

# EIAV as a Research Model for other Lentiviruses: Lessons learned and to be learnt.

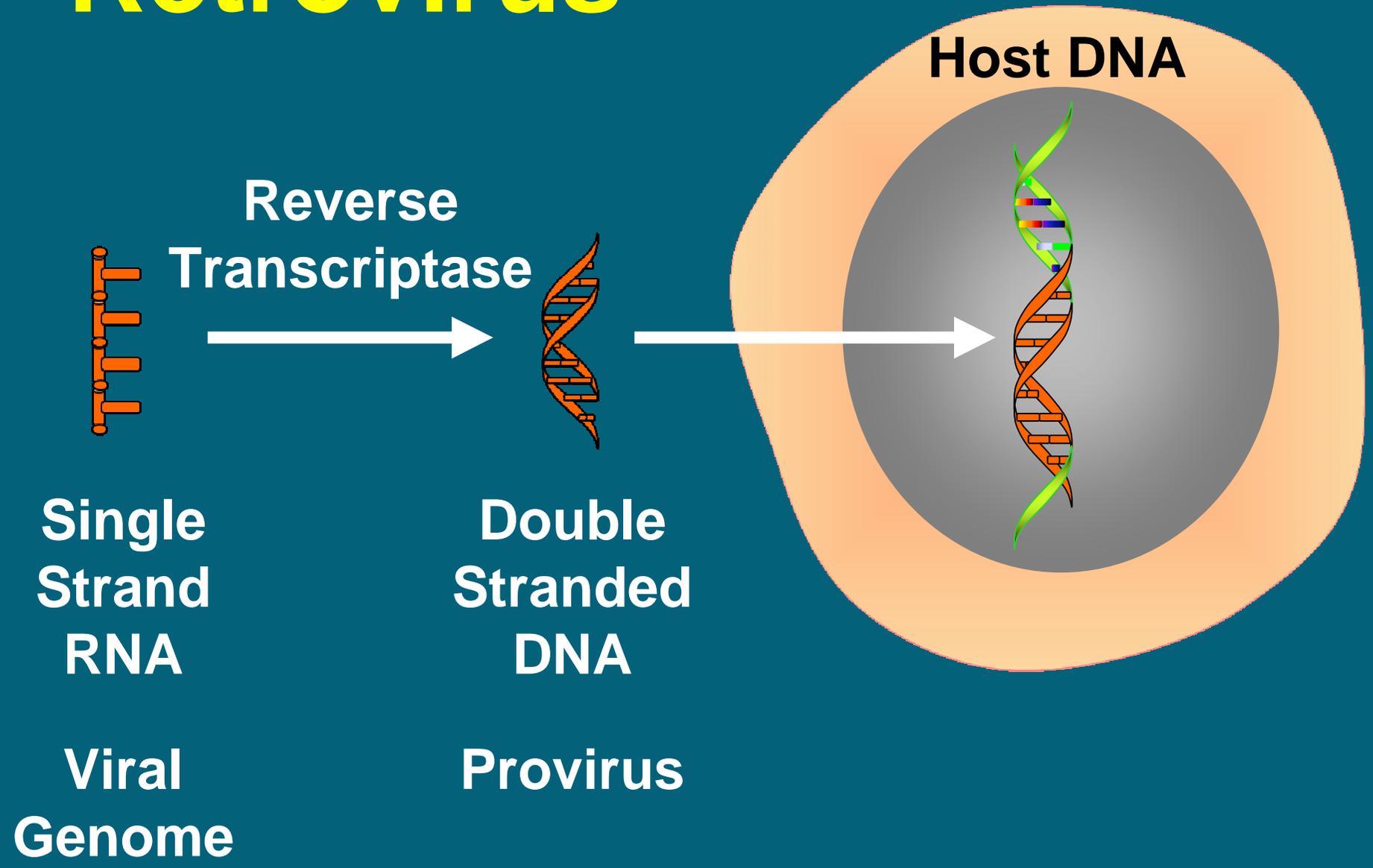


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University of Kentucky

# What is a Lentivirus?

- Family: Retroviridae
- Subfamily: Orthoretrovirinae
- Genus: Lentivirus

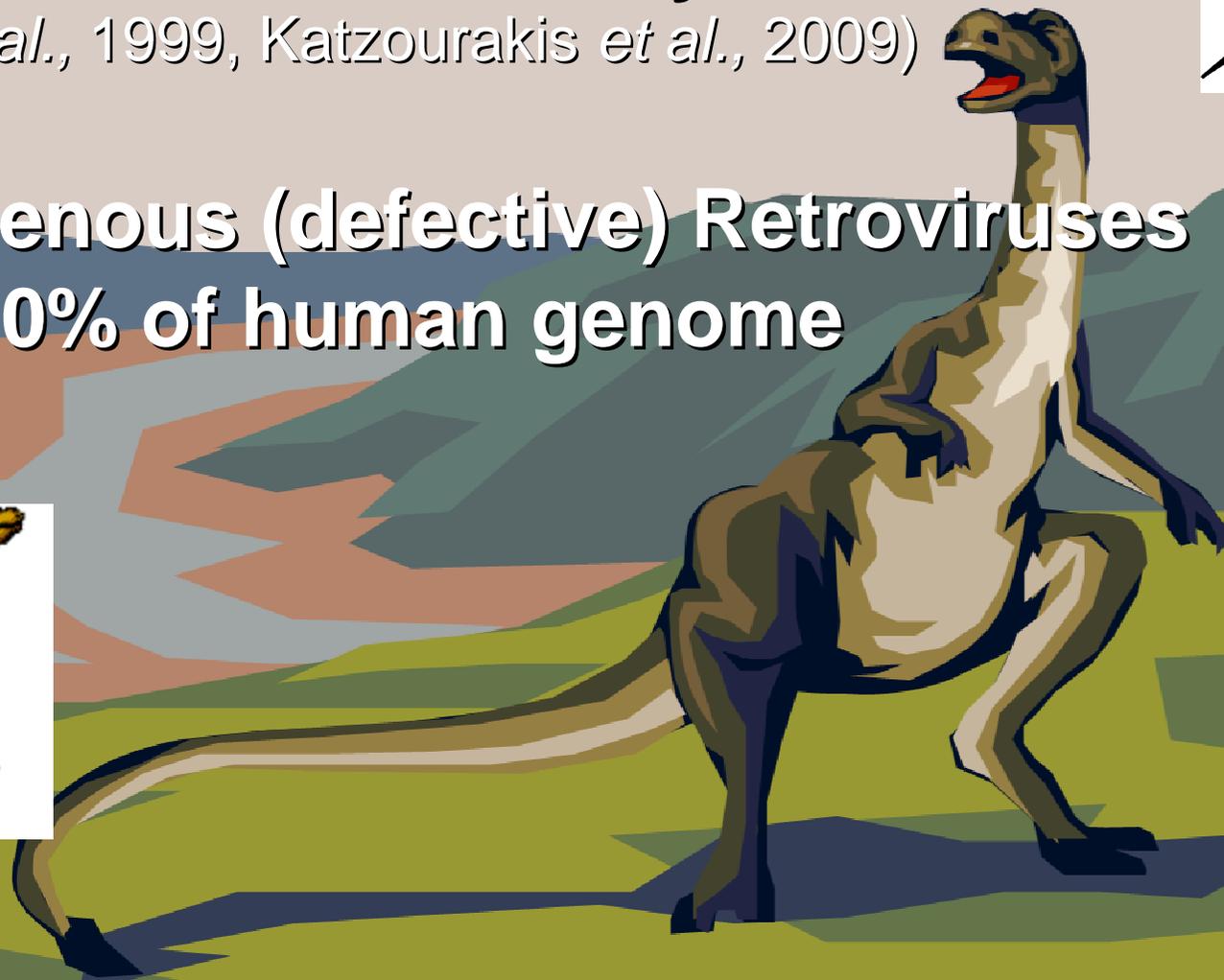
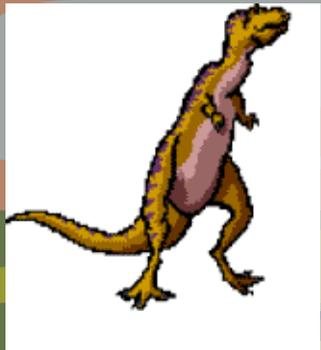
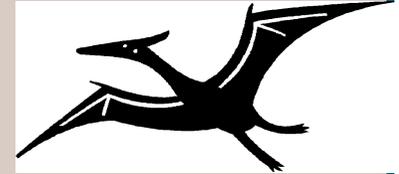
# Retrovirus



# Retroviruses

Ancient  $100 - 150 \times 10^6$  years  
(Benit *et al.*, 1999, Katzourakis *et al.*, 2009)

