

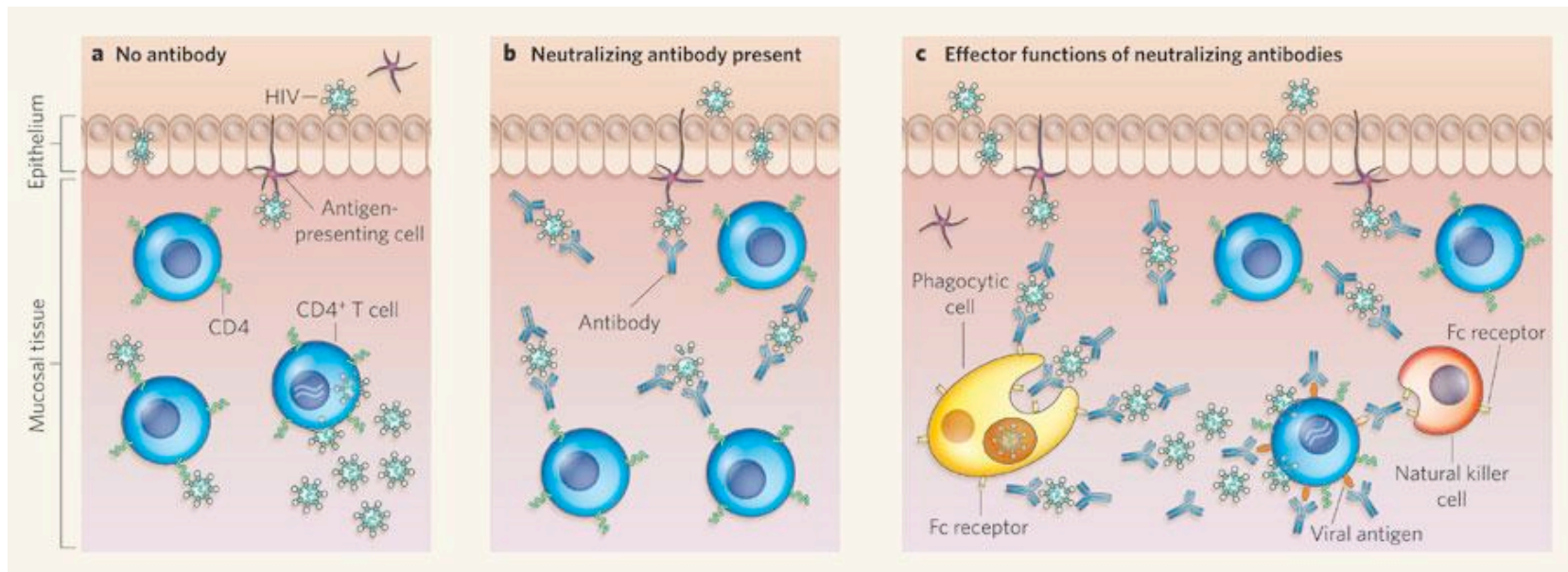
# Modeling antibody responses during viral infections

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# Antibody functions

- Neutralization of free virus
- Complement-mediated lysis of free virus and infected cells
- Opsonization of virus particles by antibodies and phagocytosis of virus particles via Fc- or complement-receptors
- Antibody-dependent cellular cytotoxicity (ADCC) of infected cells
  - Tissue damage: HIV, HBV, HCV, herpes, Dengue virus, Polio virus, LCMV



HIV-1 IC (RNA copies/ml)

