TOWARDS PRECISION MEDICINE:
MECHANISM-BASED MODELLING OF AN INHALED COMBINATION OF AZTREONAM PLUS TOBRAMYCIN DOSING REGIMENS AGAINST HYPERMUTABLE *PSEUDOMONAS AERUGINOSA* CLINICAL ISOLATES FROM PATIENTS WITH CYSTIC FIBROSIS IN *IN VITRO* BIOFILM STUDIES

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INTRODUCTION

- Antibiotic resistance, one of the greatest threats to humans, is exacerbated by suboptimal antibiotic dosing regimens
- *Pseudomonas aeruginosa* (Pa) is a Priority 1 bacterial pathogen (WHO)
- Lung infections due to Pa are a main driver of mortality in cystic fibrosis (CF)[1,2]
- 'One size fits all' dosing has been ineffective in these exacerbations, mainly due to presence of biofilms and hypermutable, multidrug-resistant Pa strains [3,4]

URGENT change in antibiotic dosing is essential

OBJECTIVES

- To evaluate inhaled dosing regimens of aztreonam (AZT) and tobramycin (TOB), in monotherapy and combination, against challenging Pa CF clinical isolates in a dynamic in vitro biofilm model.
- To characterize this experimental data through mechanism-based mathematical modelling.

METHODS

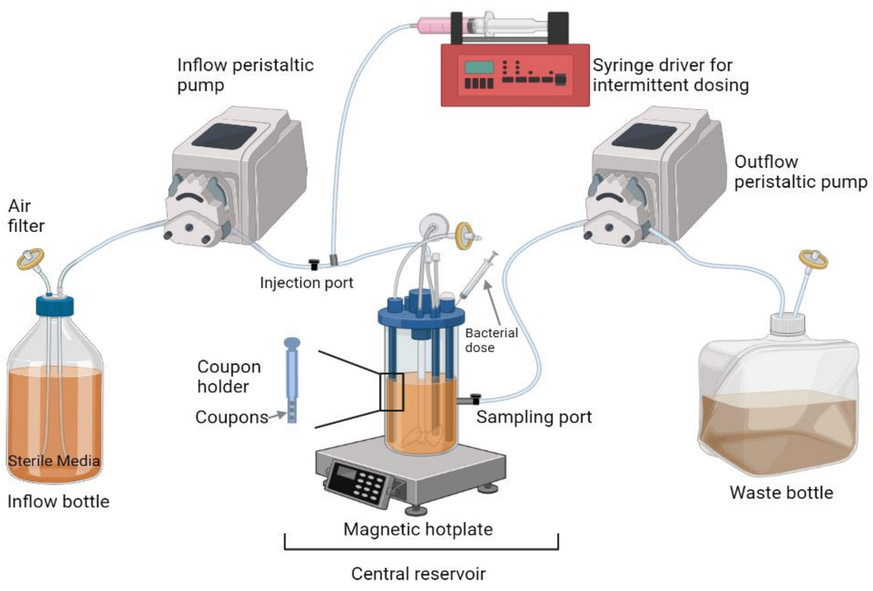


Figure 1. Biofilm model experimental set up

- Two multidrug-resistant, hypermutable clinical isolates from patients with CF, exposed to treatment for 168h (n=2±SEM)
- Biofilm model (Fig. 1) simulated the pharmacokinetics of inhaled AZT and TOB as observed in lung fluids of patients with CF ($t_{1/2}$=3h)[5]
- Concentrations of the AZT (75mg, every 8h) and TOB (300mg, every 12h) dosing regimens quantified by LC-MS/MS
- Total viable and resistant counts quantified at 8 and 5 time points
- Counts mathematically modelled (Fig. 2)