Endogenous (defective) Retroviruses  
= 8 - 10% of human genome



# Retroviruses

LT  
R

GAG

POL

ENV

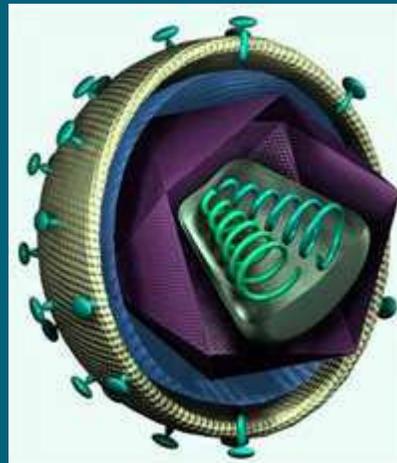
LT  
R



Structural Core Proteins  
p15, p26, p11, p9

Replicative Enzymes

Envelope Surface Glycoproteins



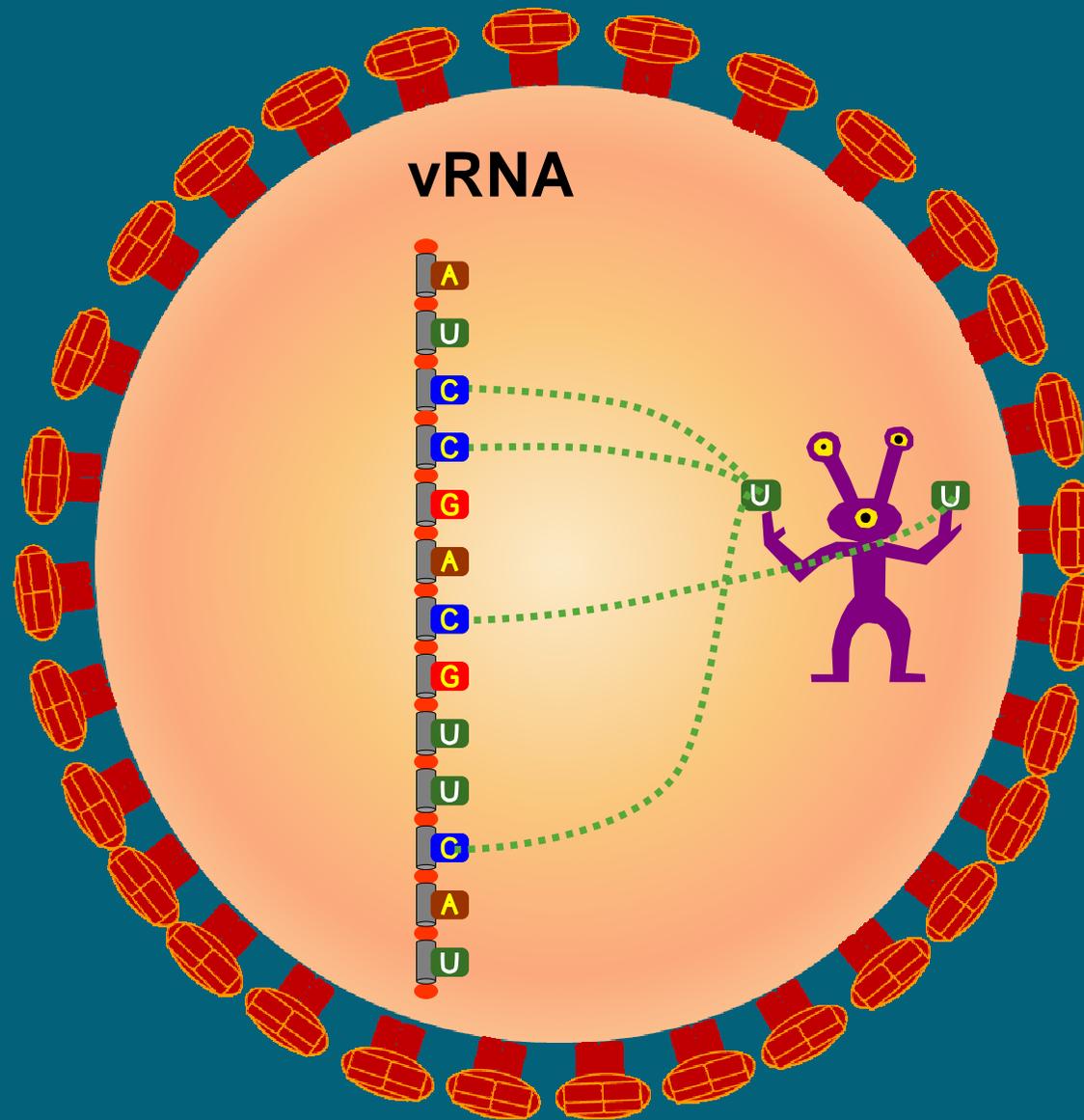
# Host Defenses

**Immune Response:** Innate  
Adaptive

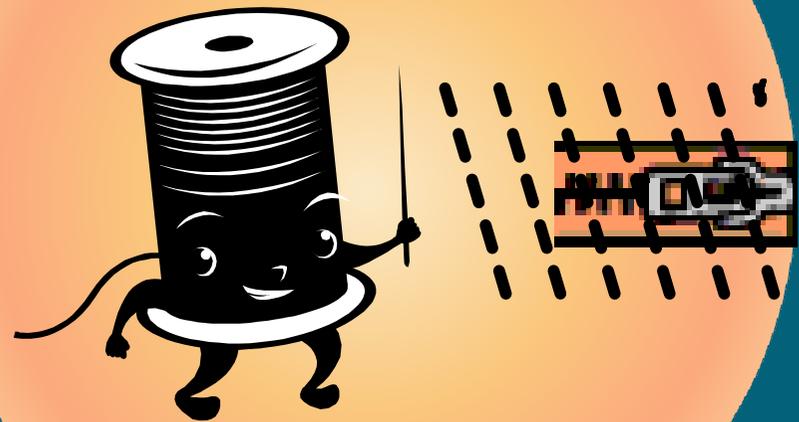
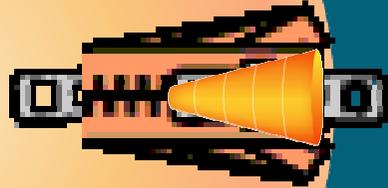
**Retroviral Restriction Factors:**

- **Apolipoprotein  $\beta$  Editing Complex 3 (APO $\beta$ EC3)**
- **Tripartite Motif-Containing Protein 5 $\alpha$  (TRIM5 $\alpha$ )**
- **Tetherin**

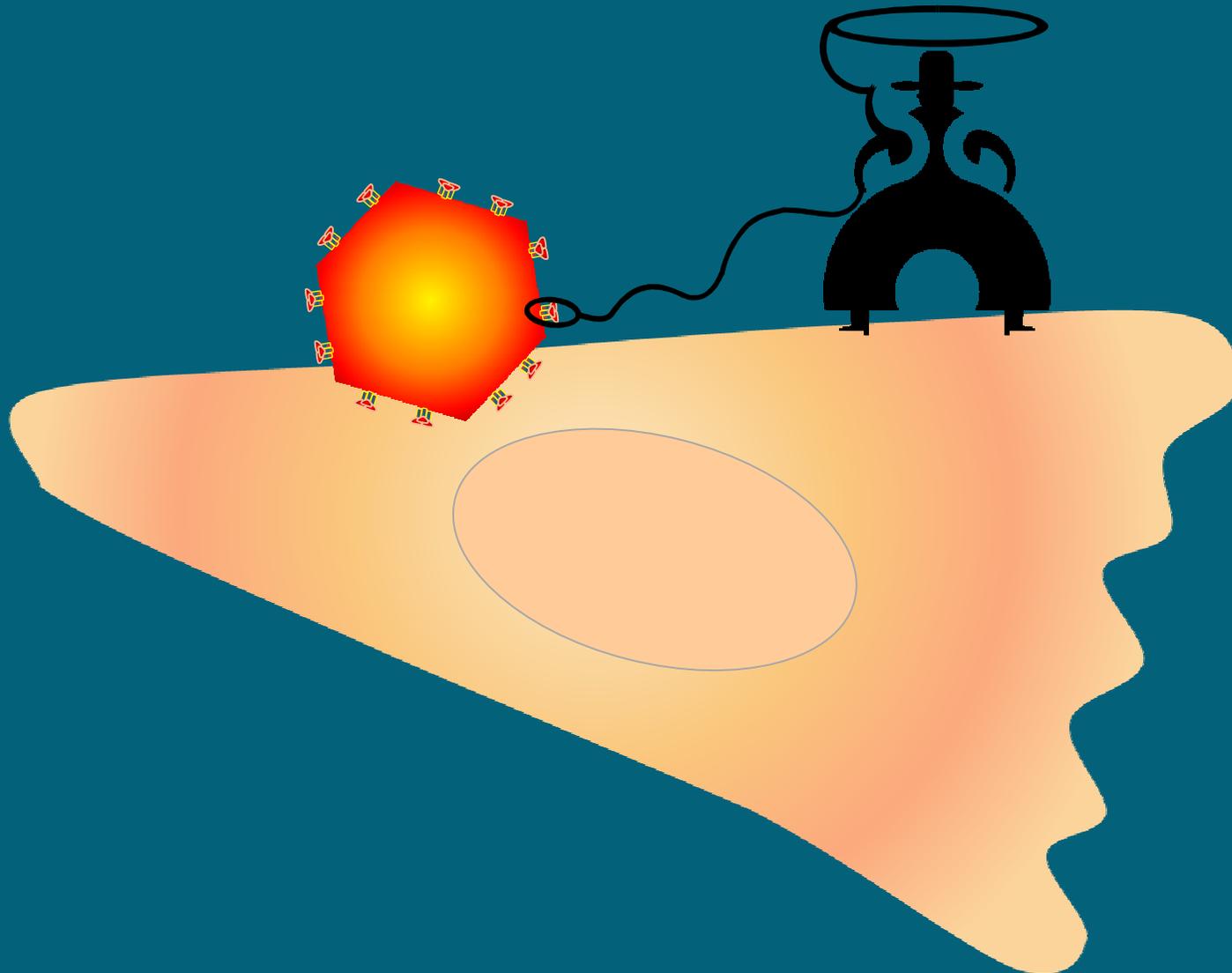
# APOBEC3 (Cytosine Deaminase)



