

# Supplemental Digital Content

Linked to the manuscript entitled “The lysis of pathogenic *Escherichia coli* by bacteriophages releases less endotoxin than betalactams” by Dufour *et al.*

**Table S1:** Nonlinear regression parameters associated with the modeling of the evolution of the free endotoxin concentration according to time obtained with strain 536 in presence of Imipenem, Ceftriaxone, 536\_P1 and Amikacin.

Sigmoid function	Imipenem
<b>Best-fit values</b>	
$V_{max}$	23616
h	2.888
K	86541
<b>Std. Error</b>	
$V_{max}$	790.4
h	0.3189
K	103758
<b>Goodness of Fit</b>	
Degrees of Freedom	9
$R^2$	0.9906
Absolute Sum of Squares	7,35E+06
$Sy.x$	903.7
<b>Constraints</b>	
h	$h > 0.0$
K	$K > 0.0$

Exponential growth function	Ceftriaxone
<b>Best-fit values</b>	
$Y_0$	447.3
K	0.02658
<b>Std. Error</b>	
$Y_0$	433.4
K	0.00539
<b>Goodness of Fit</b>	
Degrees of Freedom	10
$R^2$	0.9812
Absolute Sum of Squares	8,72E+07
$Sy.x$	2953

Reverse exponential function	536_P1	Amikacin
<b>Best-fit values</b>		
$Y_0$	429.5	429.5
Plateau	24779	8824
K	0.003985	0.01981
<b>Std. Error</b>		
Plateau	3263	245.3
K	0.0007158	0.00126
<b>Goodness of Fit</b>		
Degrees of Freedom	10	10
$R^2$	0.9937	0.9905
Absolute Sum of Squares	1,26E+06	807297
$Sy.x$	354.2	284.1
<b>Constraints</b>		
$Y_0$	$Y_0 = 429.5$	$Y_0 = 429.5$
K	$K > 0.0$	$K > 0.0$

**Table S2:** Nonlinear regression parameters associated with the modeling of the evolution of the free endotoxin concentration according to time obtained with strain LM33 in presence of Cefoxitin, Imipenem, LM33\_P1 and Amikacin.

<b>Sigmoid function</b>	<b>Cefoxitin</b>	<b>Imipenem</b>
<b>Best-fit values</b>		
$V_{max}$	13629	63504
h	1.715	1.753
K	493.9	4576
<b>Std. Error</b>		
$V_{max}$	1864	29102
h	0.5781	0.6009
K	934.1	8312
<b>Goodness of Fit</b>		
Degrees of Freedom	9	9
$R^2$	0.8919	0.9767
Absolute Sum of Squares	2.199e+007	5.588e+007
$Sy.x$	1563	2492
<b>Constraints</b>		
h	$h > 0.0$	$h > 0.0$
K	$K > 0.0$	$K > 0.0$

<b>Reverse exponential function</b>	<b>LM33_P1</b>	<b>Amikacin</b>
<b>Best-fit values</b>		
$Y_0$	1579	1579
Plateau	5888	8179
K	0.05645	0.04223
<b>Std. Error</b>		
Plateau	782.7	394.6
K	0.03751	0.007632
<b>Goodness of Fit</b>		
Degrees of Freedom	10	10
$R^2$	0.5511	0.9368
Absolute Sum of Squares	2.134e+007	4.150e+006
$Sy.x$	1461	644.2
<b>Constraints</b>		
$Y_0$	$Y_0 = 1579$	$Y_0 = 1579$
K	$K > 0.0$	$K > 0.0$

**Figure S1**

**A. Adsorption of bacteriophage 536\_P1 on its host 536.** Strain 536 grown in LB at 37 °C with shaking (100 rpm) was mixed with bacteriophage 536\_P1 at a MOI of  $10^{-4}$  and aliquots were taken at the indicated time points. Dots represent the mean of 3 independent experiments with the standard deviation.

**B. Bacteriophage 536\_P1 growth parameters.** Bacteriophage 536\_P1 was mixed with strain 536 (MOI  $10^{-1}$ ) at 37 °C with shaking. At the indicated time points, samples were analyzed in absence (grey lines) or in presence (black lines) of chloroform. The continuous lines represent the experimental measurements (mean of 2 independent experiments with standard error) while the dashed lines are the nonlinear regression obtained from these points.

