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SMR.940 - 35

**THIRD AUTUMN WORKSHOP
ON MATHEMATICAL ECOLOGY**

(14 October - 1 November 1996)

**"The dynamics of drug action on within-host pathogen
population dynamics"**

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These are preliminary lecture notes, intended only for distribution to participants.

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Pharmacokinetics?

1. PK is the measurement and modelling of drug concentrations within the body.
2. Required for licensing, efficacy and toxicity studies.
3. Evaluation of possible therapeutic dosage regimens (how much, how often?).
4. Lots of data available from both volunteer and patient studies.

Possible models

1. Single intravenous (IV) dose (first-order decay).
2. Single oral or Intramuscular (IM) dose.
3. Constant dose-rate regimens.
4. Multiple dose regimens.

Pharmacodynamics

1. PD describes the effect of a drug at the active site for a given concentration.
2. Often the exact model of action a drug is unknown (e.g. antimalarials).
3. $E_{\max}$ saturation model of drug action is commonly used
4. Data available for antibiotics and antimalarials is all *in vitro*.

Within-host pathogen models

1. Often simple exponential growth models are sufficient.
2. PD couples within-host pathogen models with PK giving treatment models.

Modelling malaria infections

1. Population biology ecological model of malaria infection.
2. Dynamics defined by parameter R_0 which measures the number of secondary infected RBCs in a naïve host produced by a single infected RBC.
3. Drug intervention makes R_0 concentration dependent.
4. Successful prophylaxis/therapy requires $R_0(C) < 1$.
5. Using PD and then PK gives the minimum doses required for success.

References for further reading

1. Rowland, M. & Tozer, T.N. (1995), *Clinical Pharmacokinetics*, Wilkins (in RSL).
2. White, N.J. (1994), Clinical pharmacokinetics and pharmacodynamics of artemisinin and derivatives, *Trans. R. Soc. Trop. Med. Hyg.*, **88**, S1, 41--43.
3. Gravenor, M.B., McLean, A.R. & Kwiatkowski, D. (1995), The regulation of malaria parasitaemia: parameter estimation for a population model, *Parasitology*, **110**, 115-122.
4. Austin, D.J., White, N.J. & Anderson, R.M. (1996), The dynamics of drug action on the within-host pathogen population growth of infectious agents, *J. Theor. Biol.*, **in press**.

provided elsewhere (N.I.S., C.A.E.D., Leeuwen, R.S., and R.J.d.B., unpublished). In phase 4 of various T cells get activated—the healthy CD4 T-cell count is ~1000 cells; resting T cells are long-lived (26)—i.e., activated T cells rapidly revert to the resting state; the infection rate is arbitrarily set to γ led particle per day; the life-time of infected cells is $1/\alpha$ —i.e., $\alpha = 0.04$, $d_T = 1/25$ —i.e., $d_T = 0.04$. Setting $\alpha = 0.04$, $d_T = 1/25$ we obtain exactly the same rates of CD4 cell decline recently reported (24, 25).

Since the mutant strains have previously been estimated to be $R_{41} = 4$, $R_{70} = 8$, $R_{215} = 16$, $R_{41/70} = 6$ (4, 27). We conservatively set the absence of the drug to $e_{215} = e_{41/215} = e_{41} = e_{70} = e_{41/70} = 0.95$ to prevent a too high of the first mutations in our model (N.I.S. *et al.*). The mutation frequencies are estimated to be 3 to A changes are preferred over other changes that transitions are more likely to occur (28). We therefore set the mutation rate of G to A changes to $\mu_1/2$, and other changes to μ_1 . The probability that no mutations occur is $(\mu_1)^{1680} = 0.95$.

RESULTS

CD4+ Cell Counts. The mean CD4+ cell count declined during the first month of treatment, but returned to baseline values during subsequent months. The changes in CD4+ cell count mirrored the changes in HIV-1 RNA load.

HIV-1 RNA Load. Serum HIV-1 RNA was detectable at all time points with a mean level at baseline of $10^{4.43}$ (Fig. 1B). A maximum decline of 0.5 log units was followed by increases during subsequent months, though still significantly below baseline values. By month 24, mean RNA load reached baseline values of treatment.

Percentages of 41, 70, and 215 Mutant Serum HIV-1 RNA. The percentage of 70 mutant RNA could not be determined in the first subject, possibly due to sequence variation of the annealing site of the probe. In the remaining subjects, the median percentage of 70 mutant RNA decreased to <5% with a concurrent increase in the percentage of 41 mutant RNA. The percentage of 215 mutant RNA was not determined within this study. Although appearing to be stable, the percentage of 215 mutant RNA was not determined.

The initial increase of serum RNA load between 1 and 3 months of treatment was not caused by the K70R amino acid change, because a similar resurgence was observed in 70 wild-type virus. However, the ultimate increase to baseline

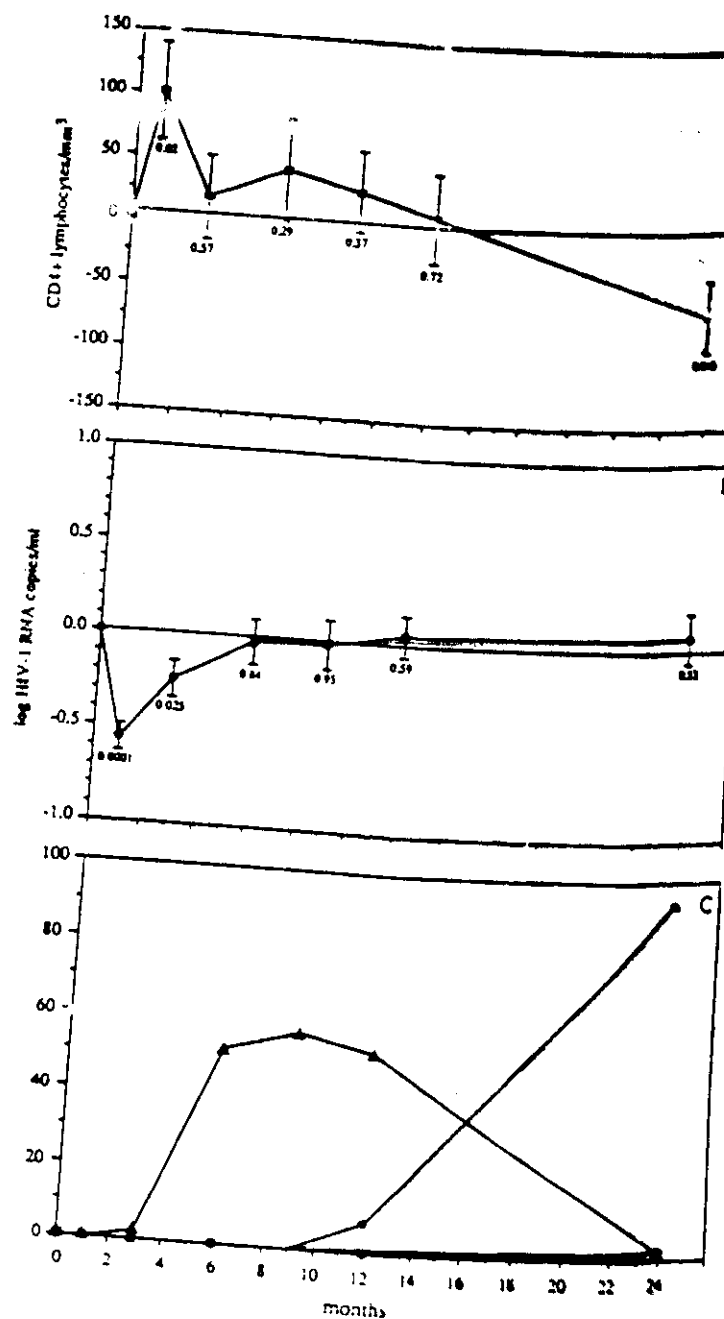


FIG. 1. Mean changes from baseline ($\pm$ SE) in (A) CD4+ cell count (B), log HIV-1 RNA load, and (C) median percentages of HIV-1 RNA containing a M41L (■), K70R (▲), and T215Y/F (●) amino acid change in HIV-1 RT during 2 years of zidovudine treatment. Numbers underneath error bars indicate the *P* values of changes (paired two-tailed *t* test).

HIV-1 RNA Load Changes and Resistance Mutations. A temporal relationship appeared to exist between the emergence of K70R mutant virus and a return to baseline values of serum RNA load (Fig. 1). Because it was not clear whether the relative amounts of 70 mutant RNA were sufficient to explain the resurgence of serum RNA load, we determined the relative amounts of 70 mutant RNA in the first 9 months of treatment. The other mutations were generally not apparent (Fig. 2).

The initial increase of serum RNA load between 1 and 3 months of treatment was not caused by the K70R amino acid change, because a similar resurgence was observed in 70 wild-type virus. However, the ultimate increase to baseline

PHARMACOKINETICS & PHARMACODYNAMICS

DAREN AUSTIN.

