

# Current concepts in virus evolution and the problem of emerging viruses

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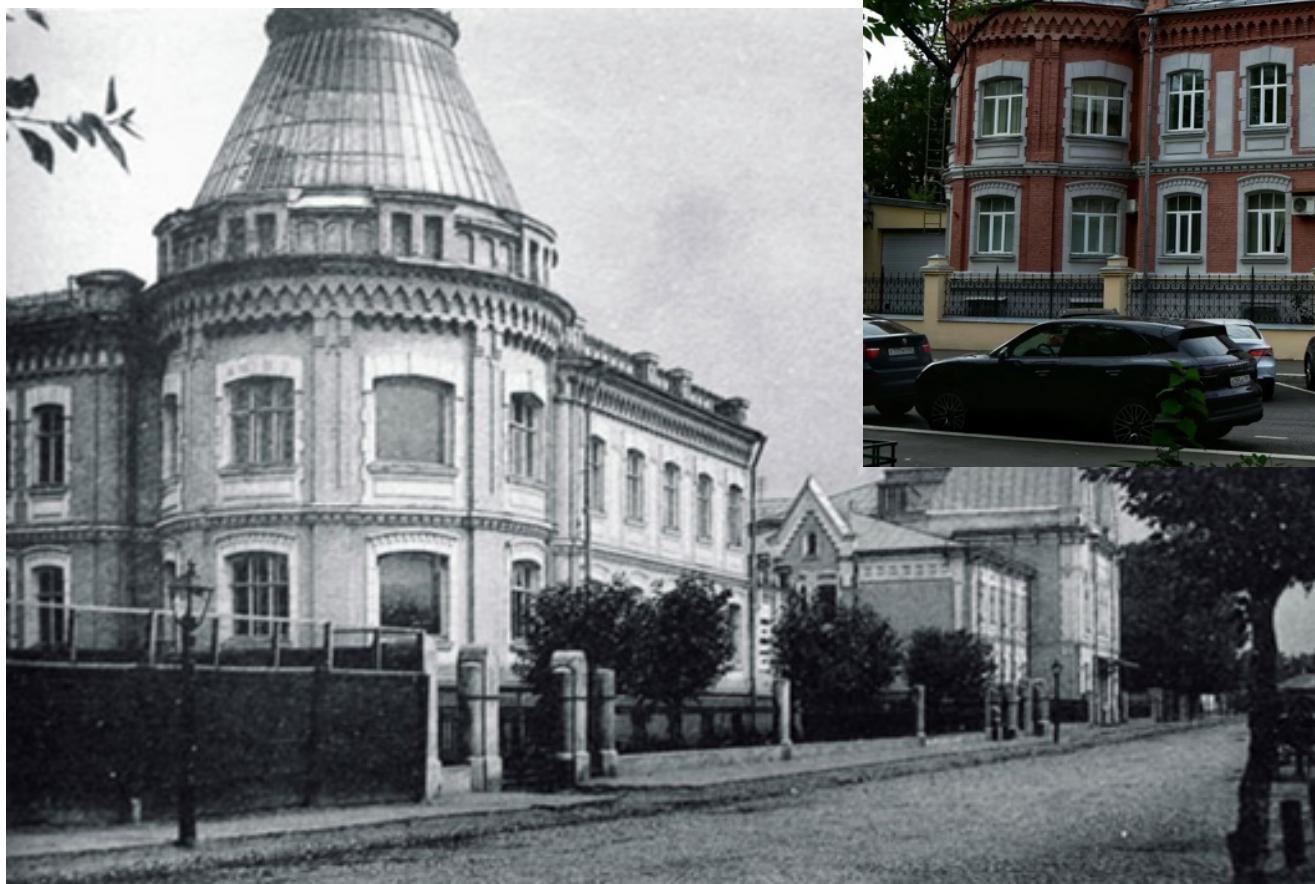
Institute for Medical Parasitology, Tropical  
and Vector-Borne Diseases,

Sechenov University

Moscow, Russia

# Martsinovsky institute of parasitology and tropical diseases

Founded 1920  
Since 2002 within  
Sechenov medical university



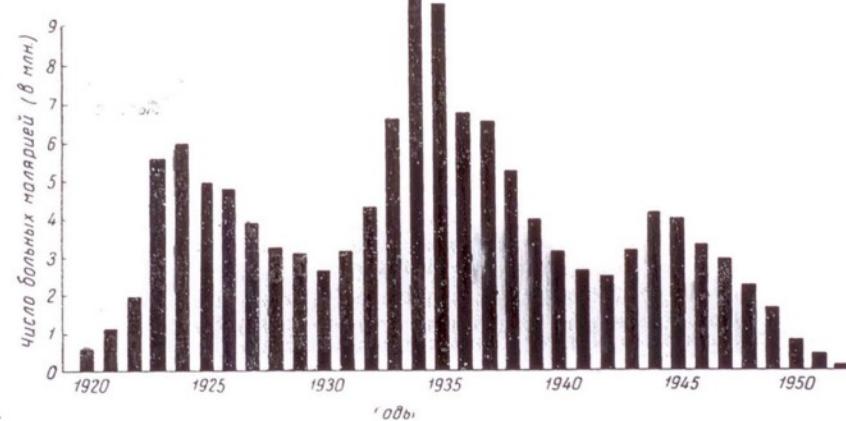
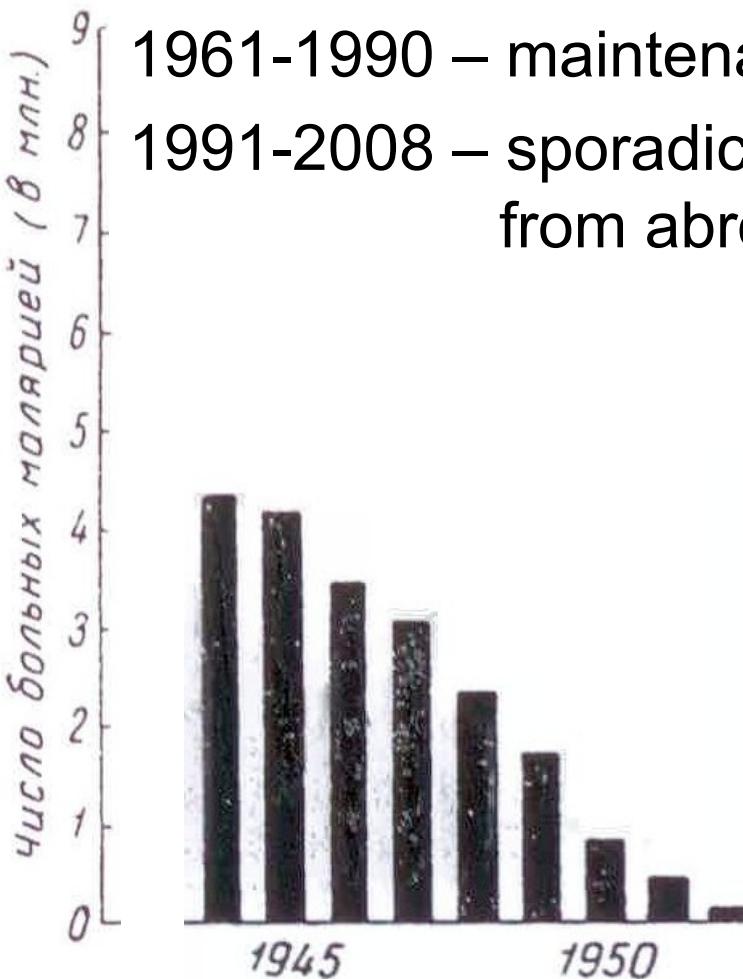
# Malaria eradication in USSR

— 1953 – incidence reached < 1/000

1954-1960 – practical eradication of malaria country-wide

1961-1990 – maintenance of results achieved

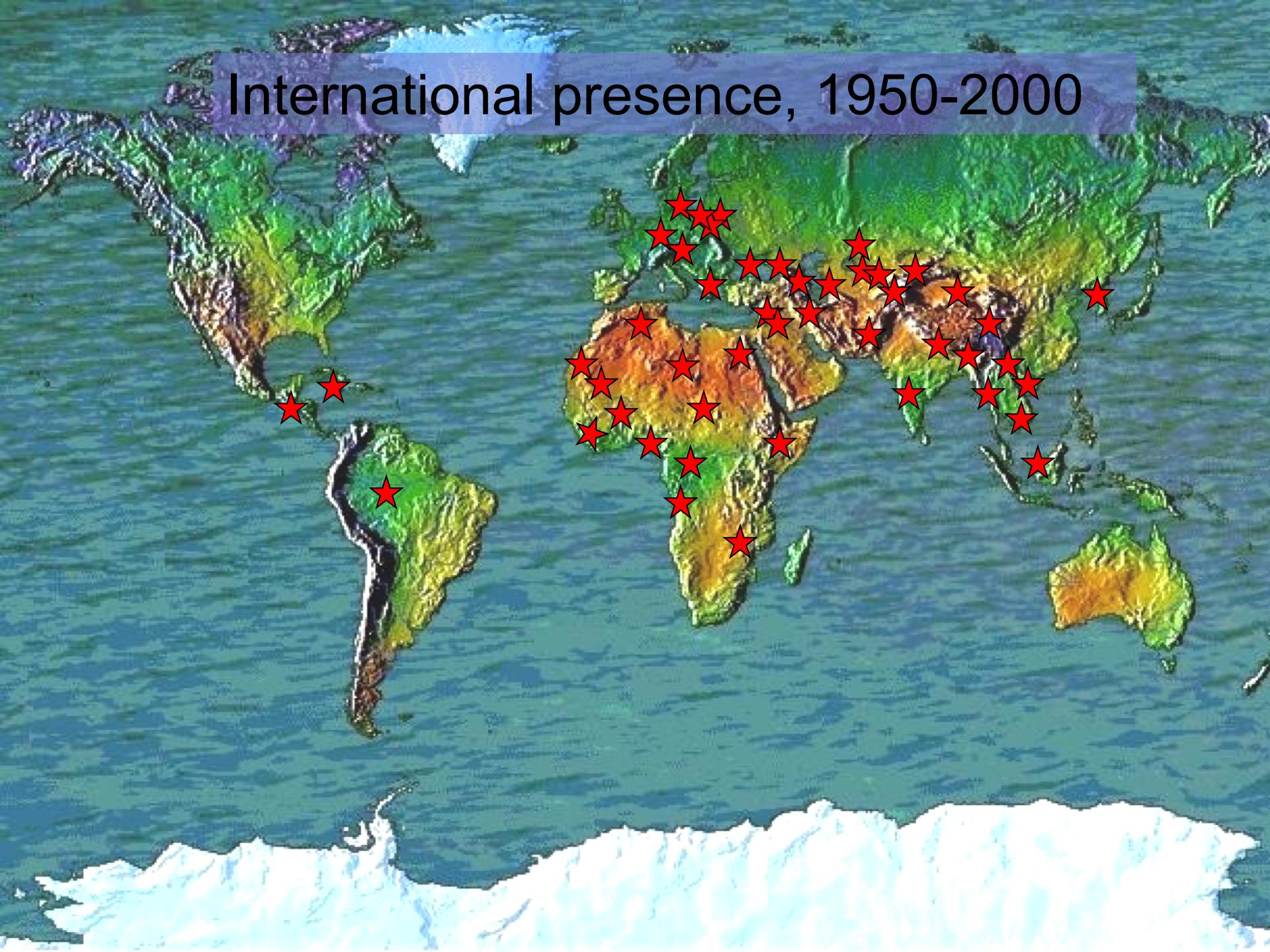
1991-2008 – sporadic introduced cases, importation cases from abroad



