

## Supplementary Material

### Pharmacodynamics of PEG-IFN alpha-2a in HIV/HCV co-infected patients: Implications for treatment outcomes

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#### Pharmacodynamic model that includes proliferation of uninfected and infected cells

We used a model [1-3] of HCV infection - that predicts various viral decline patterns such as, biphasic, triphasic and flat partial response - to fit patients' data. The equations describing the dynamics of HCV infection and treatment in this model involve uninfected hepatocytes ( $T$ ), infected hepatocytes ( $I$ ) and virus ( $V$ ). Uninfected and infected hepatocytes can proliferate with maximum proliferation rates  $r_T$  and  $r_I$ , respectively, under the control of a homeostatic process in which proliferation shuts down as the total number of susceptible hepatocytes, irrespective of whether they are infected or not, approaches a maximum number  $T_{max}$  [4]. Uninfected hepatocytes are also produced by differentiation from precursors at a constant rate  $s$  [5], die at rate  $d_T$  per cell and are infected with rate constant  $\beta$ . HCV is produced at rate  $p$  per infected cell. PEG-IFN  $\alpha$ -2a is assumed to act by partially blocking virion production, with effectiveness  $\varepsilon(t)$  (see Eq. 4 in the main text). We assume that ribavirin effectiveness  $\eta(t) = \eta_{max}(1 - \exp(-t/t_a))$ , where  $t_a = 5.6$  days and  $\eta_{max} = 0.5$ , based on the following observations: (i) it takes approximately 4 weeks for ribavirin to reach its steady-state concentration in serum [6], (ii) ribavirin

does not affect the first viral drop in combination with interferon- $\alpha$  [6, 7], and (iii) ribavirin major mode of action is suggested to reducing the rate of infection [2, 8] (see also [9]). Thus,  $0 \leq \varepsilon(t) \leq 1$  and  $0 \leq \eta(t) \leq 0.5$ ; with 0.5 or 1 meaning 50% or 100% effectiveness, respectively. The corresponding system of differential equations is

$$\begin{aligned} \frac{dT}{dt} &= s + r_T T \left(1 - \frac{T+I}{T_{\max}}\right) - d_T T - (1 - \eta(t)) \beta VT \\ \frac{dI}{dt} &= (1 - \eta(t)) \beta VT + r_I I \left(1 - \frac{T+I}{T_{\max}}\right) - \delta I \\ \frac{dV}{dt} &= (1 - \varepsilon(t)) pI - cV . \end{aligned} \quad (\text{Eq. S1})$$

The model's steady states at baseline and the baseline fraction of hepatocytes that are HCV-infected with respect to all susceptible hepatocytes,  $\pi$ , are given in the Additional File of <sup>[1]</sup>.

### **Biphasic-pharmacodynamic model**

To fit patients' data in whom a biphasic HCV RNA decline pattern was observed (as explained in Methods in the main text), we used our previously published model [10] of HCV kinetics that allows the estimation of treatment effectiveness, viral clearance and infected cell loss. The solution of our model predicts the evolution of HCV RNA over time,  $V(t)$ , as:

$$V(t) = V_0 (A e^{-\lambda_1(t-t_0)} + (1-A) e^{-\lambda_2(t-t_0)}) \quad (\text{Eq. S2})$$

where

$$\lambda_{1,2} = \frac{1}{2} (c + \delta \pm \sqrt{(c - \delta)^2 + 4(1 - \varepsilon(t))(1 - \eta(t))c\delta}) \quad \text{and} \quad A = \frac{\varepsilon(t)c - \lambda_2}{\lambda_1 - \lambda_2} .$$

Equation (S2) predicts that the viral load under treatment will always decrease to the uninfected steady state following an initial rapid viral decline (first phase) followed by a slower decay (second phase), with rates  $\lambda_1$  and  $\lambda_2$ , respectively. The parameter  $t_0$  is a delay, corresponding to the time it takes between the initiation of drug treatment and its effect in reducing HCV RNA. The solution is valid for  $t > t_0$ . For  $t < t_0$ , the solution is  $V(t) = V_0$ , where  $V_0$  is the baseline HCV RNA.  $\varepsilon(t)$  and  $\eta(t)$ ,  $c$  and  $\delta$  are as explained above for Eq. S1.

