SUPPLEMENTARY MATERIAL: Can phenotypic data complement our understanding of anti-mycobacterial effects for drug combinations?

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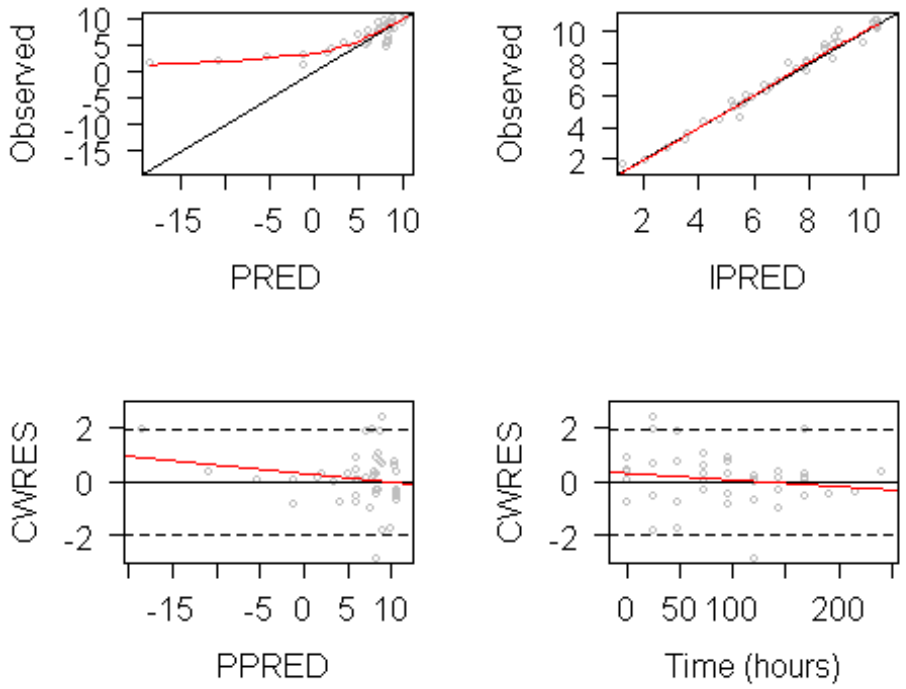
Colony Forming Units data

Table S1: Parameters from the turnover model on Colony Forming Units data

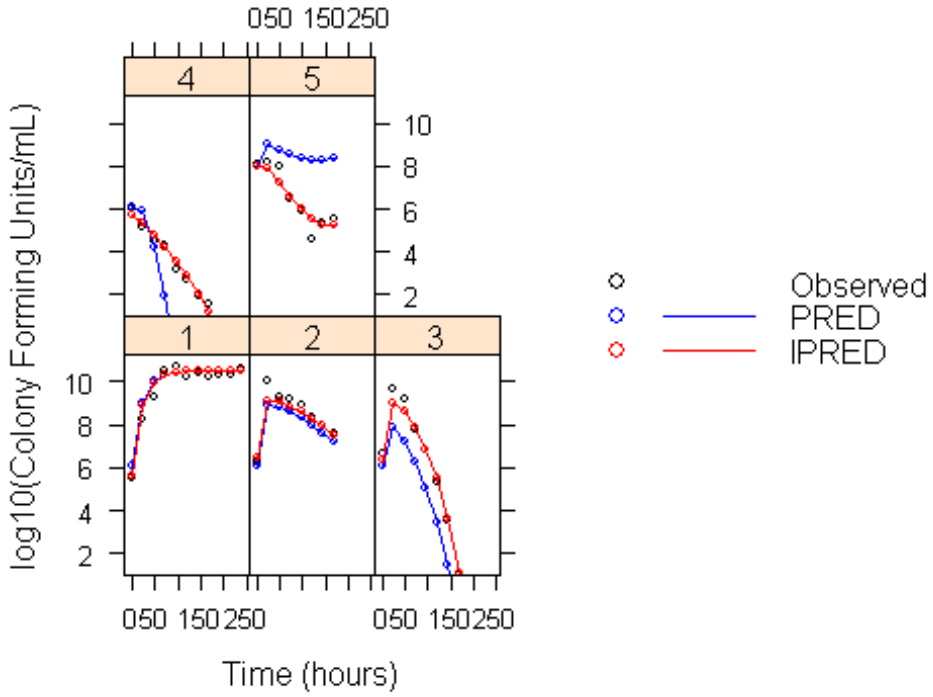
	Estimate	%RSE
Baseline CFU (10^)	6.17	3.34
knet (hr-1)	0.04	6.26
CFUMAX	10.50	0.88
IC50 (nmol/l)	3.89	163
EMAX	1.40	1.36
Time50 (hr)	28.9	9.13
LagRif50 (nmol/l)	161	846
INH on baseline CFU	0.31	16.3
T1/2 INH (hr)	438	0.06
OMEGA EC50	5.20	112
OMEGA ECLAG50	3.93	2360
Additive residual variability	0.39	2.50

