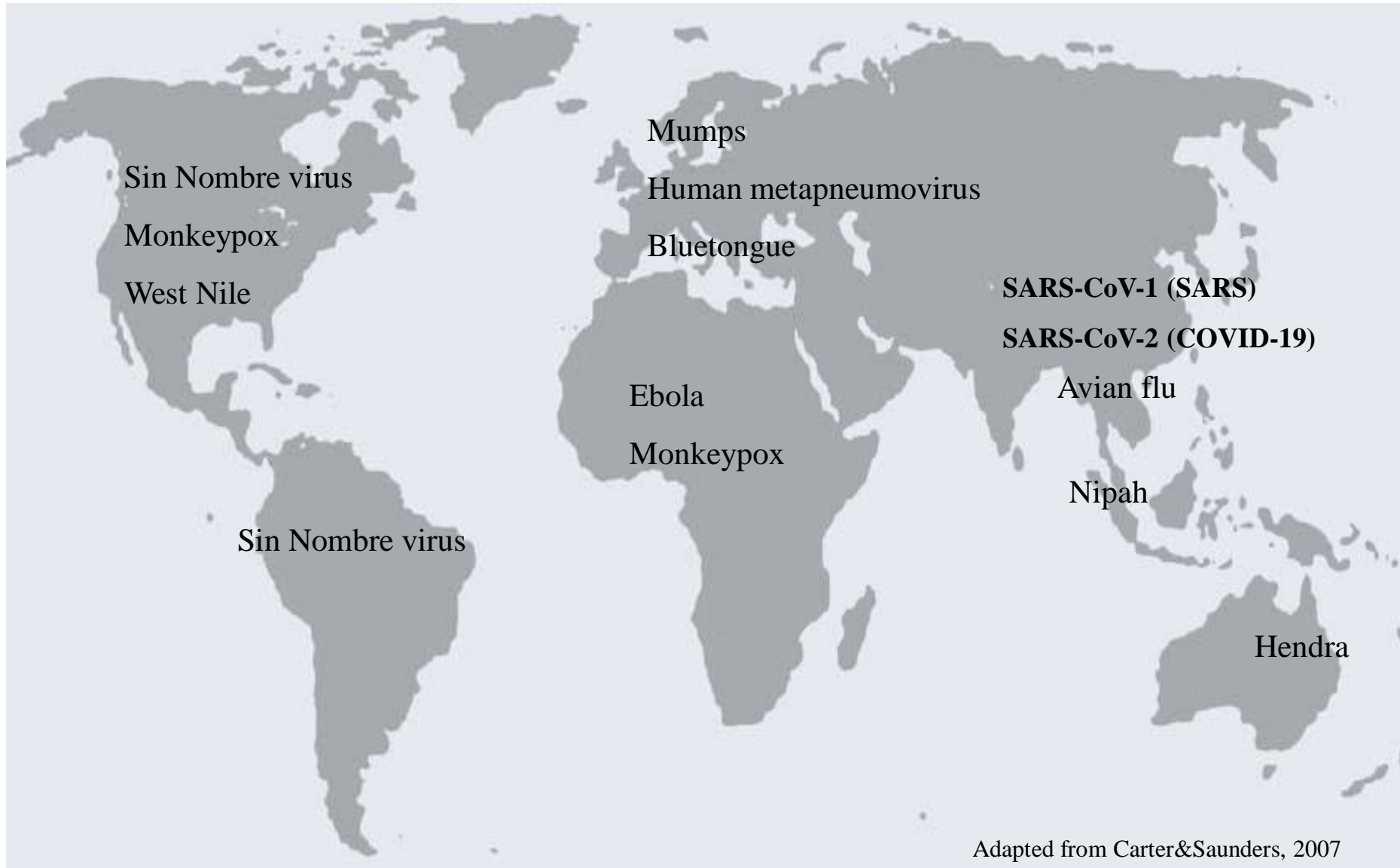


Emerging viruses



Emerging viruses comprise:

-Re-emerging of known viruses

mumps, foot and mouth disease virus

-Discovering new viruses in humans –probably present for a long time but recently noticed

HHV- 8, human metapneumovirus

-Virus emergence in a new area

West Nile (WNV) in Uganda 1937, *Flaviviridae*, emerging 1999 in NY

Bluetongue (BTV), *Reoviridae*, in 2004 found 800 km to further north than ever (HR included) and in 2007 even in Suffolk , biting midge vector (*Culicoides*) more widespread due to the global warming.



