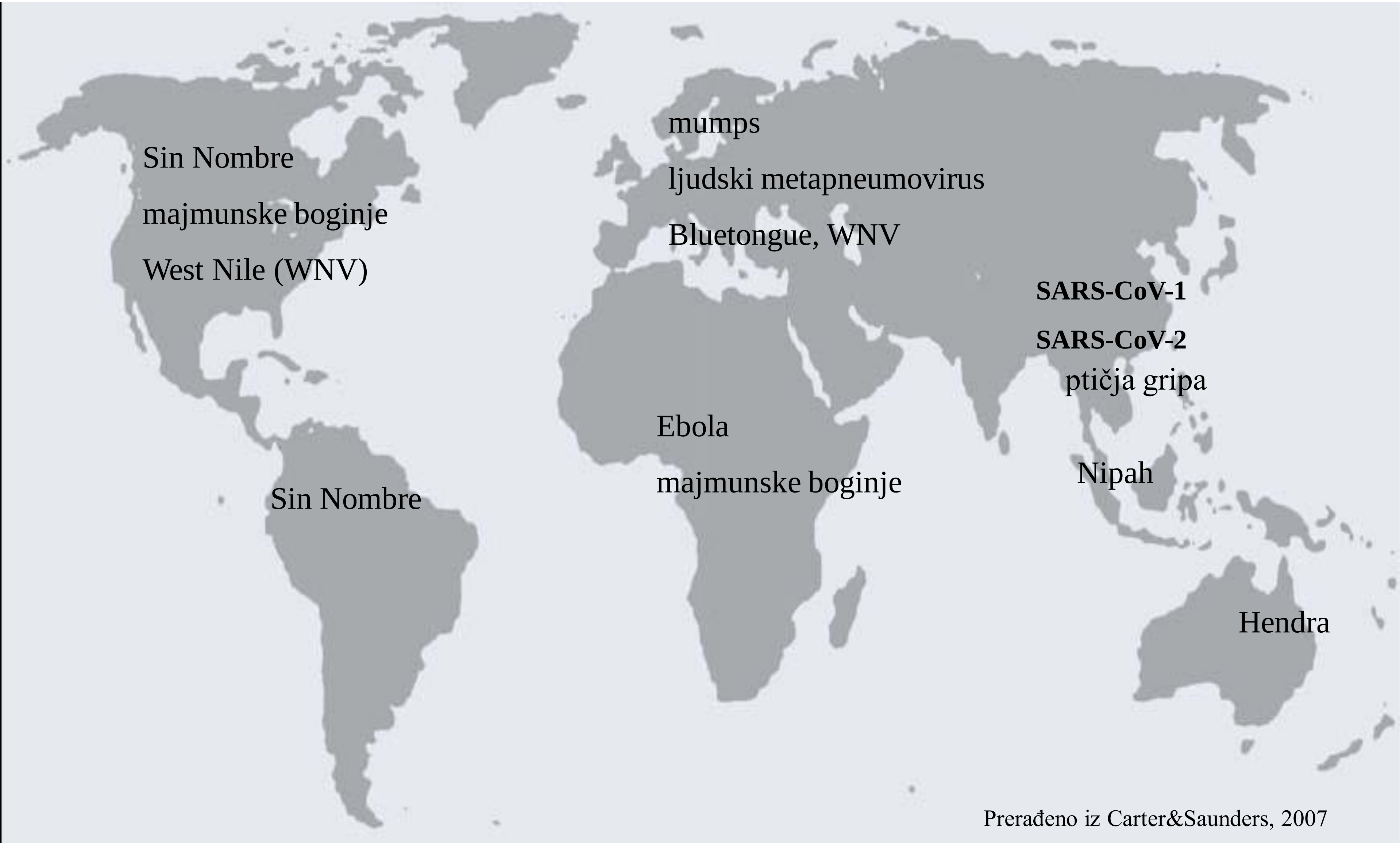
Emergentni virusi (*emerging viruses*)



Sin Nombre

majmunske boginje

West Nile (WNV)

mumps

ljudski metapneumovirus

Bluetongue, WNV

SARS-CoV-1

SARS-CoV-2

ptičja gripa

Ebola

majmunske boginje

Nipah

Sin Nombre

Hendra

Prerađeno iz Carter&Saunders, 2007

Pojam “emergentni virus” (virus koji izaziva nepoznatu, novu bolest) podrazumijeva puno toga:

-ponovna pojava (“re-emergencija”) poznatog virusa

mumps, slinavka i šap

-otkrivanje virusa koji su vjerojatno dulje patogeni npr. u čovjeka, ali tek sada smo ih uočili pa su nam novi

HHV- 8, ljudski metapneumovirus

-pojava virusa u novom području

West Nile (WNV), *Flaviviridae*, iz Ugande 1937., tek 1999. u NY

Bluetongue (BTV), *Reoviridae*, 2004. rasprostranjen 800 km sjevernije (od HR) nego ikad zbog većeg areala vektora (*Culicoides*, globalno zagrijavanje), rujan 2007. Suffolk