### **Fitting equation S1 to the experimental data**

The parameters  $t_0$ ,  $V_0$ , and  $c$  (for each patient) were estimated by equation 4 given in Neumann et al.[10] as explained in the main text. In addition, as previously described[1], we fixed  $r_T = 3 \text{ day}^{-1}$ ,  $T_{max} = 7.5 \times 10^6 \text{ cell/ml}$ ,  $d_T = 3.5 \times 10^{-3} \text{ day}^{-1}$  and  $s = 1 \text{ cell/day/ml}$ . The remaining parameters  $\delta$ ,  $r_I$ ,  $p$ ,  $Ec_{50}$ , and  $\beta$  were estimated for each patient (Table S1), using Berkeley Madonna (<http://www.berkeleymadonna.com>). As previously described [1], we let  $\delta$ ,  $r_I$ ,  $p$ , and  $\beta$  to be estimated within the following parameter space:  $0.2 \leq r_I \leq 3.0 \text{ day}^{-1}$ ,  $1 \leq p \leq 15 \text{ day}^{-1}$ ,  $d_T \leq \delta \leq 3 \text{ day}^{-1}$ ;  $10^{-8} \leq \beta \leq 10^{-6} \text{ ml/day/virions}$ . Fitting results for the first 5 weeks of treatment are shown in Fig. S1.

### **Baseline characteristics and viral kinetics of the *discontinued* patients**

Five patients have discontinued therapy after 11 or 12 weeks (three asked to leave, one went to jail, and one died for a cause not related to the study). Their baseline characteristics and viral kinetics are shown in Table S2 and Fig. S2, respectively.

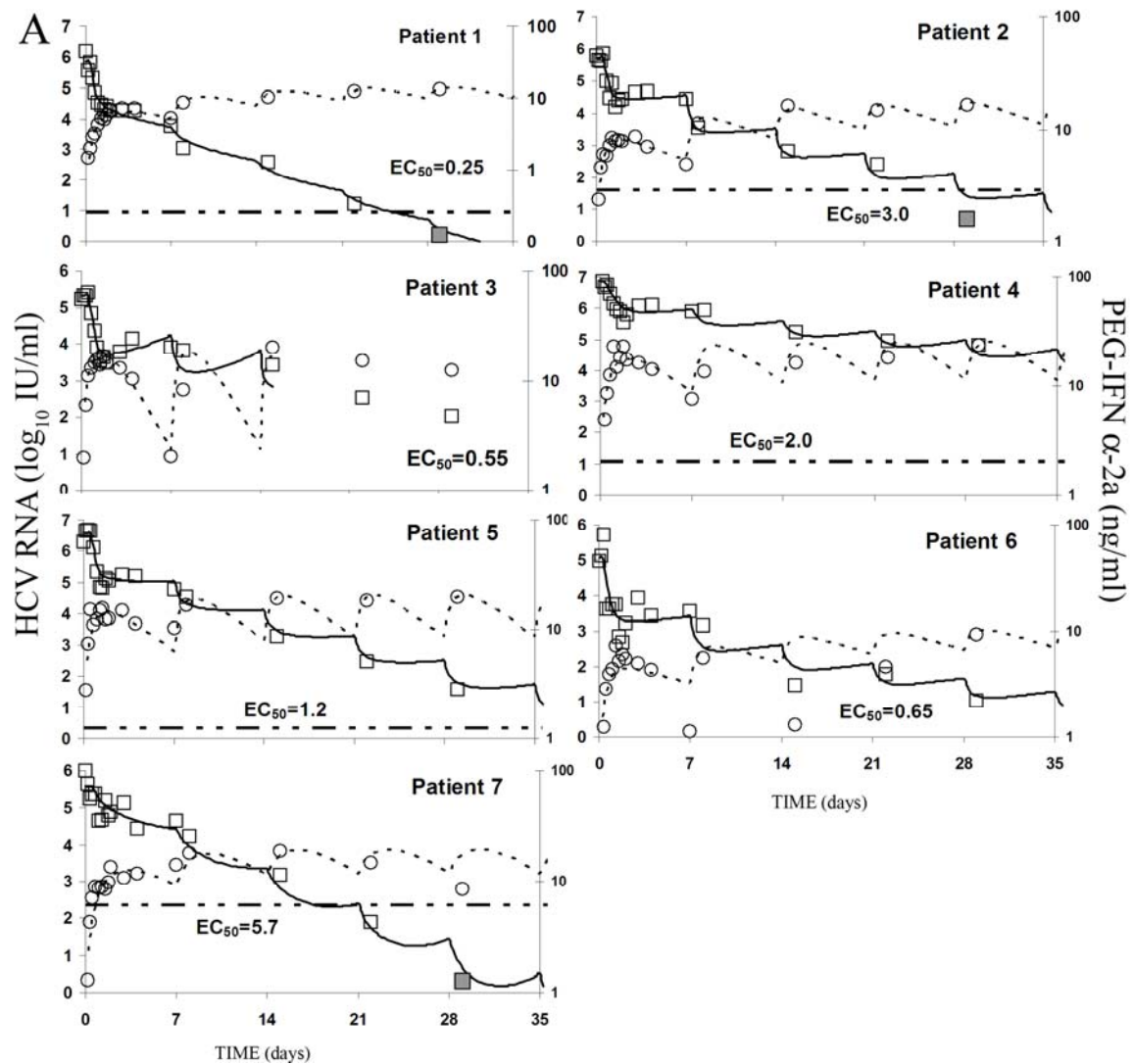
**Table S1. Parameter estimates obtained by fitting equation S1 to patients' data.**