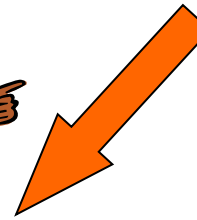
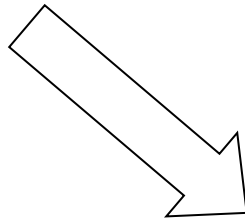
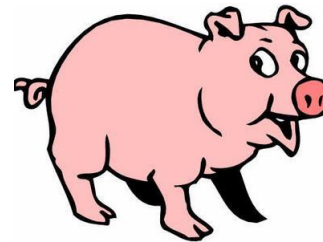
-Viruses emerging in a new hosts

Sin Nombre (1993, new hantavirus – pulmonary syndrome, *Bunyaviridae*)

Paramyxoviridae

Hendravirus (from horses in 1994, Brisbane, SE-Australia)

Nipahvirus (from pigs in 1997, Malaysia)



respiratory infection,
encephalitis



-Viruses in new hosts and in new areas

filoviruses

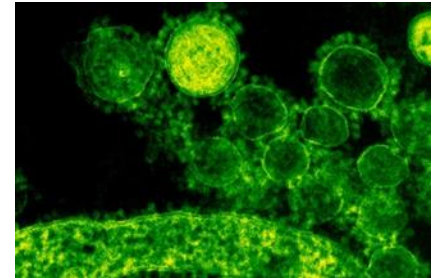
monkeypox (*Poxviridae*)

-New viruses

SARS - new coronavirus in 2002/3, SARS-CoV-1 now,

SARS-CoV-2 caused COVID-19 pandemic,

new strains of influenzavirus A



“New” viruses can be grouped according to their reservoir hosts in nature.

Originally, many human viruses are zoonotic, some are still emerging as such.

Natural sources of viruses:

Bats – rhabdoviruses, henipaviruses, coronaviruses, filoviruses

Birds – WNV, influenza (AH5N1, AH7N7, AH9N2)

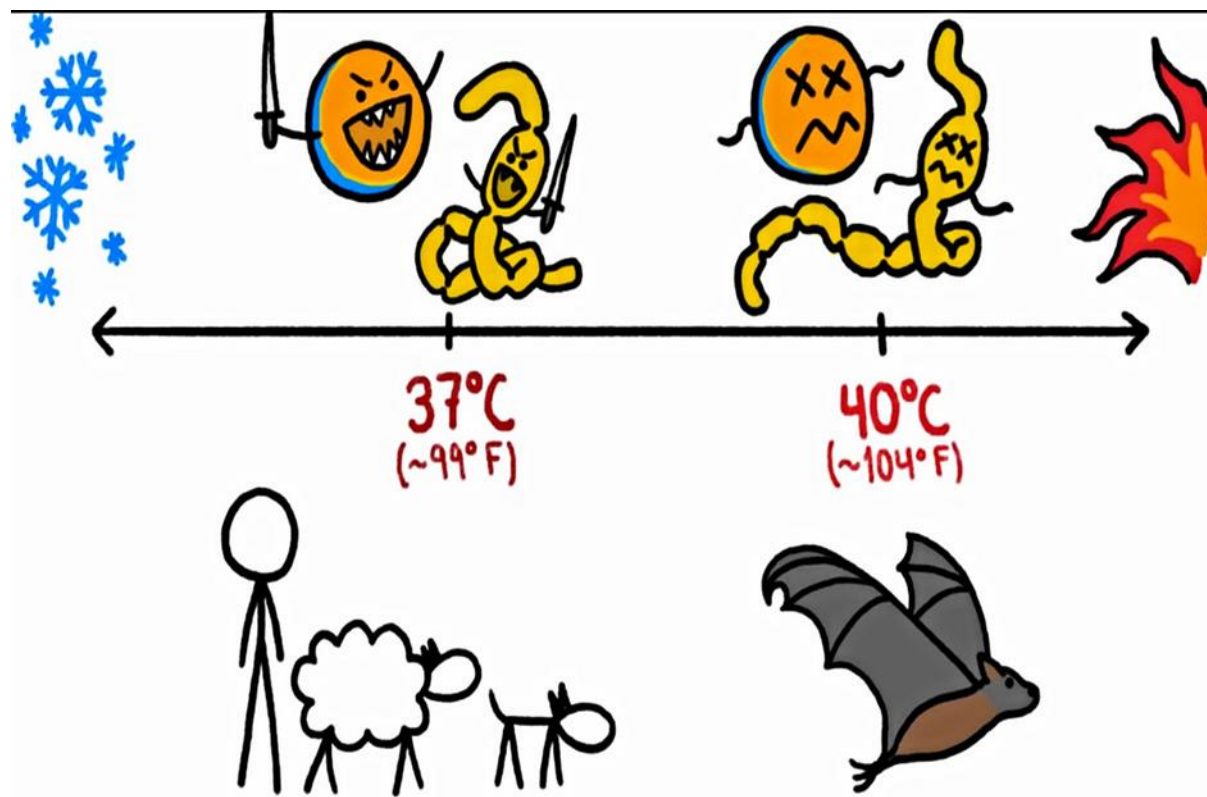
Rodents – hantaviruses

Primates - Dengue,

HIV-1, HIV-2 (repetitive introductions 50-100 years ago)