-pojava virusa u novim domaćinima

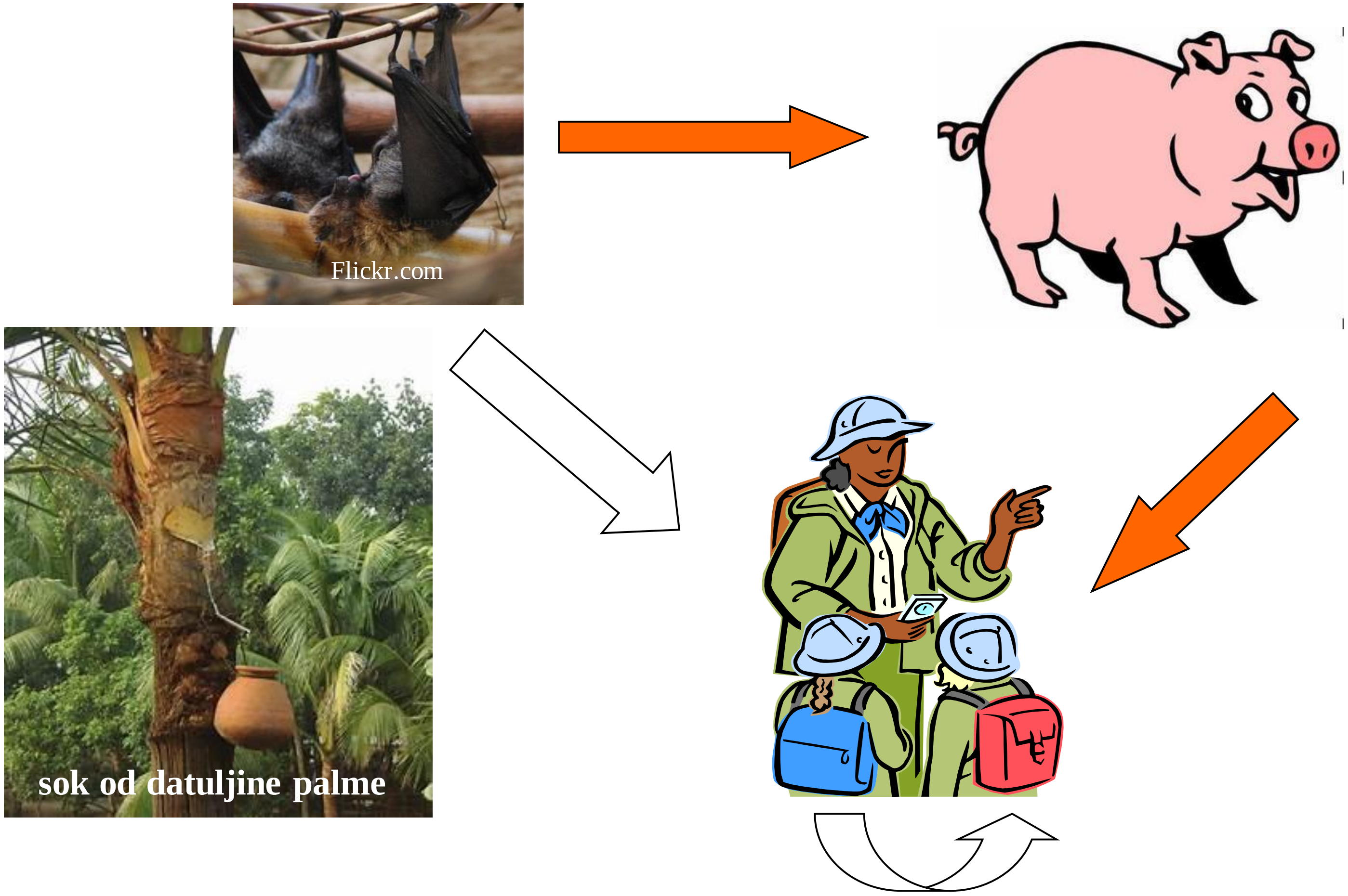
Bunyaviridae

Sin Nombre (1993., hantavirus pulmonarnog sindroma)

Paramyxoviridae

Hendravirus (iz konja 1994, ji-Australija, Brisbane)

Nipahvirus (iz svinja 1997, Malezija)



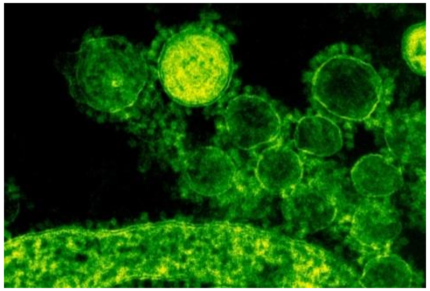
respiratorna bolest,
encefalitis

-pojava virusa u novim domaćinima i u novim područjima

  filovirusi
  majmunske boginje (*Poxvirus*)

- pojava sasvim novih virusa za čovjeka

  novi sojevi virusa gripe A (H7N9, Kina 2013.)
  SARS - tada novi koronavirus, sada SARS-CoV-1
  (slučajevi u UAE, Kataru, Jordanu, UK – pojava 2012.)
  SARS-CoV-2 uzročnik pandemije COVID-19



"Nove" viruse možemo dijeliti i prema rezervoarima u prirodi. Izvorno su mnogi ljudski virusi zoonotski, još uvijek prelaze iz životinjskih rezervoara.

Izvor virusa u prirodi:
šišmiši – rabdovirusi (bjesnoća), henipavirusi, koronavirusi,
filovirusi (Ebola)

ptice – WNV, ptičja gripa (AH5N1, AH7N7, AH9N2)

glodavci – hantavirusi

primati- Dengue,

HIV-1, HIV-2 (repetitivne introdukcije prije 50-100 godina)

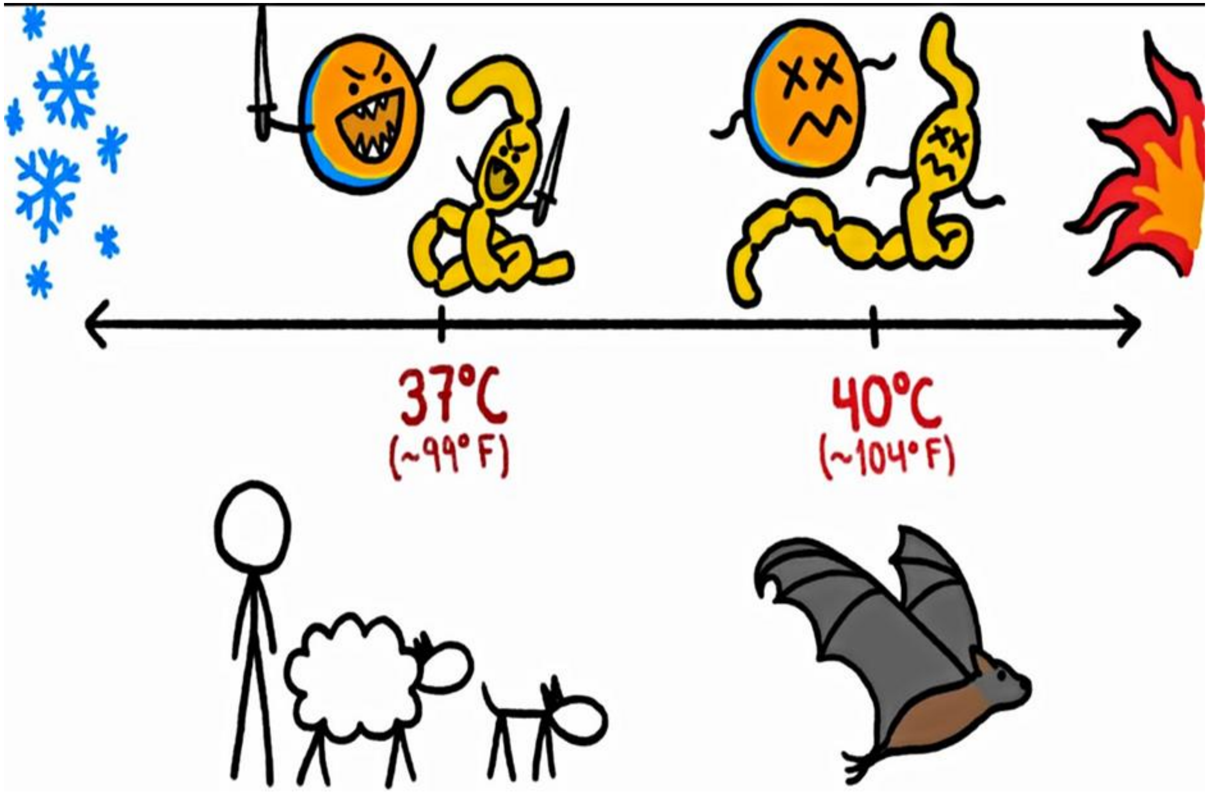
Ebola – epidemija u Gvineji 2021. – sumnje u održanje virusa u čovjeku jer je soj isti kao Makona ZEV 2013-16. kad je stradalo 11000 ljudi.