# RUSSIA-WHO COURSES



# International presence, 1950-2000



# Current concepts in virus evolution and the problem of emerging viruses

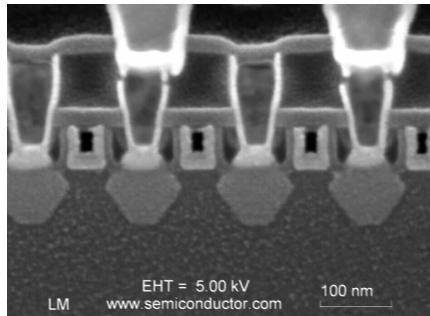
# Hepatitis B virus genome

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4 genes, ~ 100 million infected

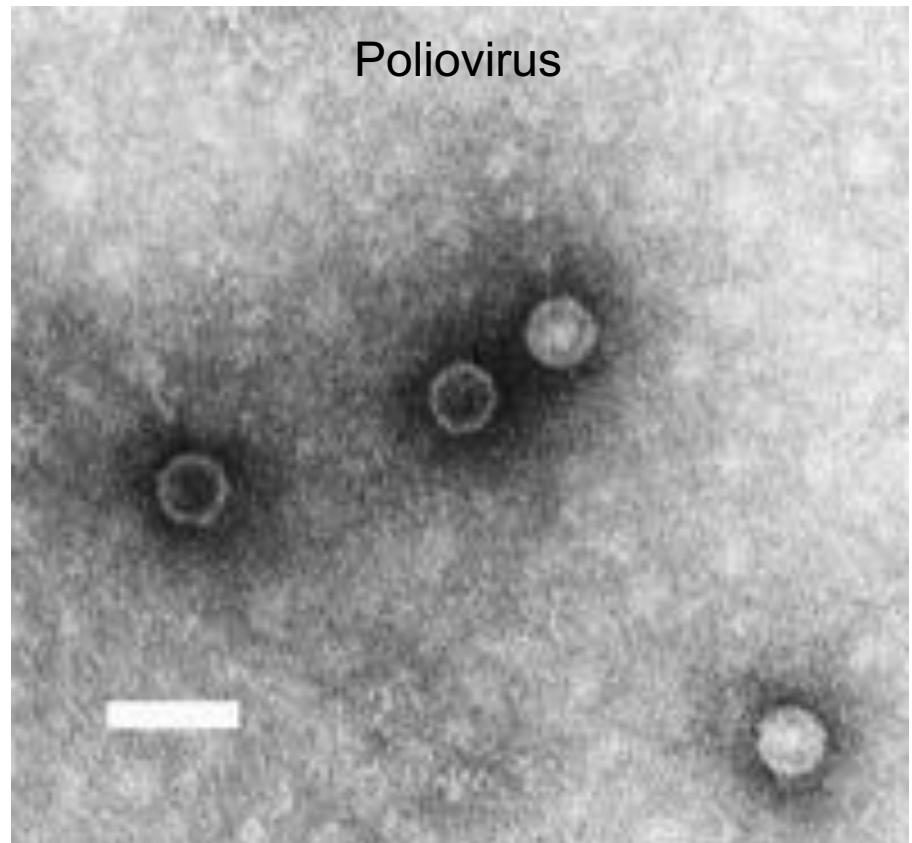
# More efficient than anything created by humans

Microprocessor element



1 bit of information

Poliovirus



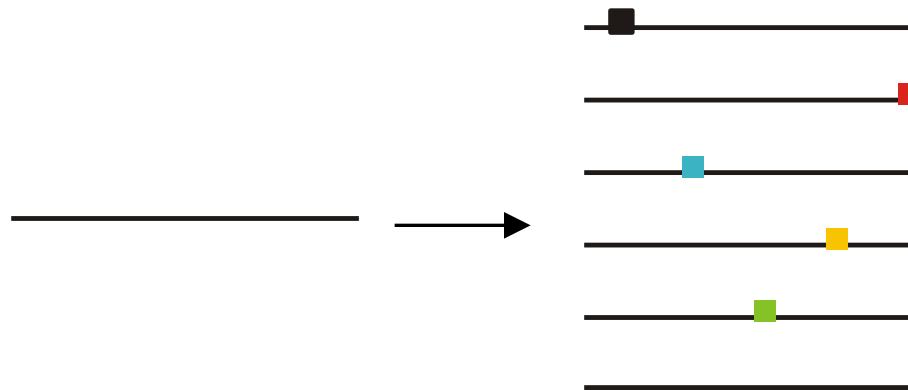
15 000 bit + protection in the  
environment, penetration and hijacking  
of cellular defenses

# Virus replication systems

- In most viruses do not have error correction function
- in RNA viruses ~ one new mutation per genome
- Replication cycle takes 8 – 72 hours, one virus makes 1000 – 100 000 new ones

# Quasiapartes

On average, each new genome has a new substitution

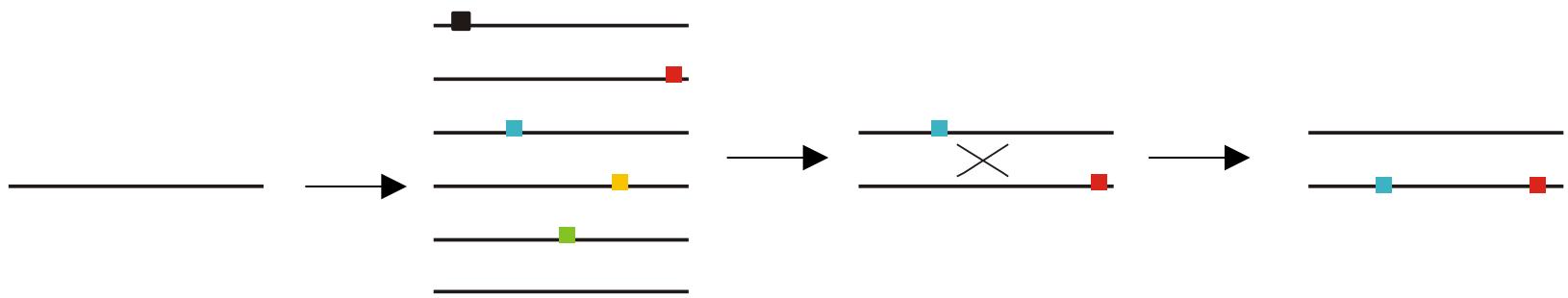


Most mutants are crippled, but few optimal provide virus survival and adaptation.

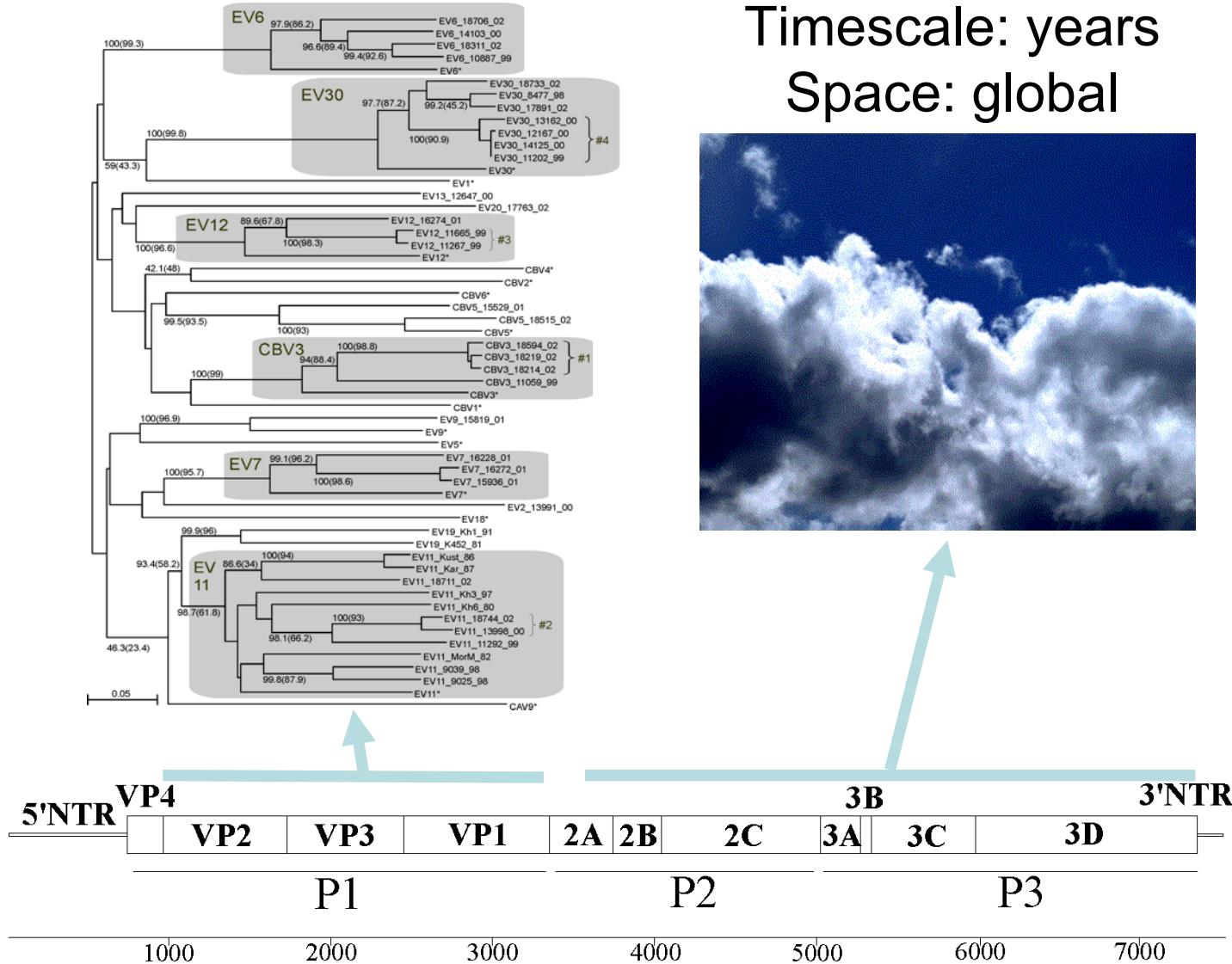
Examples:

