

The successful eradication of sylvatic rabies by oral vaccination of foxes in Slovenia

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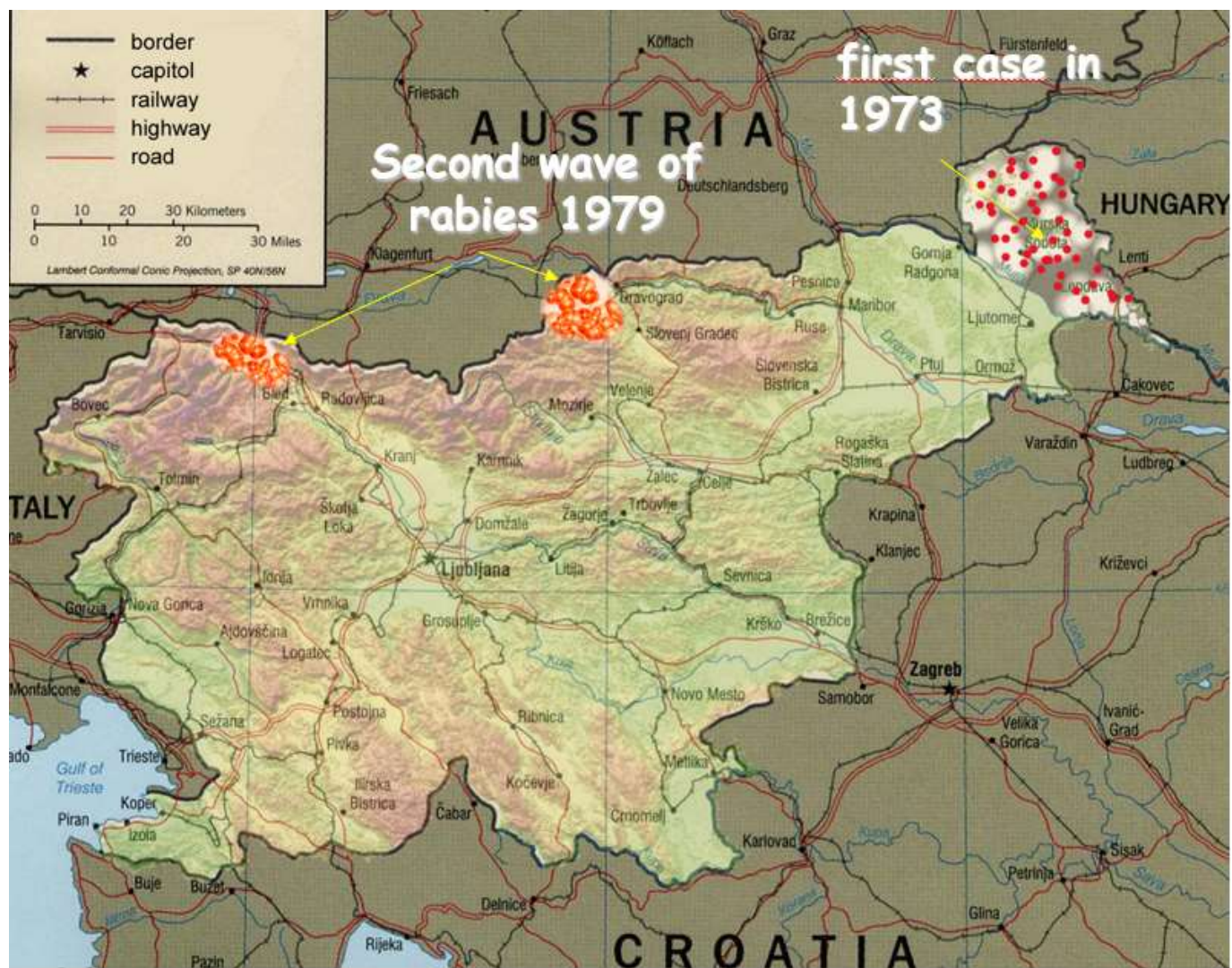