<https://youtu.be/Ao0dqJvH4a0>

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

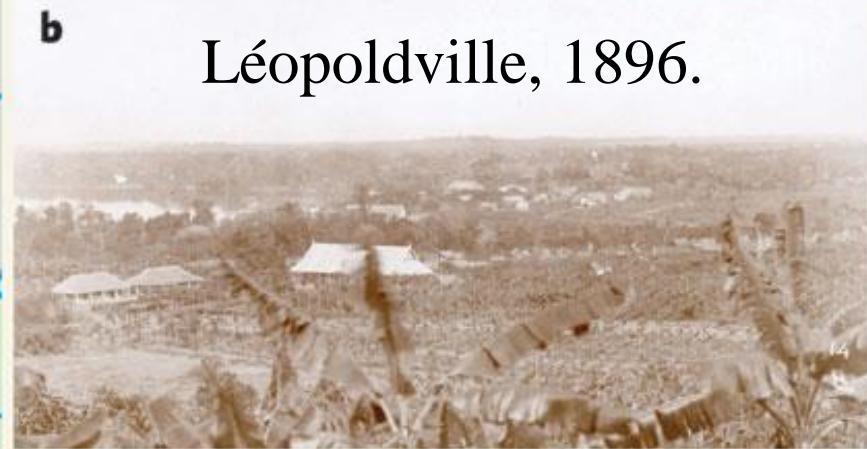
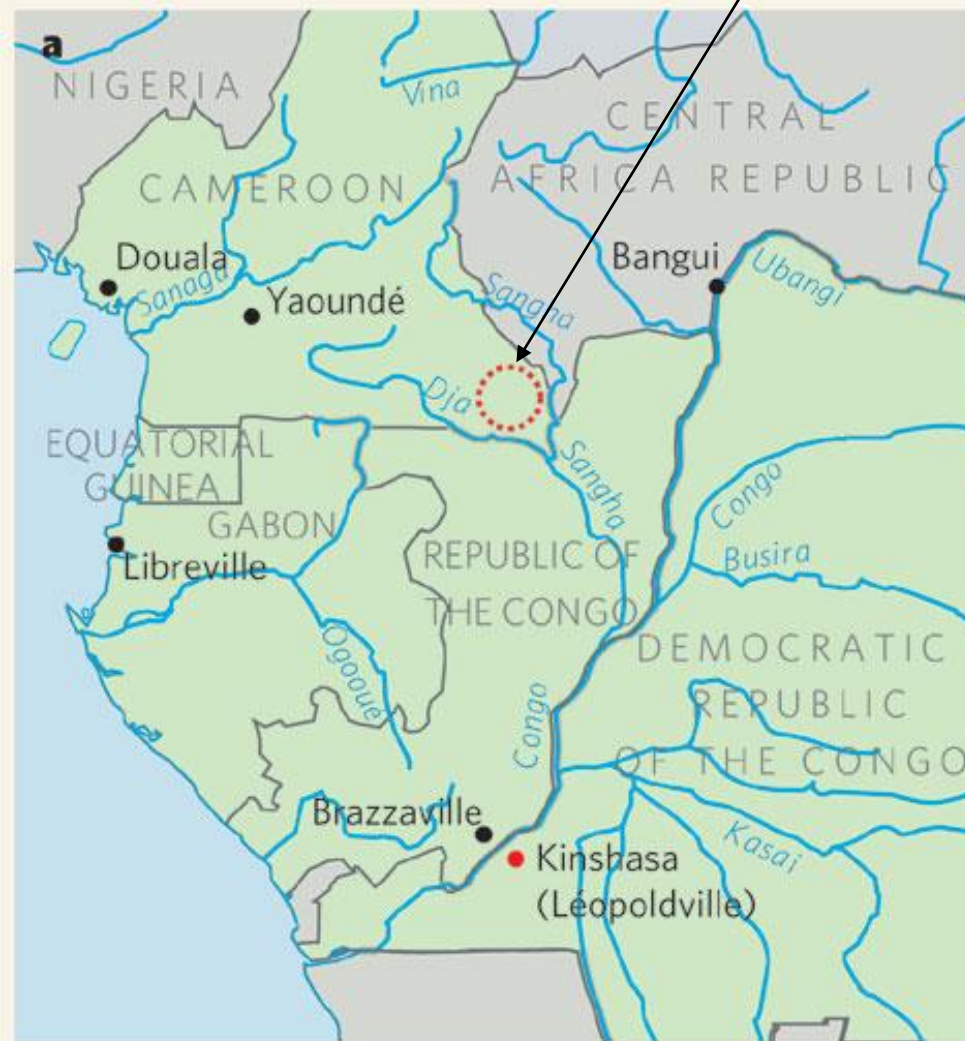


Why are bats so important virus reservoirs?