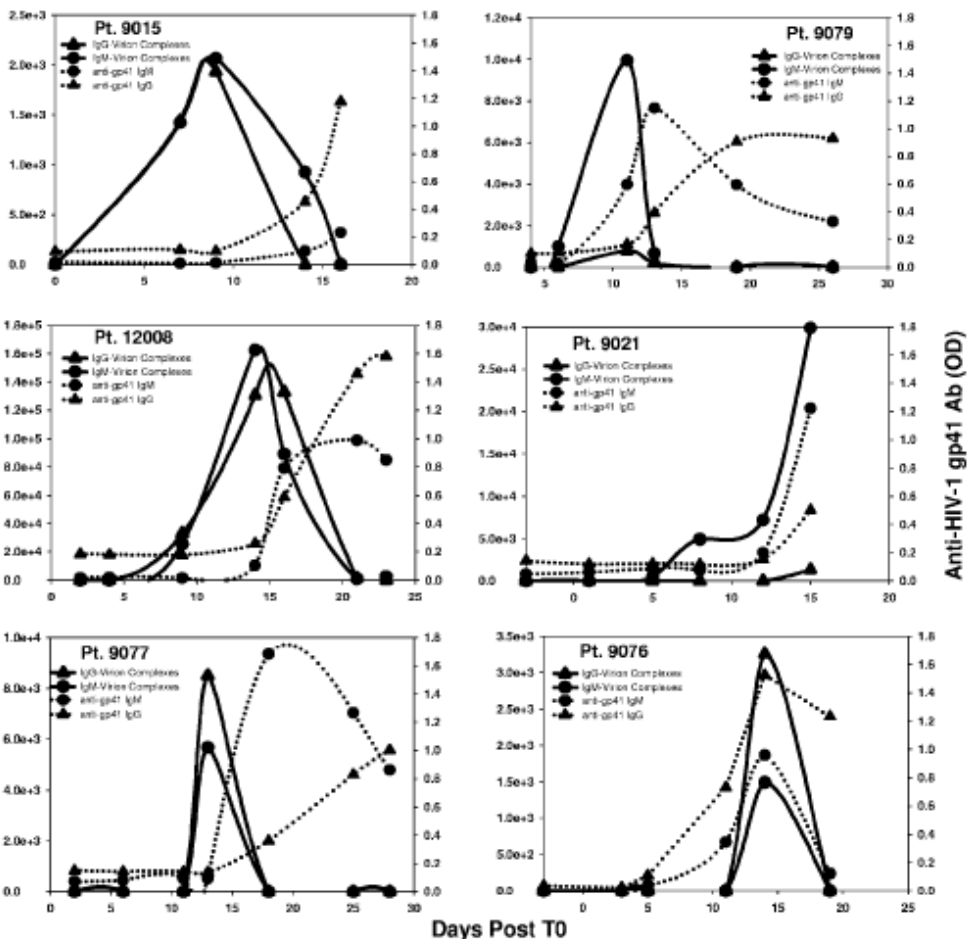


FIG. 5. HIV immune complexes produced at a median time of 8.0 days after  $T_0$ . The detection of immune complexes for patients (Pt) 9015, 12008, 9077, 9079, 9021, and 9076 are aligned to  $T_0$  and plotted in comparison to the detection of free antibody (Ab) responses.

# Competition

- Antibodies can compete with each other for
  - antigen
  - space in the lymph nodes
  - T cell conjugates and/or kinetic prolongation
- 1. Competition between strain-specific and broadly specific neutralizing antibody in HIV infection.
- 2. Competition between antibodies directed to virus particles and those directed to empty particles in Hepatitis B infection.

# 1. HIV infection

## ■ Broadly neutralizing antibodies

- Monoclonal Ab: IgG1b12, 2F5, 2G12, 4E10, Z13, PG9, PG16
- VRC01 (neutralizes 90% HIV strains)

## ■ Vaccines

### □ AIDSVax

- Rocombinant gp120 protein as vaccine vector
- Induced strain-specific Ab but failed to induce broadly neutralizing Ab

### □ STEP

- Induction of cellular mediated immune responses
- Recombinant adenovirus serotype 5
- Suppressed by pre-existing AD5-specific Ab
- Enhanced HIV infection

### □ RV 144

- ALVAC-HIV recombinant canarypox + AIDSVax
- Successful in reducing infectivity rates
- Believed inefficient for clade C

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# What are the challenges?

## Virus

- ❑ Extensive viral clade and sequence diversity
- ❑ Early establishment of latent viral reservoirs
- ❑ Viral evasion of humoral and cellular immune responses

## Antibody

- Responses are strain-specific (ssAb)
  - No method exists to elicit broadly reactive neutralizing antibodies in vivo
    - ❑ Deleted during selection [Haynes, *Science* 2005, *Nat Struct Mol Biol* 2010]
    - ❑ Wrong conformation
    - ❑ High rate of mutation (VRC01) [Kwong *Science* 2010]
    - ❑ Competition [Zhang, *PNAS* 2009, Clarke, *Evol Applic* 2009]
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# Competition

## Hypothesis

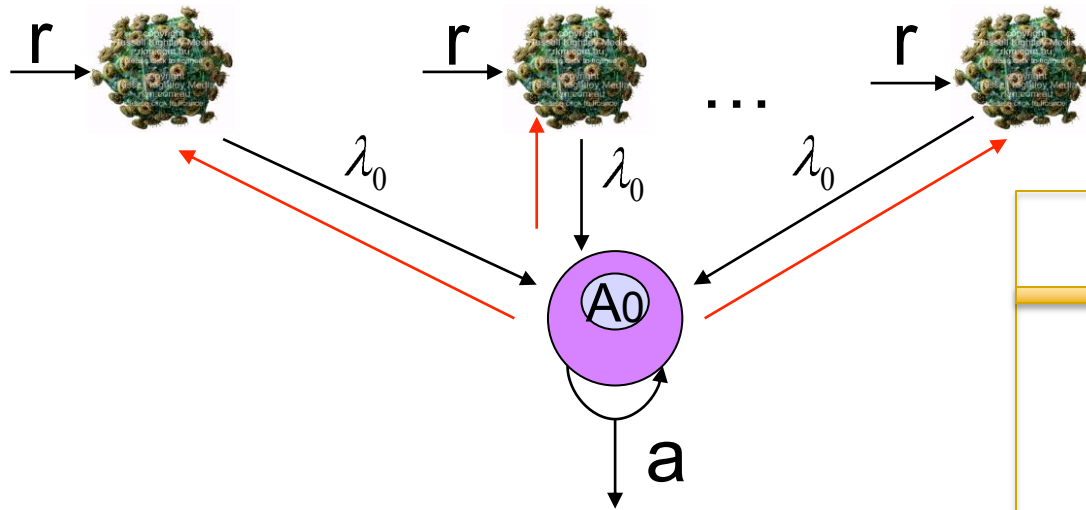
- Presence of strain-specific antibodies doesn't have to exclude the presence of broadly neutralizing ones

## Model

- Competition between the two antibody types.
  - Find the parameter region where bnAb is made inefficient by ssAb
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# Model without competition