1947 –
compulsory
vaccination
of dogs

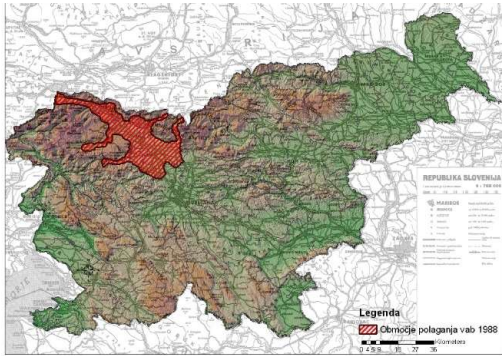
1950 – last
case in
humans

1973 – first
case of
rabies in fox

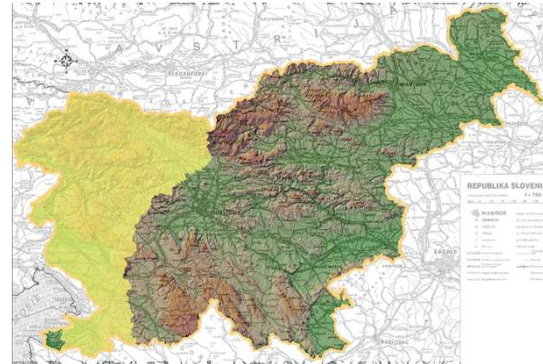
1988 –
carrying out
oral
vaccination
of foxes