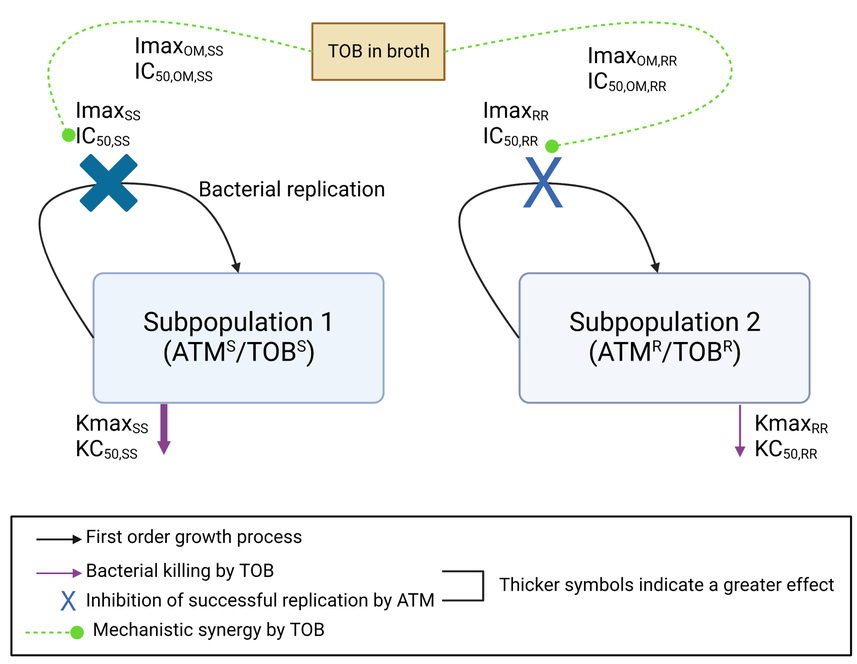
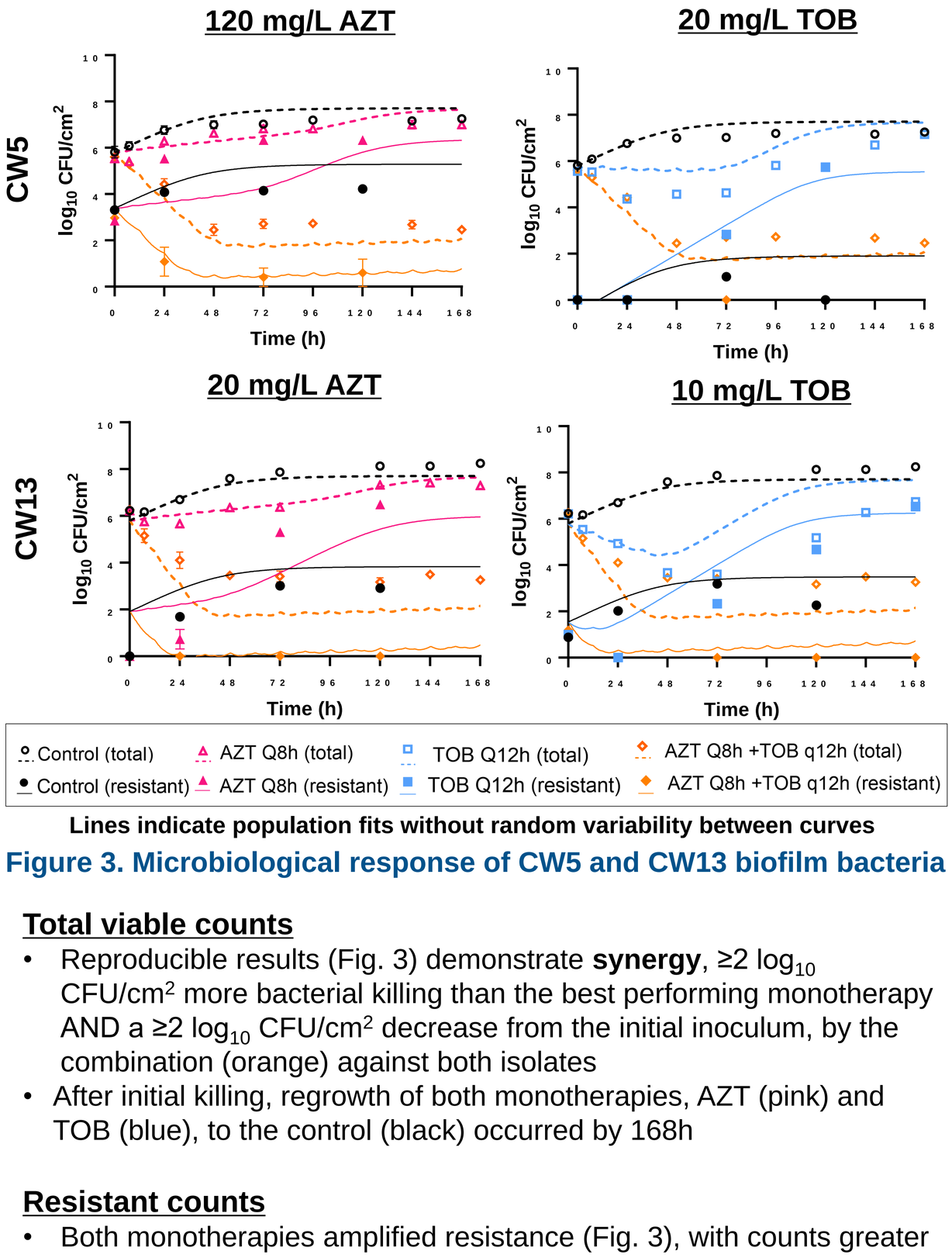


Figure 2. Simplified mechanism-based model (MBM) structure

RESULTS



Lines indicate population fits without random variability between curves

Figure 3. Microbiological response of CW5 and CW13 biofilm bacteria

Total viable counts

- Reproducible results (Fig. 3) demonstrate **synergy**, ≥2 log$_{10}$ CFU/cm^2 more bacterial killing than the best performing monotherapy AND a ≥2 log$_{10}$ CFU/cm^2 decrease from the initial inoculum, by the combination (orange) against both isolates
- After initial killing, regrowth of both monotherapies, AZT (pink) and TOB (blue), to the control (black) occurred by 168h

Resistant counts

- Both monotherapies amplified resistance (Fig. 3), with counts greater than the baseline resistance that is shown in the control population
- Monotherapies resulted in the total viable bacterial population at 168h showing increased resistance
- The combination suppressed resistance compared to the control

MBM

- The simultaneously modelled biofilm data was well characterised by the model (Fig. 3)
- The combination was modelled with the inclusion of mechanistic synergy

CONCLUSIONS

As well as performing synergistically, the inhaled AZT and TOB combination was required to supress resistance against both Pa clinical isolates from patients with CF. The MBM could be utilised to inform translation of regimens to *in vivo* or ultimately clinical studies in the future. This MBM could be extended with the use of population pharmacokinetics to adjust the dosing regimen for a patient based on their specific characteristics that affect the antibiotic pharmacokinetics in the lungs. This could also be paired with identifying bacterial characteristics which impact the antibiotic exposure in the lung fluid. This promising combination regimen warrants further investigation.

ACKNOWLEDGEMENTS

This work was supported by NHMRC Project and Ideas grants GNT1159579 and GNT1184428.

REFERENCES

1. *Touw et al. Pharmacy World and Science 1998; 20:149-160.*
2. *Monogue et al. J Antimicrob Chemother 2016; 60:6578-6584.*
3. *Rees et al. J Antimicrob Chemother 2019; 63:e02538-18.*
4. *Oliver et al. International Journal of Medical Microbiology 2010*
5. *El Hassani et al. Clinical Pharmacokinetics 2021; 60:447-470.*