Social, flying, globally distributed animals (all ecological niches), huge biodiversity and abundance, specific physiology (temperature and metabolic rate high during flight) selects robust viruses (and other pathogens) that can defeat immune system and spill-over to other mammals.

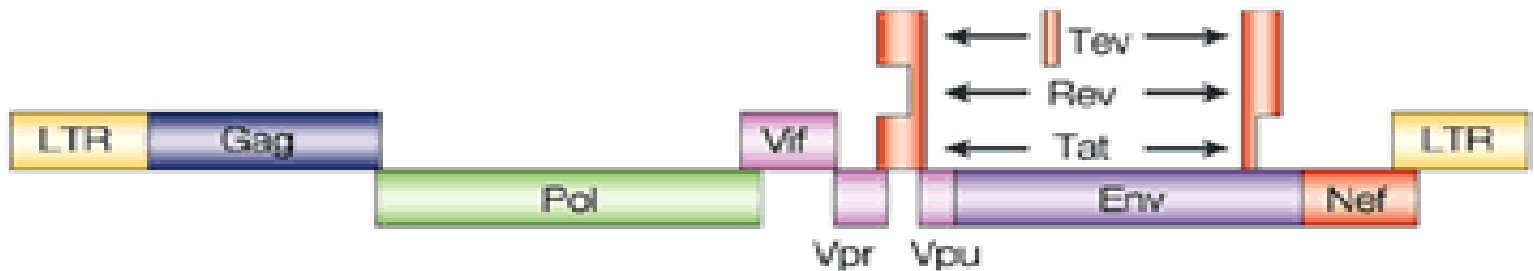
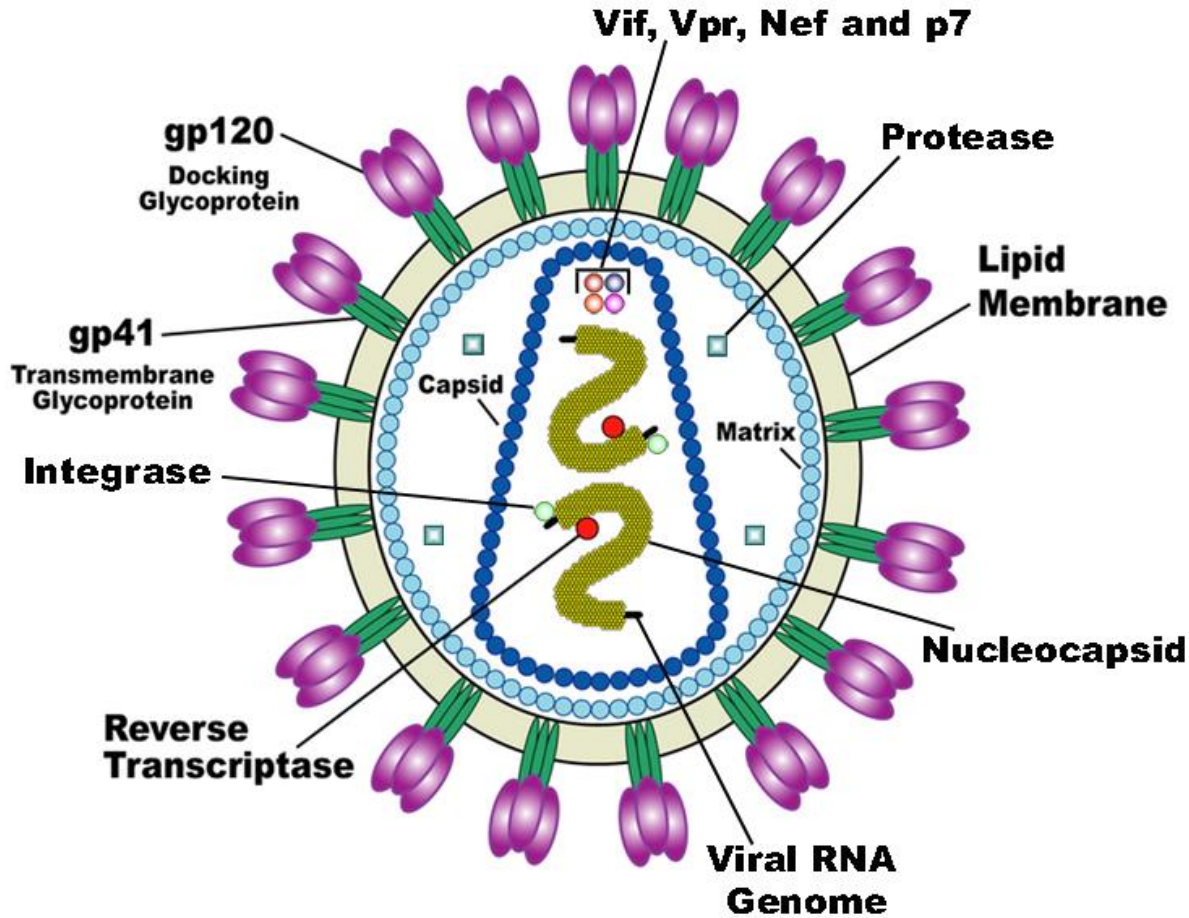
HIV-1 homeland

SIV from chimpanzees the most related to the HIV-1, group M – cosmopolite, the cause of most human infections.