## -continuous immunization



Model equations:

$$\frac{dV_i}{dt} = (r - K_0 A_0) V_i$$

$$\frac{dA_0}{dt} = \lambda_0 \sum_{i=1}^n V_i + A_0 (a - \beta A_0)$$

$$V_i(t_i) = V_0, \quad A_i(t_i) = 0, \quad A_0(0) = 0.$$



# Basic reproduction number

$$R_0 = \frac{r}{K_0 \frac{a}{\beta}}$$

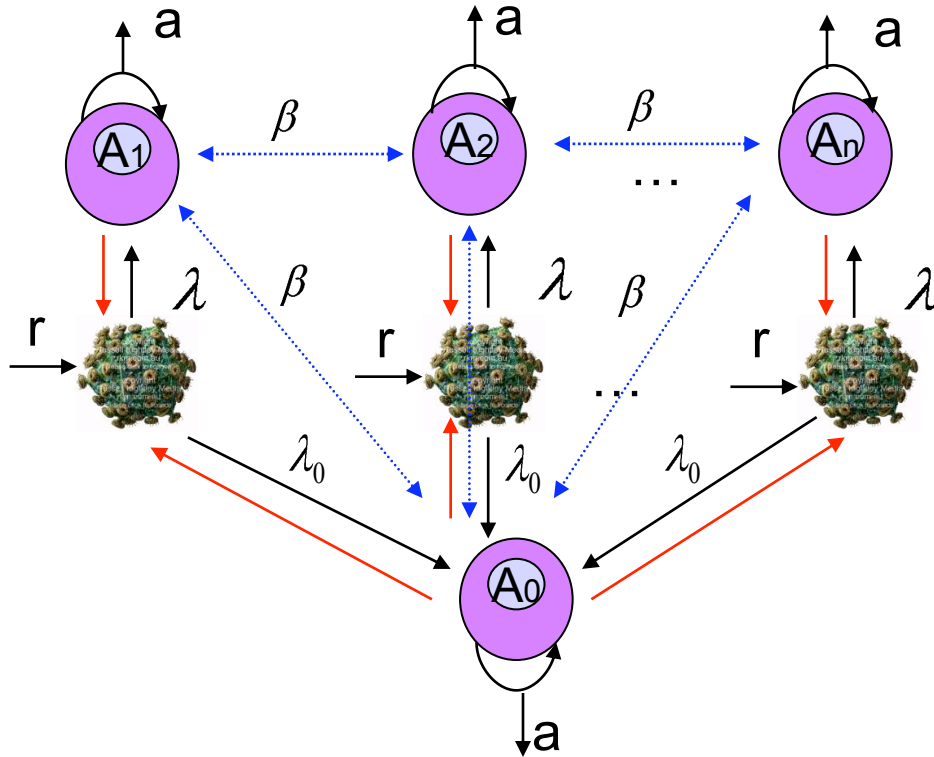
If  $R_0 < 1$  then all viruses will be cleared.

If  $R_0 > 1$  then at least one virus will persist.

**Biological interpretation:** When the virus replication rate is smaller than the product between the bnAb affinity rate and the antibody life span, viruses will be cleared, otherwise some persist.

# Model with competition

## -continuous immunization



Model equations:

$$\frac{dV_i}{dt} = (r - K A_i - K_0 A_0) V_i$$

$$\frac{dA_i}{dt} = \lambda V_i + A_i(a - \beta A_i)$$

$$\frac{dA_0}{dt} = \lambda_0 \sum_{i=1}^n V_i + A_0(a - \beta A_i)$$

$$V_i(t_i) = V_0, \quad A_i(t_i) = 0, \quad A_0(0) = 0.$$

# Basic reproductive number

$$R_0 = \frac{r}{\frac{m\lambda_0 K_0 + \lambda K}{m(\lambda + \lambda_0)} \frac{a}{\beta}} \text{ dependent on } m.$$

If  $R_0 < 1$  for  $m = n$  then all viruses will be cleared.

If there exist an  $m > 1$  such that  $R_0 > 1$  then all viruses will persist.