- HIV and receptor switch. No mutation=no AIDS
- neurovirulence of poliovirus.  
No mutation=no neurological lesions

# Recombination further enhances variability of virus genomes

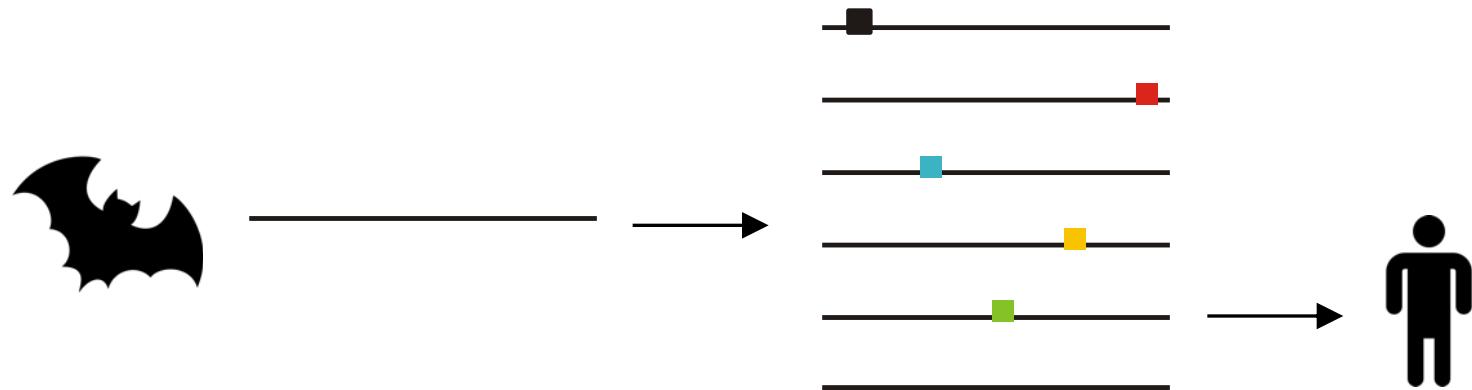


# Virus genomes: the whole, but so divided



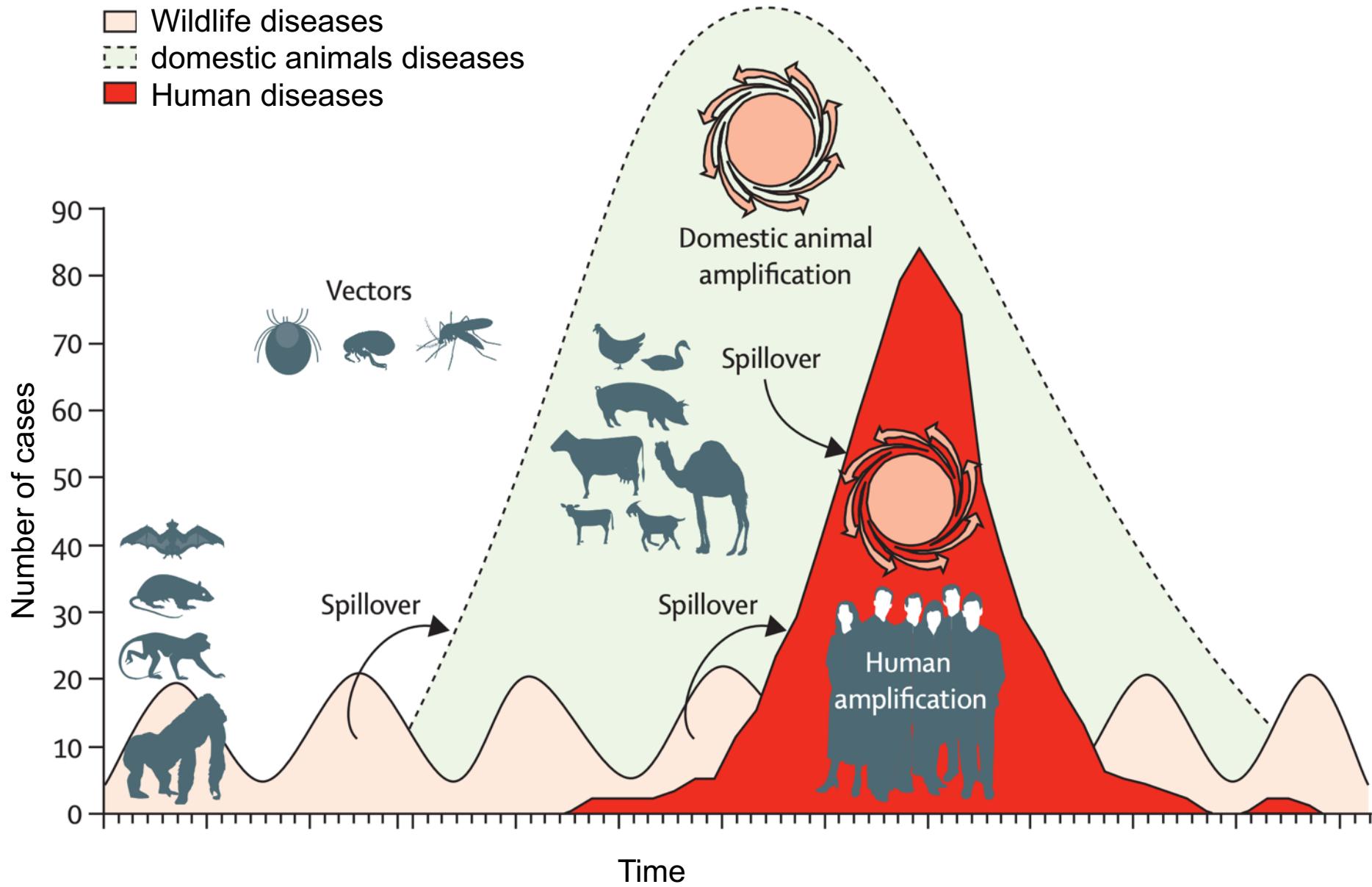
# Quasiappecies

Adaptation reserve

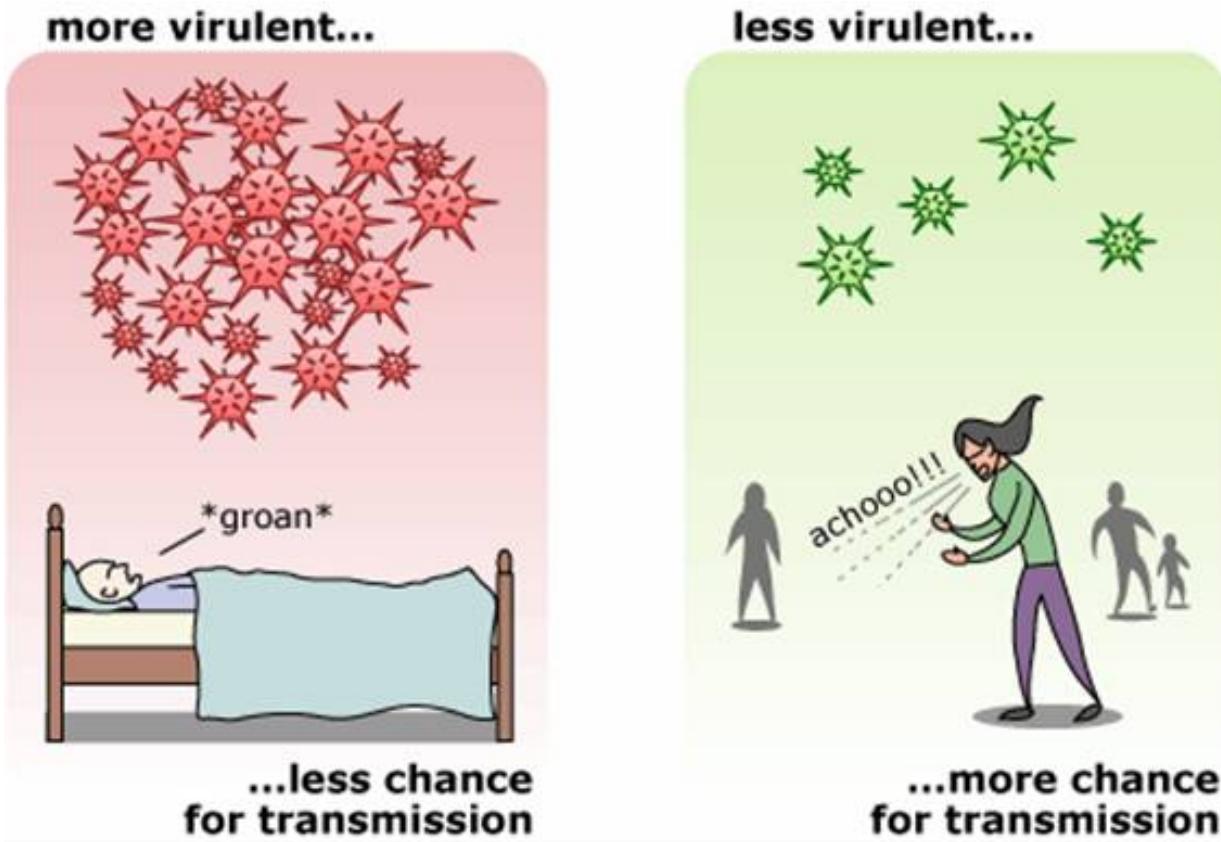


# Emerging virus infections

- Wildlife diseases
- domestic animals diseases
- Human diseases



# Virulence ≠ fitness



«Bird flu»: severe infection of lower respiratory tract.  
Lethal pneumonia = low infectivity

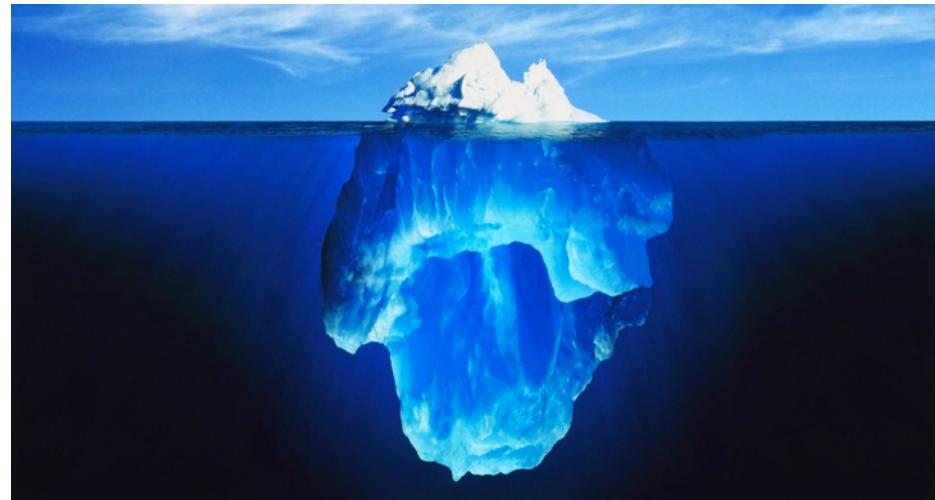
# Some of the well-known emerging infections