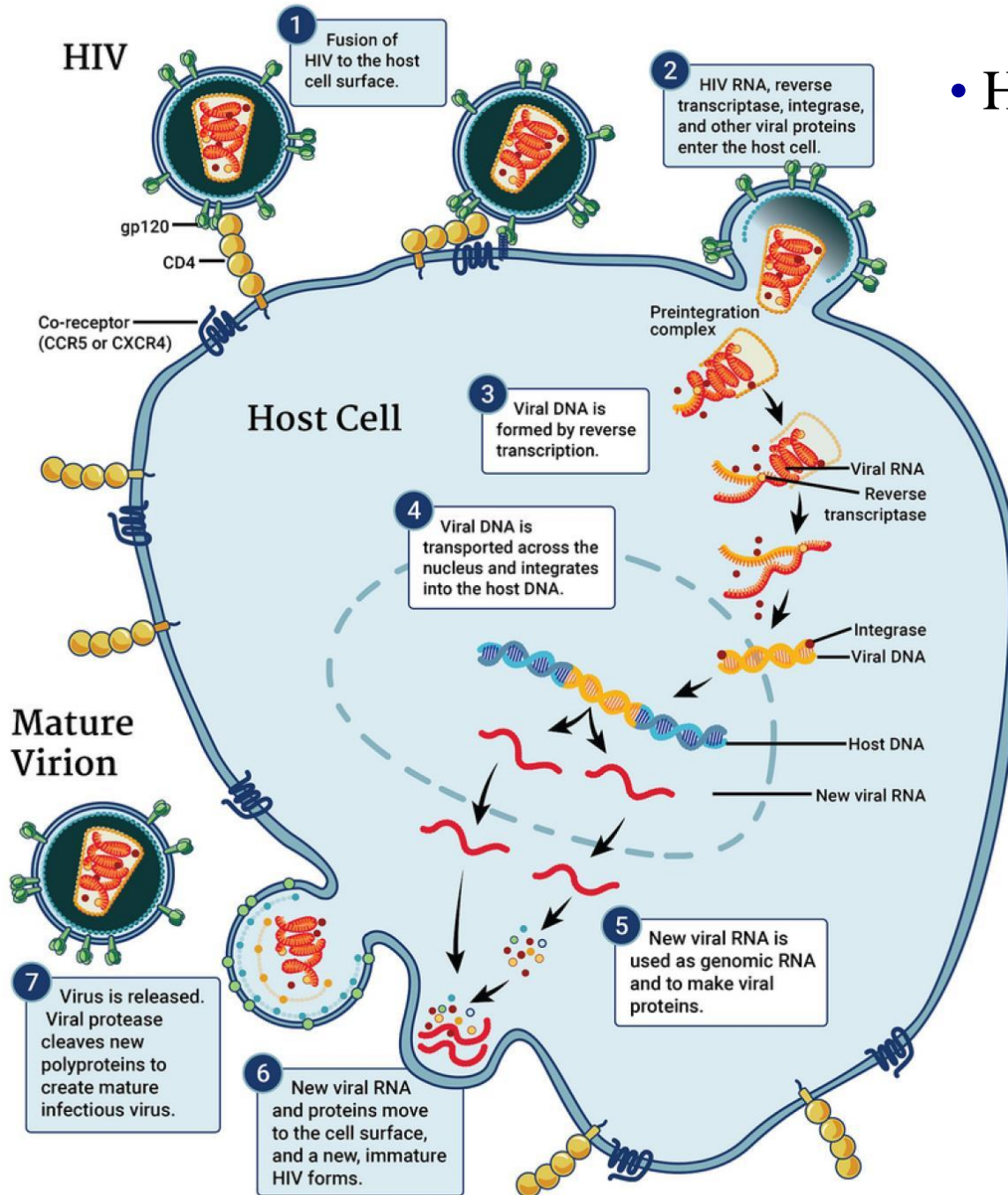


Sharp & Hahn, Nature 455: 605-6, 2008. Worobey *et al.*, Nature 455: 661-4, 2008.