I PHARMACOKINETICS

- MEASUREMENT AND MODELLING OF DRUG CONCENTRATIONS WITHIN THE BODY.
- REQUIRED FOR LICENSING, EFFICACY AND TOXICITY STUDIES.
- EVALUATION OF POSSIBLE DOSAGE REGIMENS.
- LOTS OF DATA.

MODELS

- SINGLE I.V. DOSE (FIRST-ORDER ELIMINATION).

• VOLUME OF DISTRIBUTION $V = \frac{\text{AMOUNT OF DRUG IN BODY}}{\text{PLASMA DRUG CONCENTRATION}}$

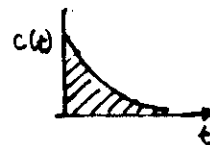
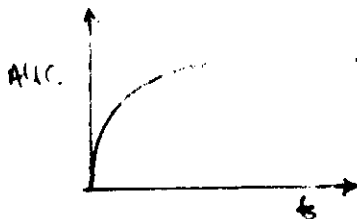
$$V = \frac{A}{C}$$

$$\frac{dC}{dt} = -kC \Rightarrow C(t) = C(0) \exp(-kt) \quad \text{--- } \times V$$

$$A(t) = \text{DOSE} \exp(-kt)$$

• $t_{1/2} = \frac{\ln 2}{k} \Rightarrow$ ESTIMATION OF k FROM $t_{1/2}$.

• AREA UNDER CURVE $AUC = \int_0^{t_1} dt' C(t')$

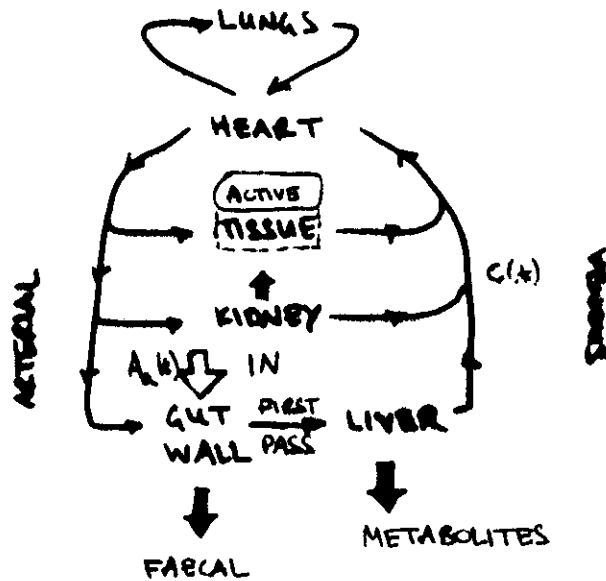


• CLEARANCE = RATE OF DRUG ELIMINATION

$$CL = \frac{\text{DOSE}}{AUC}$$

- SINGLE ORAL / I.M. DOSE (FIRST-ORDER ABSORPTION)

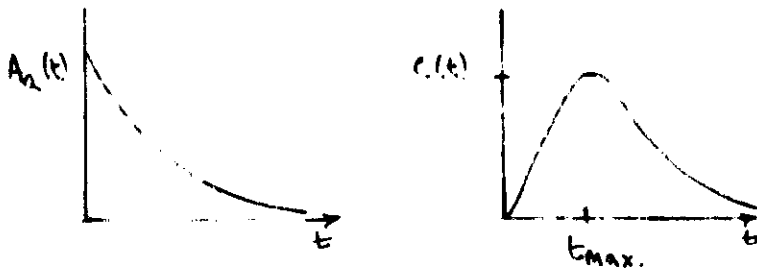
- BIOAVAILABILITY F = FRACTION OF DOSE ABSORBED INTACT;



$$\frac{dA_a}{dt} = -k_a A_a \quad \frac{dC}{dt} = \frac{k_a A_a}{V} - k C$$

$$A_a(t) = F \cdot \text{DOSE} \cdot \exp(-k_a t)$$

$$C(t) = \frac{F \cdot \text{DOSE}}{V} \cdot \frac{k_a}{k_a - k} \left[\exp(-kt) - \exp(-k_a t) \right]$$



- MULTIPLE COMPARTMENT MODELS.

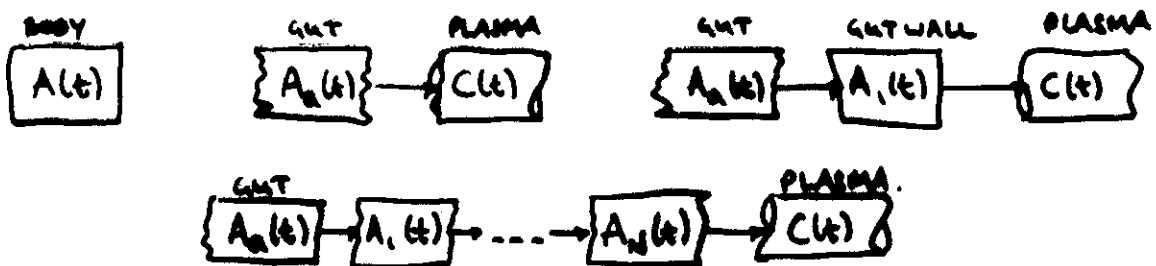
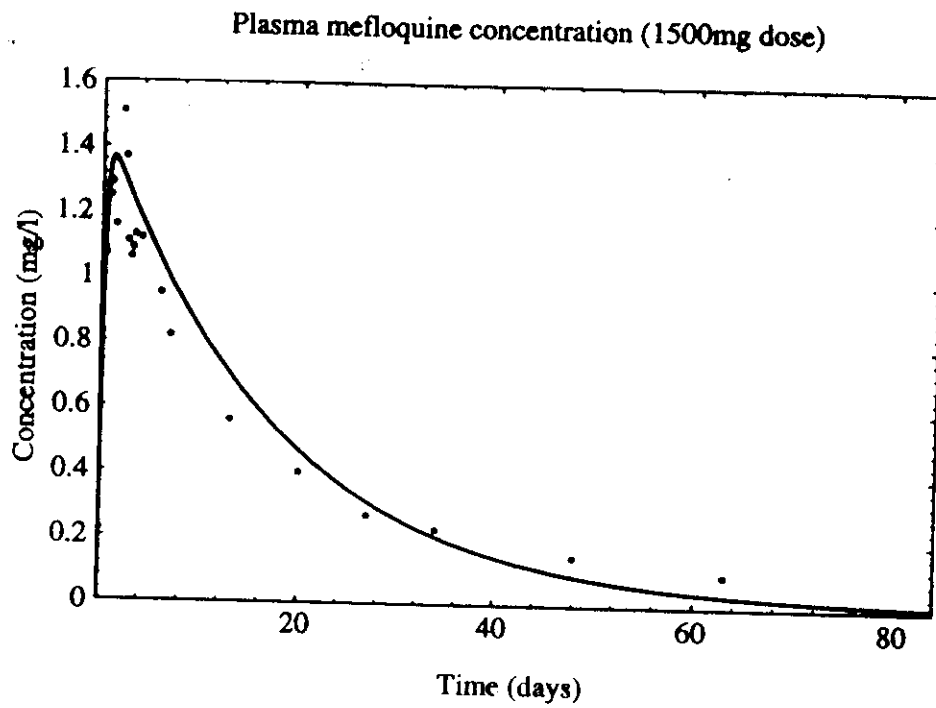
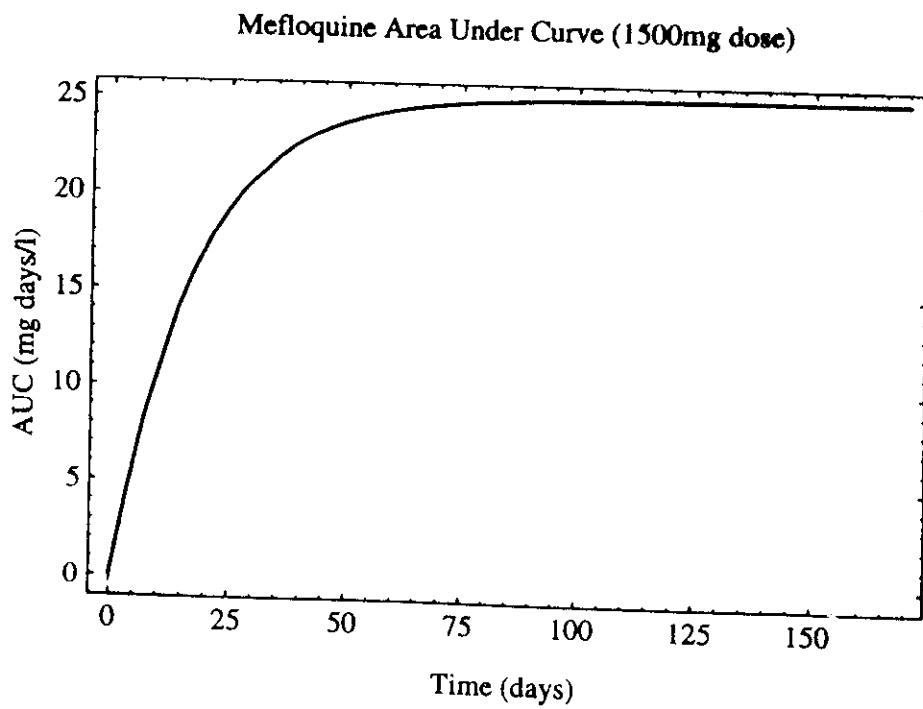


Figure 1.

a/



b/



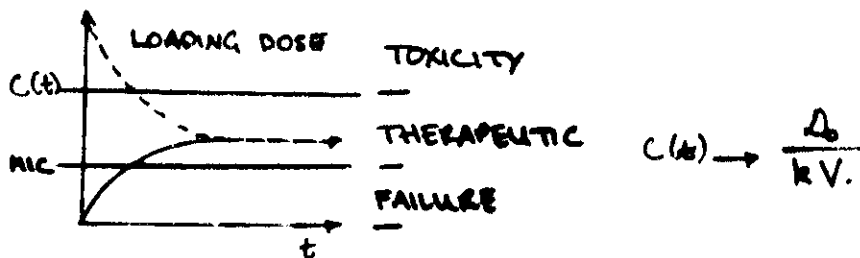
① — CONSTANT DOSE-RATE REGIMENS.