# TRIM 5α



# Tetherin



# Lentiviral Characteristics

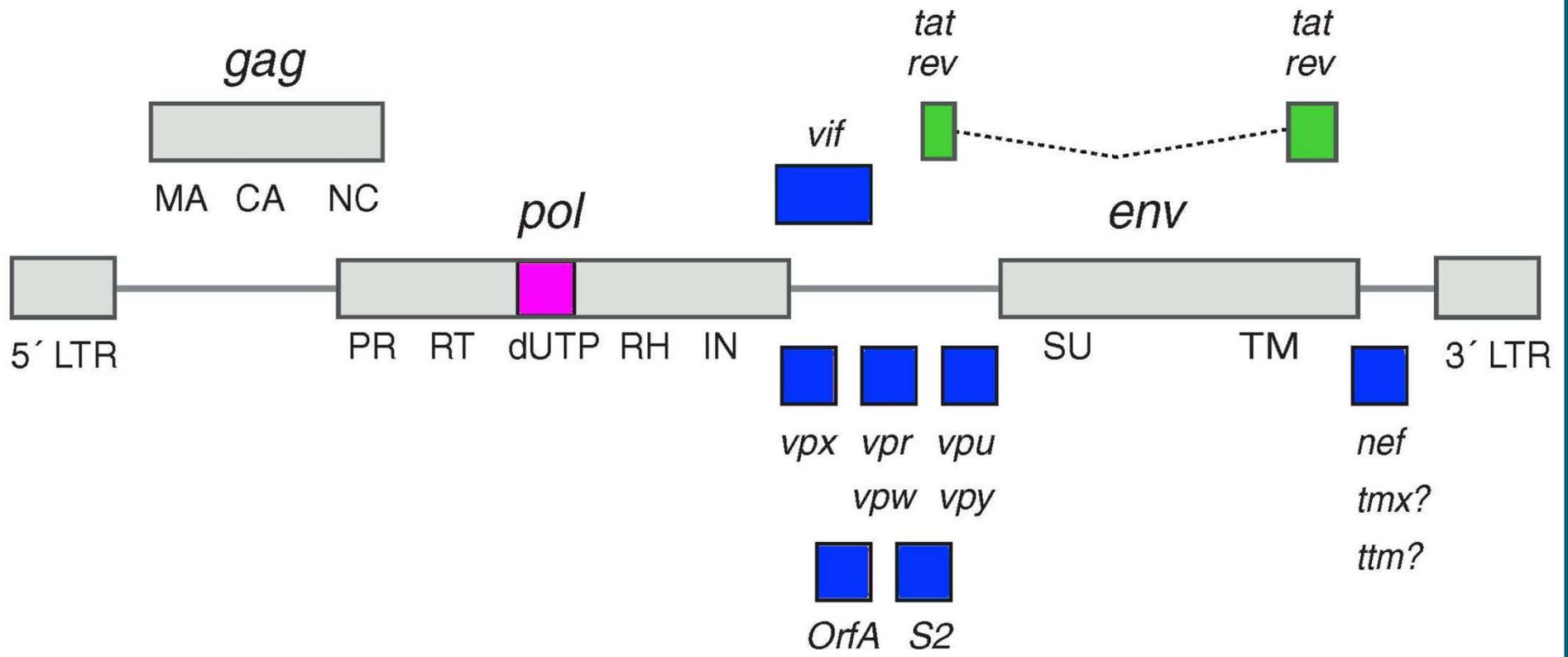
Genetically, Morphologically Distinct  
Infect Non-Dividing Cells

Hostile environment

Low dNTP (SAMHD1) High dUTP

Evolved Additional ORFs to GAG,  
POL, ENV

Complex Retroviruses



# Additional / Ancillary Lentiviral Genes

|                |                                  |             |                            |
|----------------|----------------------------------|-------------|----------------------------|
| <b>Tat</b>     | Transactivator for replication   | <b>Vpu</b>  | CD4 ↓<br>Tetherin ↓        |
| <b>Rev</b>     | Export of viral RNA from nucleus | <b>OrfA</b> | CD134 ↓                    |
| <b>dUTPase</b> | dUTP → dUMP                      | <b>nef</b>  | CD4 –<br>signaling         |
| <b>S2</b>      | Binds cellular proteins          |             | –intracellular trafficking |
|                | Inflammatory cytokine ↑          |             | –cell migration            |
| <b>Vif</b>     | APOβEC3 degradation              |             | –apoptotic pathways        |
| <b>Vpr</b>     | SAMHD1 degradation               |             |                            |

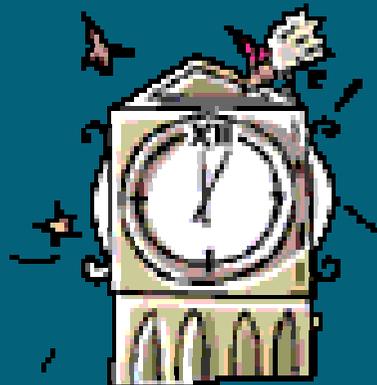
# Timeline of Lentiviral Evolution

## Molecular Clock Estimate

Entire Genus = < 1 million years

Individual Lentiviruses = 100's to 1000's

|            |        | years       |
|------------|--------|-------------|
| Human      | HIV-1M | 1908 – 1933 |
| Gorilla    | SIVgov | 1818 – 1906 |
| Chimpanzee | SIVcp2 | 1266 – 1685 |