Figure S1: Goodness of fit plots for the turnover model



Popupation (PRED) and individual (IPRED) predictions against observations, and conditonal weighted residuals (CWRES) versus PRED and time after start of the experiment. Dots represent observations, the black line represents the line of unity and the red line represents the Local Polynomial Regression Fitting.

Figure S2: Individual data fits for the turnover model



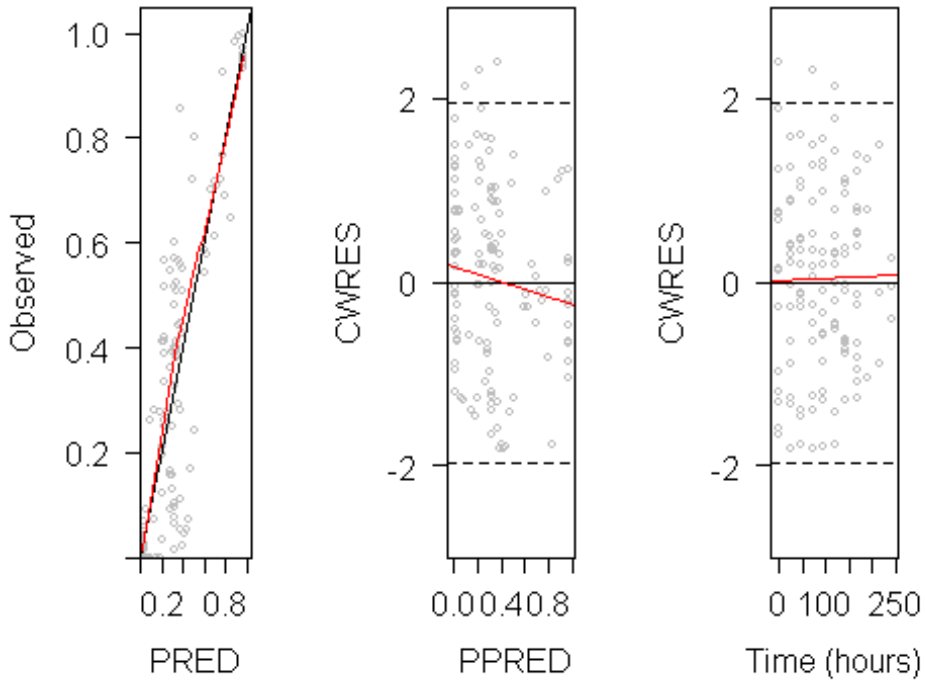
Population (PRED) and individual (IPRED) predictions of the observed CFU data with the turnover model. 1: Growth curve, 2: Rifampicin C_{MAX} = 0.14 mg/l, 3: Rifampicin C_{MAX} = 0.4 mg/l, 4: Rifampicin C_{MAX} = 1.47 mg/l, and 5: Rifampicin C_{MAX} = 0.4 mg/l & isoniazid C_{MAX} = 1.2 mg/l.