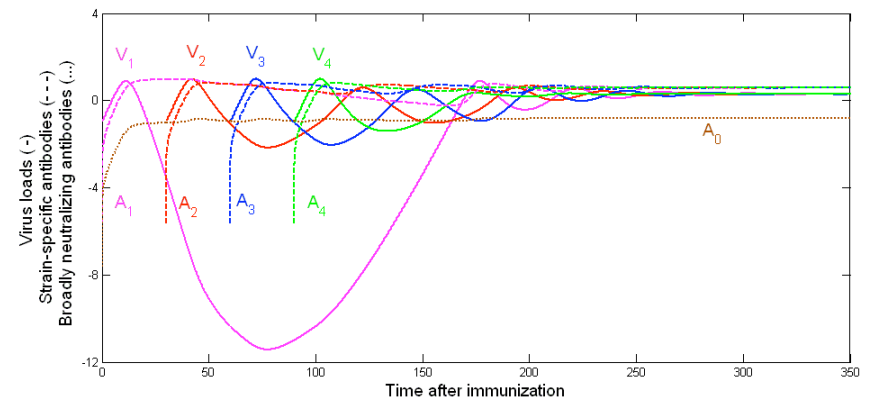
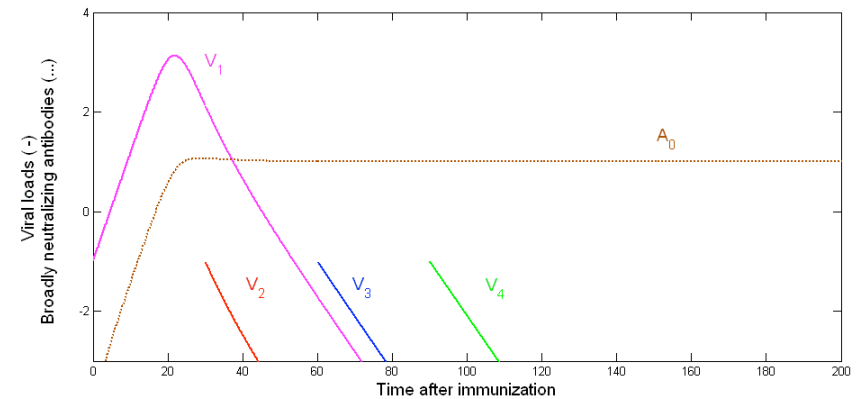
**Biological interpretation:** When the virus replication rate is smaller then the product between the combined ssAb and bnAb affinity rate and the antibody life span viruses will be cleared, otherwise some persist.

# Model prediction

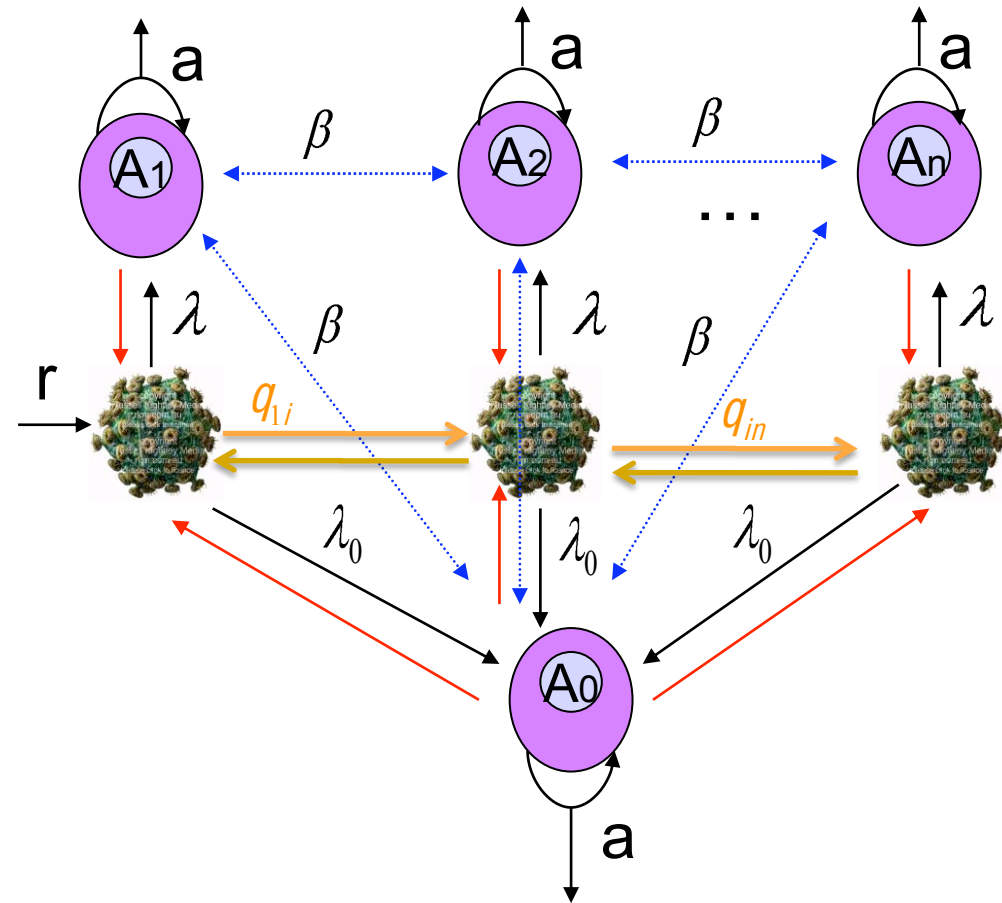
For any  $m \geq 2$  for which

$$\frac{a}{\beta} \frac{mK_0\lambda_0 + K\lambda}{m(\lambda + \lambda_0)} < r < K_0 \frac{a}{\beta}$$

- Viruses are cleared with no competition.
- Viruses persist with competition.



# Natural infection - mutations



Model equations:

$$\frac{dV_i}{dt} = r \sum_{j=1}^n q_{ij} V_j - (KA_i + K_0 A_0) V_i$$

$$\frac{dA_i}{dt} = \lambda V_i + A_i(a - \beta A_T)$$

$$\frac{dA_0}{dt} = \lambda_0 \sum_{i=1}^n V_i + A_0(a - \beta A_T)$$

$$V_1(0) = V_{1,0}$$

$$V_j(0) = A_j(0) = A_0(0) = A_1(0) = 0.$$

$Q = \{q_{ij}\}_{i,j}$  is the mutation matrix:

$$0 \leq q_{ij} \leq 1 \text{ and } \sum_{i=1}^n q_{ij} = 1.$$

# No competition

Let  $V = (V_1, V_2, \dots, V_n)$  interact with  $A_0$ .