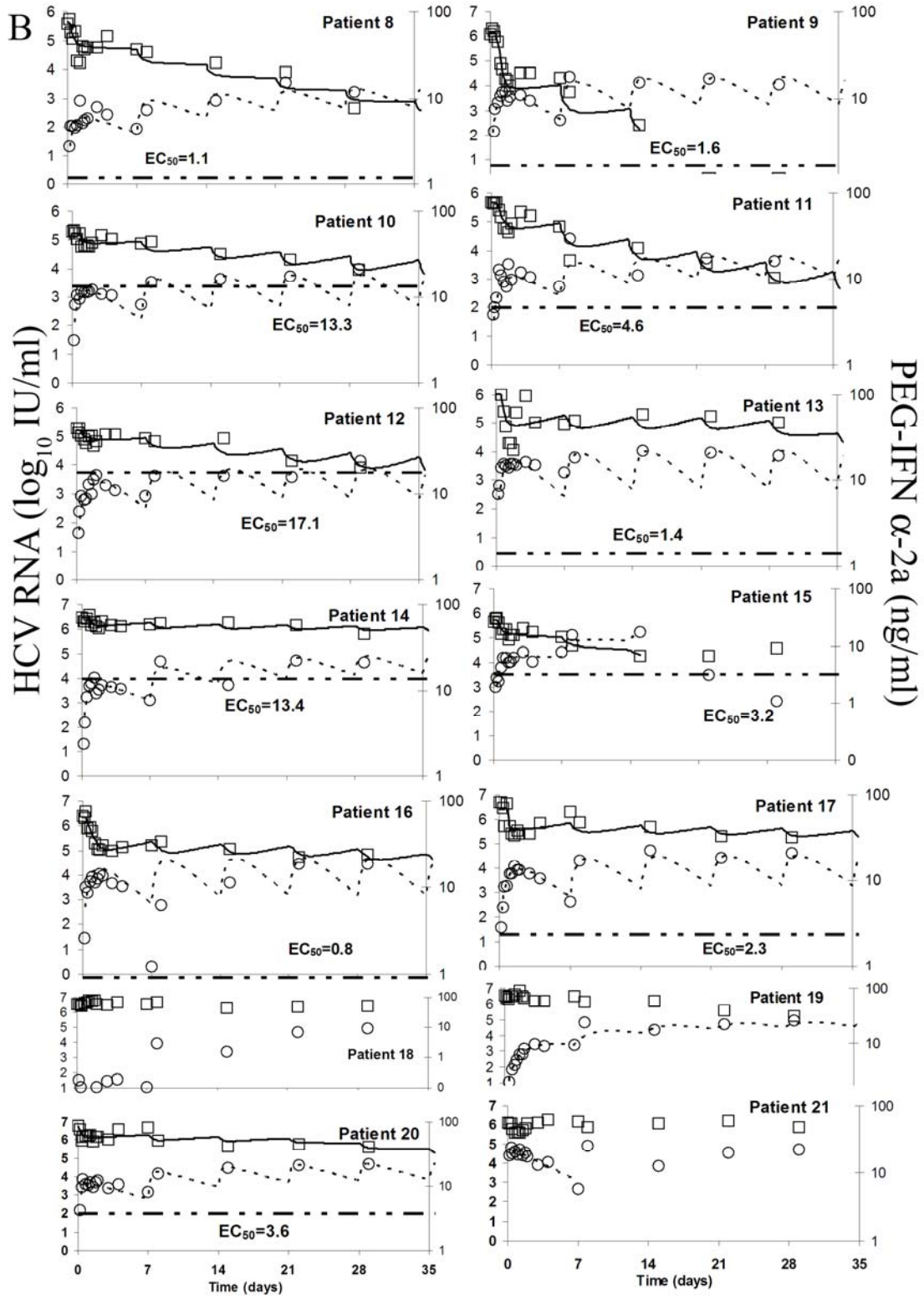
Patient No.	$r_I$	$\beta$	$\delta$	$p$	$n$	$\pi$	$EC_{50}$	$\varepsilon_{7max}$	$\varepsilon_{max}$
1*	0.96	9.9	0.34	0.90	1.0	86%	0.19	0.974	0.985
2*	3.00	1.7	0.18	0.80	2.6	39%	2.60	0.953	0.993
3* <sup>@</sup>									
6*	2.97	1.8	0.14	0.60	2.0	13%	0.67	0.987	0.996
7*	2.97	1.9	0.46	1.97	1.0	13%	6.90	0.632	0.676
4*	0.51	2.6	0.27	4.10	1.0	99%	1.97	0.908	0.925
5*	0.57	3.4	0.30	7.40	1.2	95%	0.66	0.975	0.983
<b>Median (IQR)</b>	<b>2.0 (2.4)</b>	<b>2.3 (3.3)</b>	<b>0.29 (0.20)</b>	<b>1.4 (4.8)</b>	<b>1.1 (1.2)</b>	<b>63 (83)</b>	<b>1.3 (3.1)</b>	<b>0.964 (0.140)</b>	<b>0.984 (0.130)</b>
8	2.97	3.9	0.18	0.38	1.0	86%	1.08	0.856	0.911
9	2.97	0.3	0.26	6.20	1.0	16%	1.70	0.868	0.884
13	1.38	9.9	0.26	1.00	1.0	99%	1.40	0.917	0.935
10	0.51	0.2	0.07	2.95	1.0	6%	5.71	0.672	0.759
11	0.00	1.6	0.11	0.70	2.0	45%	2.90	0.938	0.972
12	0.63	1.0	0.10	1.20	1.0	13%	21.46	0.380	0.480
14	1.26	0.9 <sup>&amp;</sup>	0.11	2.60 <sup>&amp;</sup>	1.0	99%	13.40	0.469	0.624
15 <sup>@</sup>									
16	2.22	0.7	0.11	0.89	1.0	98%	0.78	0.946	0.961
17	2.67	0.5	0.11	3.10	1.0	98%	2.27	0.856	0.892
18**	NF	NF	NF	NF	NF	NF	NF	NF	NF
19**	NF	NF	NF	NF	NF	NF	NF	NF	NF
20	0.75	1.1	0.15	5.20	1.0	99%	3.60	0.757	0.841
21**	NF	NF	NF	NF	NF	NF	NF	NF	NF
<b>Median (IQR)</b>	<b>1.3 (2.1)</b>	<b>1.0 (1.7)</b>	<b>0.11 (0.09)</b>	<b>1.9 (2.8)</b>	<b>1.0 (0.2)</b>	<b>92 (84)</b>	<b>2.6 (6.3)</b>	<b>0.856 (0.300)</b>	<b>0.888 (0.220)</b>
<b>P value</b>	<b>NS</b>	<b>0.034</b>	<b>0.01</b>	<b>NS</b>	<b>NS</b>	<b>NS</b>	<b>NS</b>	<b>0.039</b>	<b>0.039</b>