② — MULTIPLE DOSE REGIMENS.

} THERAPEUTIC RANGE

① DOSE RATE = D_0 (mg/h).

$$\frac{dC}{dt} = \frac{D_0}{V} - kC \rightarrow C(t) = \frac{D_0}{kV} (1 - \exp(-kt)).$$



② CONSTANT DOSE TAKEN EVERY τ HOURS.

ASSUME I.V. DOSING.

TIME $A(t)$ / DOSE

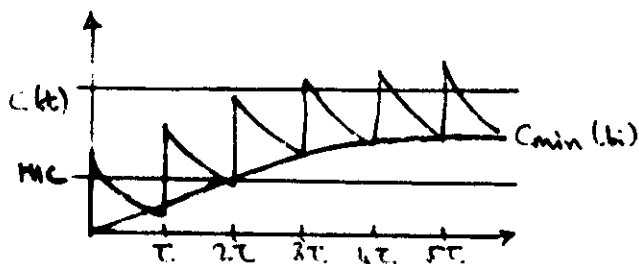
0 0

$\tau \exp(-k\tau)$

$2\tau \exp(-k\tau) [1 + \exp(-k\tau)]$

$N\tau \exp(-k\tau) [1 + \exp(-k\tau) + \dots + \exp(-(N-1)k\tau)]$

$$A_{min}(t_i) = \text{DOSE} \frac{(1 - \exp(-i k \tau))}{(1 - \exp(-k \tau))} \exp(-k \tau)$$



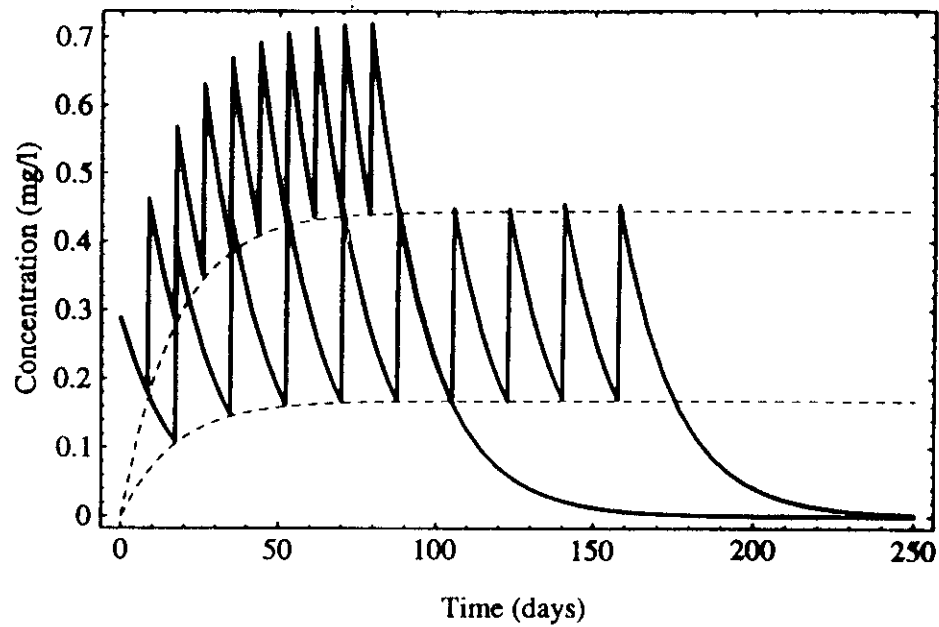
$$A_{min} \rightarrow \text{N.S.E.}, \frac{\exp(-k\tau)}{1 - \exp(-k\tau)} \approx \frac{D_0}{k}$$

$\Rightarrow$ EQUIVALENT WHEN $D_0 = k \text{ DOSE} \exp(-k\tau) \cdot R$.

• R = ACCUMULATION FACTOR FOR THE REGIMEN.

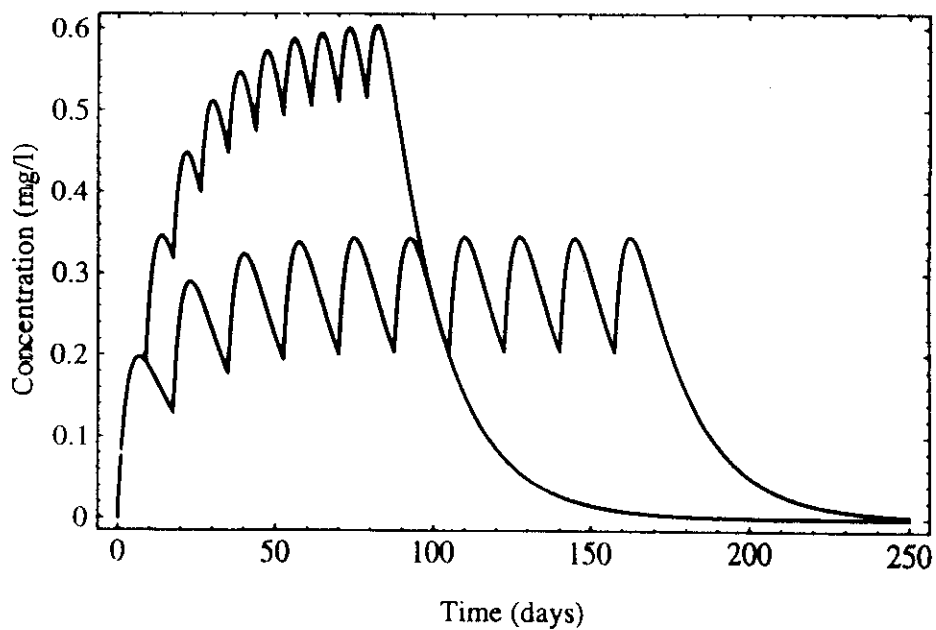
a/

Plasma mefloquine concentration (250mg oral dose)



b/

Plasma mefloquine concentration (250mg slow absorption)



II PHARMACODYNAMICS.

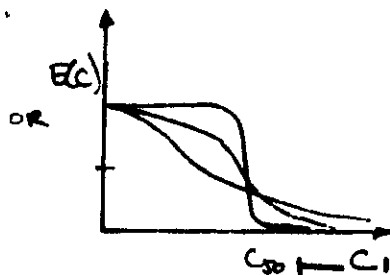
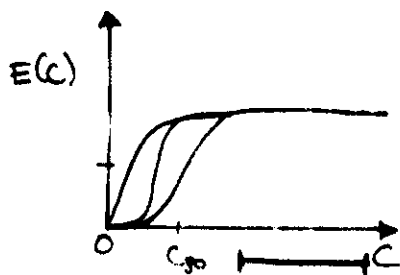
— DESCRIBES THE CONCENTRATION - EFFECT RELATIONSHIP AT THE ACTIVE SITE.

— EXACT MODE OF ACTION IS OFTEN UNKNOWN.

— E_{MAX} MODEL.

$$\bullet \text{ EFFECT } (C) = \frac{E_{MAX} C^n}{C_{50}^n + C^n} \quad \text{INCREASED EFFECT.}$$

$$= \text{NO DRUG} - \frac{E_{MAX} C^n}{C_{50}^n + C^n} \quad \text{DECREASED.}$$



— THERAPEUTIC.

— ANTIMALARIAL DRUGS KILL INFECTED RBC. (INCREASE)

— ANTIBIOTICS INHIBIT REPLICATION (REDUCE).

— DATA IS FROM *IN VITRO* STUDIES ONLY.