Zna se da 500 dana može ostati u spermijima.

Je li čovjek također postao izvor virusa?

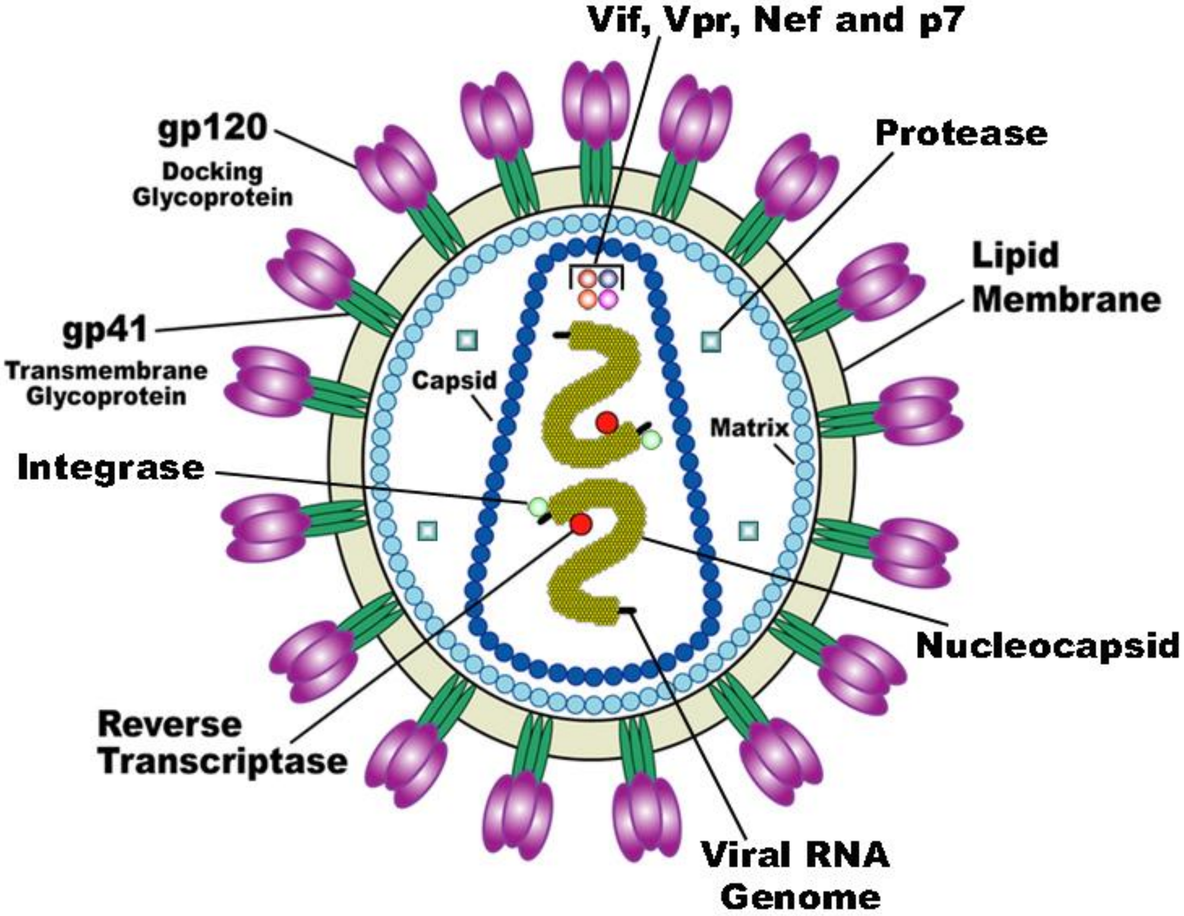
https://youtu.be/Ao0dqJvH4a0

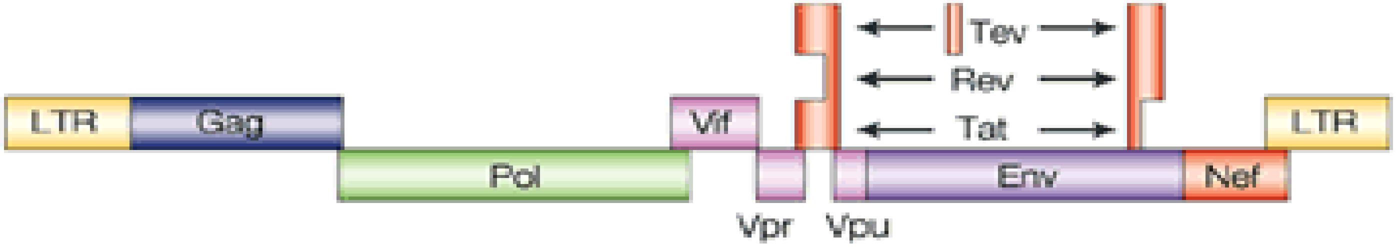
https://www.youtube.com/watch?v=Ao0dqJvH4a0#action=share



Zašto su šišmiši tako važni izvori zoonoza?
Žive u skupinama, lete, ima ih po cijelom svijetu (sve ekološke niše), ogromna im je bioraznolikost i brojnost, specifičnosti fiziologije (porast tjelesne temperature za vrijeme leta) probire viruse (i ostale patogene) koji mogu opstati i za vrijeme povišene tjelesne temperature u ljudi i životinja (aktivacije imunosnog sustava). Nova hipoteza – imunosna prilagodba.