- 1895 – Paralytic polio
- 1918 – Spanish flu\*
- 1950s – Ebola\*
- 1990e – West Nile fever\*
- 2003 – SARS\*
- Hantavirus respiratory syndrome\*
- Monkey pox\*
- Bird flu\*
- Henipaviruses \*

\* - emerged by zoonotic transfer

# Emerging infections of the 21<sup>st</sup> century

- 2003 – SARS
- 2009 – SFTS (Severe Fever with Trombocytopenia Syndrome)
- 2011 – Schmallenberg
- 2012 – MERS
- 2014 – Ebola
- 2015 – Zika
- 2019 – COVID-2019



# How can we peek into the past of virus evolution?

- Virus polymerases make errors
- Rate of mutation accumulation for a given virus is relatively constant over time

like tree rings



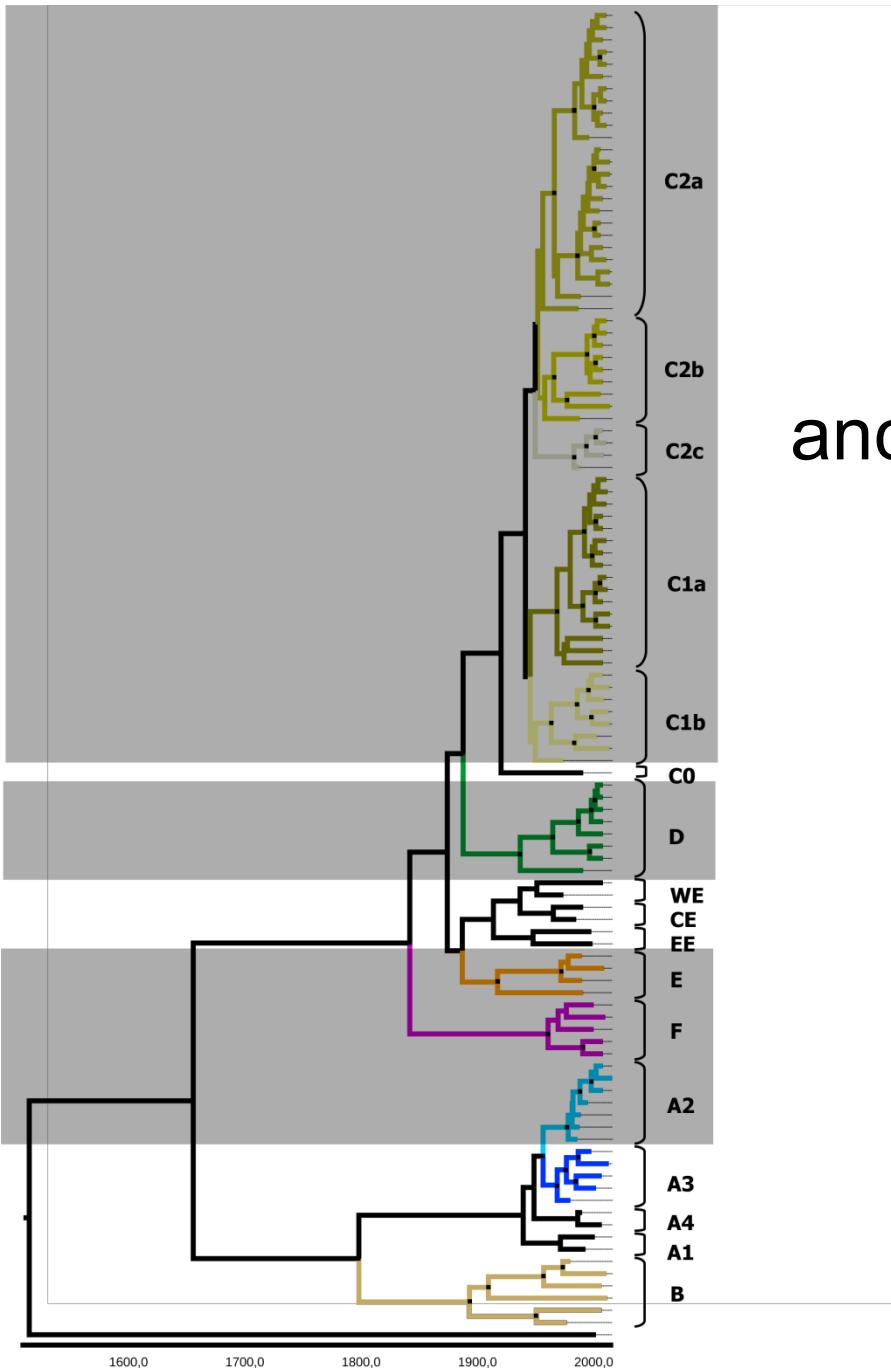
- Using genomic sequences of modern viruses one can infer their evolution in the past

# Even typical zoonoses and «bibleic» infections are actually emerging viruses

- Rabies of carnivores: described 3000 years ago, molecular evidence suggests that all current strains on earth have a common ancestor ~700 years ago
- Crimean Congo hemorrhagic fever: described in Central Asia 1000 years ago, emerged in South Russia 250 years ago
- Tick-borne encephalitis: emerged probably after the Ice Age, most of the spread in Eurasia after 1600 and due to human activity
- Polio – emerged around 100-150 years ago

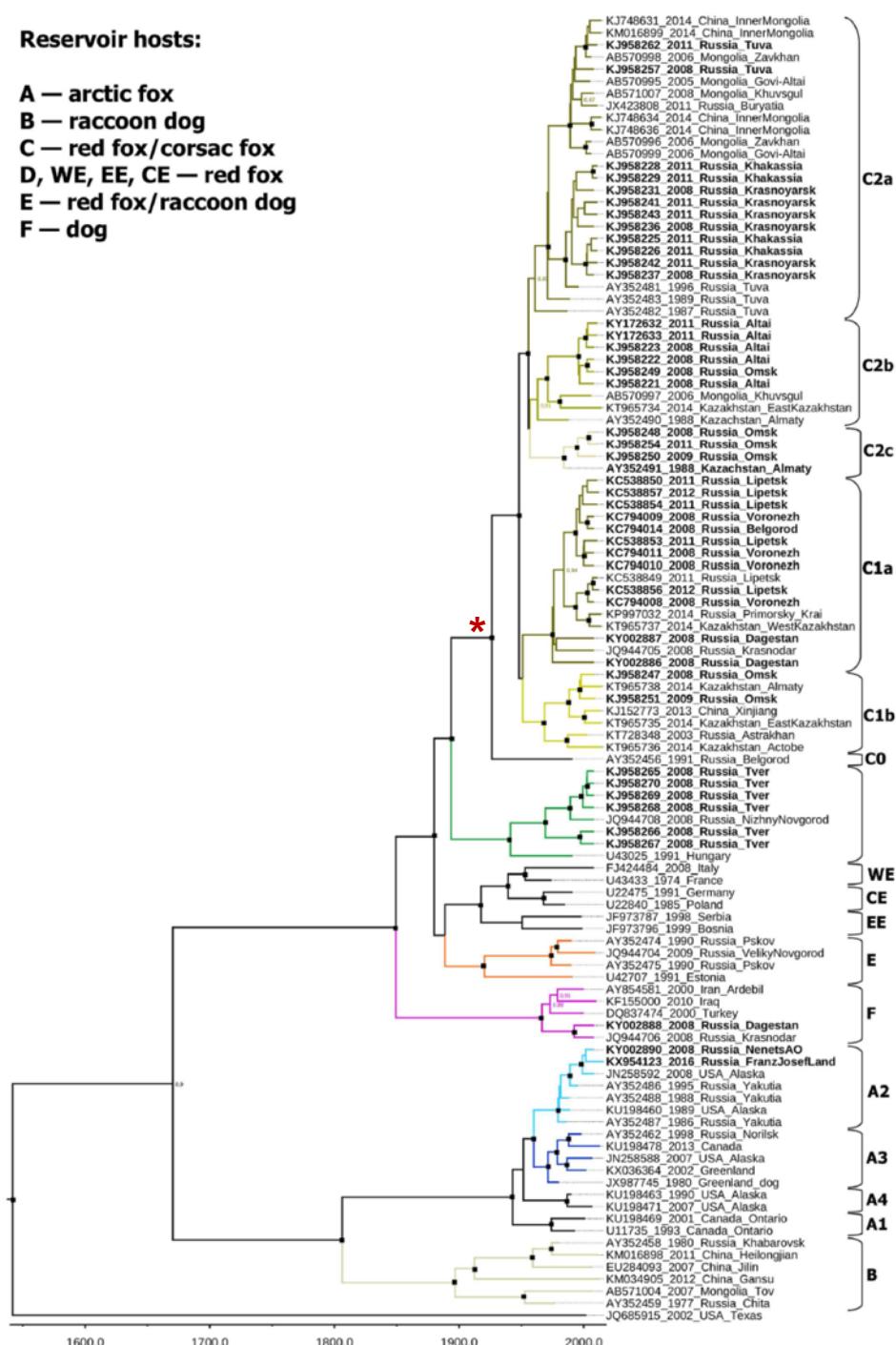
# Rabies

The most recent common ancestor of all viruses in Russia existed in ~1850



## Reservoir hosts:

- A — arctic fox
- B — raccoon dog
- C — red fox/corsac fox
- D, WE, EE, CE — red fox
- E — red fox/raccoon dog
- F — dog



Can we trust these calculations?

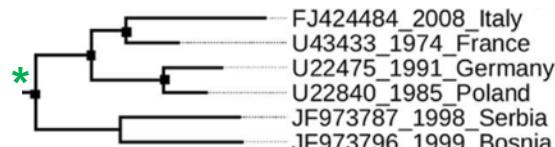
Correspondence of inferred and actually recorded events

\* 1948 [1929–1964]

1946 recorded emergence of rabies in steppe foxes.

\*1939 [1919–1958]

1939 – West-ward migration of rabid foxes described in the area.