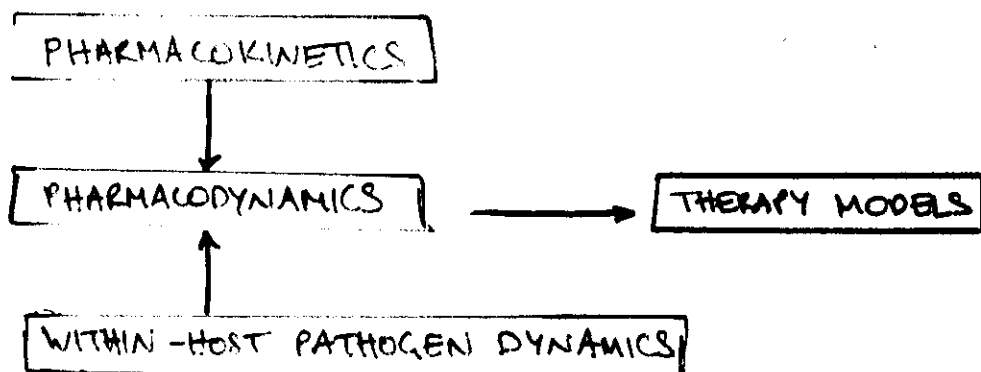
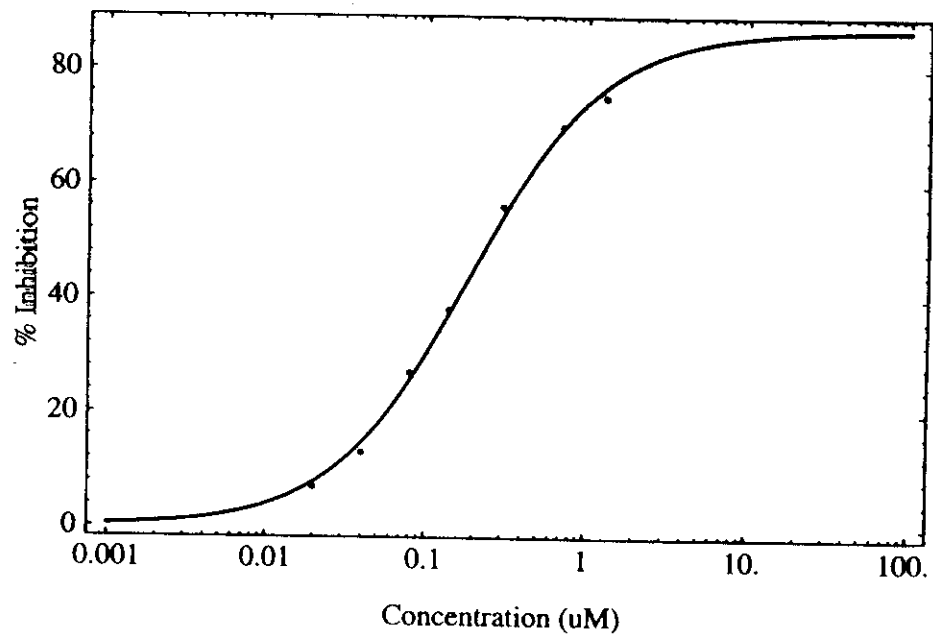


Figure 2

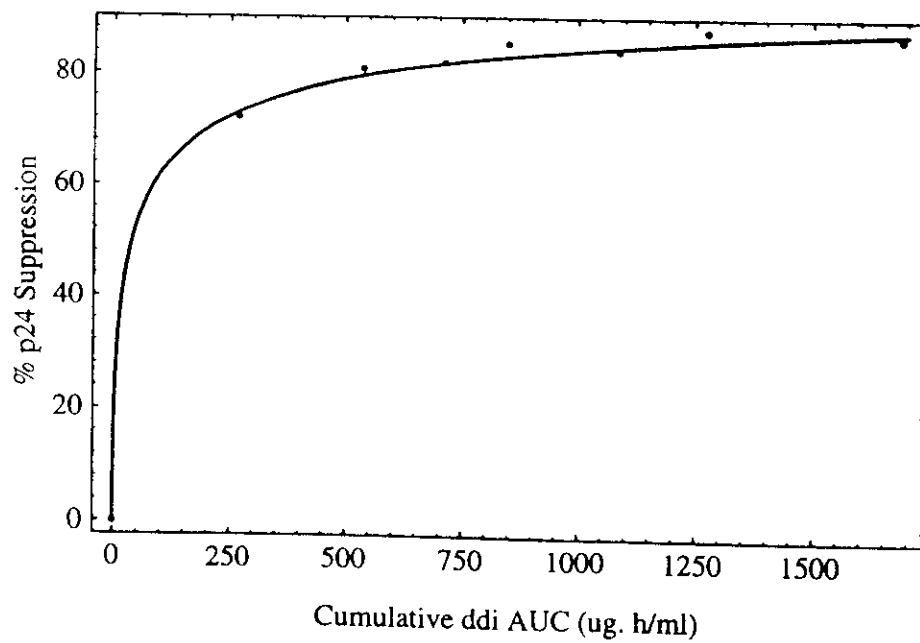
a/

Mefloquine inhibition of T996 *P. falciparum*



b/

ddI suppression of p24 HIV antigen



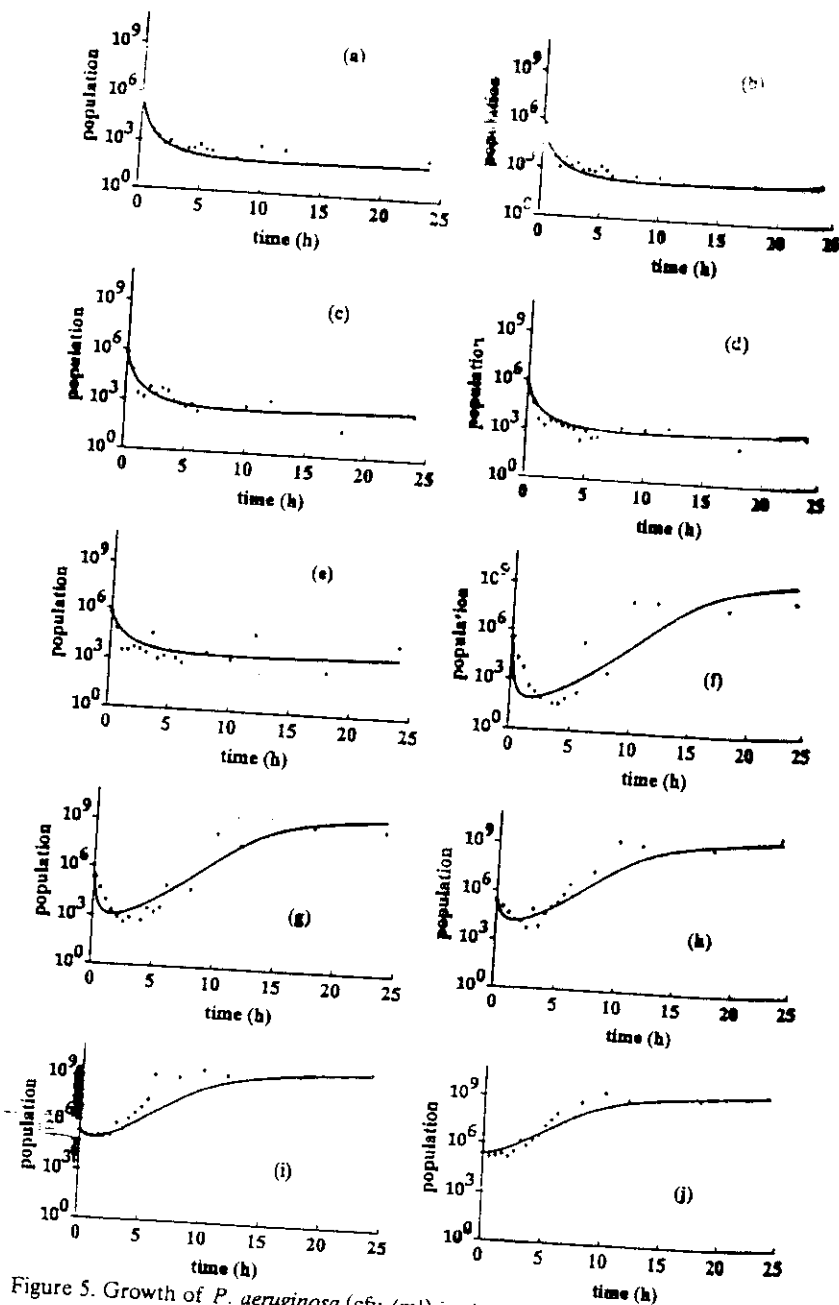
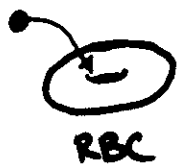


Figure 5. Growth of *P. aeruginosa* (cfu/ml) in the presence of imipenem. Initial concentrations of (a) 64, (b) 32, (c) 16, (d) 8, (e) 4, (f) 2, (g) 1, (h) 0.5, (i) 0.25 and (j) 0.125 $\mu\text{g/ml}$. Parameter values for U5 are used for graphs (a)–(e); parameter values for L5 are used for graphs (f)–(j). The points show the experimental data; the solid line shows the fitted curve.

IV MALARIA.