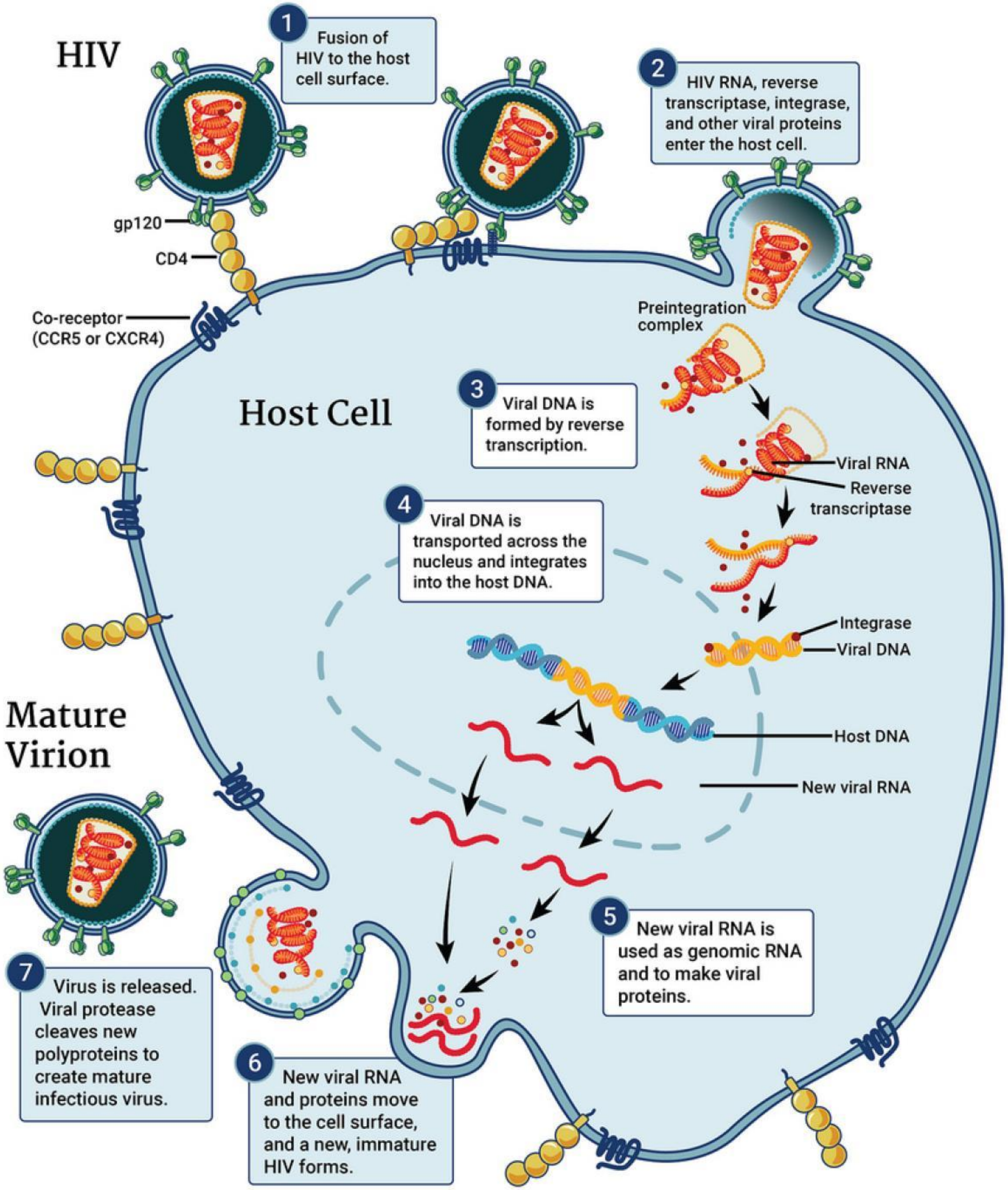
- HIV i njegovo porijeklo





en.wikipedia.org/wiki/HIV

- Replikacijski ciklus HIV-a



1 Fusion of HIV to the host cell surface.

2 HIV RNA, reverse transcriptase, integrase, and other viral proteins enter the host cell.

3 Viral DNA is formed by reverse transcription.

4 Viral DNA is transported across the nucleus and integrates into the host DNA.

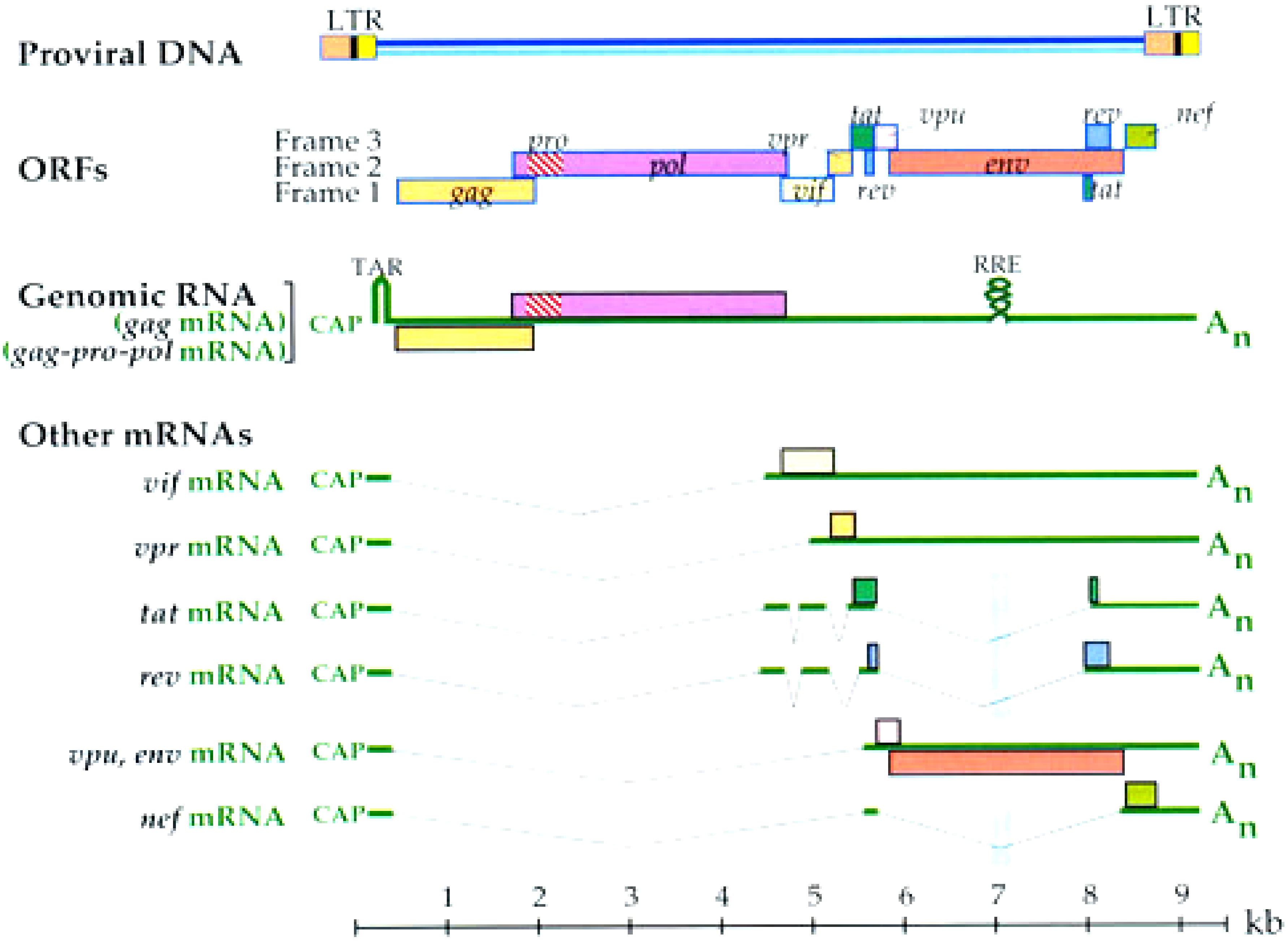
5 New viral RNA is used as genomic RNA and to make viral proteins.