$\beta$ , viral infection rate [ $10^{-7}$  mL/virions/day];  $r_I$ , HCV-infected cell proliferation rate constant [1/day];  $p$ , viral production rate constant [virions/cell/day];  $EC_{50}$ , PEG-IFN concentration that decreases HCV production by 50%;  $n$ , Hill coefficient;  $\varepsilon_{7max}$ , maximum effectiveness during first dose of PEG-IFN;  $\varepsilon_{max}$ , 4 to 12-week PEG-IFN effectiveness.  $\pi$ , estimated baseline percentage of hepatocytes that are HCV-infected;  $\pi = \bar{I} / (\bar{I} + \bar{T})$ , where an over bar denotes a baseline value (see Additional File of our recent publication[1]).  $V_0$ ,  $c$ , and  $t_0$  values for each patient are shown in Table 3 in the main text.

<sup>&</sup>, these parameter values were fixed during fit to allow model convergence. NF, model cannot not be fitted to the data. NA, in these patients PEG-IFN concentration declined from day 15 (see Fig. 2 in main text). <sup>@</sup>, in these patients PEG-IFN concentration dropped from day 15, thus parameter estimates were not performed with Eq. S1 but with Eq. S2 (see Table 3 in the main text).

**Figure S1.** PEG-IFN- $\alpha$ -2a serum concentrations and HCV-RNA levels during the first five weeks of treatment in **(A)** SVRs and **(B)** non-SVRs. Graphs show drug concentration data (circles) and best-fit theoretical curve (Eq. 3 (see main text), dashed line; right axis, ng/ml) and HCV RNA data (squares) and best-fit curve (solid line) (left axis,  $\log_{10}$  IU/mL) from our combined triphasic or biphasic pharmacodynamic models (Eqs. S1 or S2, respectively; see also Table 3 in the main text). Estimated  $EC_{50}$  is represented by horizontal dotted-dashed line.



