16. Odds FC. 2003. Synergy, antagonism, and what the checkerboard puts between them. *J Antimicrob Chemother* 52:1. <https://doi.org/10.1093/jac/dkg301>.
17. Fouquier J, Guedj M. 2015. Analysis of drug combinations: current methodological landscape. *Pharmacol Res Perspect* 3:e00149. <https://doi.org/10.1002/prp2.149>.
18. Koh WJ, Jeon K, Lee NY, Kim BJ, Kook YH, Lee SH, Park YK, Kim CK, Shin SJ, Huitt GA, Daley CL, Kwon OJ. 2011. Clinical significance of differentiation of *Mycobacterium massiliense* from *Mycobacterium abscessus*. *Am J Respir Crit Care Med* 183:405–410. <https://doi.org/10.1164/rccm.201003-0395OC>.
19. Park J, Cho J, Lee CH, Han SK, Yim JJ. 2017. Progression and treatment outcomes of lung disease caused by *Mycobacterium abscessus* and *Mycobacterium massiliense*. *Clin Infect Dis* 64:301–308. <https://doi.org/10.1093/cid/ciw723>.
20. Bruniera FR, Ferreira FM, Saviolli LR, Bacci MR, Feder D, da Luz Goncalves Pedreira M, Sorgini Peterlini MA, Azzalis LA, Campos Junqueira VB, Fonseca FL. 2015. The use of vancomycin with its therapeutic and adverse effects: a review. *Eur Rev Med Pharmacol Sci* 19:694–700.
21. Clinical and Laboratory Standards Institute. 2011. Susceptibility testing of mycobacteria, Nocardiae, and other aerobic actinomycetes; approved standard—2nd ed. CLSI document M24-A2. Clinical and Laboratory Standards Institute, Wayne, PA.