Cell viability data

Table S2: Parameter estimates from the unordered multinomial response model

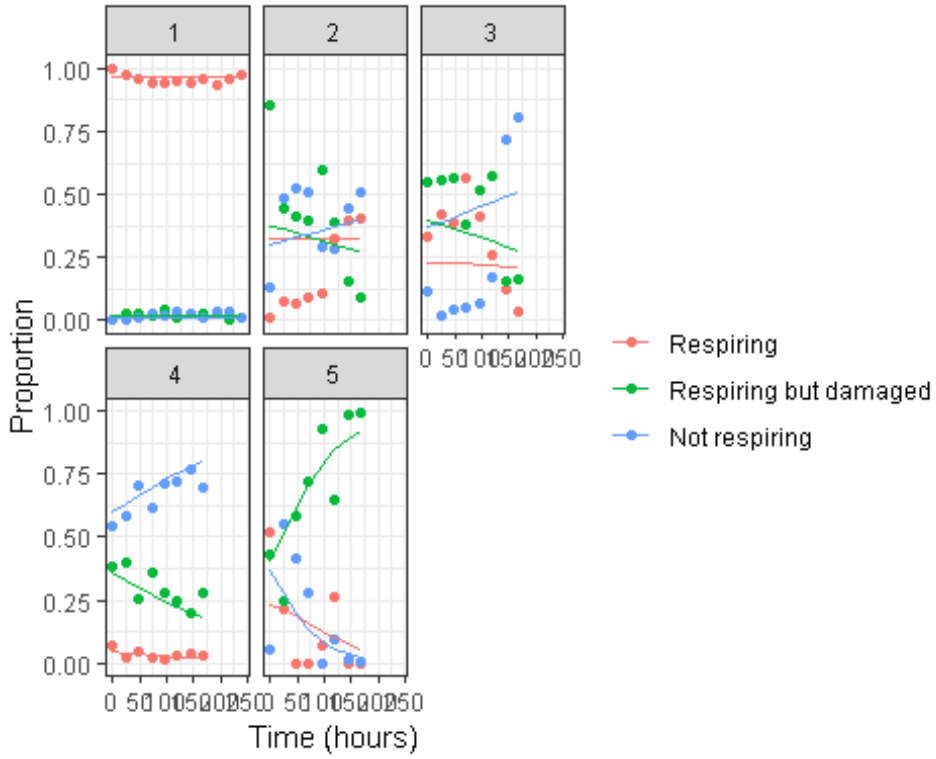
	Estimate	Std. Error
THETA1	3.86e+00	1.71e-01
THETA2	-3.81e+00	6.17e-01
THETA3	-2.61e-02	1.03e-02
THETA4	-3.00e-07	6.00e-07
THETA5	2.34e-03	6.06e-03
THETA6	-8.84e+00	2.74e+01
THETA7	9.65e-03	4.35e-03
THETA8	-2.96e-01	2.73e-01
THETA9	2.00e-07	3.00e-07
THETA10	3.35e-03	3.04e-03
THETA11	-5.41e+00	3.80e+00
Additive	7.19e-01	2.04e-01

Figure S3: Goodness of fit plots for the unordered multinomial response model.



Model predictions (PRED) against observed proportions, and conditonal weighted residuals (CWRES) versus PRED and time after start of the experiment. Dots represent observations, the black line represents the line of unity and the red line represents the Local Polynomial Regression Fitting.

Figure S4: Individual data fits for the unordered multinomial response model.



Model predictions (blue, green and red lines) of the observed proportional data (blue, green and red dots). 1: Growth curve, 2: Rifampicin C_{MAX} = 0.14 mg/l, 3: Rifampicin C_{MAX} = 0.4 mg/l, 4: Rifampicin C_{MAX} = 1.47 mg/l, and 5: Rifampicin C_{MAX} = 0.4 mg/l & isoniazid C_{MAX} = 1.2 mg/l. Model predictions for the Rifampicin C_{MAX} = 0.14 mg/l and Rifampicin C_{MAX} = 0.4 mg/l experiment were less accurate when compared to the model predictions for the growth curve, Rifampicin C_{MAX} = 0.14 mg/l, and Rifampicin C_{MAX} = 0.4 mg/l & isoniazid experiment due to the noise in the data.