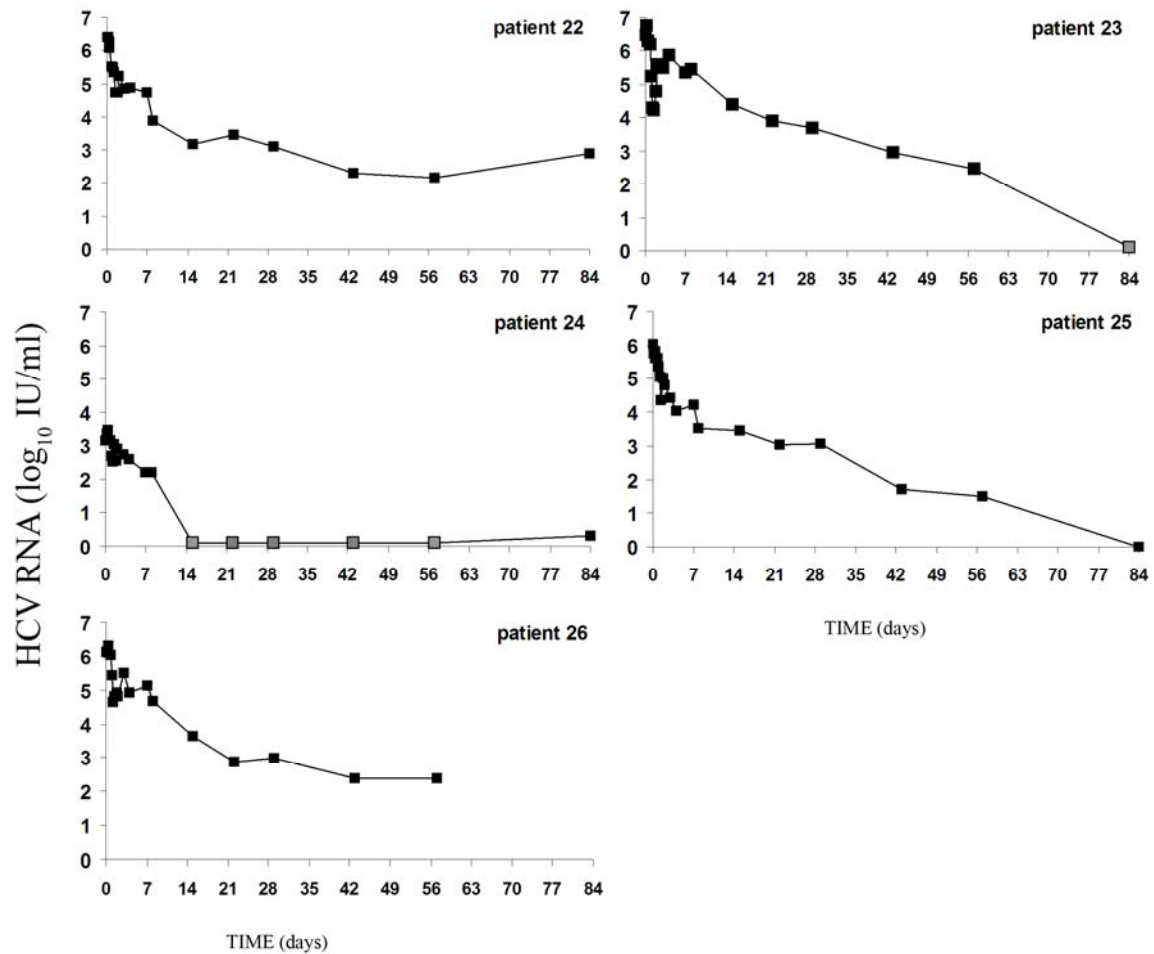


**Table S2.** Baseline Characteristics of the *discontinued* patients.

Patient No.	Genotype	race	Age (yr)	gender	Weight (kg)	CD4 (cells/m <sup>3</sup> )	Metavir
22	1	W	38	M	71	486	F1A1
23	1	B	47	M	78	524	F1A1
24	3	B	39	M	67	455	F4A3
25	3	W	49	M	71	424	F2A3
26	3	B	34	M	65	658	F1A1

W, white; B, black; M, male.

**Figure S2.** HCV RNA levels during 12 weeks of treatment. Gray squares indicate undetectable HCV RNA (<10 IU/ml). Solid lines were used to emphasize phases of viral decline.



## References

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