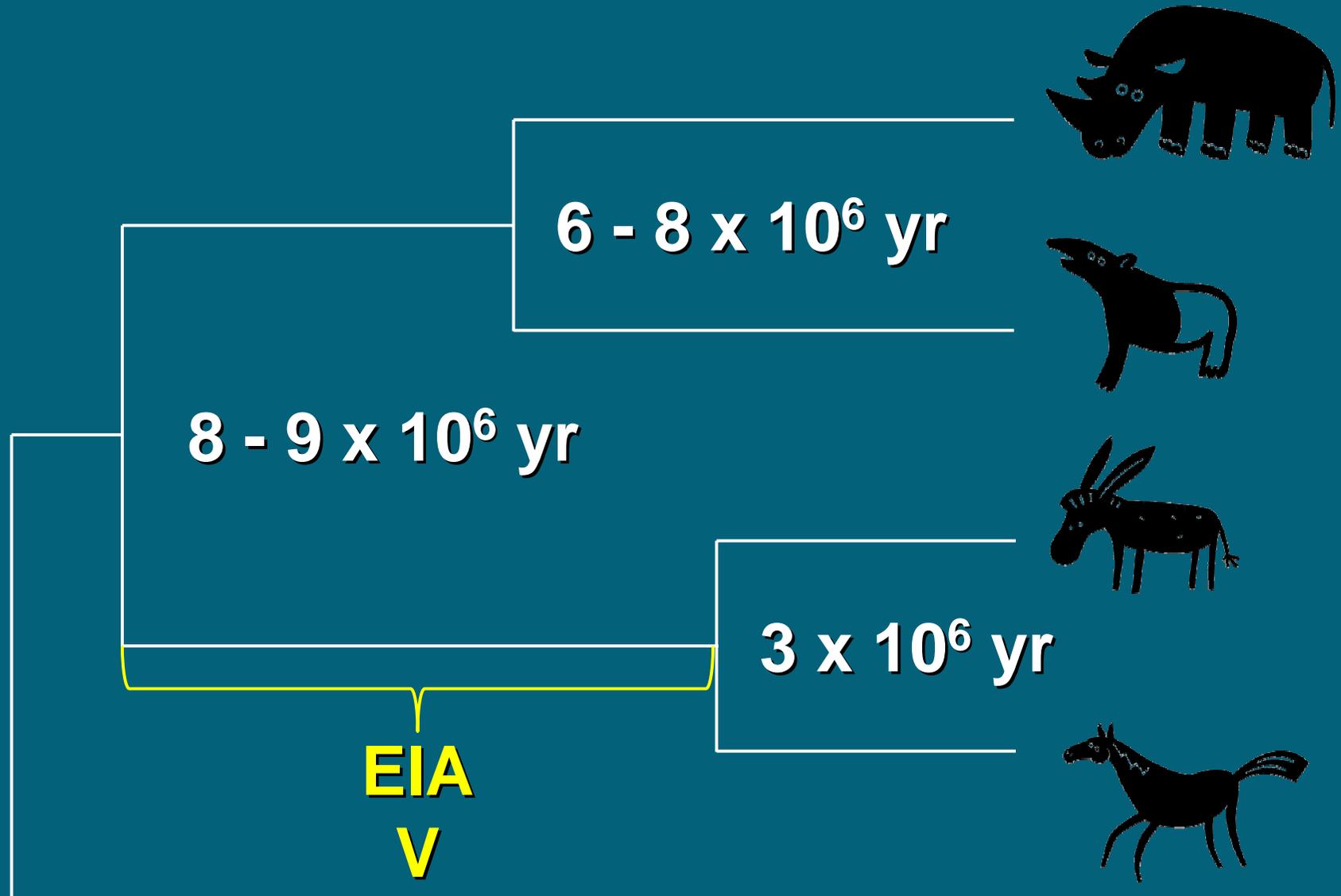
*Wertheim et al.,  
2009*

# Lentivirus Distribution

Retroviruses All Vertebrates

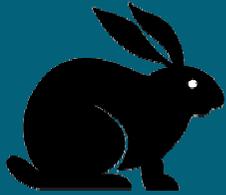


# Perissodactyla



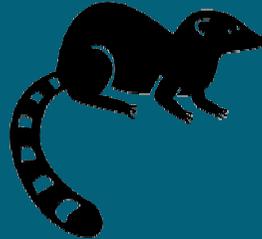
# Revised Timeline of Lentiviral Evolution

Defective



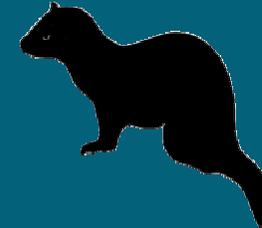
**RELIK**  
 $12 \times 10^6$  yr

Endogenous



**PSIV**  
 $4.2 \times 10^6$   
yr

Lentiviruse



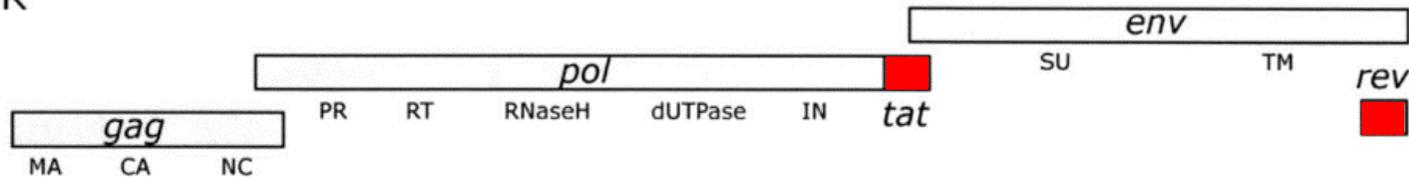
**ELVmpf**  
 $12 \times 10^6$  yr

# Endogenous Lentiviruses

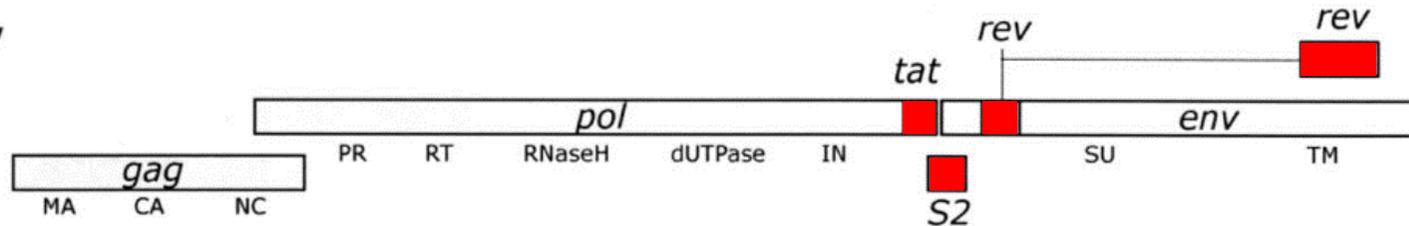
- Older
- Expand Host Range
  - Lagomorph
  - Prosimian
  - Carnivore
- Extinction

# Lentiviral Genome Organization

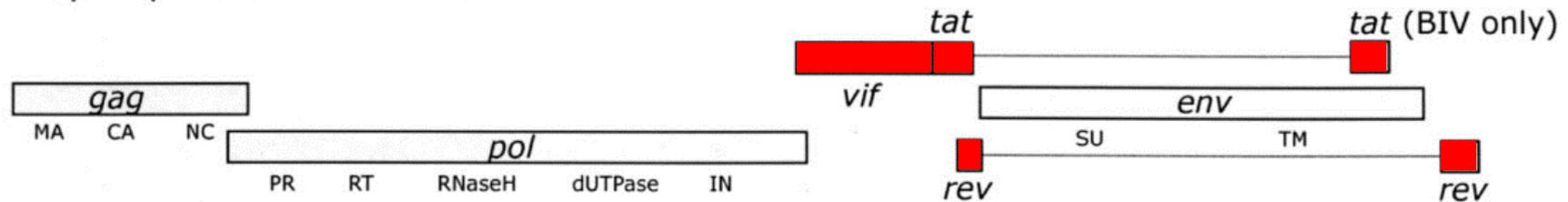
RELIK



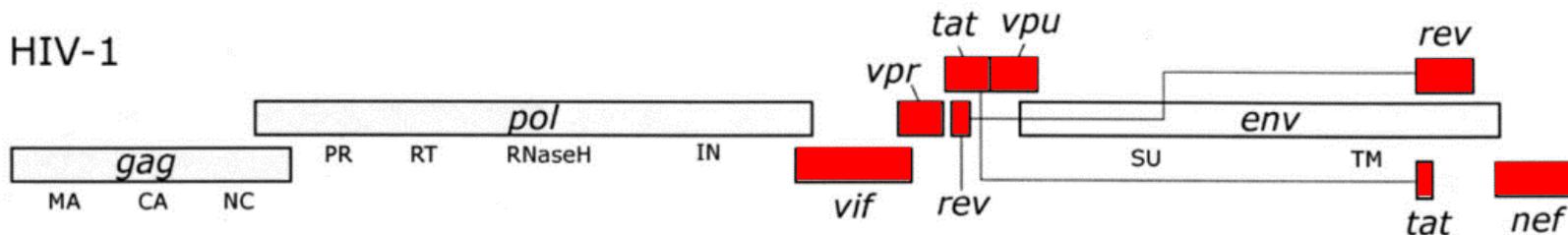
EIAV



FIV/BIV/OMVV



HIV-1





# EIAV

- Infects ALL Equidae
- Persistent Infection – NOT eliminated by host responses
- Simplest genome organization of any extant Lentivirus
  - dUTP
  - TAT
  - REV
  - S2
- Only extant Lentivirus - VIF

# EIAV and Retroviral Restriction Factors

**APO $\beta$ EC3** – Horse more genes than any other non-primate species

- Not blocked by EIAV
- Packaged in virions
- ?