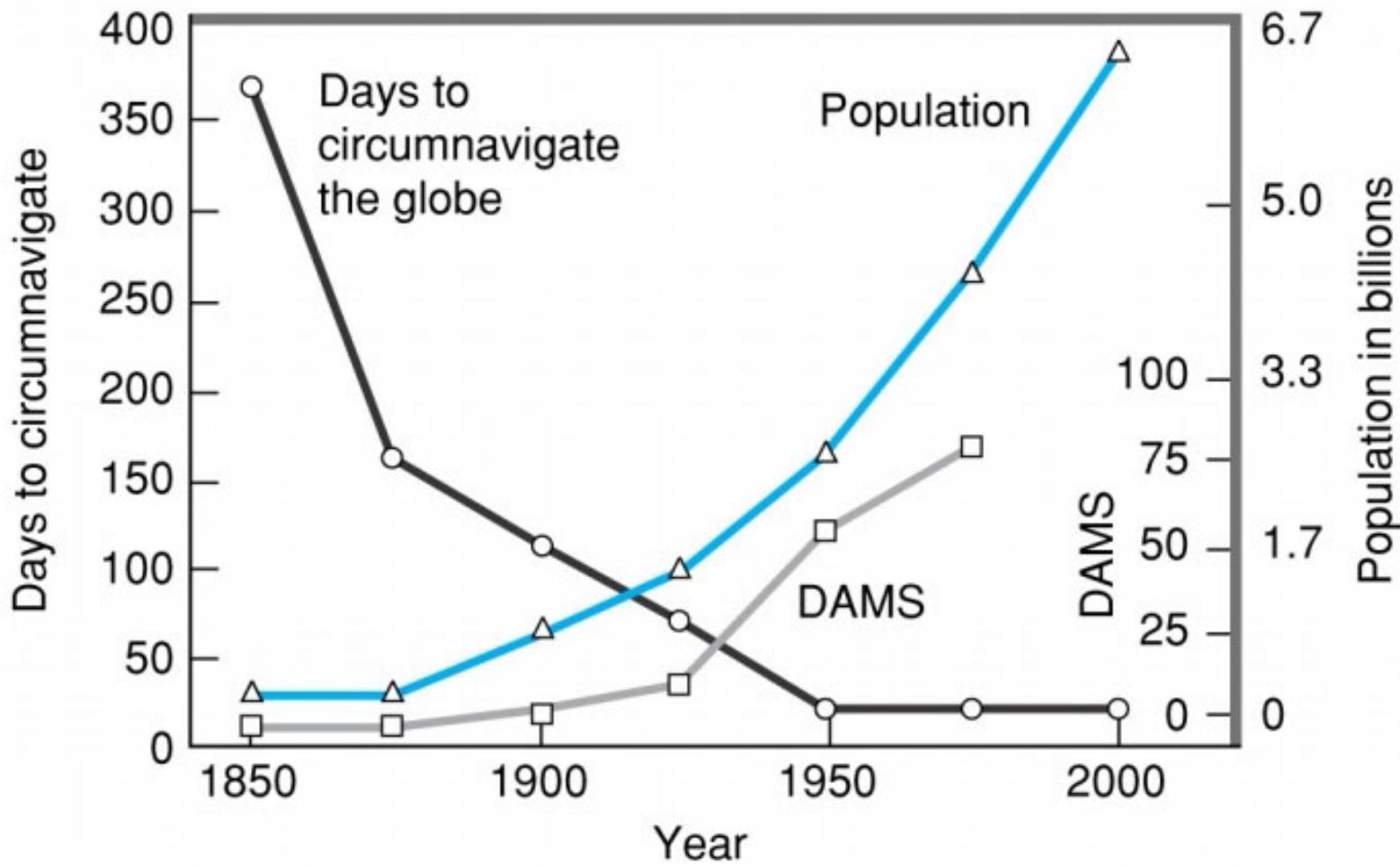


WE  
CE  
EE

# **Two *modus vivendi* of enterovirus genes**



# Probability of disease emergence is increasing



# «Judgement day virus»

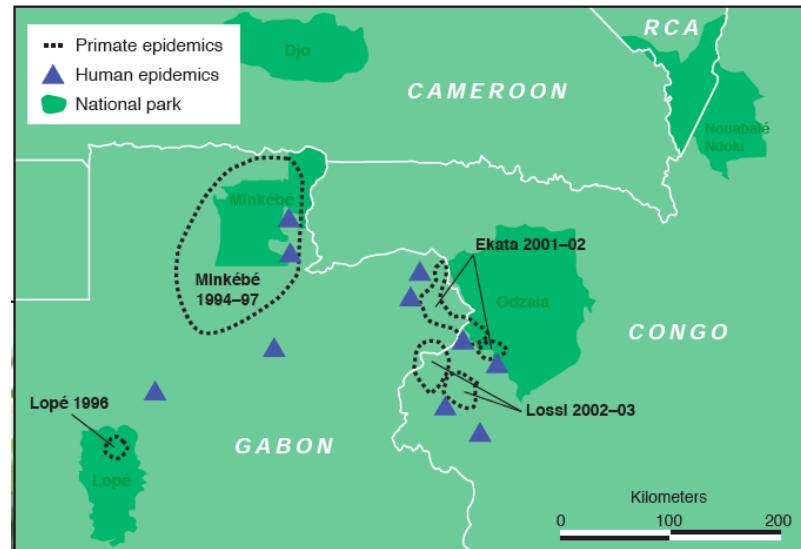
- Viruses that are adapted to humans are generally not a threat
- Emerging zoonoses can cause high lethality
- In natural conditions they do not spread outside of small groups (a village, for example)
- Some contagious and lethal viruses failed to establish in human population (SARS)
- Yet cities are an ideal and biologically unprecedented environment for virus spread
- Even SARS-CoV-2 causes limited mortality on ecological scale

# «Judgement day virus»

rabbit

- Rabbit myxomatosis virus was used in 1950 in Australia to control rabbit populations
- In two years rabbit population decreased from 600 to 100 million
- Remaining rabbits developed partial resistance; the virus, in its turn, became less virulent
- Virus was introduced to France in 1952; 90% of rabbits were dead to 1953
- Virus was introduced to the UK in 1953; 95% of rabbits were dead to 1955

# Epizooties in primates

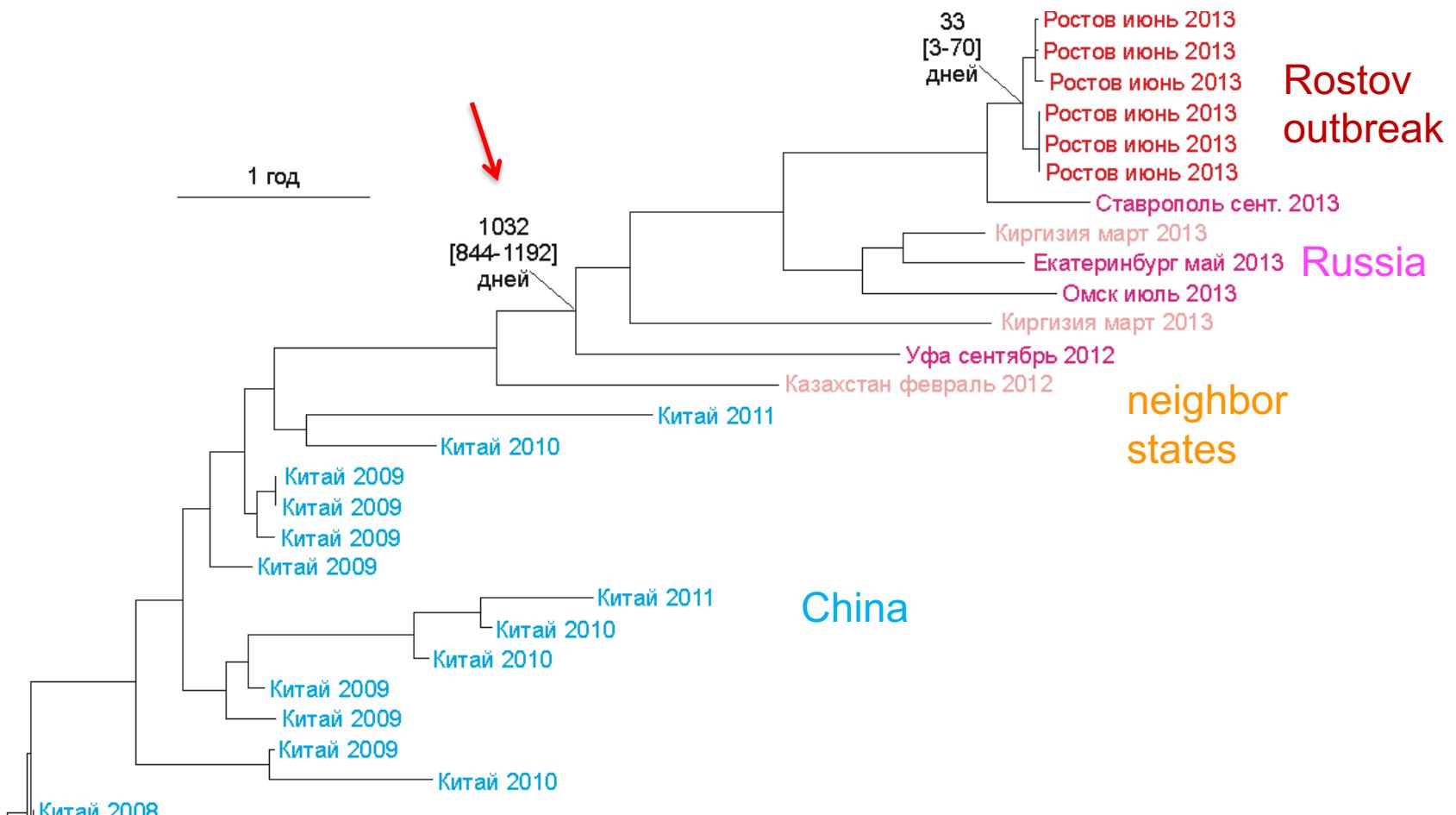


- Gabon: >50% reduction of ape population in 1983 due to Ebola

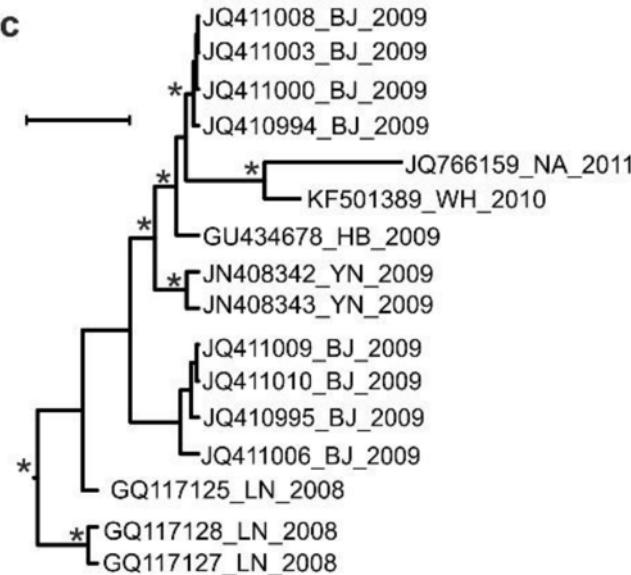
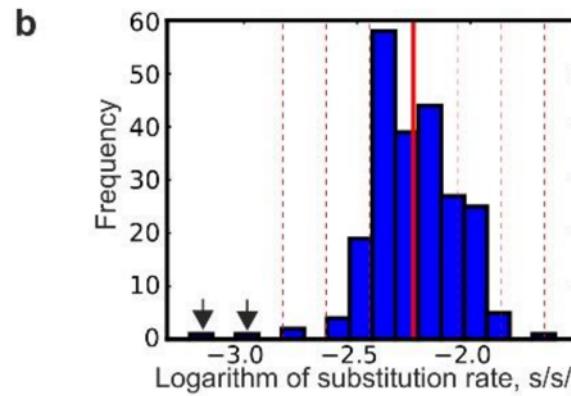


**Remains of the day.** Veterinary scientist Annelisa Kilbourn (who died last November in a plane crash) holds a femur from a lowland gorilla that died in an Ebola outbreak.

