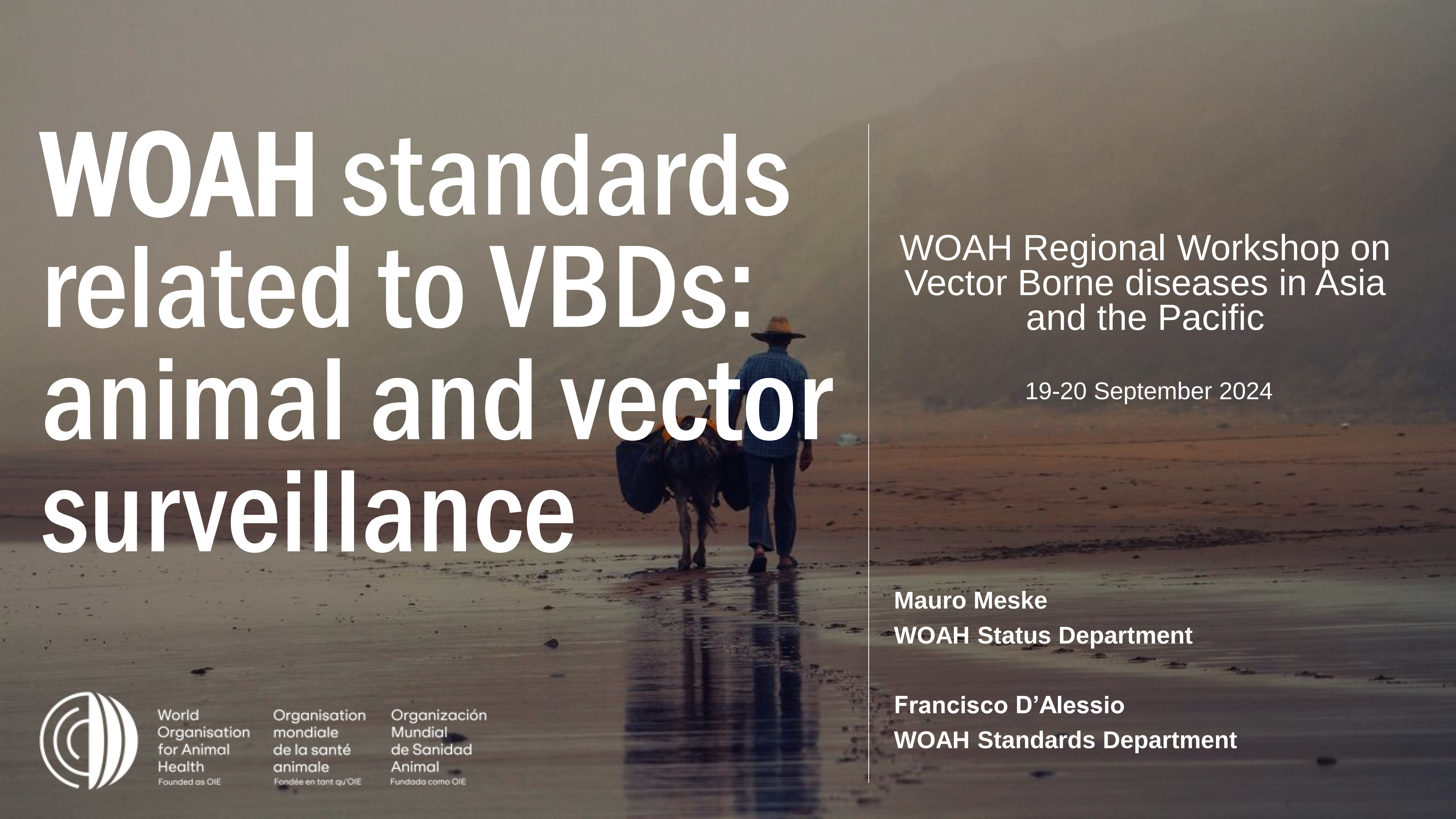


WOAH standards related to VBDs: animal and vector surveillance

WOAH Regional Workshop on Vector Borne diseases in Asia and the Pacific

19-20 September 2024

Mauro Meske
WOAH Status Department

Francisco D’Alessio
WOAH Standards Department

World
Organisation
for Animal
Health
Founded as OIE

Organisation
mondiale
de la santé
animale
Fondée en tant qu’OIE