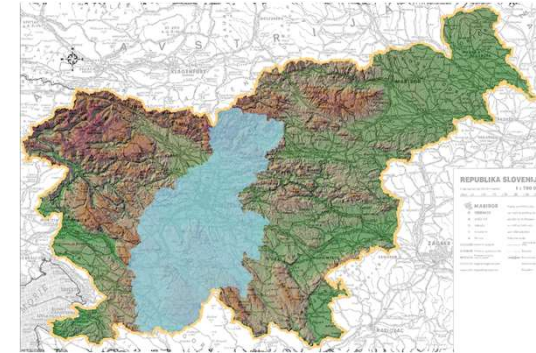
The first ORV in period 1988 - 1994



1988

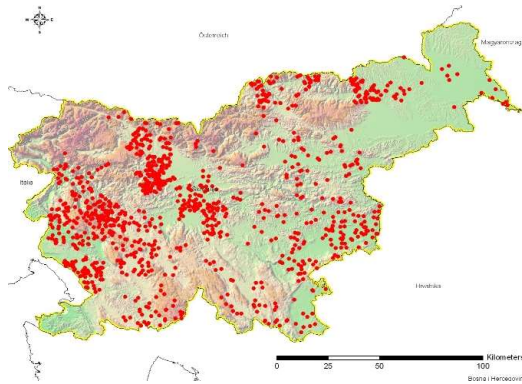


1990

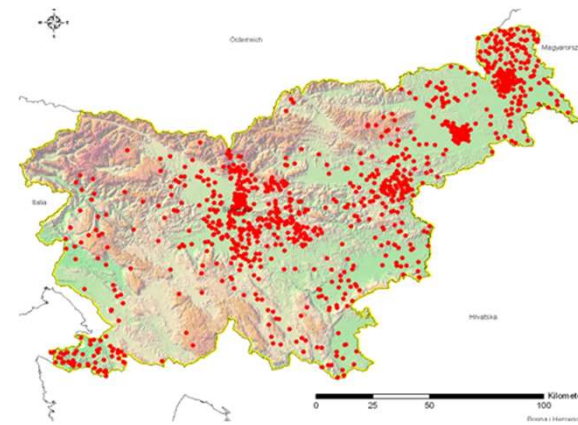


1991

The strategy of gradually pushing rabies from west to east did not work



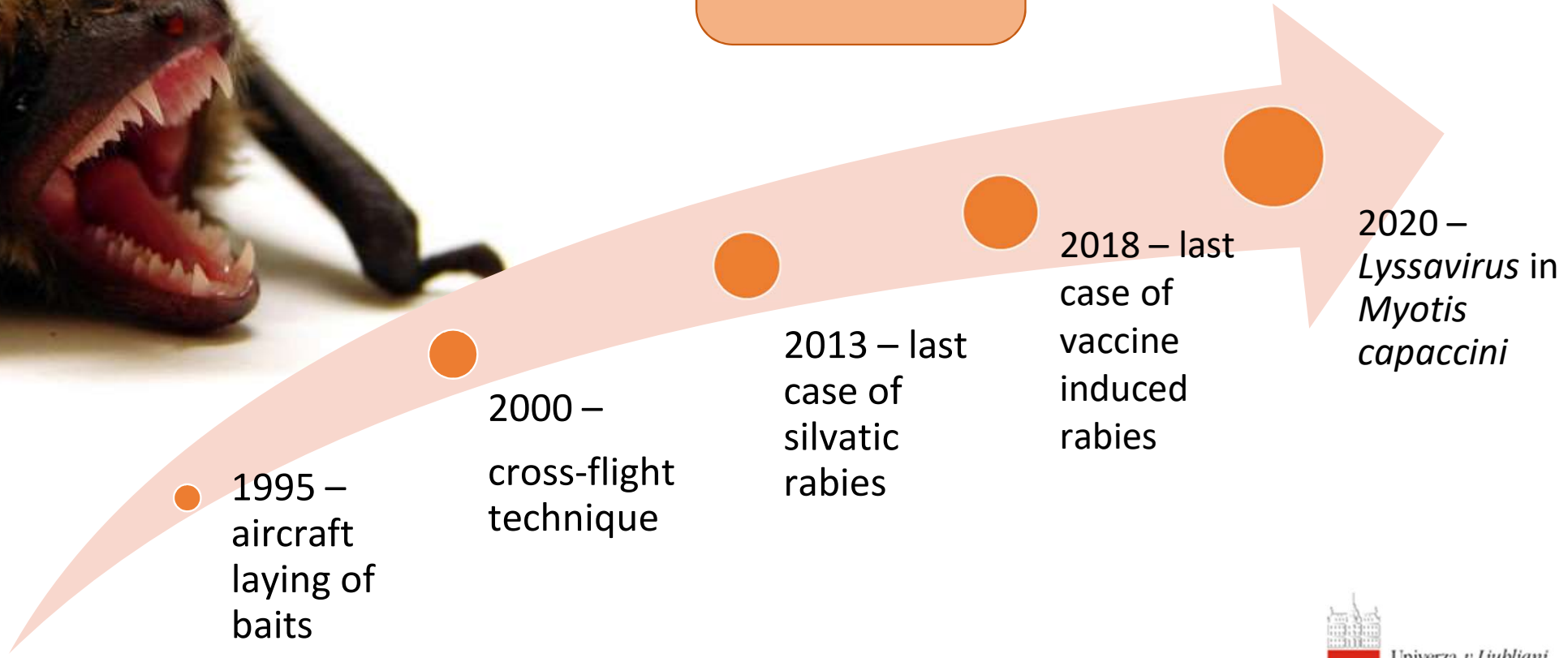
1988; 1.067 rabies cases



1995; 1.089 rabies cases



2016 – SLOVENIA
DECLARED FREE
FROM RABIES

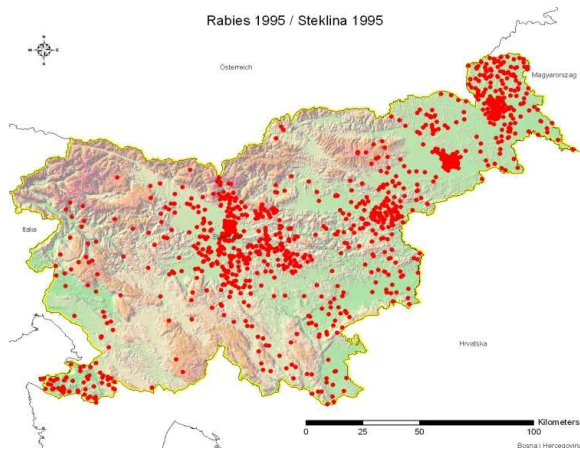