The dynamics of the systems (1) and (2) are equivalent

$$(1) \quad \frac{dV}{dt} = (rQ - K_0 A_0 / n) V$$

$$\frac{dA_0}{dt} = \lambda_0 V_T + A_0(a - \beta A_0)$$

$$(2) \quad \frac{dV_T}{dt} = (r - K_0 A_0) V_T$$

$$\frac{dA_0}{dt} = \lambda_0 V_T + A_0(a - \beta A_0)$$

when the dominant eigenvalue of  $Q = \{q_{ij}\}$  is simple, with corresponding eigenvector  $Z \geq 0$  s.t.  $QZ = Z$ .

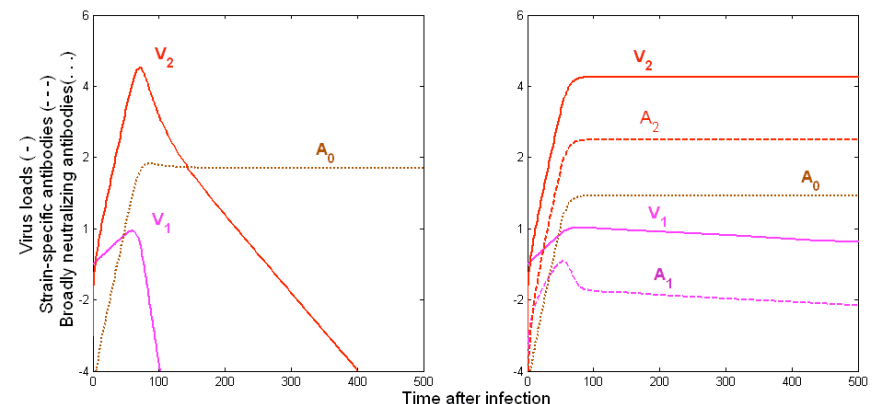
# For example

1.  $Q$  is irreducible.

$$2. \quad Q = \begin{pmatrix} 1 - q_{12} & 0 & 0 & \dots & 0 & 0 \\ q_{12} & 1 - q_{23} & 0 & \dots & 0 & 0 \\ \dots & & & & & \\ 0 & 0 & 0 & & q_{n-1n} & 1 \end{pmatrix}.$$

Then  $R_0 = \frac{r}{K_0 \frac{a}{\beta}}$  is independent of  $n$  and  $Q$ .

When  $R_0 < 1$  all virus strains are cleared and when  $R_0 > 1$  all (dominant) viruses persist.



# Competition

$$R_0 = \frac{r}{\Omega K_0 \frac{a}{\beta}}$$

If  $R_0 < 1$  then all viruses are cleared, otherwise some viruses persist.

For  $n = 2$  and  $\mu_{11} = 1 - \alpha$ ,  $\mu_{12} = \alpha$ ,  $\mu_{21} = \mu_{22} = 0$

$$\Omega = \frac{\frac{K}{K_0} \left( \frac{\lambda}{\lambda_0} + \frac{K_0}{K} \right) \left( \frac{\lambda}{\lambda_0} + 2 \frac{K_0}{K} \right)}{\left( 1 + \frac{\lambda}{\lambda_0} \right) \left\{ \left( 3 \frac{\lambda}{\lambda_0} + 4 \frac{K_0}{K} \right) - \alpha \left( 2 \frac{\lambda}{\lambda_0} + 4 \frac{K_0}{K} \right) + \sqrt{\left( \left( 3 \frac{\lambda}{\lambda_0} + 4 \frac{K_0}{K} \right) - \alpha \left( 2 \frac{\lambda}{\lambda_0} + 4 \frac{K_0}{K} \right) \right)^2 - 8 \left( \frac{\lambda}{\lambda_0} + \frac{K_0}{K} \right) \left( \frac{\lambda}{\lambda_0} + 2 \frac{K_0}{K} \right) (1 - \alpha)^2} \right\}}$$