6 New viral RNA and proteins move to the cell surface, and a new, immature HIV forms.

7 Virus is released. Viral protease cleaves new polyproteins to create mature infectious virus.

https://www.niaid.nih.gov/diseases-conditions/hiv-replication-cycle

- Genom HIV-a


LTR
LTR
Proviral DNA
ORFs
Frame 3
Frame 2
Frame 1
pro
pol
gag
vpr
vif
tat
vpu
rev
env
tat
rev
nef
TAR
RRE
Genomic RNA
(gag mRNA)
(gag-pro-pol mRNA)
CAP
A n
Other mRNAs
vif mRNA CAP
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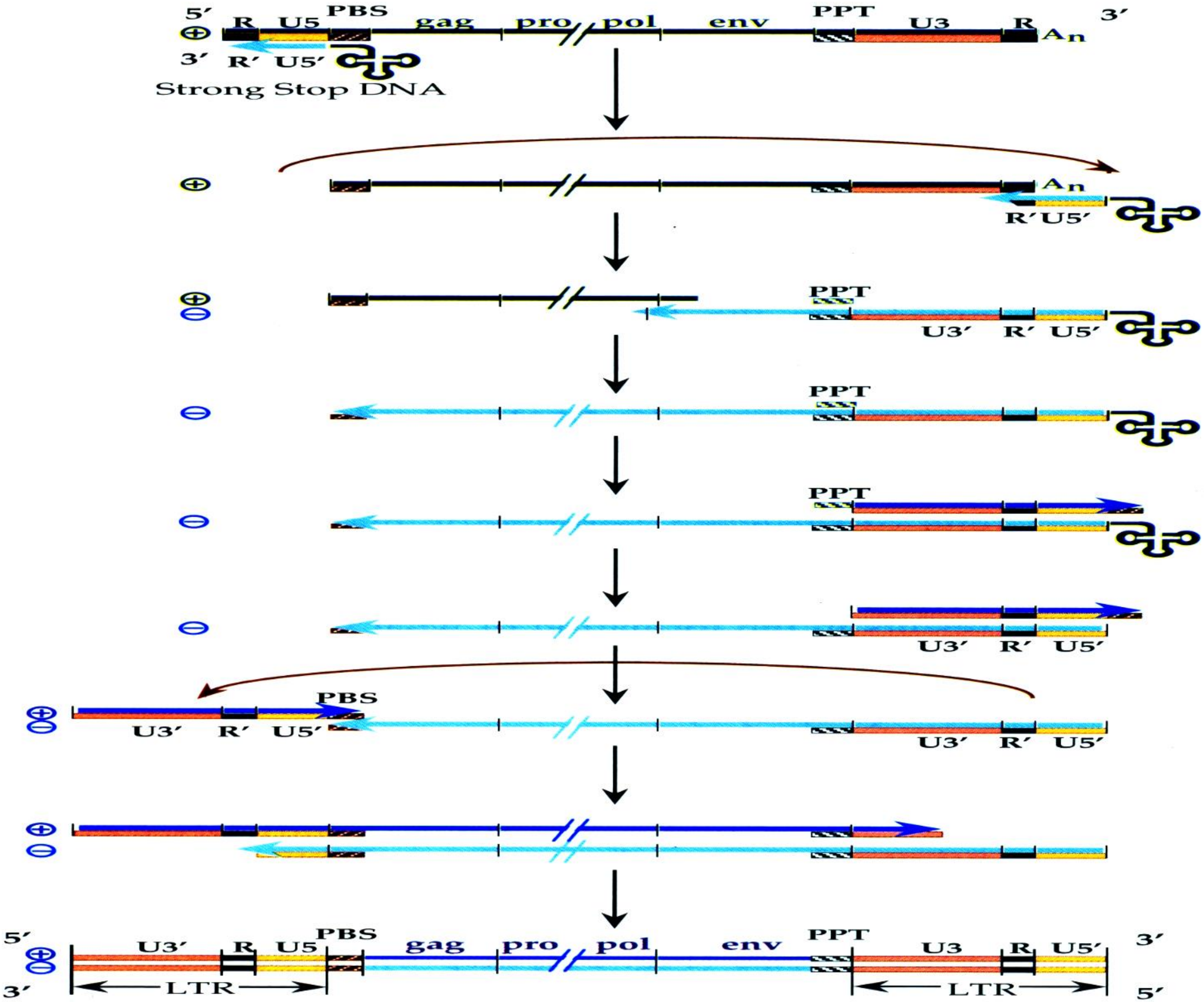
5′
⊕