Organización
Mundial
de Sanidad
Animal
Fundada como OIE

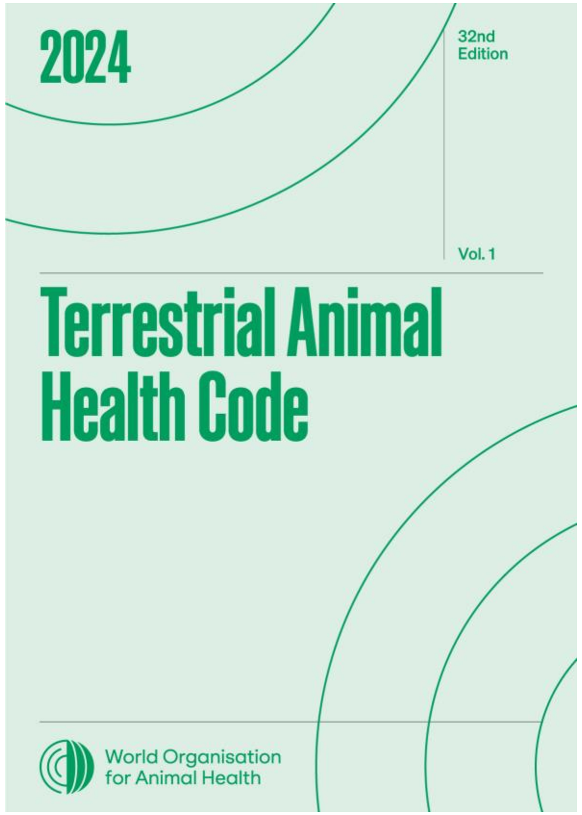
WOAH international standards

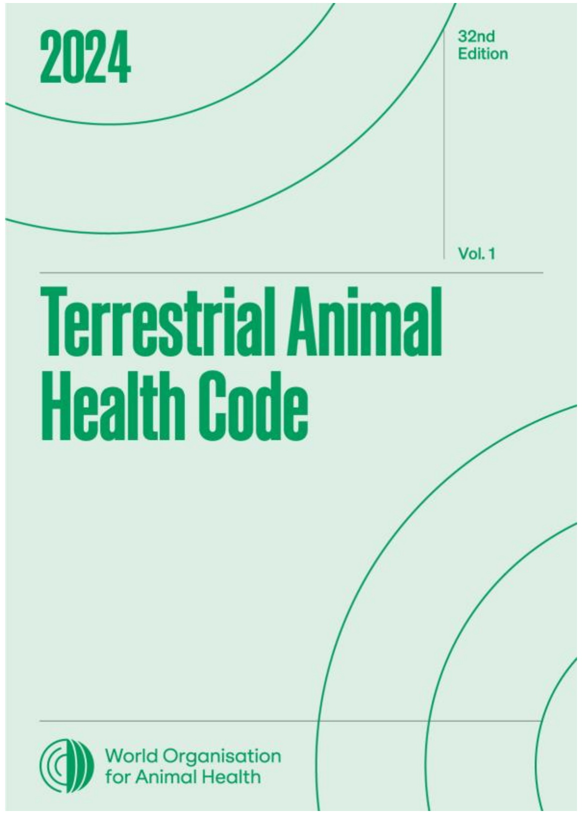
WOAH establishes standards for the improvement of animal health and welfare and veterinary public health worldwide, including the prevention of disease spread through international trade of animals and animal products.