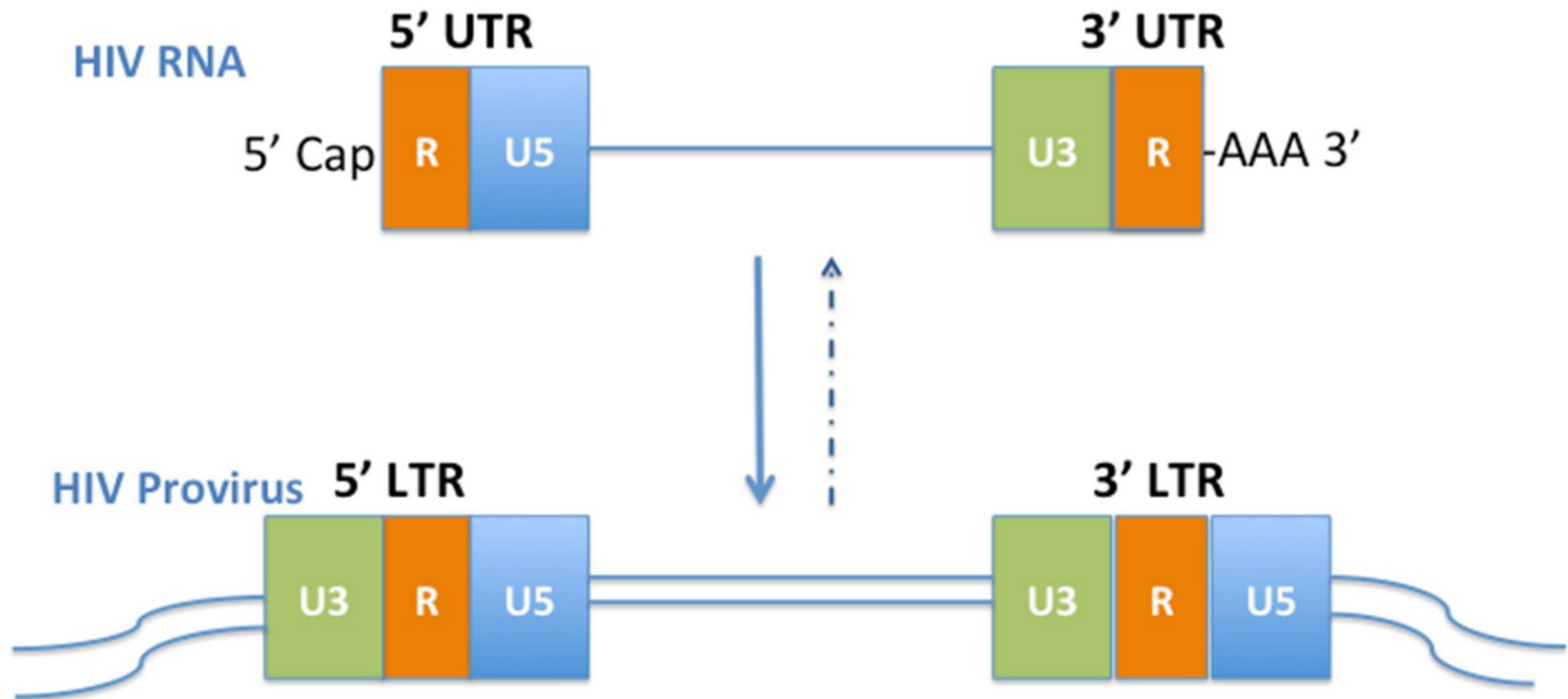
- HIV virion



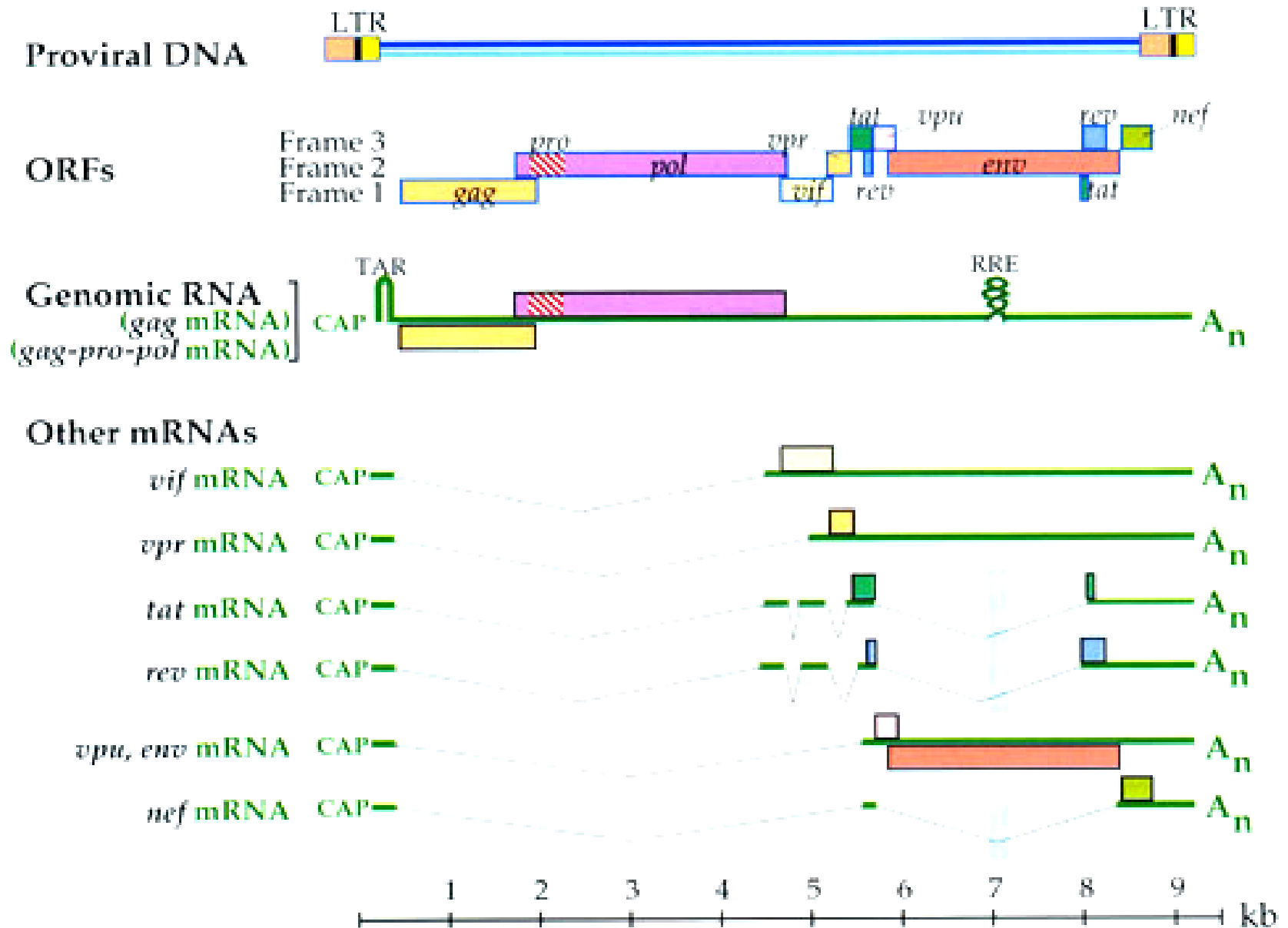
- HIV replication cycle



- HIV RNA genome and proviral DNA form



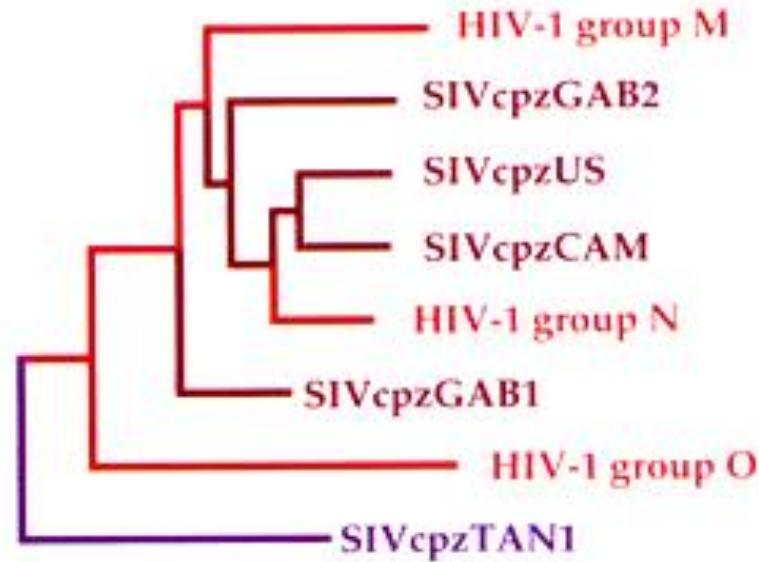
- HIV genome expression (Strauss&Strauss, 2002)



HIV evolutionary origin on the bases of *pol*, *env* genes:

Central Africa (Zaire 1959), 1970s in other African countries, 1980s – Haiti, and then in USA & Europe.