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PBS
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PPT
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Strong Stop DNA
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R′U5′
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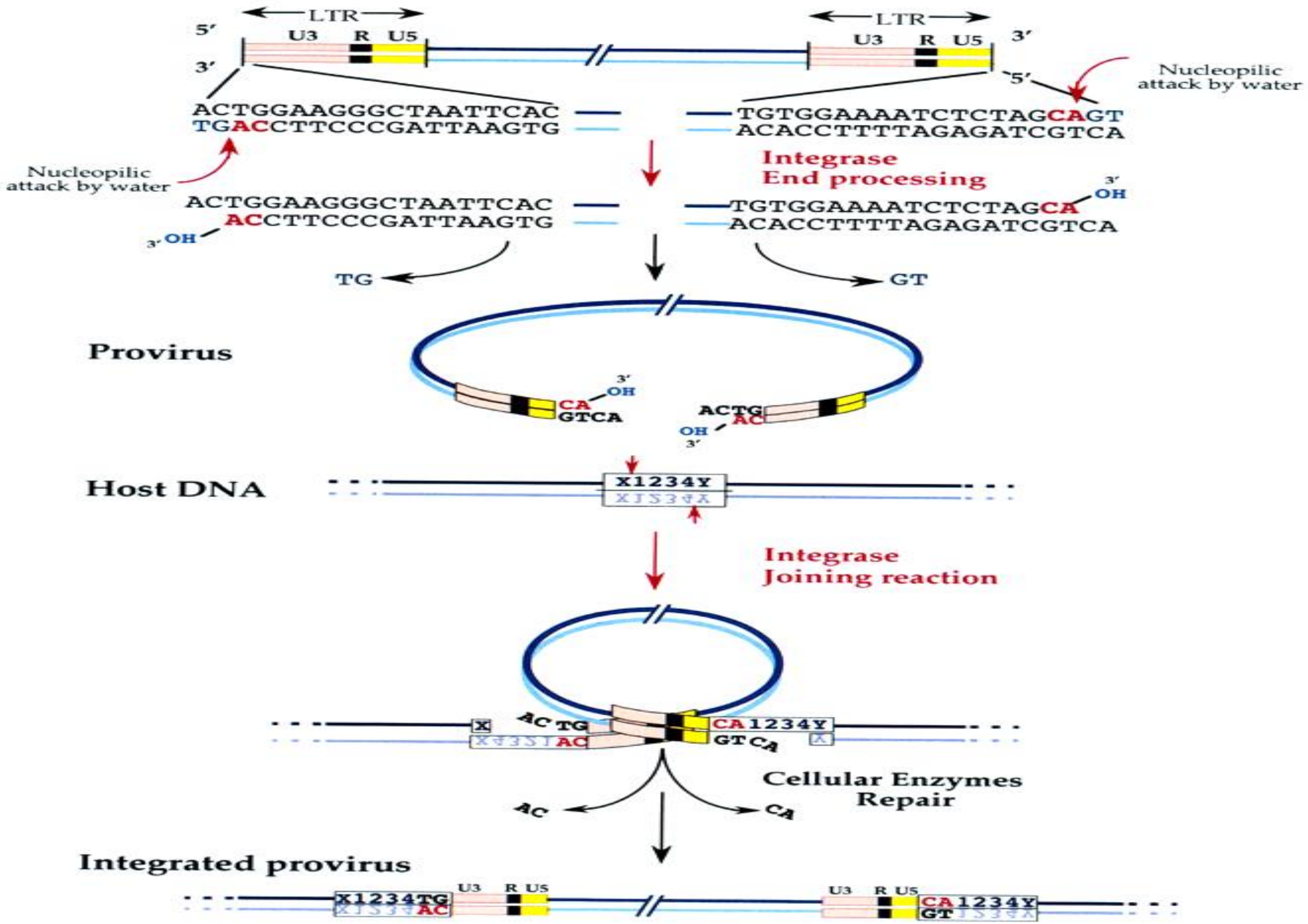
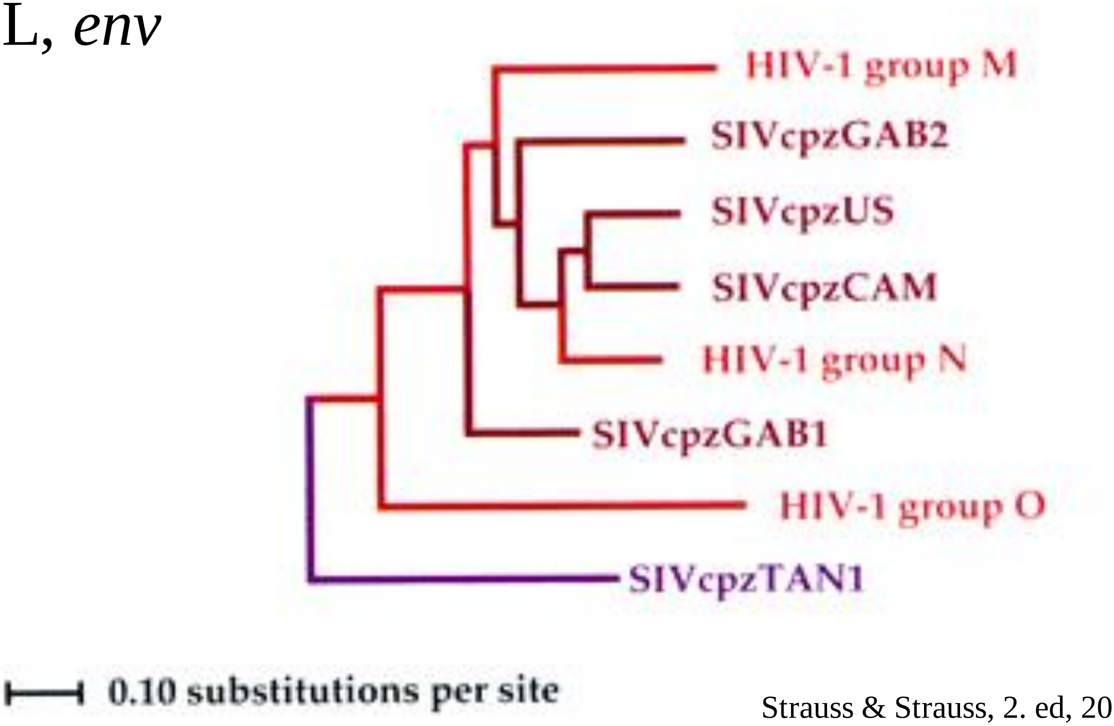
- Integracija HIV-a u genom domaćinske stanice



Porijeklo virusa HIV na temelju gena *pol*, *env*:

Centralna Afrika (Zair 1959.), ’70-tih u drugim Afričkim zemljama, ’80-tih – Haiti, a zatim USA i Europa.

