

Mathematical Modeling of *Escherichia coli* Kinetics to Predict Growth and Rifampicin-dependent Killing Profile

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October 8, 2022

Abstract

Antibiotic resistance is a global health threat. To combat against infections, we urgently need better strategies. Currently there are limited number of antibiotics in the treatment repertoire of existing bacterial infections. Among them rifampicin is a broad-spectrum antibiotic against various bacterial pathogens. Efficacy of rifampicin decreases by time due to appearance of rifampicin persister or resistant phenotypes in the population. To benefit more from rifampicin, its current standard dosage might be reconsidered and deeply explored using both computational tools and experimental or clinical studies. In this study, we present the mathematical relationship between the concentration of rifampicin and the growth and killing kinetics of *Escherichia coli* cells. We generated time-killing curves of *Escherichia coli* cells in the presence of 4 µg/ml, 16 µg/ml, and 32 µg/ml rifampicin exposures. We fitted time-killing curve data using the *lsqcurvefit* function in MATLAB to model rifampicin responses of *Escherichia coli* cells.

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