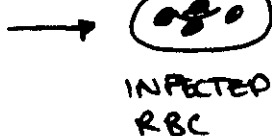
- NO IMMUNITY MODEL;

MEROZOITES



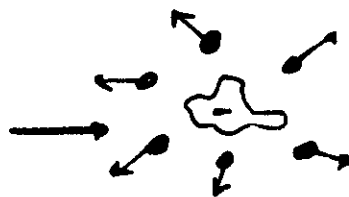
RBC

$X(t)$



INFECTED RBC

$Y(t)$



FREE

MEROZOITES

$M(t)$

$$\frac{dX}{dt} = \Lambda - \mu X - \frac{\beta X M}{\text{INFECTION}}$$

$$\frac{dY}{dt} = \beta X M - \alpha Y$$

INCREASED DEATH RATE WHEN INFECTED

$$\frac{dM}{dt} = \frac{\gamma \alpha Y}{\text{CELL RUPTURES}} - \delta M - \beta' X M$$

$\alpha(c)$ WITH DRUGS.

$\gamma(c)$ WITH DRUGS.

- MALARIA INVADDES IF

$$R_0 = \frac{\Lambda}{\mu} \frac{\beta(\mu)}{\delta} > 1$$

$\frac{\Lambda}{\mu} = \text{HAEMATOCRIT.}$

- PROPHYLAXIS REQUIRES $R_0 < 1$.

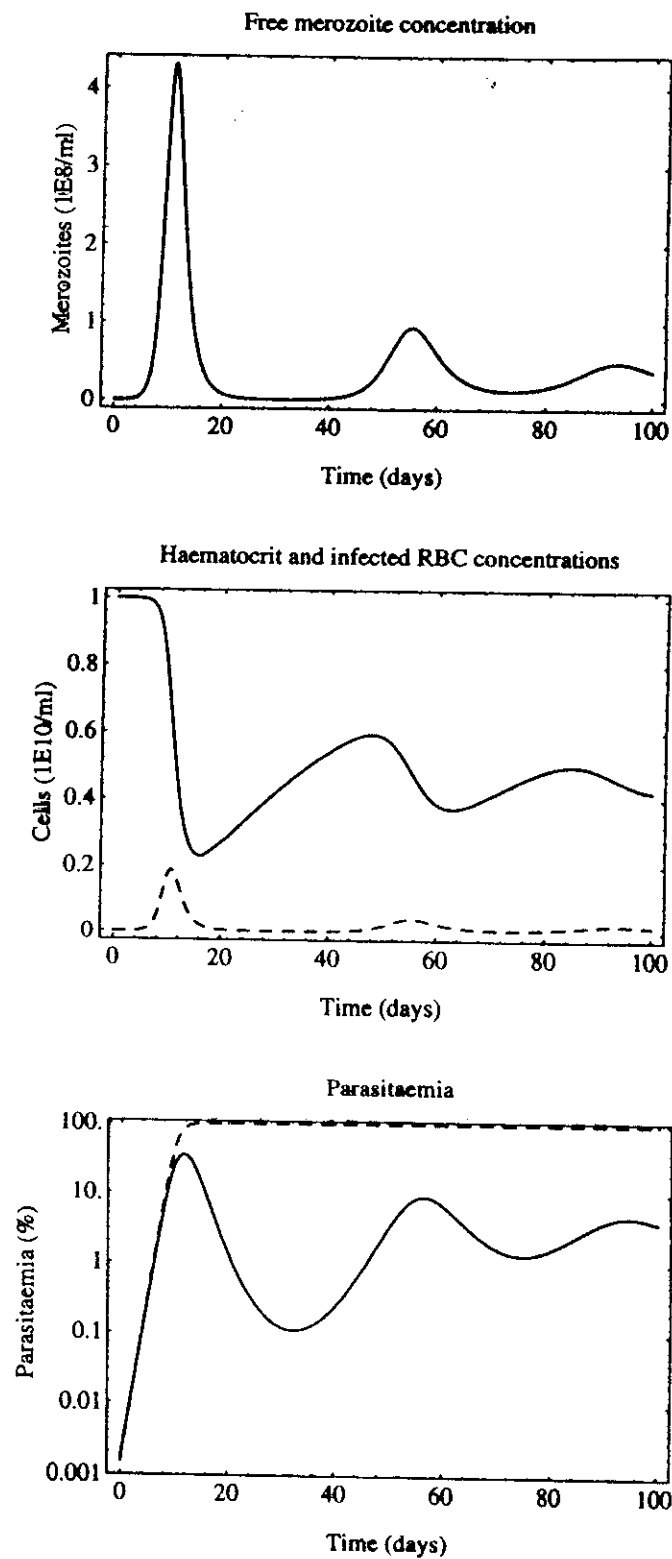
- CHEMOPROPHYLAXIS MAKES $R_0(c)$, CONCENTRATION DEPENDENT.

- CALCULATE PLASMA DRUG CONCENTRATION REQUIRED SUCH THAT $R_0(c) < 1$

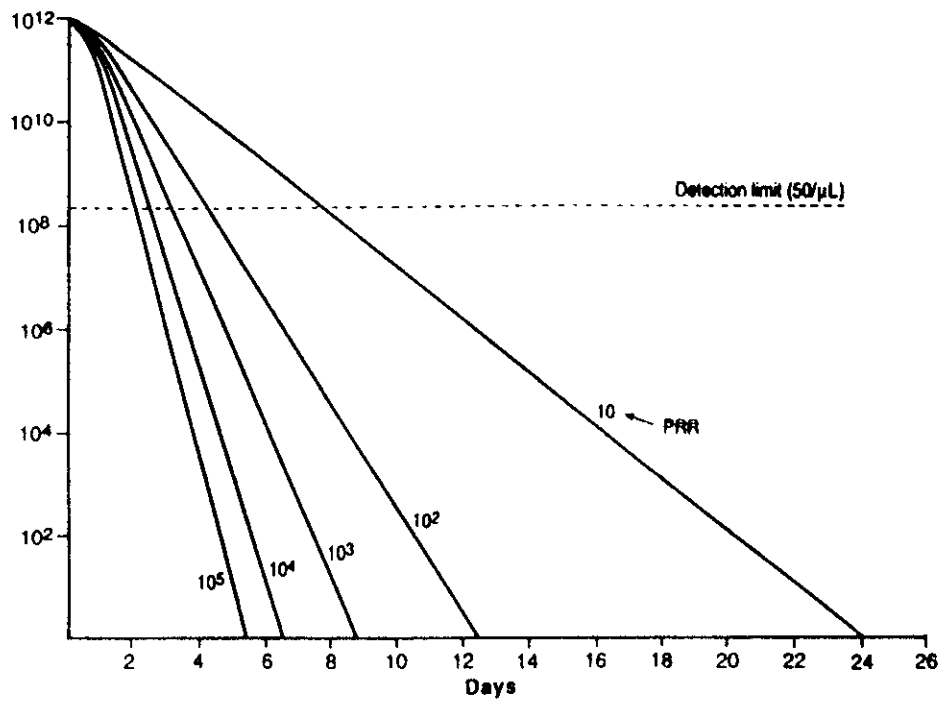
- IMMUNITY REDUCES R_0 .

$$R_0 = \frac{\Lambda}{\mu} \frac{\beta(\gamma - 1 - I)}{\delta(1 + I)} \approx 1 \quad \text{DEPENDENT ON } I$$

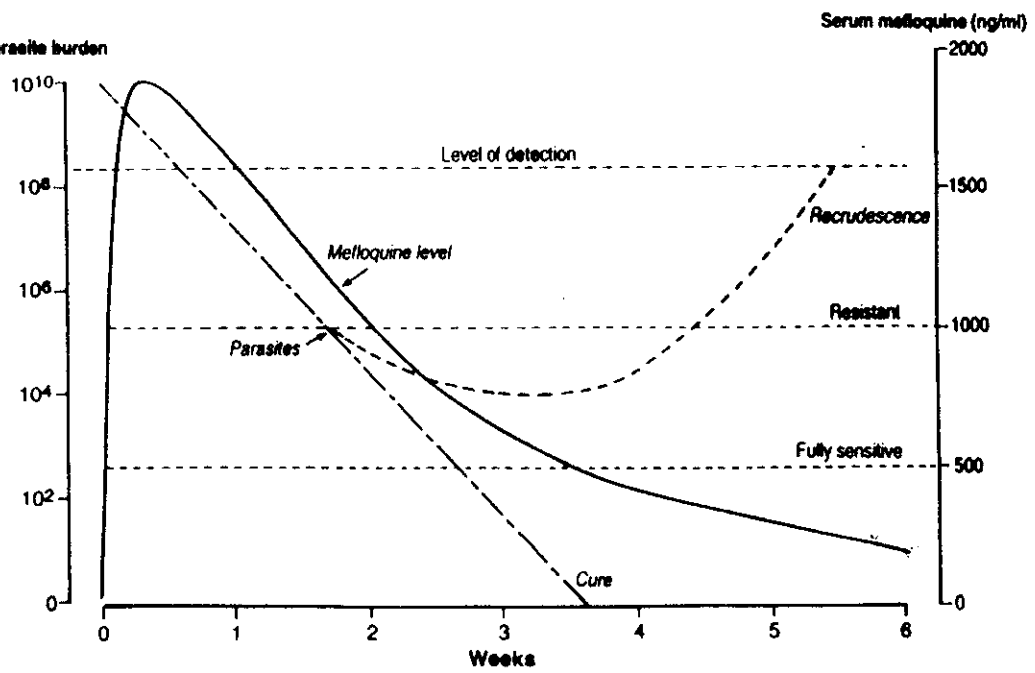
Figure 9.