# Practical application of evolution studies outbreak investigation



# Investigation of a lab enterovirus release in China in 2008 r.



# Echovirus 11

## Virus trafficking patterns

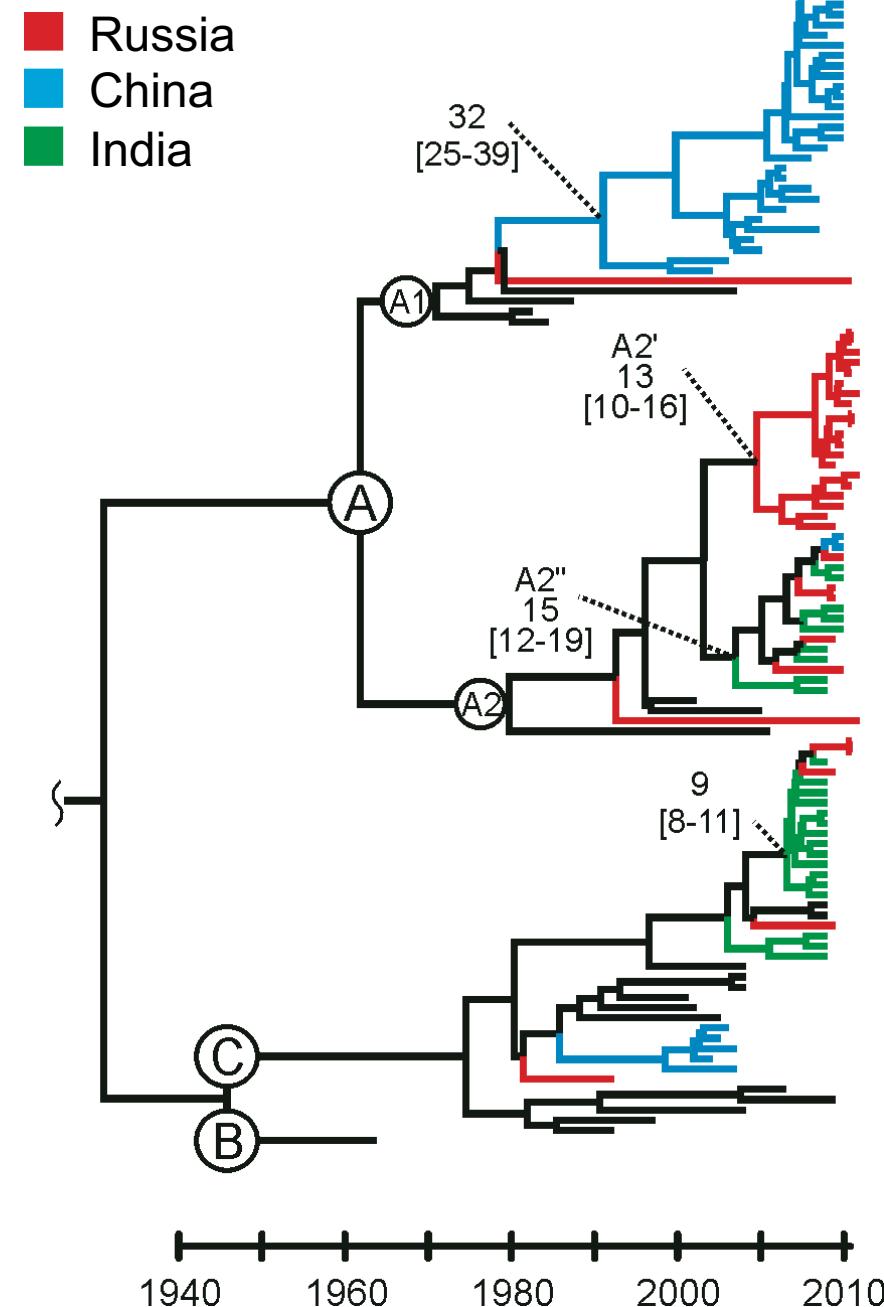
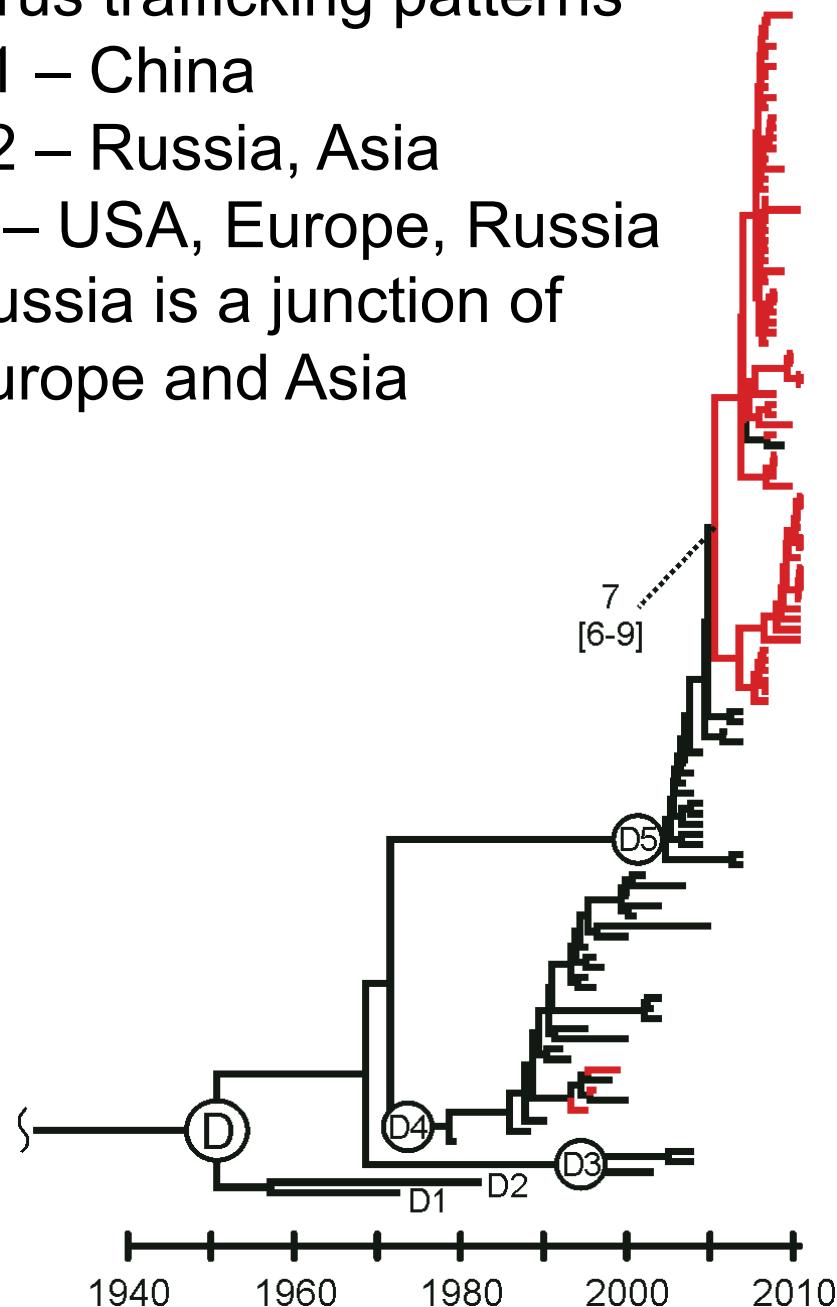
A1 – China