- **Ensuring transparency** and **enhancing knowledge** of the **worldwide animal health situation.**
- Development of **national policies and national sanitary systems**
- **Assessment of potential trading partners** and **their health situation**
- Drafting of **import sanitary measures**, according to the commodity and their origin
- **Veterinary certification** and **export/import procedures**

WOAH international standards

Terrestrial Code





Volume I
User's guide and
Horizontal chapters

Volume II
Disease-specific
chapters

- New version every year
- Latest version publicly available on the WOAH website
- Previous editions are also available

Terrestrial Code - content

Volume I: Horizontal chapters

- User’s Guide
- Glossary
- Animal disease diagnosis, surveillance and notification
- Risk analysis
- Quality of Veterinary Services
- Disease prevention and control
- Trade measures, import-export procedures and veterinary certification
- Veterinary public health
- Animal welfare

Volume II: Disease-specific chapters

- **Definition of infection/ infestation** and specific epidemiological considerations
- **Safe commodities** where appropriate
  - Safe commodities = based on absence of the pathogenic agent in the traded commodity OR inactivation by processing or treatment that the commodity has undergone
  - Importing countries should not apply trade restrictions to safe commodities with respect to the pathogenic agent concerned
- **Determination of the animal health status** of a country, zone or compartment
  - Official status recognition
  - Self declaration of animal health status
- **Recommendations on safe trade** for live animals, genetic material, other products of animal origin (meat, milk, eggs, skins, etc.)
- **Specific management** of commodities, e.g.
  - Recommendations on inactivation
  - Vector-protection during transport
- **Recommendations on surveillance**
  - Surveillance strategies specific to infection/ infestation
  - Link to Chapter 1.4 and 1.5 on animal health and vector surveillance

Glossary

- **Vector**

means an insect or any living carrier that transports an infectious agent from an infected individual to a susceptible individual or its food or immediate surroundings. The organism may or may not pass through a development cycle within the vector.

- **Infestation**

means the external invasion or colonisation of animals or their immediate surroundings by arthropods, which may cause clinical signs or are potential vectors of pathogenic agents.

- **Official control programme**

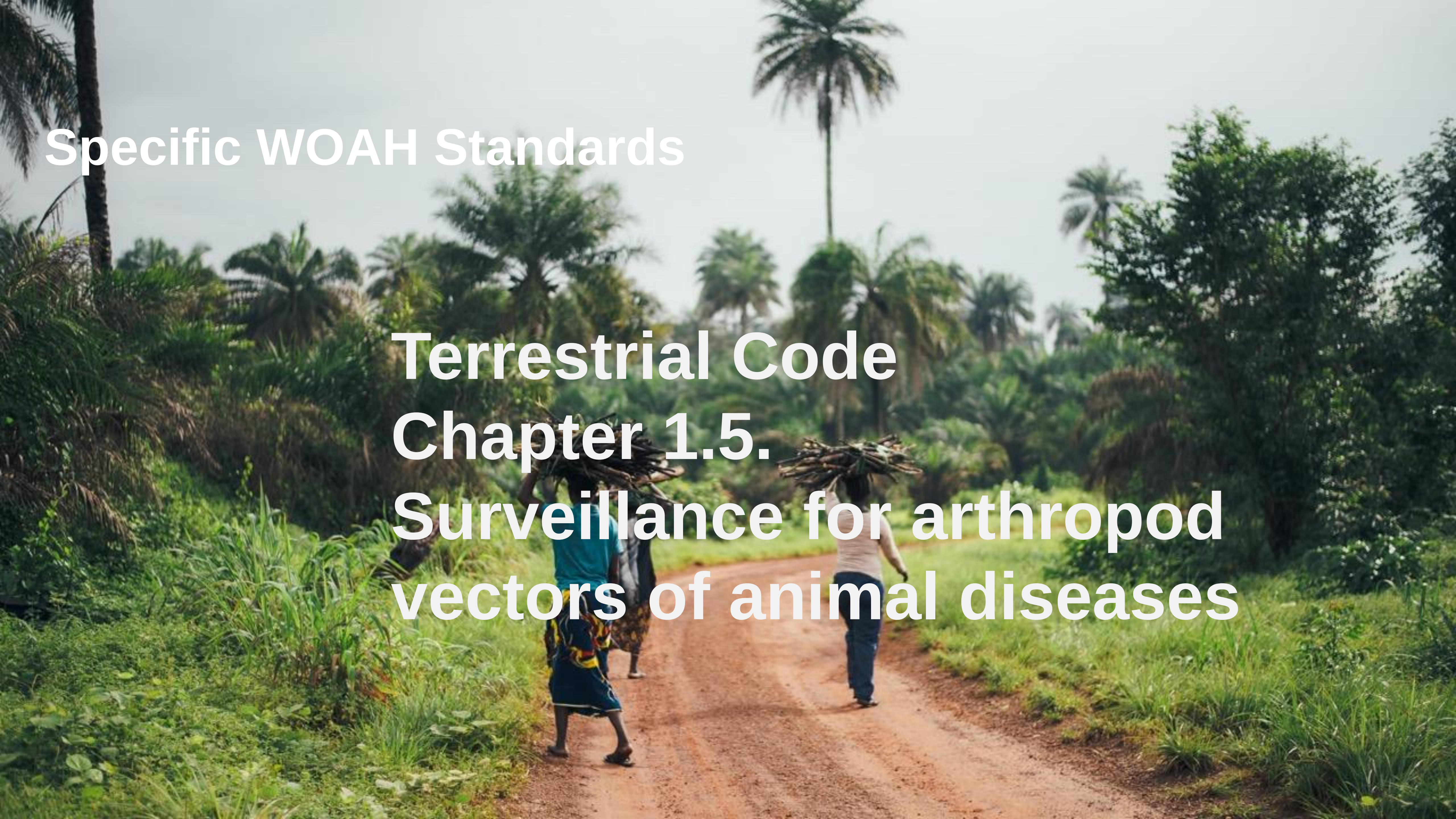
means a programme which is approved, and managed or supervised by the Veterinary Authority of a Member Country for the purposes of controlling a vector, pathogenic agent or disease by specific measures applied throughout that Member Country, or within a zone or compartment of that Member Country.