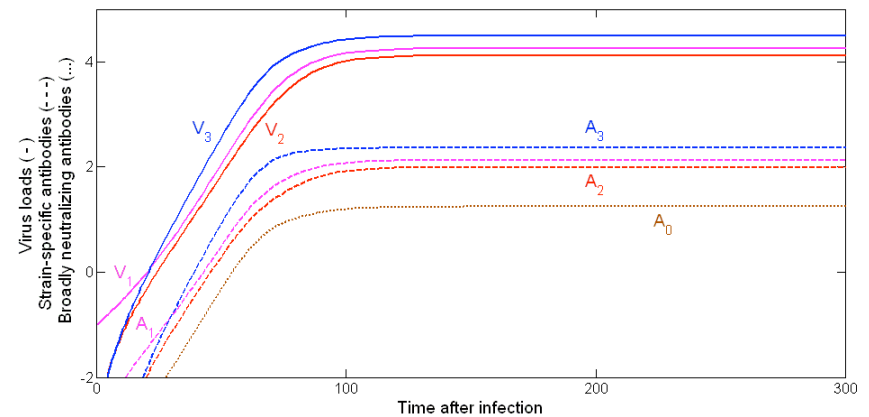
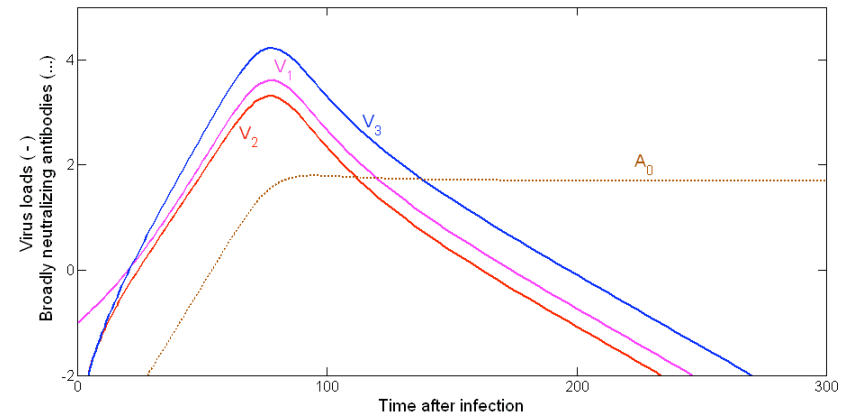


# Model prediction

For parameters

$$\Omega K_0 \frac{a}{\beta} < r < K_0 \frac{a}{\beta}$$

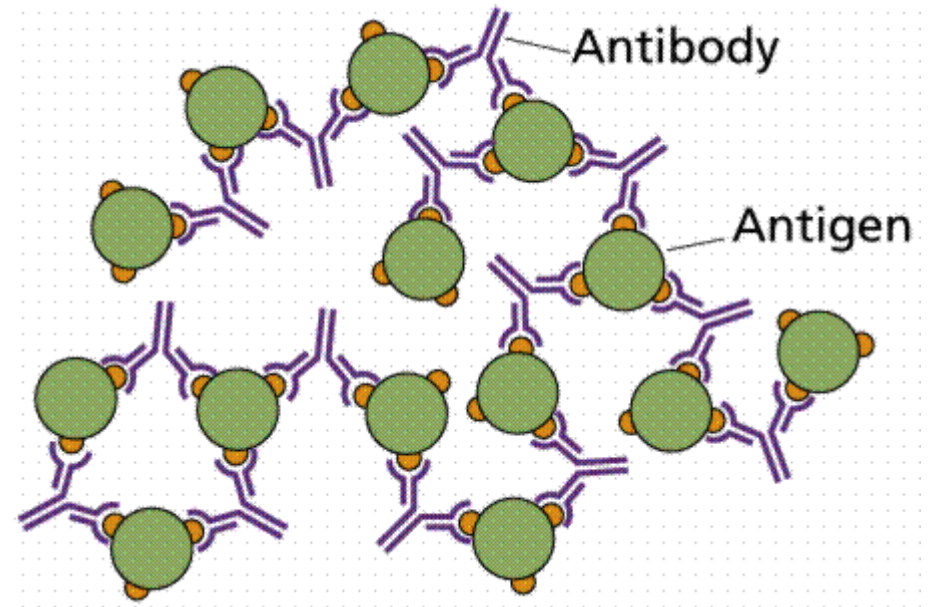
- Viruses are cleared with no competition.
- Viruses persist with competition.



# Summary

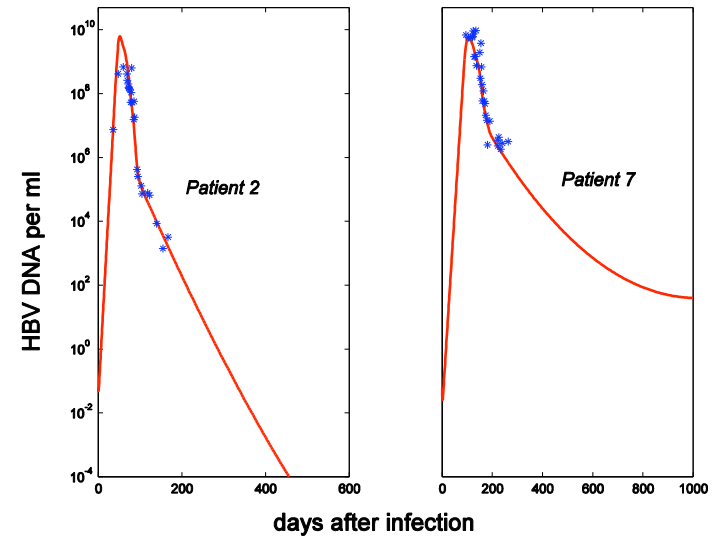
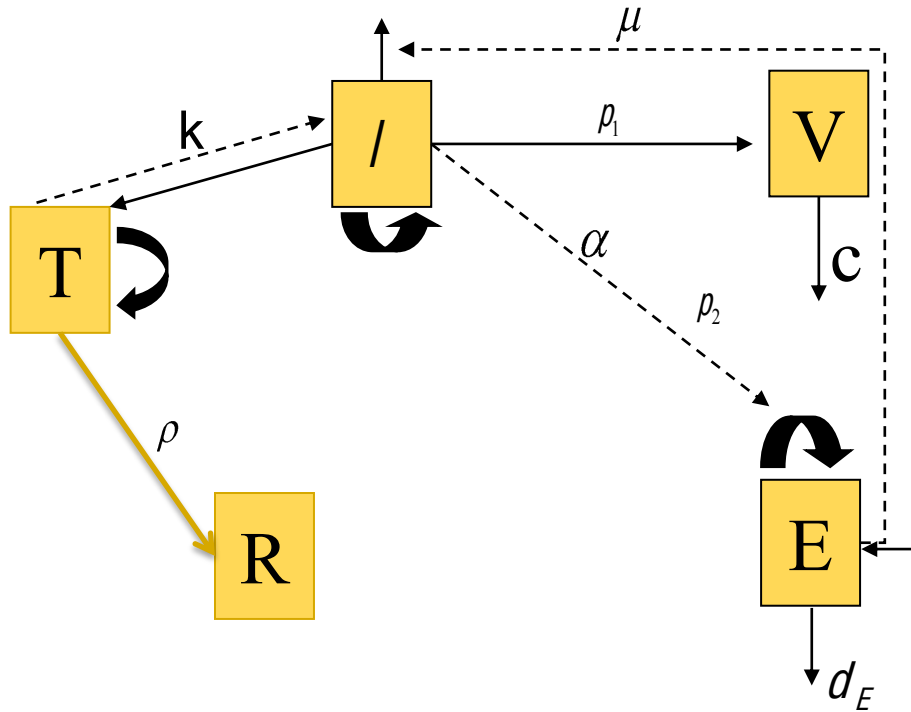
- Broadly neutralizing antibodies alone can control multiple HIV infections.
- Additional immune events directed against specific HIV viral strains weaken the immune system defense, by limiting the growth of B cells producing broadly neutralizing antibodies.
- Under global resource limitation, HIV will be controlled only when there is no delay in a viral-specific antibody response. We know that this is not achieved in vivo.
- Inferences:
  - Increase in  $K_0$ .
  - Decrease in  $\lambda_0$ .