ML, *env*



Strauss & Strauss, 2. ed, 2008

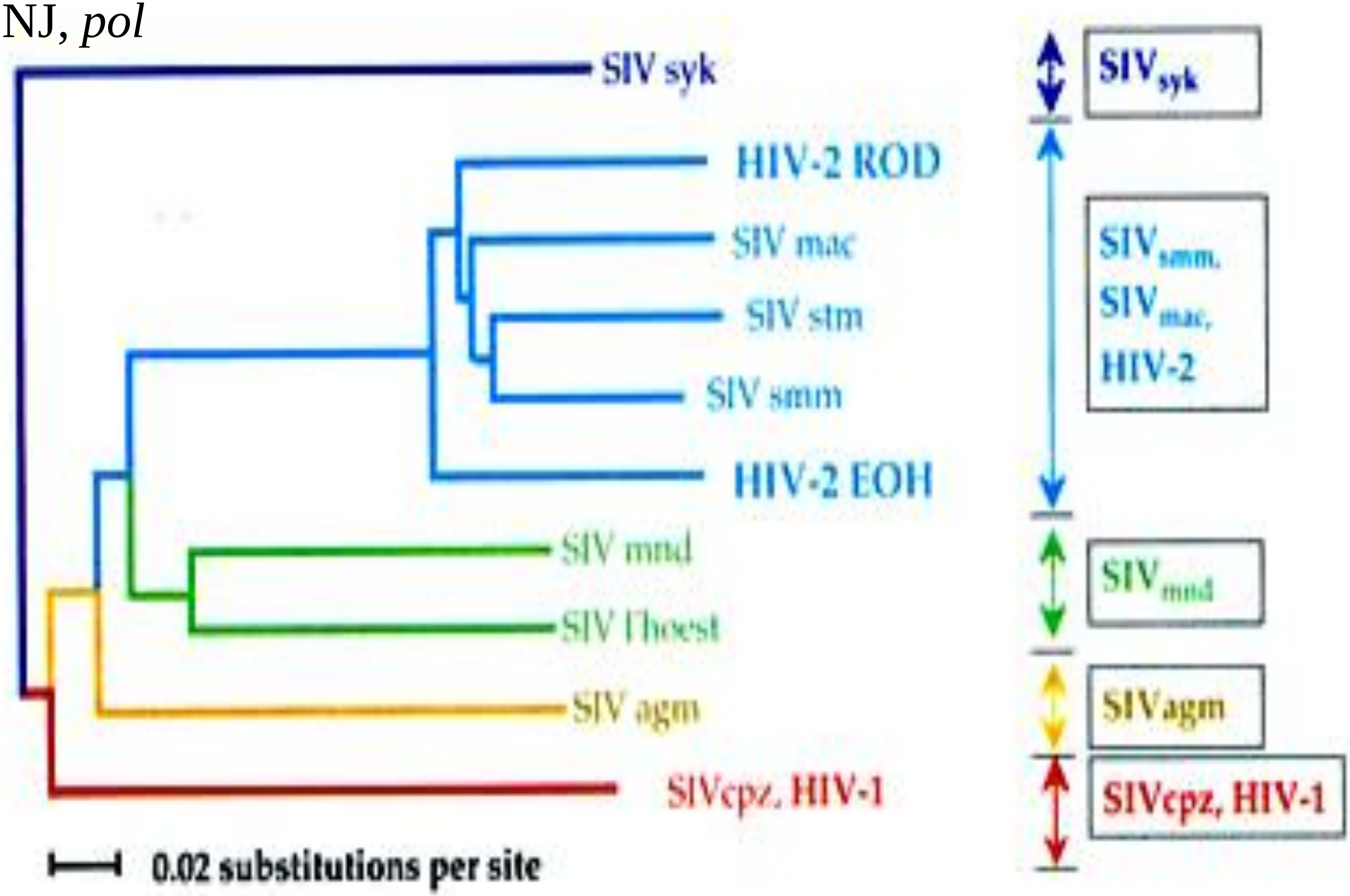
Majmunski T-limfotropni virus (STLV-3, SIV, HTLV-3):

HIV-1 iz čimpanze (SIVcpz, *Pan troglodytes*) kroz barem 3 “ulaza”,

HIV-2 iz mangabi majmuna (SIVsmm, *Cercocebus atys).*

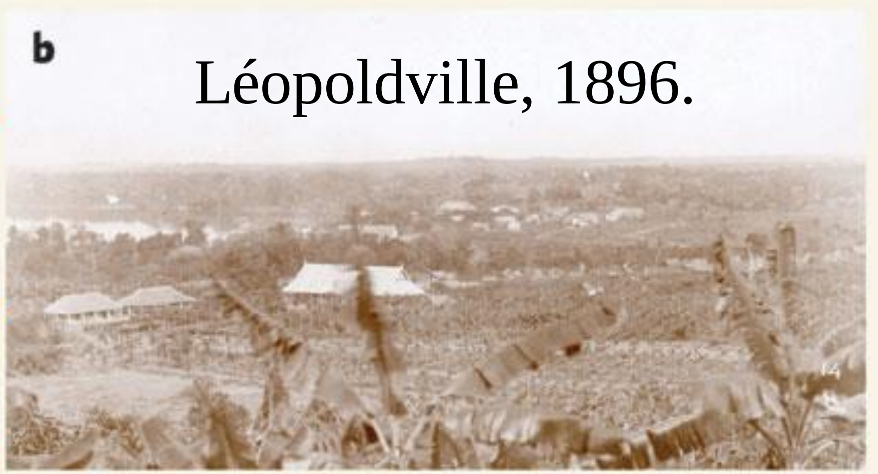
Strauss & Strauss, 2. ed, 2008

NJ, *pol*



Domovina HIV-1

SIV u čimpanzama najsličniji HIV-1, skupina M – kozmopolitska, odgovorna za većinu zaraza ljudi.



Léopoldville, 1896.

1955.

Sharp & Hahn, Nature 455: 605-6, 2008. Worobey *et al*., Nature 455: 661-4, 2008.

Majmunski retrovirusi i dalje prelaze na čovjeka (ukupno ih je barem 6) – studije na lovcima iz Kameruna.

HTLV-I (1978.), uzrokuje leukemiju odraslih T-stanica (ATL) i neurološki poremećaj (HAM - *HTLV-1 associated myelopathy*) virusi leukemija T-stanica ili limfotropni virusi, nova imena PTLV-…

PTLV-II – benigna varijanta leukemije (1982.), veza s leukemijom “dlakavih” stanica (zrele B-stanice)?