**TRIM5 $\alpha$**  – EIAV p26 resistant?

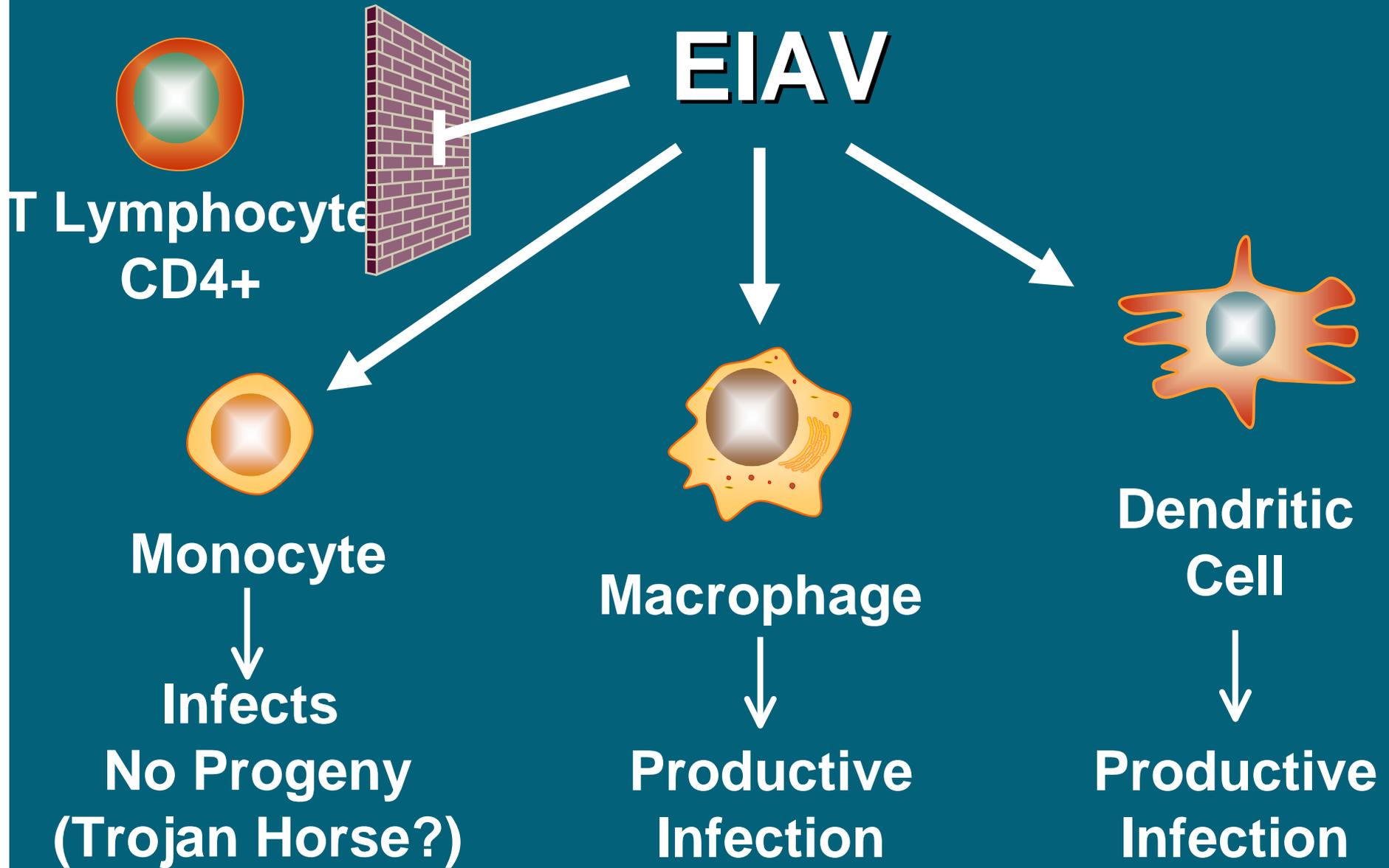
- Expression in horses?

( $\Delta$ TRIM5 $\alpha$  in Canidae)

**Tetherin** – EIAV Env resistant?

**Is EIAV a primitive lentivirus?**

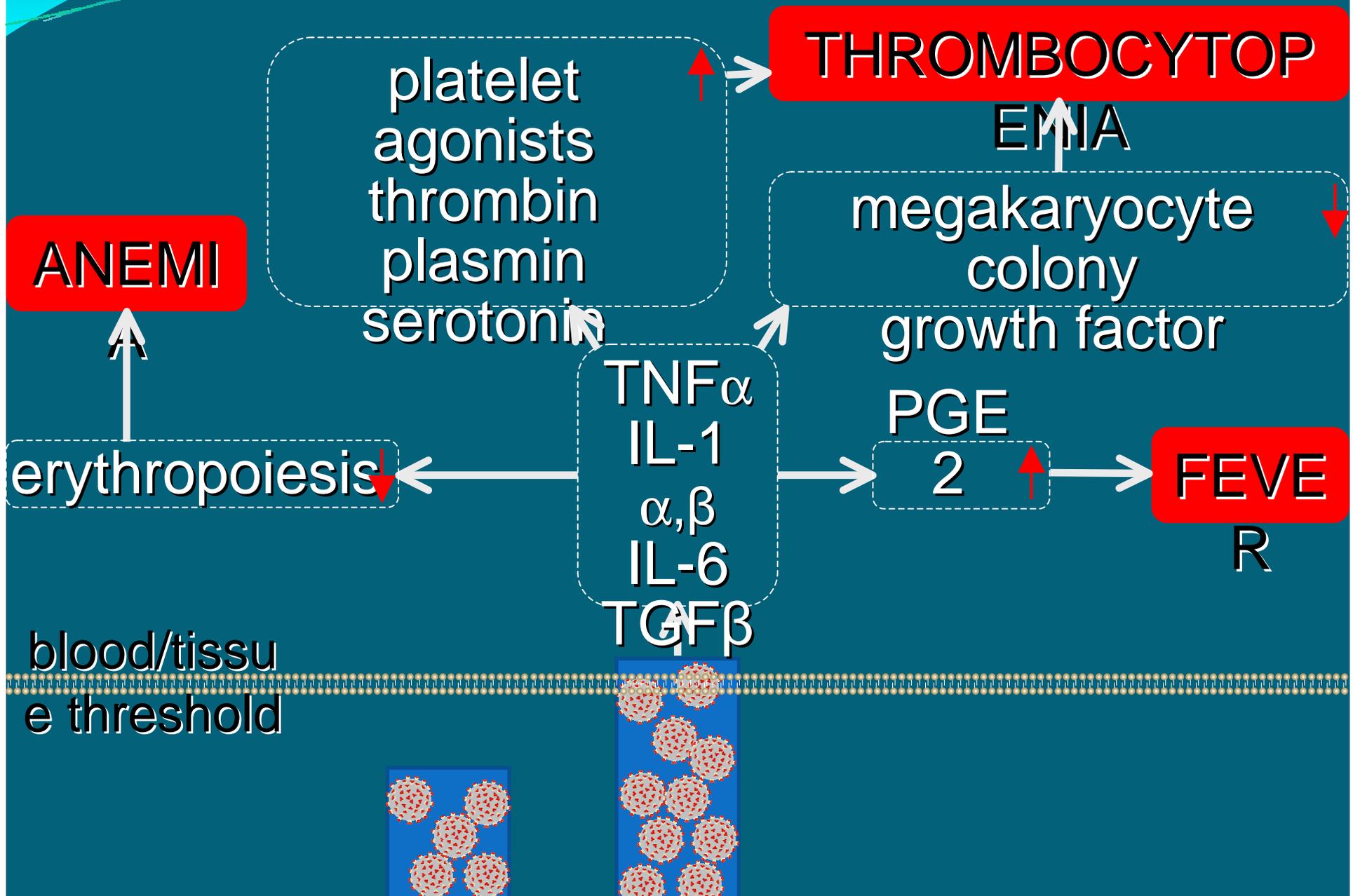
# Host Cell Types



# EIA Clinical Signs

| Stage                     | Signs                                                                              | Viral Loads |
|---------------------------|------------------------------------------------------------------------------------|-------------|
| Acute                     | Fever (>39°C)<br>Thrombocytopenia<br>Lethargy                                      | High        |
| Chronic<br>(12-24 months) | Fever<br>Thrombocytopenia<br>Petechial hemorrhaging<br>Anemia<br>Edema<br>Cachexia | High        |
| Inapparent                | None                                                                               | Low         |

# Pathogenesis of Acute EIA

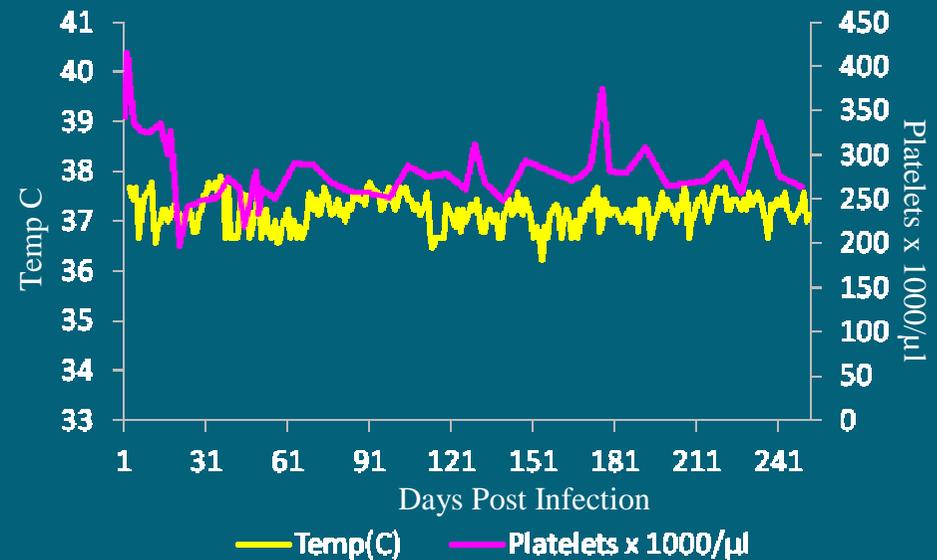
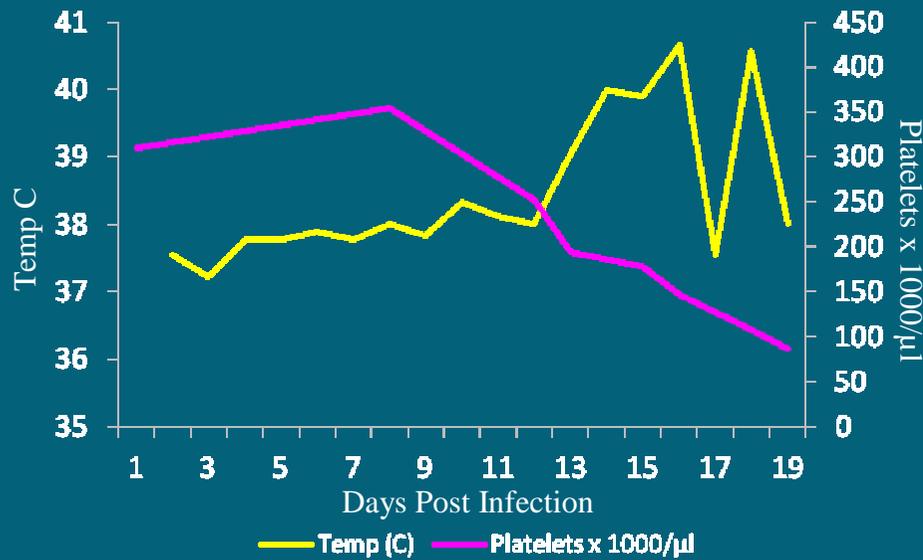