ML, *env*



— 0.10 substitutions per site

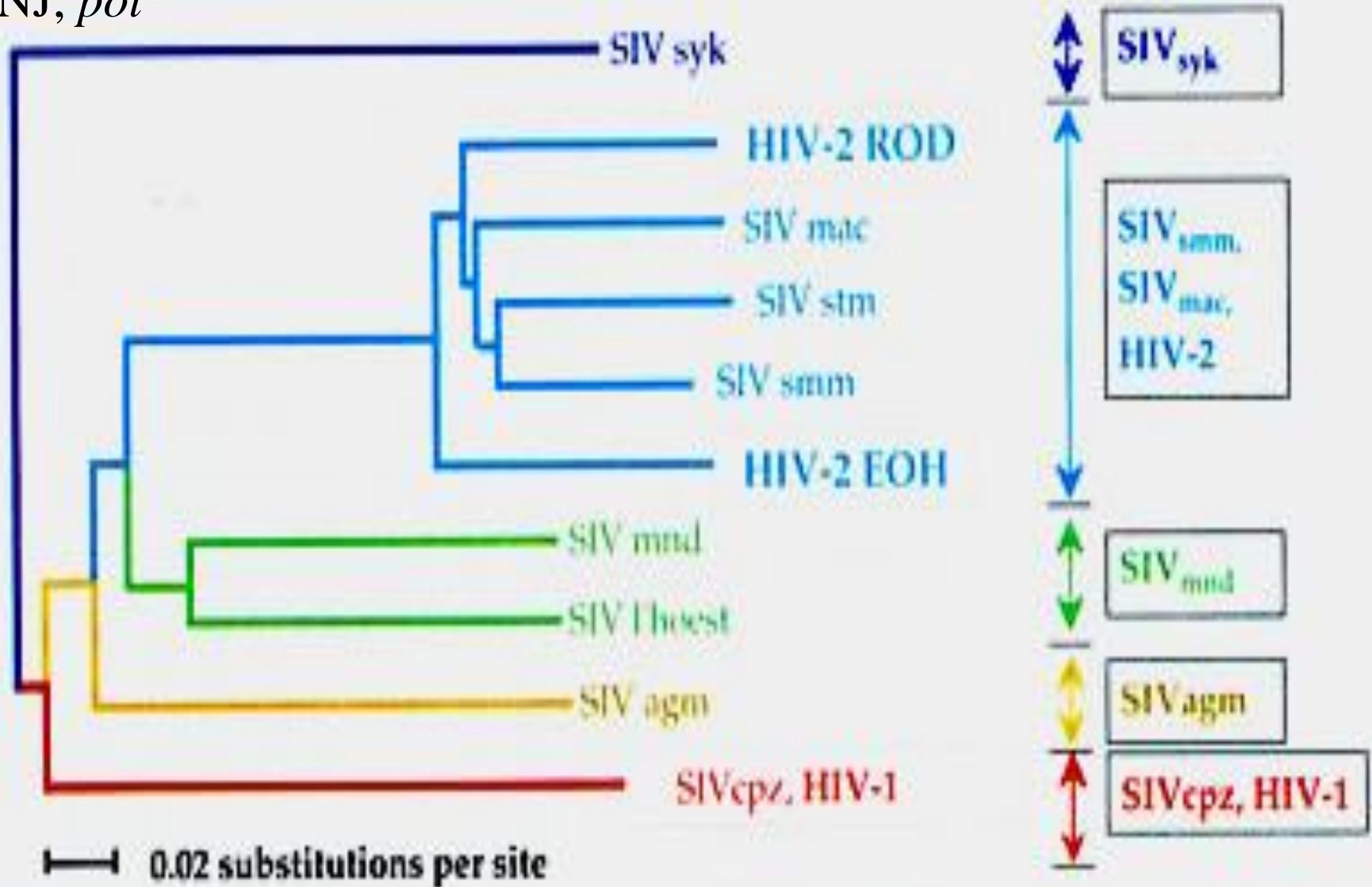
Strauss & Strauss, 2. ed, 2008

Monkey T-lymphotropic viruses (STLV-3, SIV, HTLV-3):

HIV-1 from chimpanzee (SIVcpz, *Pan troglodytes*) through at least 3 “introductions”,

HIV-2 from sooty mangabeys (SIVsmm, *Cercocebus atys*).

NJ, *pol*



Monkey retroviruses continue to jump to humans.

At least 6 crossed the species barrier already – studies on bush meat hunters and handlers from Cameroon.

T-cell leukemia or lymphotropic viruses, new names
primate...PTLV

PTLV-1 (1978.), adult T-cell leukemia and neurological disorder
(HAM - *HTLV-1 associated myelopathy*),

PTLV-2– benign leukemia variant (1982.), link with “hairy”-cell
leukemia (mature B-cells)?

Why new viruses emerge?

Ecological changes

- of natural (meteorological changes-temperature, rainfall, humidity, climate changes, habitat changes, food availability for reservoir and/or vector animals, animals migrations)
- or human origin (deforestation edge effect, reforestation, agricultural practice and food production changes),

Demographic changes

human population expansion and encroachment, uncontrolled urbanization, deforestation, reforestation, pollution, climatic changes, travel of humans, transportation of goods, travel of animals aided by humans (wild, domestic), recreational activities (hiking, camping, hunting, etc...), sexual habits, eating habits.

The power to choose is often in our hands!