SECTION 1. ANIMAL DISEASE DIAGNOSIS, SURVEILLANCE AND NOTIFICATION

Chapter 1.1.	Notification of diseases and provision of epidemiological information
Chapter 1.2.	Criteria for the inclusion in the OIE list
Chapter 1.3.	Diseases, infections and infestations listed by the OIE
Chapter 1.4.	Animal health surveillance
Chapter 1.5.	Surveillance for arthropod vectors of animal diseases

SECTION 4. DISEASE PREVENTION AND CONTROL

Chapter 4.4.	Zoning and compartmentalisation
Chapter 4.5.	Application of compartmentalisation
Chapter 4.18.	Official control programmes for listed and emerging diseases



Specific WOAH Standards

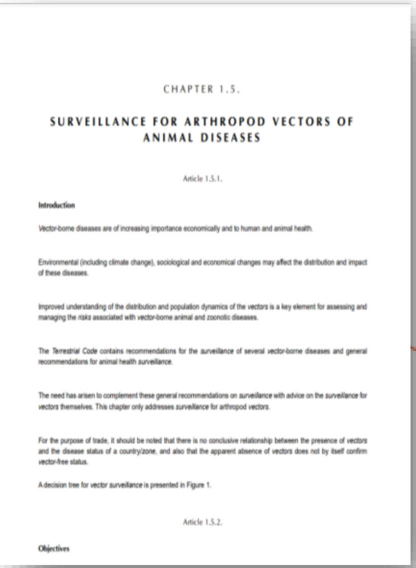
Terrestrial Code
Chapter 1.5.
Surveillance for arthropod vectors of animal diseases

Chapter 1.5. Surveillance for arthropod vectors of animal diseases

Chapter 1.5.

Article 1.5.1. Introduction

- The Terrestrial Code contains recommendations for the surveillance of several vector-borne diseases and general recommendations for animal health surveillance.
- The need has arisen to complement these general recommendations on surveillance with advice on the surveillance for vectors themselves. This chapter only addresses surveillance for arthropod vectors.
- For the **purpose of trade**, it should be noted that there is no conclusive relationship between the presence of vectors and the disease status of a country/zone, and also that **the apparent absence of vectors does not by itself confirm vector-free status**.