The second ORV in period 1995 - 2020

1995

Tested: 3787

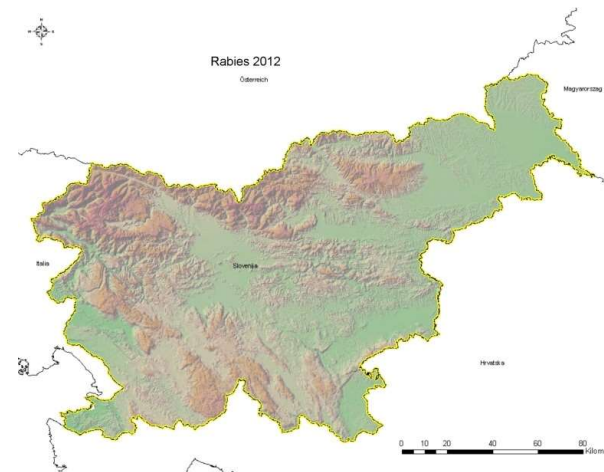
Rabies positive: 1089

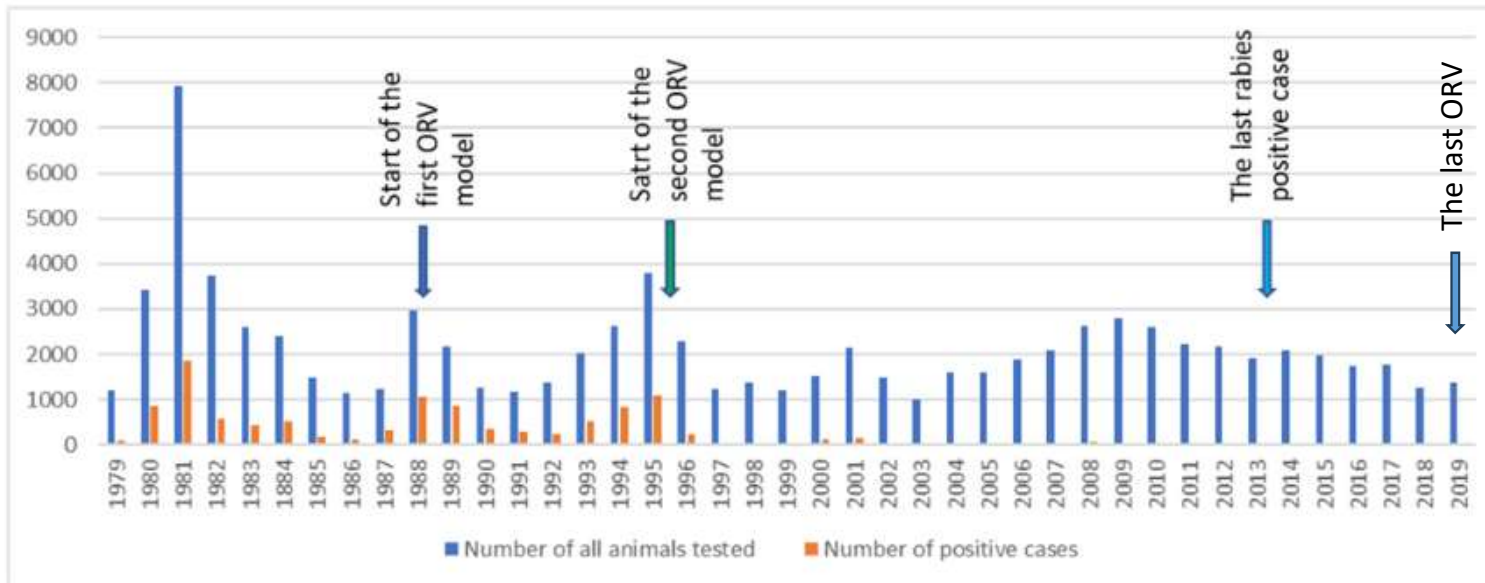


2013

Tested: 1918

Rabies positive: 0



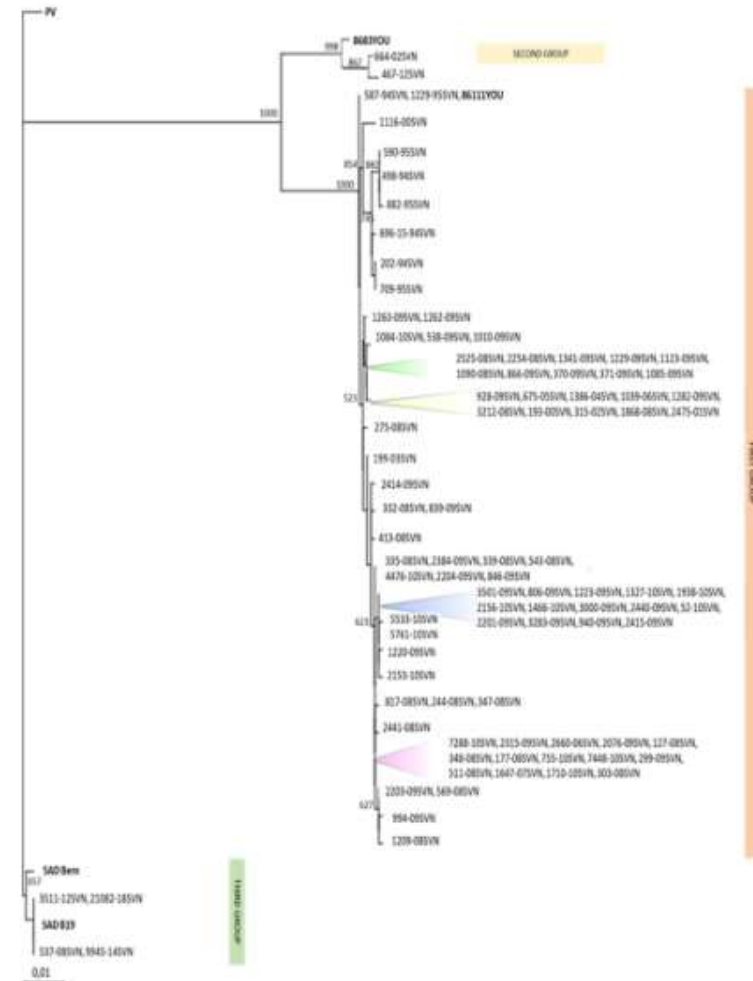


Number of tested animals in period 2010 – 2020: 10,2 animals/100 km²

Genetic Characterization of Rabies virus in Slovenia

(Černe D. et al. *Viruses* 2021, 13, 405)