A2 – Russia, Asia

D – USA, Europe, Russia

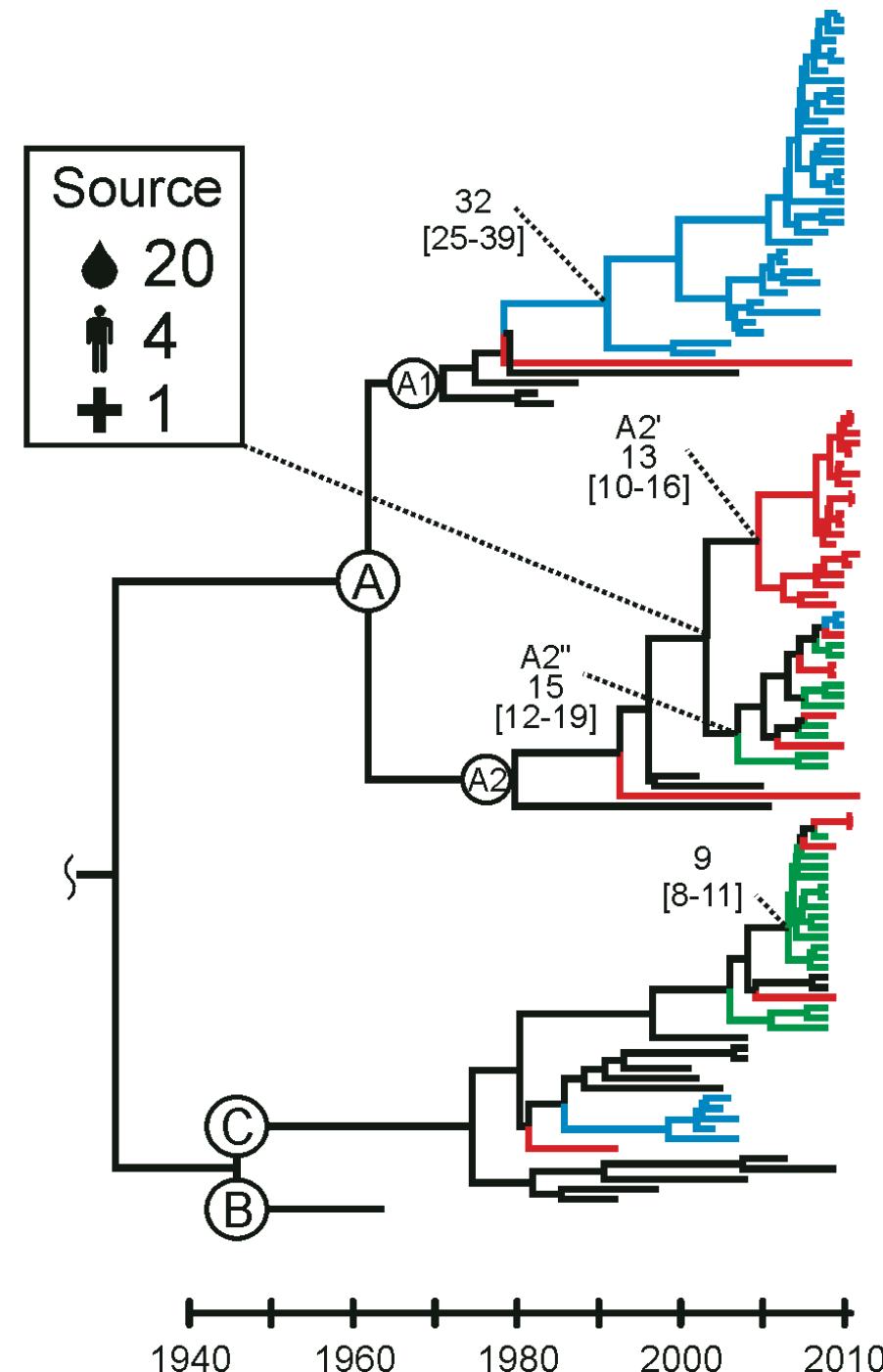
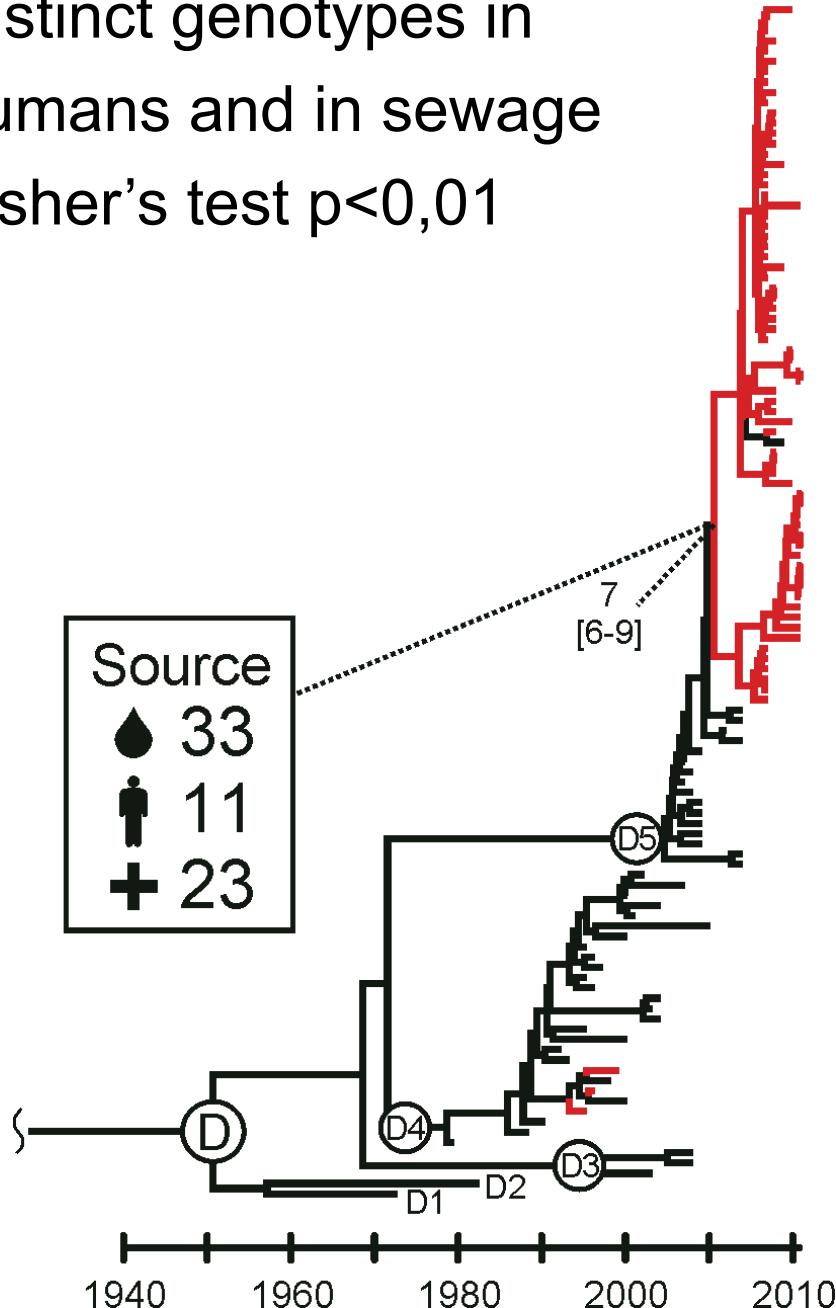
Russia is a junction of

Europe and Asia



# Echovirus 11

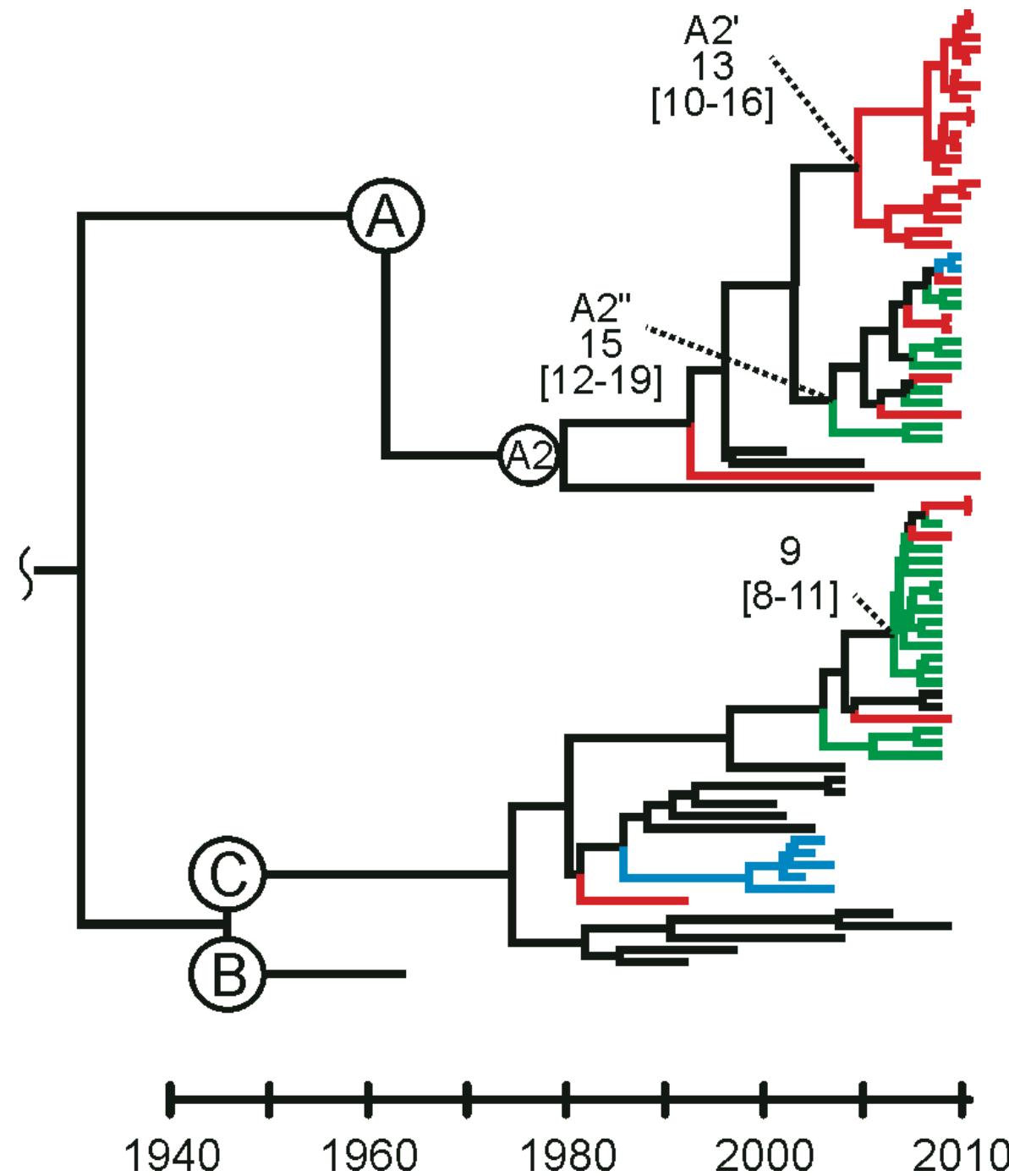
Distinct genotypes in  
humans and in sewage  
Fisher's test p<0,01



Echovirus 11

Different long-distance  
transmissibility of distinct  
groups?