CHAPTER 1.5.

SURVEILLANCE FOR ARTHROPOD VECTORS OF
ANIMAL DISEASES

Article 1.5.1.

Introduction

Vector-borne diseases are of increasing importance economically and to human and animal health.

Environmental (including climate change), sociological and economical changes may affect the distribution and impact of these diseases.

Improved understanding of the distribution and population dynamics of the *vectors* is a key element for assessing and managing the *risks* associated with *vector*-borne animal and zoonotic diseases.

The *Terrestrial Code* contains recommendations for the *surveillance* of several *vector*-borne diseases and general recommendations for animal health *surveillance*.

The need has arisen to complement these general recommendations on *surveillance* with advice on the *surveillance* for *vectors* themselves. This chapter only addresses *surveillance* for arthropod *vectors*.

For the purpose of trade, it should be noted that there is no conclusive relationship between the presence of *vectors* and the disease status of a country/*zone*, and also that the apparent absence of *vectors* does not by itself confirm *vector*-free status.

A decision tree for *vector surveillance* is presented in Figure 1.

Article 1.5.2.

Objectives

First adopted in 2009;

Most recent update adopted in 2010.

Chapter 1.5.

Article 1.5.2. Objectives

1) **gathering up-to-date information** on the spatial and temporal distribution and abundance of vectors of the arthropod-borne listed diseases and emerging diseases;

2) **monitoring changes** in the spatial and temporal distribution and abundance of these vectors;

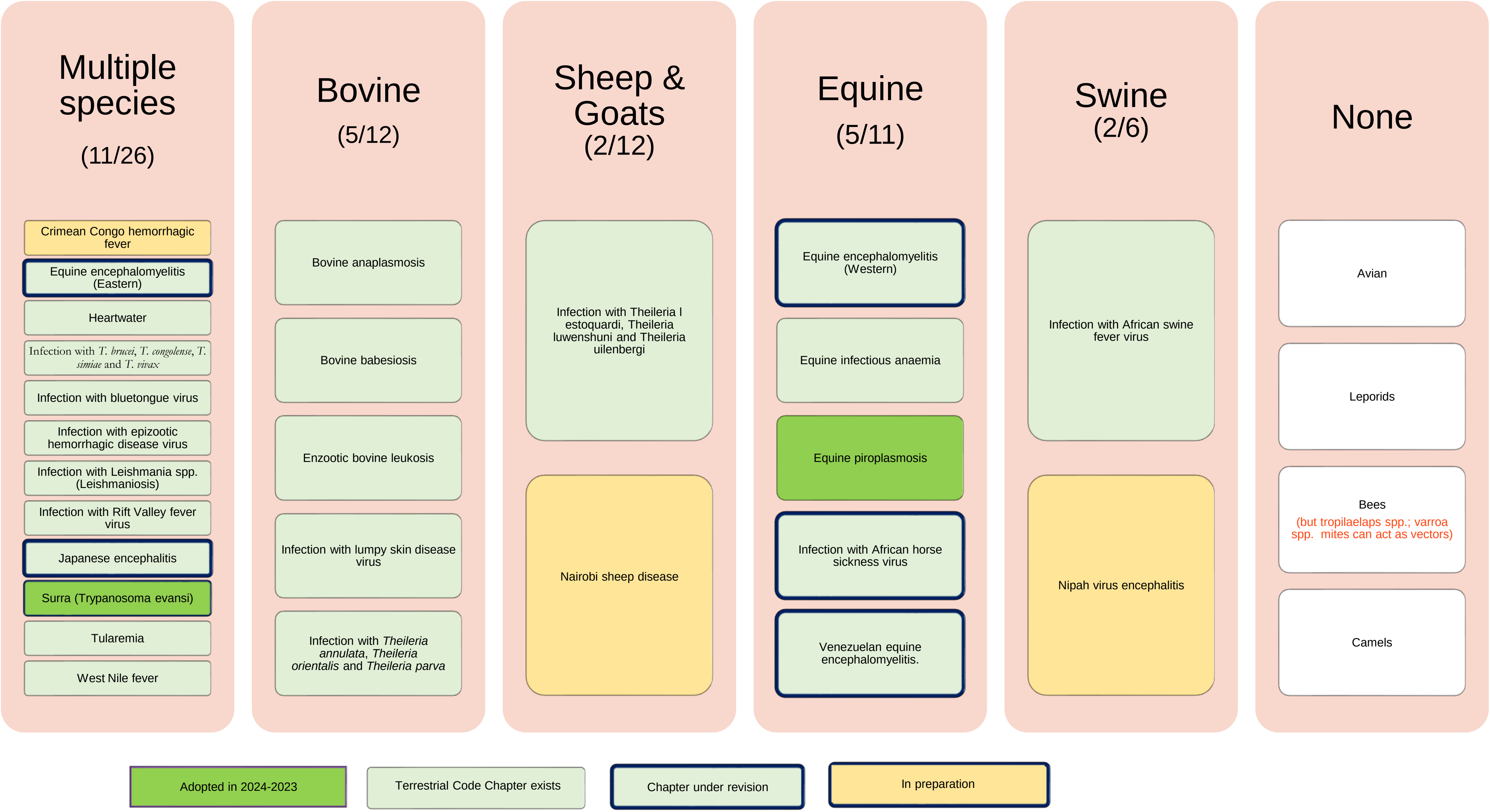
3) collecting relevant data to **inform risk assessment** (including vector competency) and risk management of these vector-borne diseases;