- How much antibody is needed for protection?
  - vitro/vivo
- How many surface antigens have to be occupied by antibodies?



<http://gened.emc.maricopa.edu>

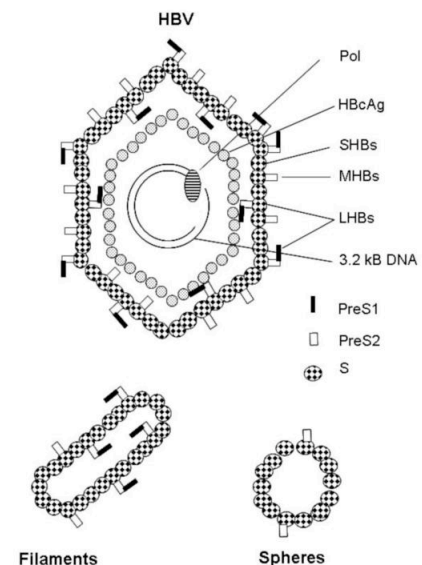
## 2. Hepatitis B



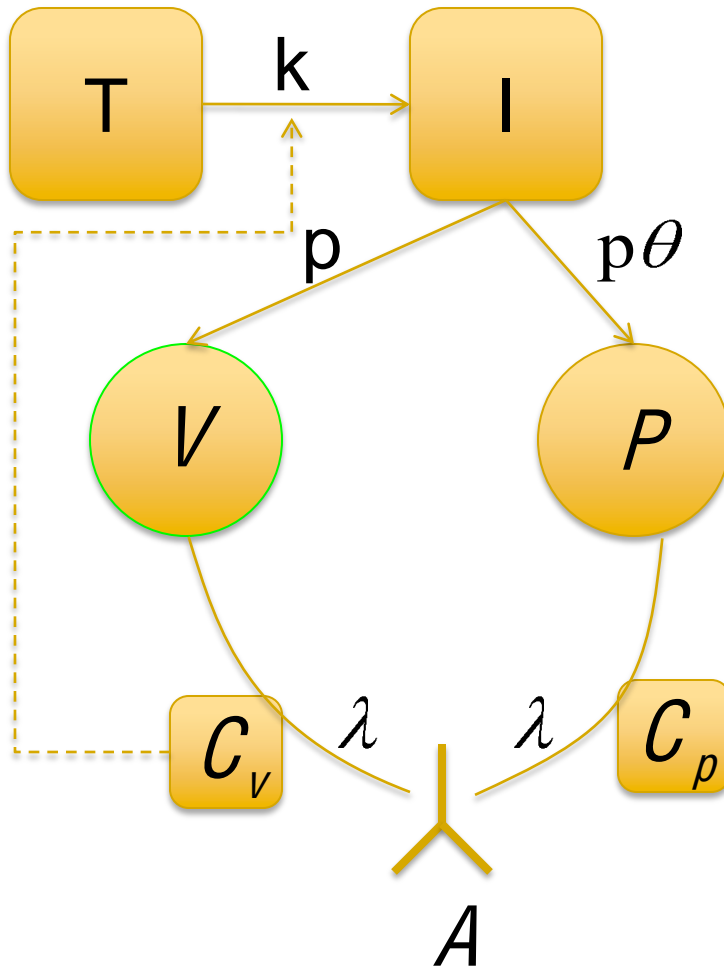
[Ciupe et al, *JTB* 2007, *PNAS* 2007]

# Antibody responses

- Efficient vaccine that induces *anti-HBsAg* antibodies and immune system memory.
- For people already infected
  - Role of antibody in disease pathogenesis.
  - Anti-HBs antibody is detectable after the resolution of acute infection.
  - Inhibit the spread of infection, but do not affect viral replication (Zhang, *J. Virol*, 2004).
  - Subviral particles (1000-10,000 more than virus) may serve as a decoy.