Total parasite burden

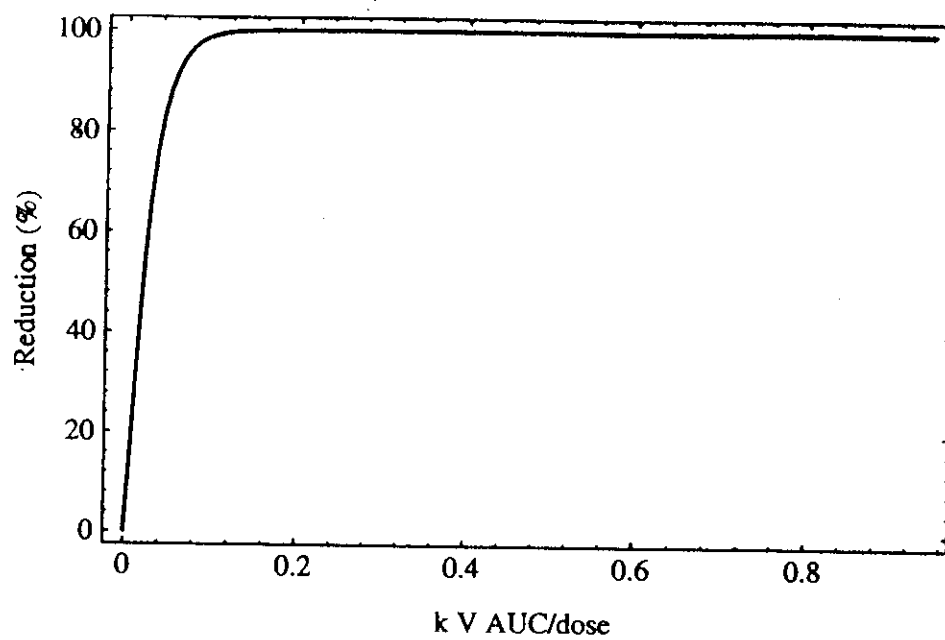


Total parasite burden



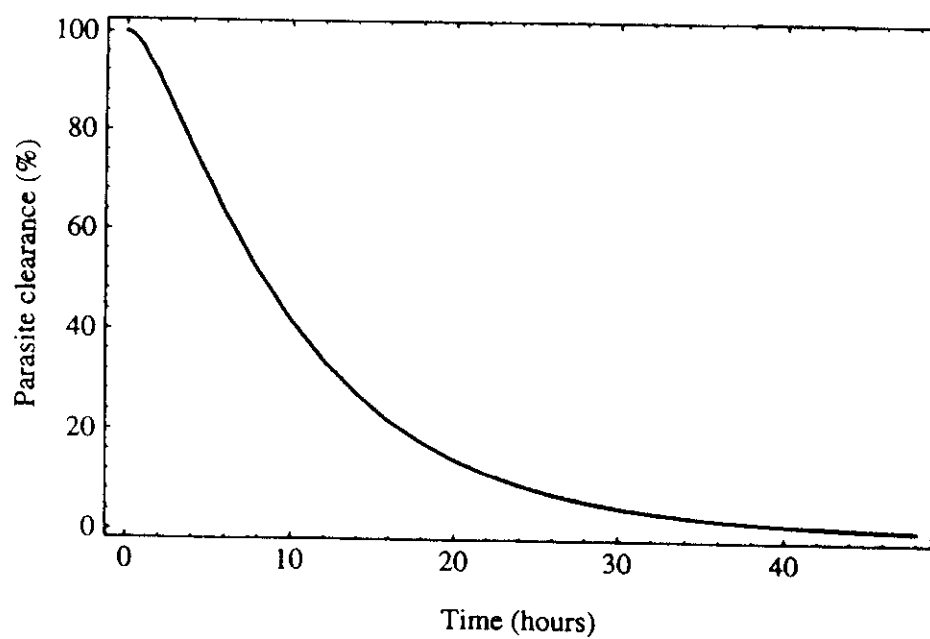
a/

Percentage parasite reduction



b/

Population parasite clearance curve



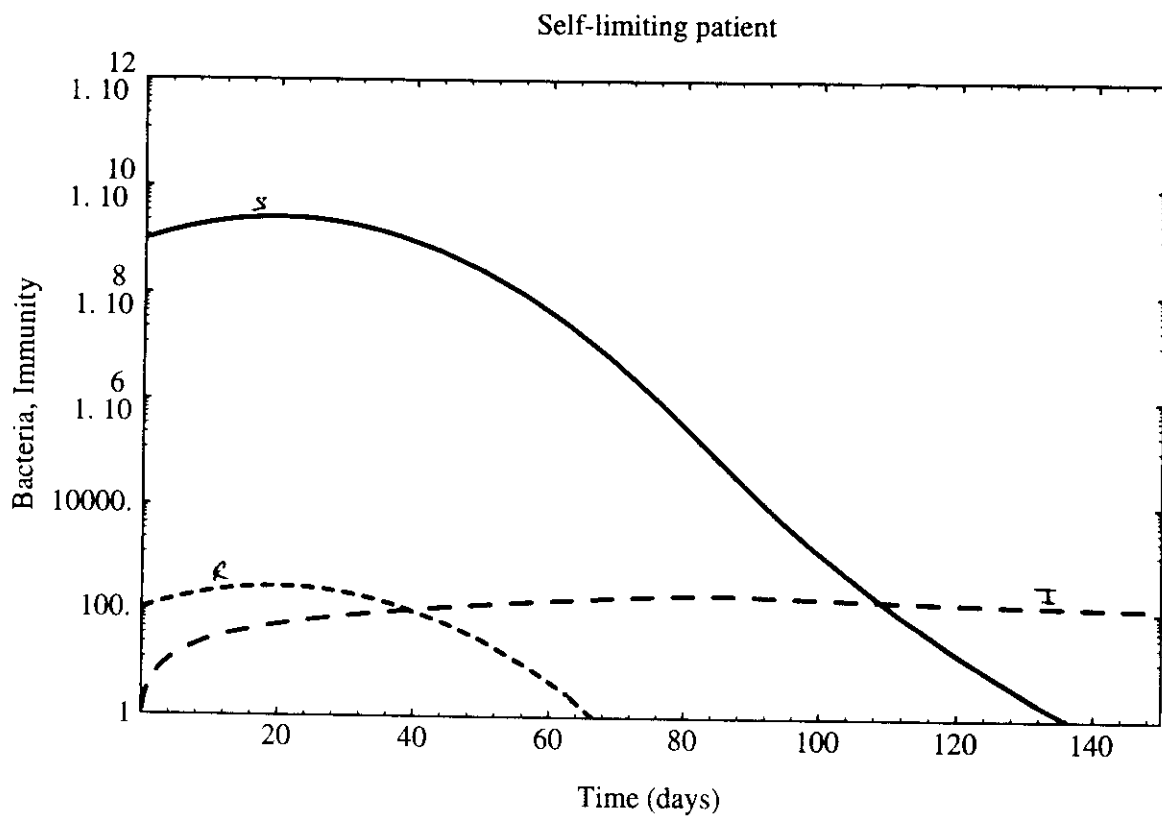
Simple Model of Bacterial Infection

$$\frac{dS}{dt} = (\lambda_S - \gamma I)S \quad \text{Sensitive}$$

$$\frac{dR}{dt} = (\lambda_R - \gamma I)R \quad \text{Resistant}$$

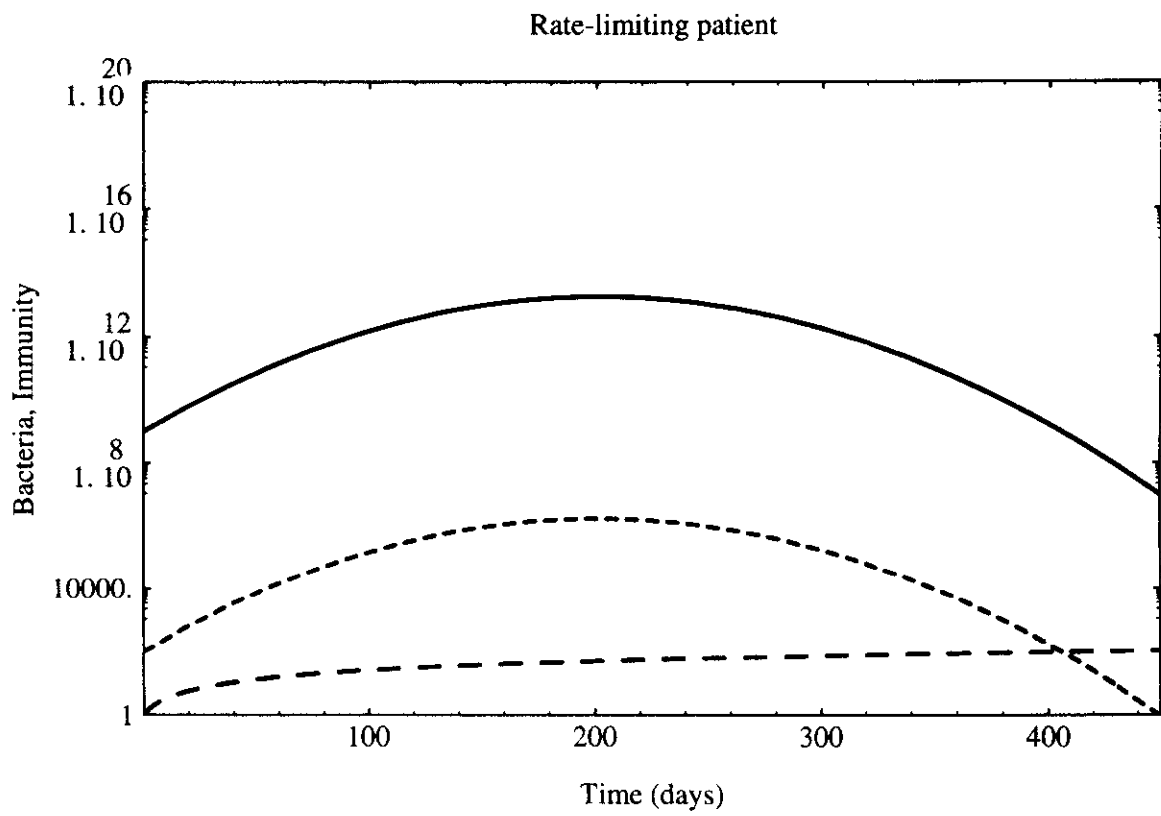