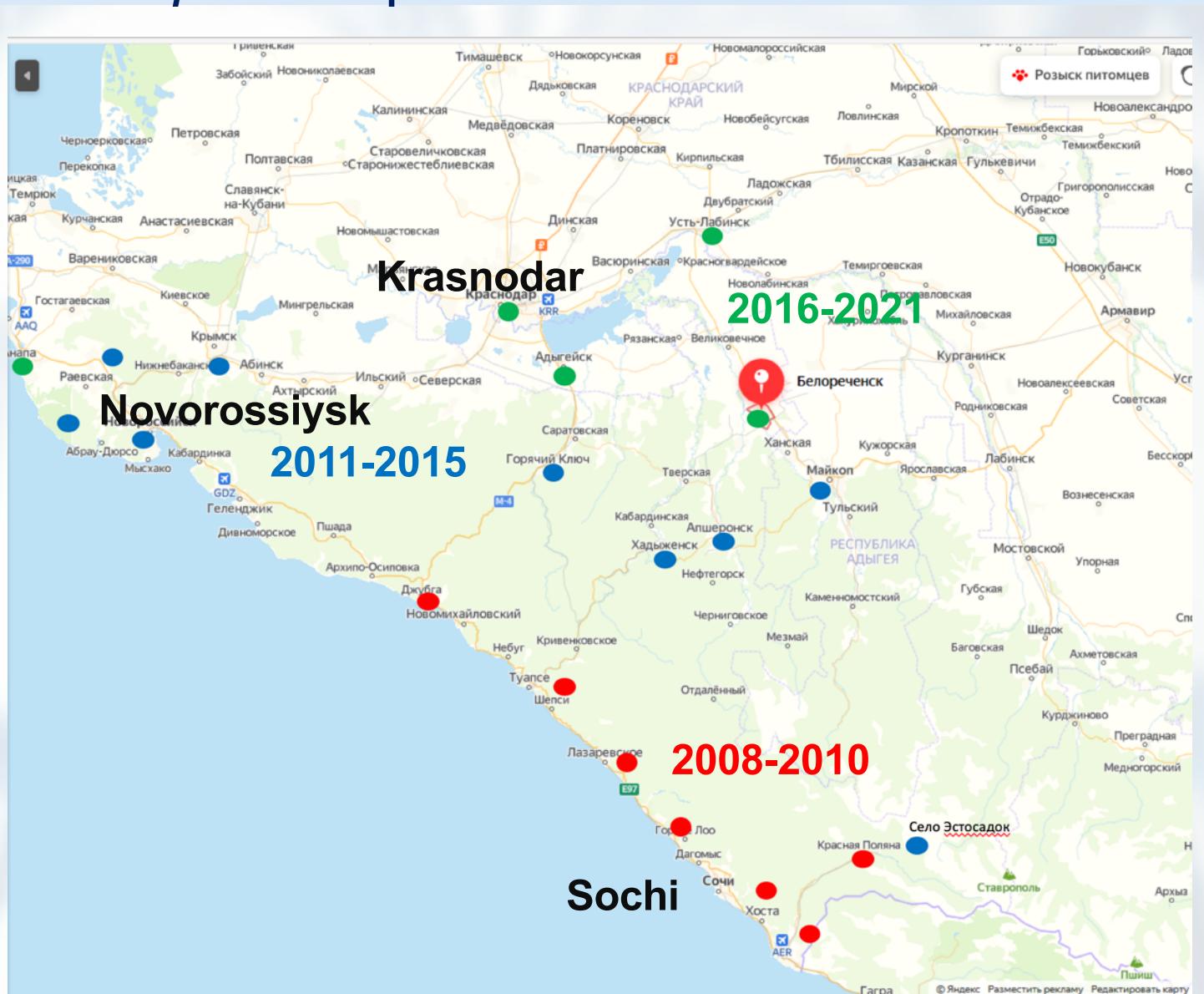
Fisher's test p<0,01



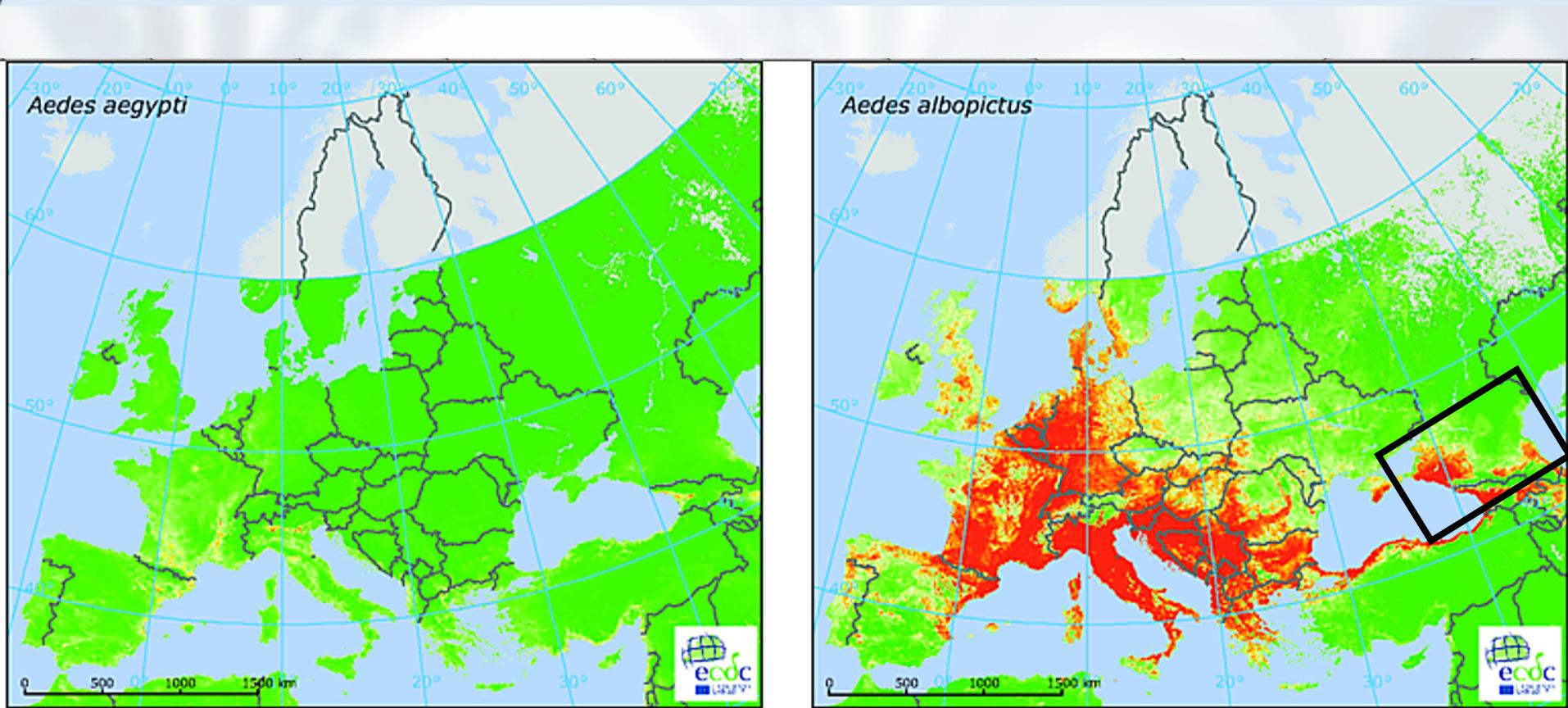
# Besides viruses...

## *Aedes albopictus* spread in South Russia

- First detected in 2008
- Over the coast and then inland
- Displaced remnant *Ae. aegypti* populations

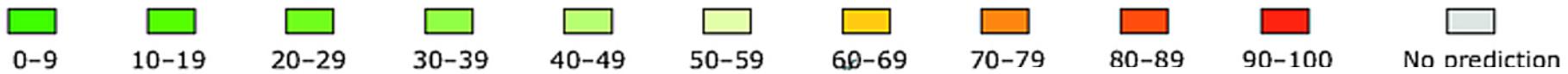


# In full accordance with climate forecasts



Climatic suitability for *Aedes aegypti* and *Aedes albopictus* (Asian tiger mosquito) in Europe

Suitability (%)



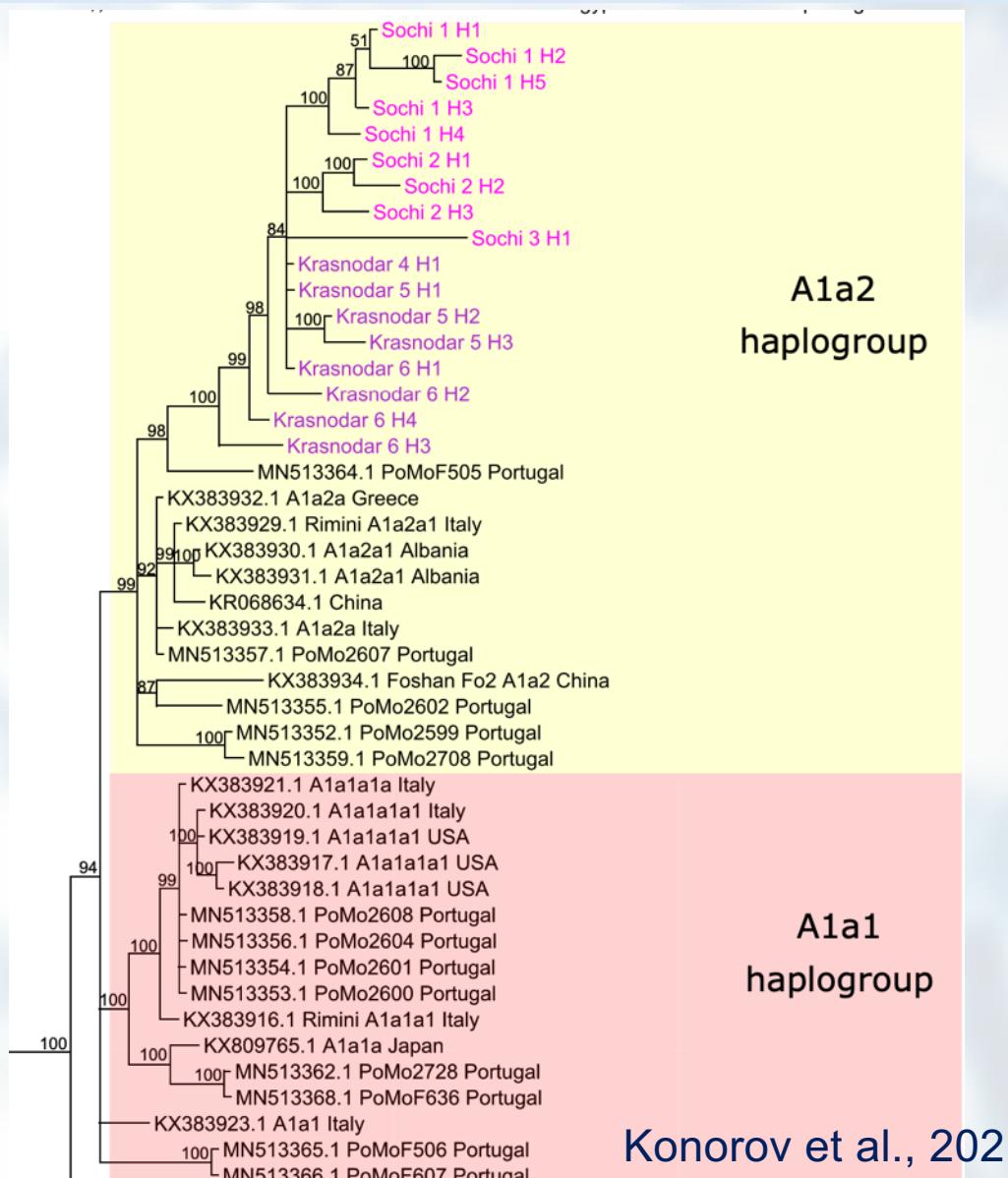
# A single-source introduction?

Full mitochondrial genome phylogeny

South Russia mosquitoes are monophyletic

Awesome genetic diversity generated in 10 years (200 genomes sequenced)

"adaptation on each meadow"



# Thank you for your attention

## Thank you for invitation



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