# EIA Clinical Signs

Highly variable  
Sub-clinical – Death  
Individual  
Equid Species



# EIAV Differences between Equid Species



# Host Management of Lentiviral Infections



**Natural:**

SIV / African Non-Human

Primates

Subclinical

Viral Replication – High

Immune Control – Ineffective

Limit Pathogenesis, CD4 Depletion

NEF  $\rightarrow$  CD3-TCR $\downarrow$

**Non-Natural:**

HIV / Humans, SIV /

Asian Macaques

AIDS

Viral Replication – High

Immune Control – Limited, Transient

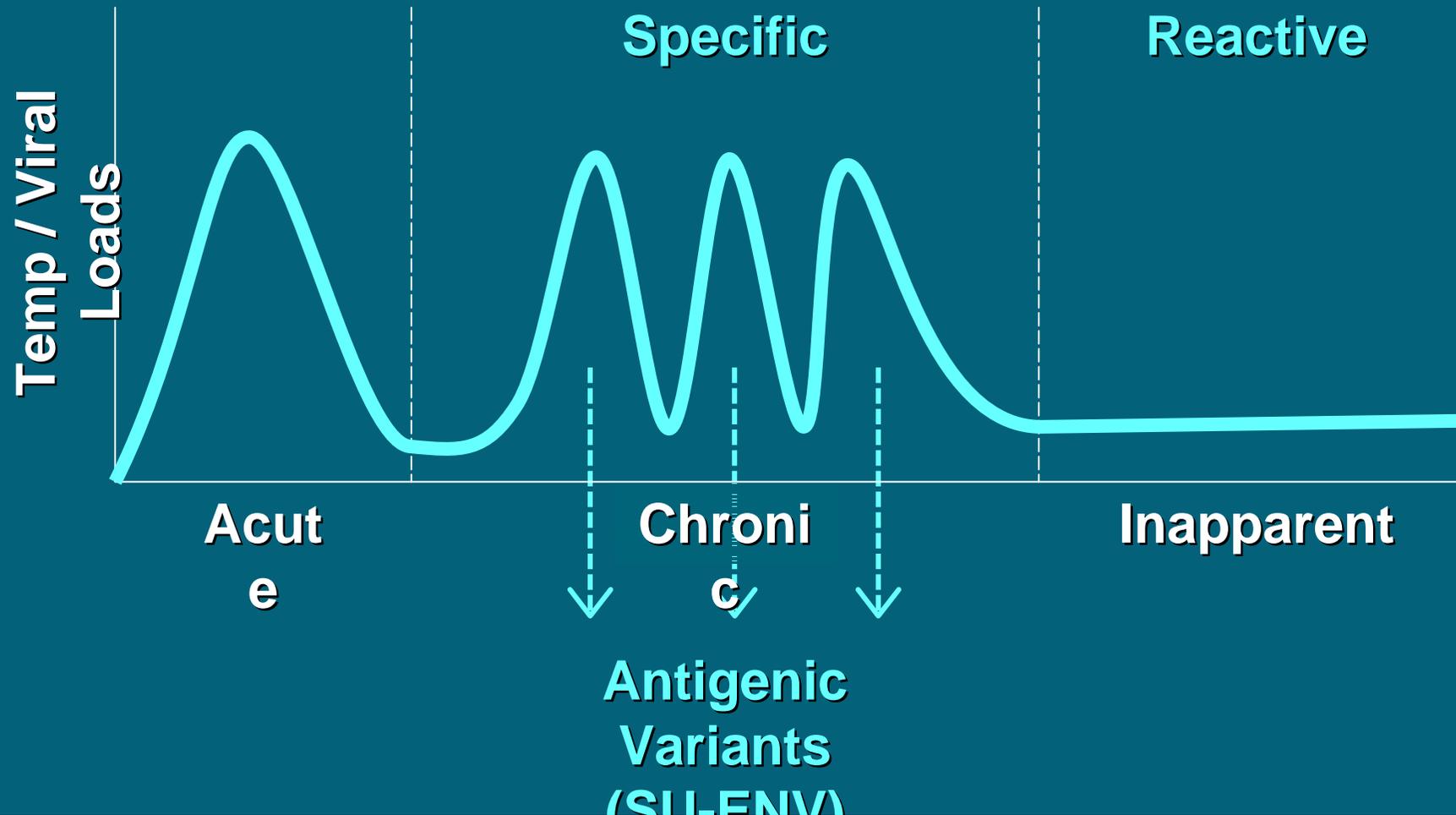
(Exception – elite controllers?)

# EIAV / Horse

Natural Immune Suppression: Viral Load  $\uparrow$

Disease  
Transient  
Strain  
Specific

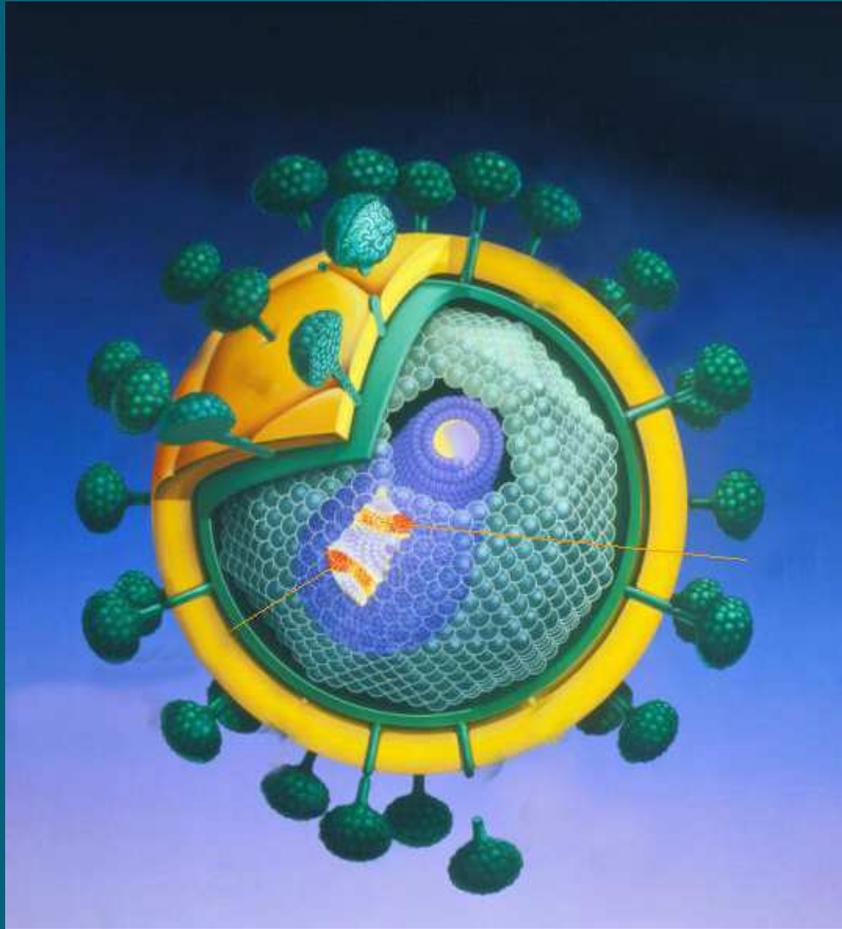
Long Term  
Cross-  
Reactive



# Immunological Control of EIAV

- No simple correlate of protection
- Differences between individual horses
- Model for Elite Control of HIV in humans?
- Other mechanisms?