- 95 rabies positive samples
- strains were clustered into three genetically groups
 - Western Europe group
 - Eastern Europe group
 - SAD B19 vaccine-associated group
- The four vaccine-induced cases (3 foxes an 1 marten)
 - unusual behaviour
 - aggressiveness
 - uncoordinated movements
 - not afraid of dogs and people



Bats *Lyssavirus* surveillance in Slovenia

Period 2008 -2012: first active and passive surveillance program for bat lyssaviruses:

913 oropharyngeal swabs

806 blood samples

171 brain samples

Period 2020 – 2022: active and passive surveillance program for bat lyssaviruses:

256 oropharyngeal swabs

235 blood samples

74 brain samples

Retrospective study: dead bats collected for Slovenian museum of natural history in period 2012 – 2019:

225 dead bats

21 bat species



Retrospective bat lyssavirus study: Methods



- 225 dead bats were collected by biologists
- Samples were stored more years in freezer ($-20\text{ }^{\circ}\text{C}$)
- Identification of bat species using morphological keys and molecular characterization
- Brain samples were collected through the foramen occipitale
- Samples were tested by pan-lyssavirus specific real-time RT-PCR method:
 - 1.) brain tissue homogenates
 - 2.) automated RNA extraction
 - 3.) real time RT-PCR (WHO 2019)

Retrospective bat lyssavirus study: Results

All samples collected in active and passive surveillance program were negative to *Lyssavirus*.

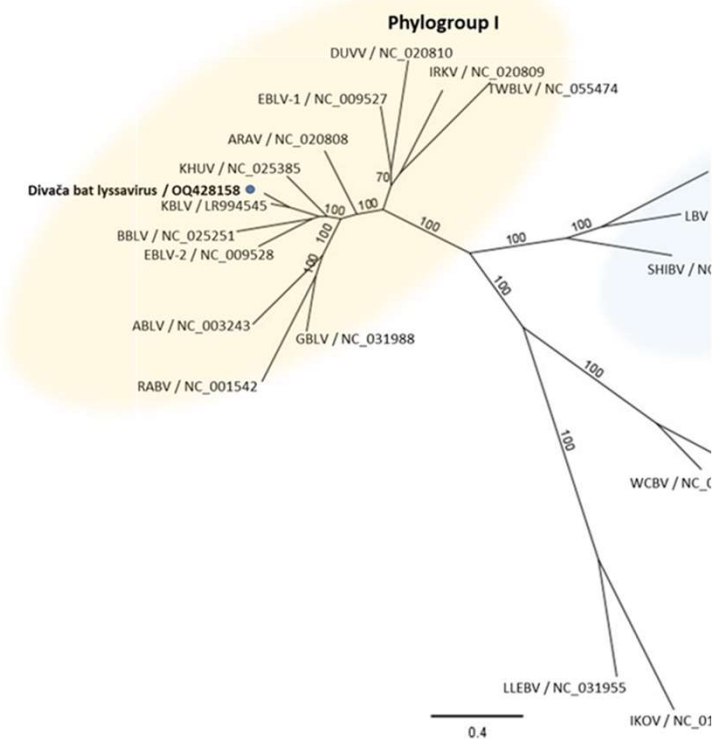
In retrospective surveillance study (225 dead bats), only one sample PP-0868/2014 were positive to Lyssavirus

Sample PP-0868/2014:
(*Myotis capaccinii*)

RTq-PCR	positive
FAT	positive
RTCIT	negative

Divača bat lyssavirus: genome determination by NGS

- The nearly complete genome of Divača bat lyssavirus from Slovenia was determined by NGS (Illumina, USA).
- Genome consists 11,871 nucleotides and reflects the characteristic gene organization known for lyssaviruses.
- Phylogenetic analysis of Divača bat lyssavirus revealed that it belongs to phylogroup I lyssaviruses and is most closely related to **Kotalahti bat lyssavirus (KBLV)** with **87.20% nucleotide and 99.22% amino acid identity**.
- Together with **KBLV, Khujand virus, European bat lyssavirus 2, Bakeloh bat lyssavirus, and Aravan virus**, Divača bat lyssavirus was detected in the bat genus *Myotis*
- Lyssavirus was first time detected in *Myotis capaccinii*
- Lyssavirus was first time detected in bat in Slovenia



THANKS FOR THE ATTENTION