HTLV- 3 (HIV) 1982/3

PTLV-4 (1987.) nije patogen za čovjeka, postoji serološka srodnost

Zašto se pojavljuju novi virusi?

Ekološki faktori

-prirodne promjene (meteorološke-temperatura, oborine, vlažnost, klimatske promjene, promjene staništa, dostupnosti hrane za rezervoarne domaćine i/ili vektore, migracije životinja)

- uzrokovane (efekt rubova kod deforestacije, reforestacije, promjene u poljoprivrednoj praksi i uzgoju hrane),

Demografski faktori

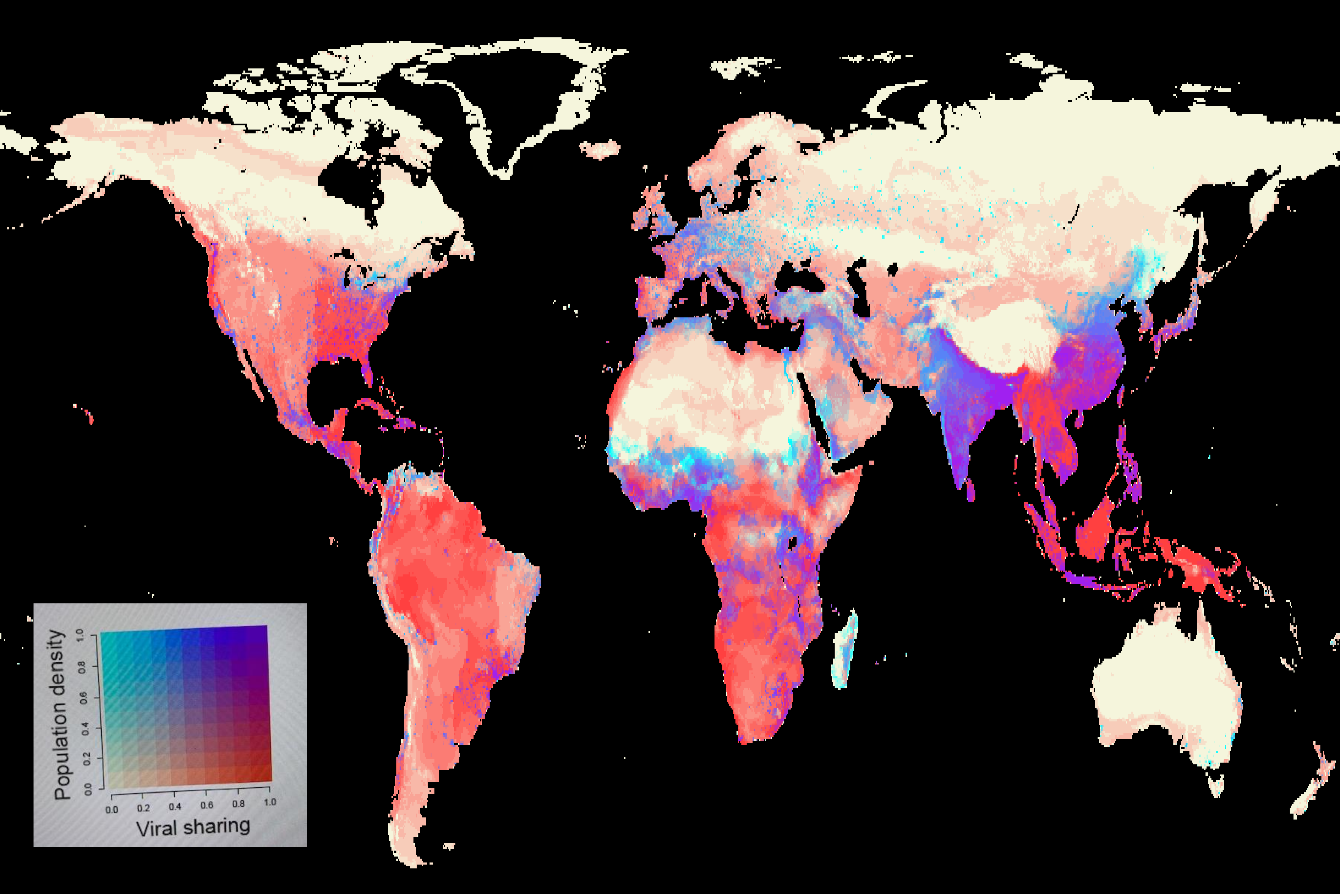
- rast populacije i zadiranje u prirodni okoliš, nekontrolirana urbanizacija, deforestacija i reforestacija, zagađenje, klimatske promjene, transport ljudi i roba, prijevoz životinja (divljih, domaćih),

rekreacijske aktivnosti (planinarenje, kampiranje, lov, itd.), promjene seksualnih, prehrambenih navika.

Biramo li ekonomske strategije i politike razvoja tako da ostanemo zdravi?!

Carlson et al. 2022, Climate change increases cross-species viral transmission risk. Nature (April 28, published online) https://doi.org/10.1038/s41586-022-04788-w

At least 10,000 virus species have the capacity to infect humans, but at present, the vast majority are circulating silently in wild mammals. However, climate and land use change will produce novel opportunities for viral sharing among previously geographically-isolated species of wildlife. In some cases, this will facilitate zoonotic spillover—a mechanistic link between global environmental change and disease emergence. Here, we simulate potential hotspots of future viral sharing, using a phylogeographic model of the mammal-virus network, and projections of geographic range shifts for 3,139 mammal species under climate change and land use scenarios for the year 2070. We predict that species will aggregate in new combinations at high elevations, in biodiversity hotspots, and in areas of high human population density in Asia and Africa, driving the novel cross-species transmission of their viruses an estimated 4,000 times. Because of their unique dispersal capacity, bats account for the majority of novel viral sharing, and are likely to share viruses along evolutionary pathways that will facilitate future emergence in humans. Surprisingly, we find that this ecological transition may already be underway, and holding warming under 2°C within the century will not reduce future viral sharing. Our findings highlight an urgent need to pair viral surveillance and discovery efforts with biodiversity surveys tracking species' range shifts, especially in tropical regions that harbor the most zoonoses and are experiencing rapid warming.



Carlson et al. 2022, Climate change increases cross-species viral transmission risk. Nature
https://doi.org/10.1038/s41586-022-04788-w