# EIAV SU : A Critical Role



Attachment/Entry  
Neutralizing  
Epitopes

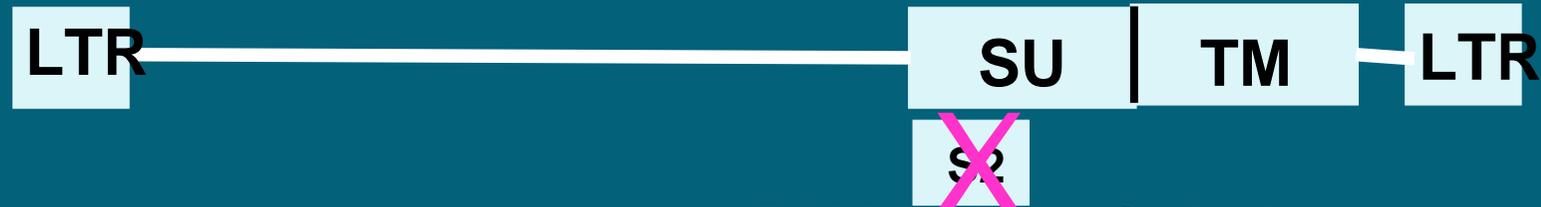
# Variation in SU PND with Time

## SU PND Amino Acid Sequence

|    | N | S | S | D | S | S | N | P | V | R | V | E | D | V | M |
|----|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| I  | • | • | • | • | • | • | • | • | • | • | • | • | • | • | • |
| II | • | • | • | • | • | • | • | S | • | • | • | • | • | • | • |
| II | • | • | G | • | • | • | • | S | • | • | • | • | • | • | • |
| I  |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
| I  | * | * | * | * | * | * | * | * | * | * | * | * | * | * | • |
| V  |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
| V  | T | • | G | P | • | • | • | S | • | • | G | • | Y | E | T |

# $\Delta S2$ EIAV Vaccine

Based on EIAV<sub>UK3</sub> infectious molecular clone (Cook et.al. Virology 313: 588-603, 2003)



RNA copies/ml plasma

EIAV  $\Delta S2$

$10^2 - 10^4$

EIAV<sub>UK3</sub>

$>10^8$

Immunize Horses EIAV $\Delta 2$ , challenge  $>6$  months

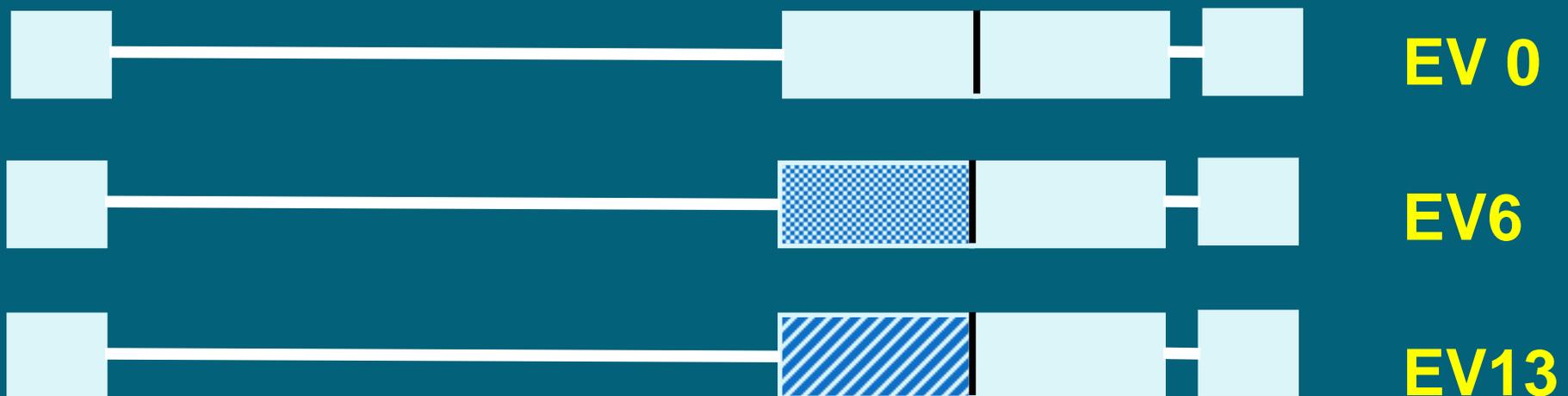
75-100% Protection from INFECTION  
from **HOMOLOGOUS challenge**

# EIAV Heterologous Challenge

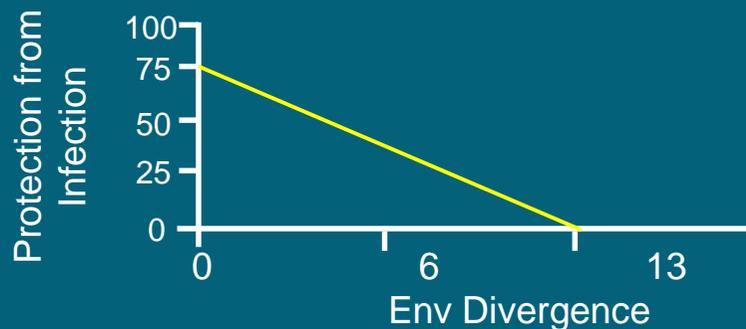
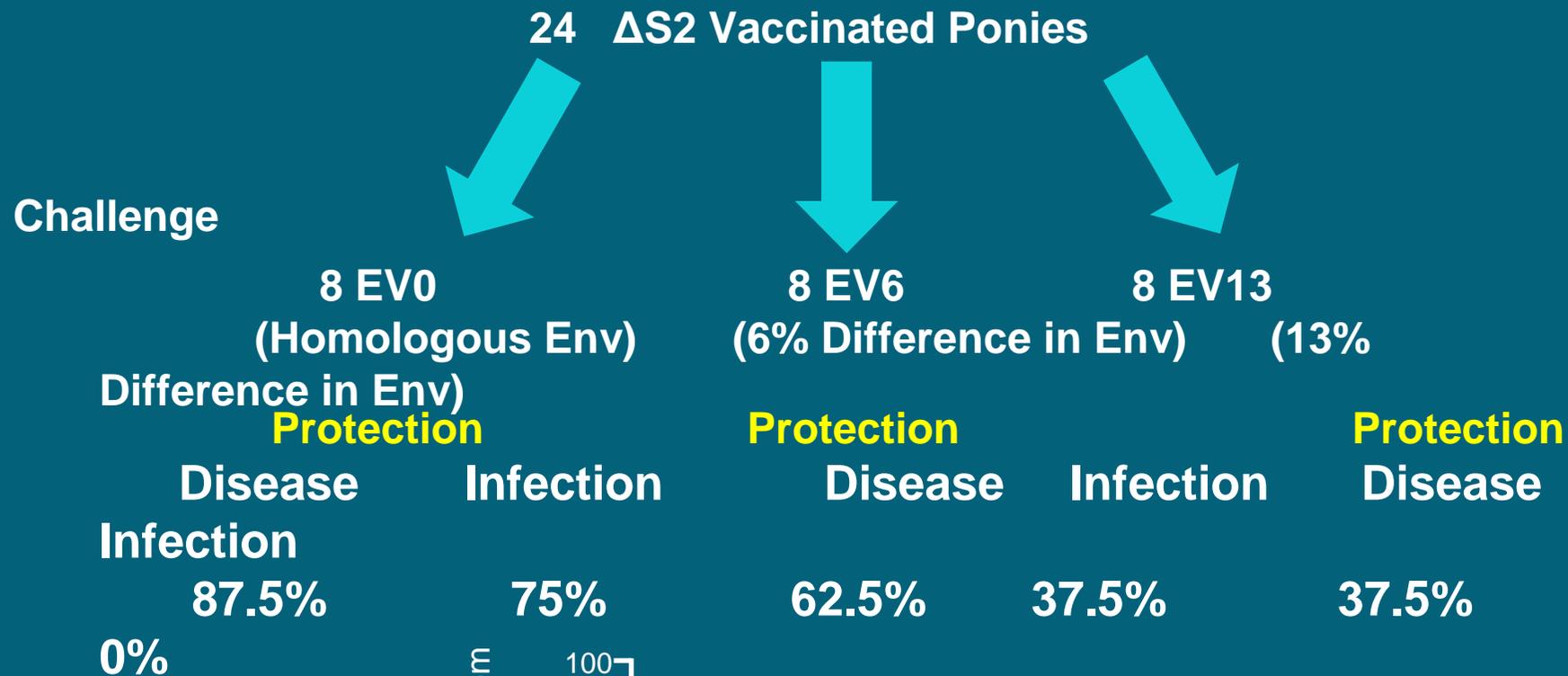
Pony 564 EIAV<sub>PV</sub> = EIAV<sub>UK3</sub> SU = EV0

Febrile episode IV @260dpi (6% divergence = SU =

Inapparent 1219dpi (13% divergence SU = EV13)



# $\Delta$ S2 Vaccine Trial



# Variation in EIAV SU

- Establishment of persistent infection
- Critical role in vaccine efficacy (related strains)
- Limited by structure and function?