$$\frac{dI}{dt} = \lambda - \mu I + \frac{p(R+S)}{h_{50} + (R+S)} \quad \text{Immune}$$

Proliferation

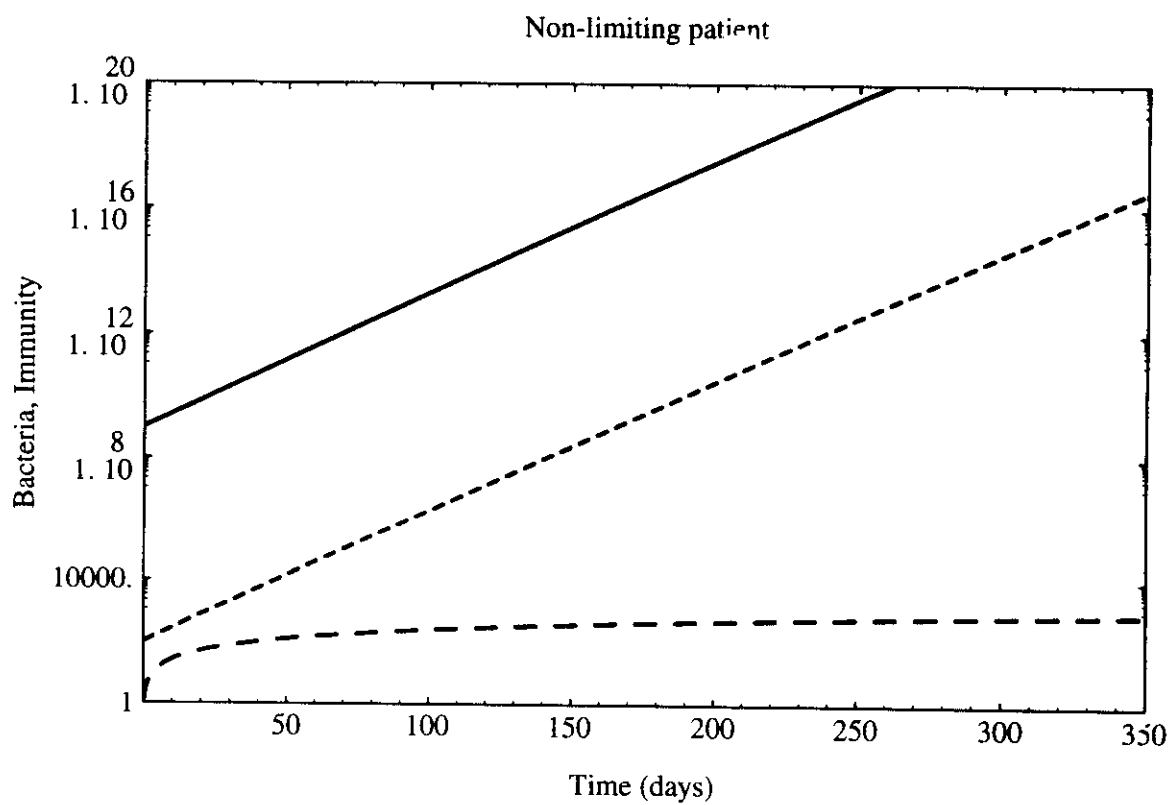


- 1/ Patient Recovers naturally.
- 2/ MOST infections are in this class!
- 3/ Resistant strains are present at low concentrations naturally in the environment (for most antibiotics)

11 rate.m



Patient recovers but only after HIGH levels of pathogen



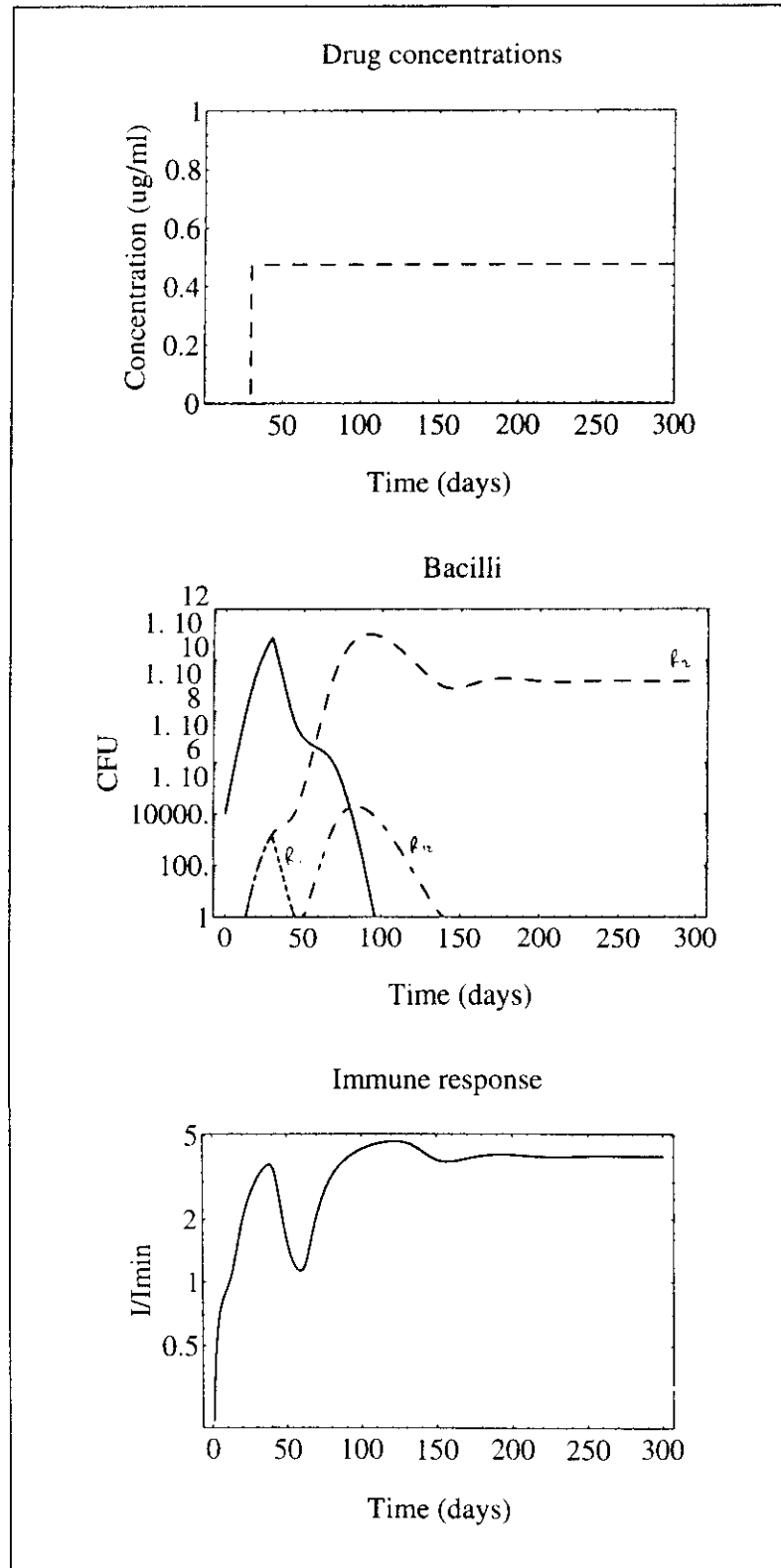
Patient cannot clear infection using immunity alone and
requires urgent treatment.