# Antibody model



Model equations:

$$\frac{dT}{dt} = rT(1 - \frac{T+I}{T_{max}}) - kVT$$

$$\frac{dI}{dt} = rI(1 - \frac{T+I}{T_{max}}) + kVT - \rho I$$

$$\frac{dV}{dt} = pI - cV + k_- C_v - k_+ AV$$

$$\frac{dP}{dt} = \theta pI - cP + k_-^p C_p - k_+^p AP$$

$$\frac{dC_v}{dt} = -k_- C_v + k_+ AV - c_{AV} C_v$$

$$\frac{dC_p}{dt} = -k_-^p C_p + k_+^p AP - c_{AV} C_p$$

$$\frac{dA}{dt} = \lambda(V + P) + A(a - \beta A)$$

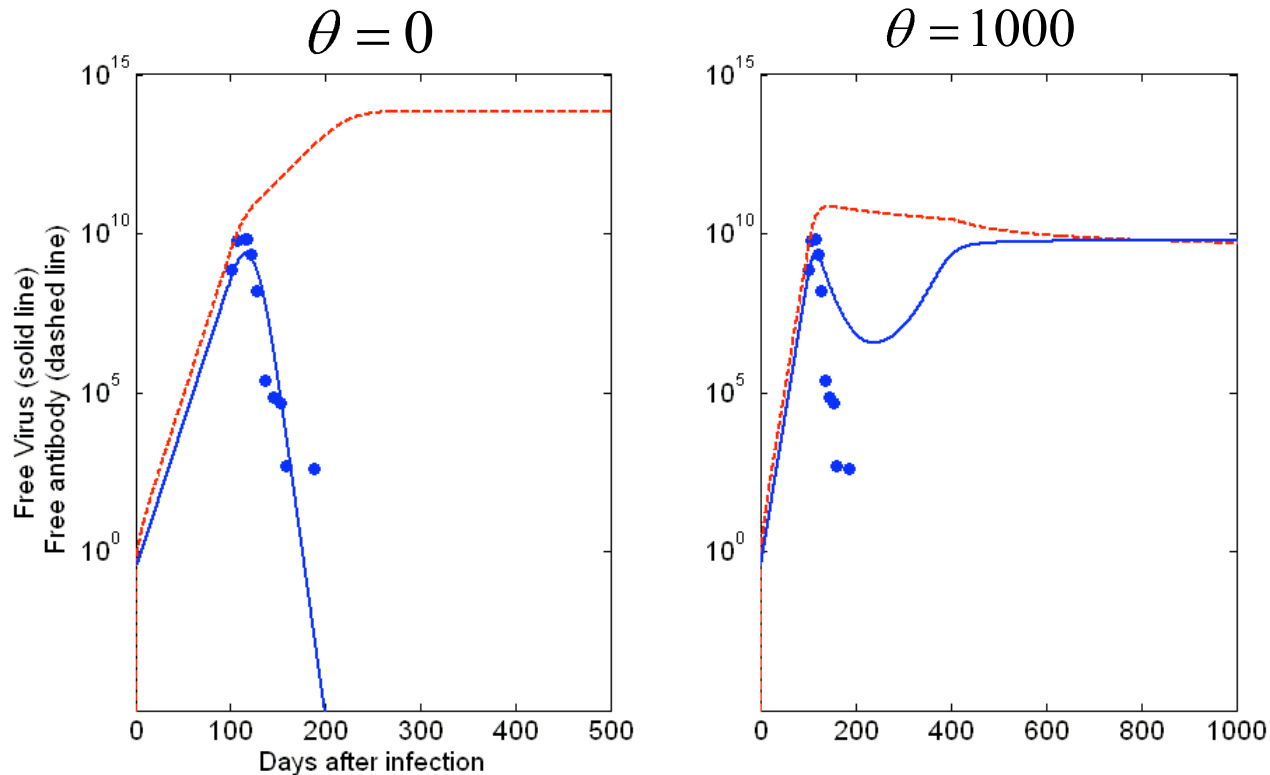
$$+ k_- C_v - k_+ AV + k_-^p C_p - k_+^p AP$$

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# Things to consider

- Different binding rates
  - Different removal rates
  - Delay in antibody production
  - Increase the binding, so that most antibodies are in complexes
  - Combined effect of immune responses
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# Numerical results



Antibody responses to subviral particles lower the responses directed at virus particles leading to chronic infections.



# Conclusions

- Competition between antibody producing B cells alone can explain the inefficacy of antibodies to control viral infection
  - Most fit antibody wins
  - Of the limited amount of antibody present, most bind non-infectious particles which exceeds virus titers.
- Use this knowledge in a vaccine trial

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# Acknowledgments

- Thomas Kepler, Duke University
  - Patrick DeLeenheer, Univ of Florida
  - Alan Perelson, LANL
  - Ruy Ribeiro, LANL
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