# Lesson Learned

- Lentiviruses: complex  $>12 \times 10^6$  YR
- Few mammalian hosts – Extinct
- EIAV : Least complex genome
  - Successful/Persistent
  - Integration
  - MØ host cell
  - Neutralization Ab resistant
  - Antigenic variation

# Lesson Learned

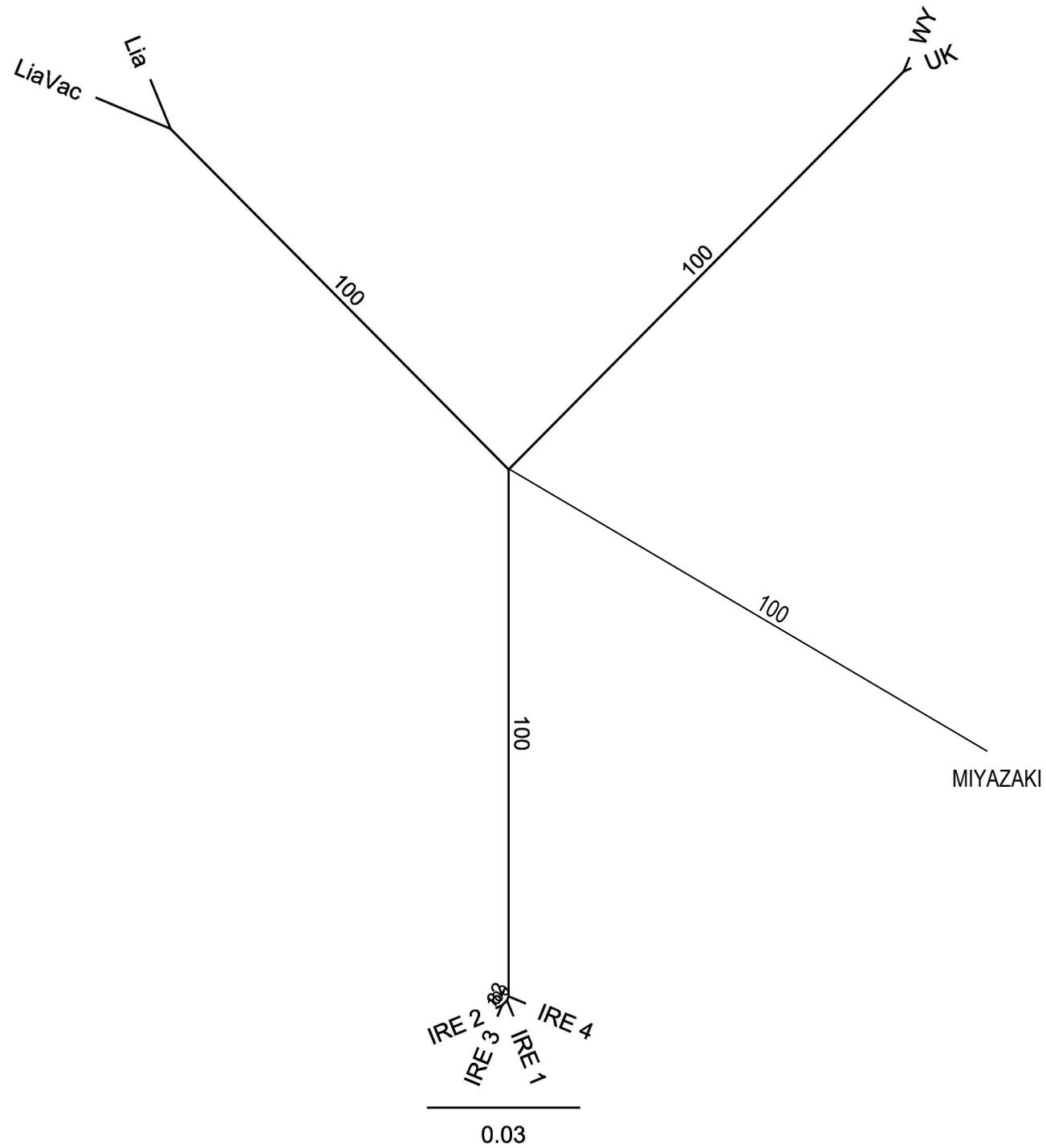
- Disease = High Viral Loads
- Inapparent Carrier = Low Viral Loads
  - Immunological Control
  - Horse = Model for Elite HIV Control?
- Vaccine Efficacy : Variation in SU

# Lessons to be Learned

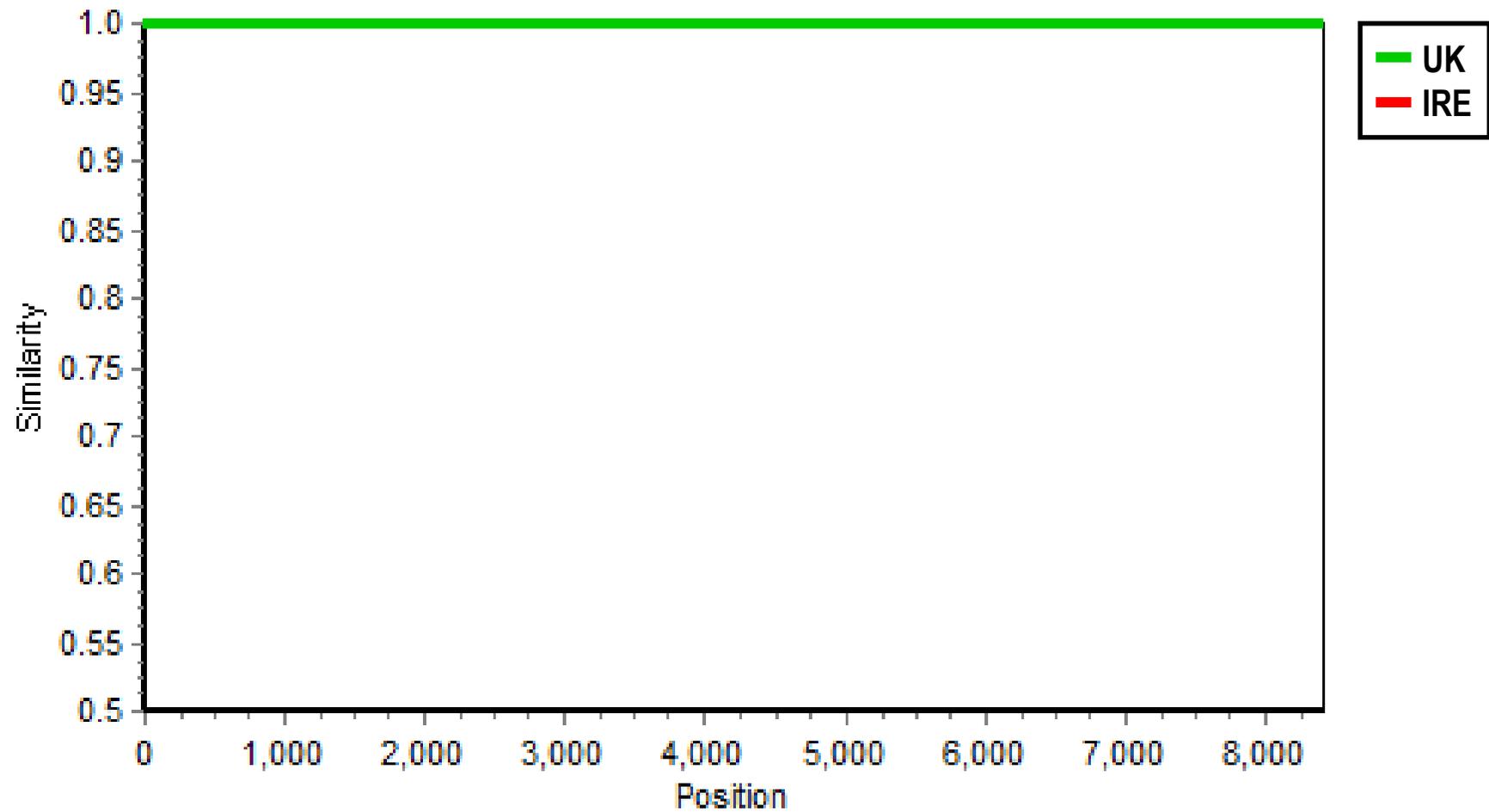
- ? Extent of EIAV Diversity
  - ❖ Molecular Diagnostics
  - ❖ Vaccines
- ? EIAV Persistence Mechanisms
- ? Evasion of Host Restriction factors
  - ❖ NO VIF/VPU

# Lessons to be Learned

- Immunological Control Mechanisms
  - ❖ NO Simple correlations
  - ❖ Other mechanisms
- ? Differences between Horses in Disease and Control
- ? Differences between Equid species



SimPlot - Query: AF016316\_UK  
FileName: D:\My Documents\EIAV IRE\UK vs IRE.fasta



Window: 200 bp, Step: 20 bp, GapStrip: On, Kimura (2-parameter), T/t: 2.0

# Acknowledgements:

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