These 5 models of TB infection in an immunocompromised patient show how MULTIPLE resistance is difficult to avoid

$$\frac{dS}{dt} = (\lambda_S - \gamma I)S, \quad \frac{dR_1}{dt} = (\lambda_{R_1} - \gamma I)R_1, \quad \frac{dR_2}{dt} = (\lambda_{R_2} - \gamma I)R_2, \quad \frac{dR_{12}}{dt} = (\lambda_{R_{12}} - \gamma I)R_{12}$$

↑ multiply resistant

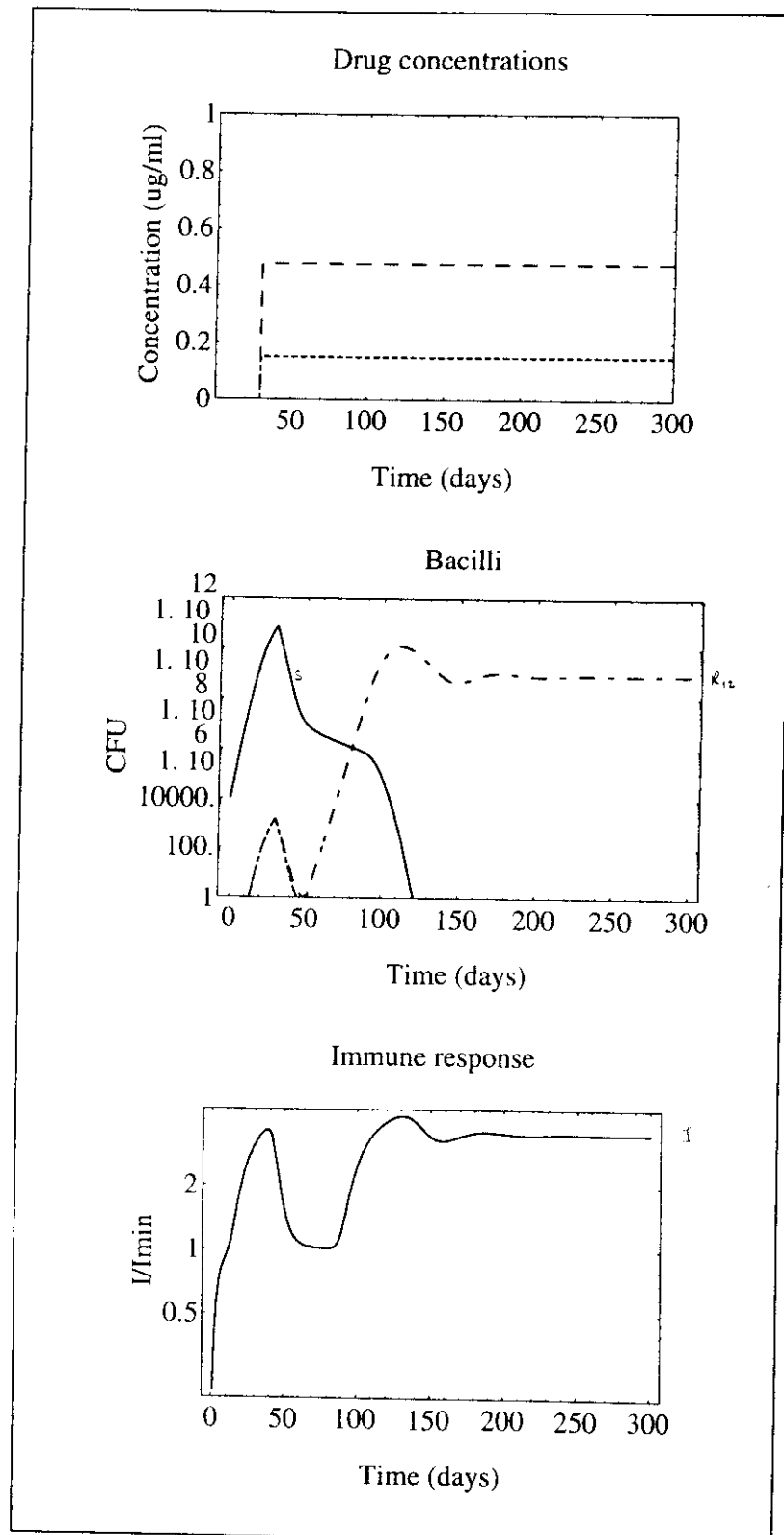
Continuous Rifampin treatment



Continuous
monotherapy

Resistant to
Drug 2

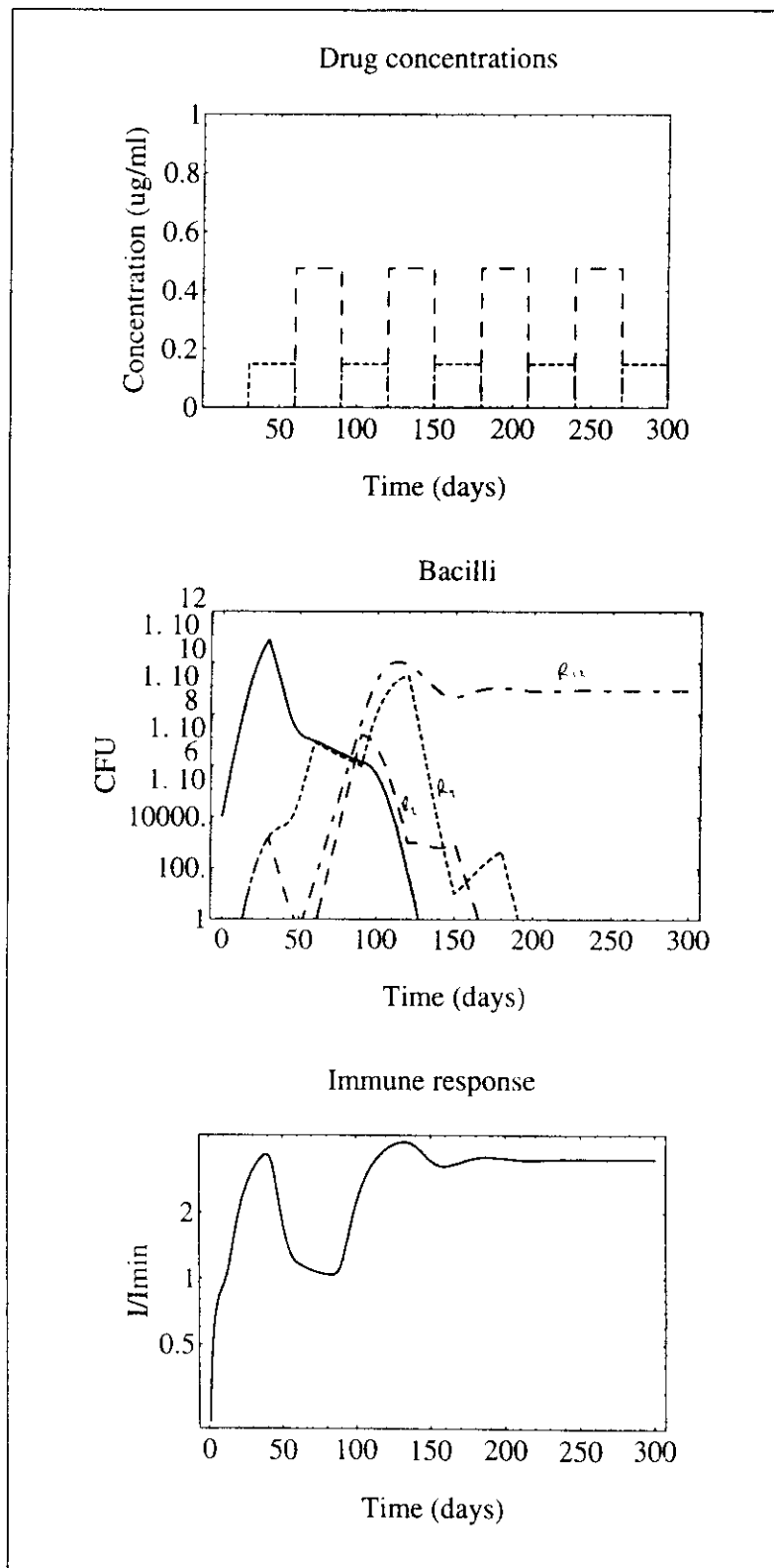
Continuous INH and Rifampin treatment



continuous
dual therapy

Multiply
Resistant

Alternate INH and Rifampin treatment



Modulated
Treatment

Multiply
Resistant