4) **detecting the presence of specific vectors or confirming their absence**;

5) understanding **pathways of entry** for vectors and vector-borne pathogenic agents.

Article 1.5.3. Sampling methodology: Sampling methods- Data management, analysis and interpretation

WOAH Listed diseases & Vector borne – State of play



Multiple species

(11/26)

- Crimean Congo hemorrhagic fever
- Equine encephalomyelitis (Eastern)
- Heartwater
- Infection with *T. brucei*, *T. congolense*, *T. simiae* and *T. vivax*
- Infection with bluetongue virus
- Infection with epizootic hemorrhagic disease virus
- Infection with Leishmania spp. (Leishmaniosis)
- Infection with Rift Valley fever virus
- Japanese encephalitis
- Surra (Trypanosoma evansi)
- Tularemia
- West Nile fever

Bovine

(5/12)

- Bovine anaplasmosis
- Bovine babesiosis
- Enzootic bovine leukosis
- Infection with lumpy skin disease virus
- Infection with *Theileria annulata*, *Theileria orientalis* and *Theileria parva*

Sheep & Goats

(2/12)

- Infection with Theileria lestoquardi, Theileria luwenshuni and Theileria uilenbergi
- Nairobi sheep disease

Equine

(5/11)

- Equine encephalomyelitis (Western)
- Equine infectious anaemia
- Equine piroplasmosis
- Infection with African horse sickness virus
- Venezuelan equine encephalomyelitis.

Swine

(2/6)

- Infection with African swine fever virus
- Nipah virus encephalitis

None

- Avian
- Leporids
- Bees (but tropilaelaps spp.; varroa spp. mites can act as vectors)
- Camels

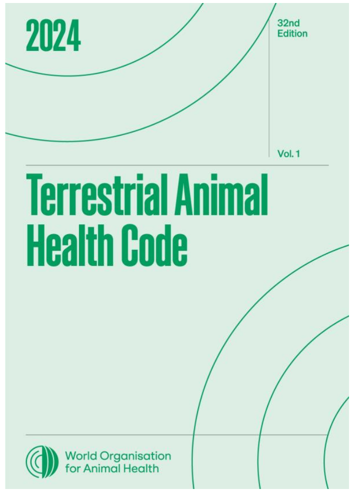
Adopted in 2024-2023

Terrestrial Code Chapter exists

Chapter under revision

In preparation

Volume II: Disease-specific chapters



1. Definition of infection/ infestation, its occurrence and specific epidemiological considerations (including relevant vectors)
2. Determination of the animal health status of a country, zone or compartment
3. Recommendations on safe trade for live animals, genetic material, other products of animal origin (meat, milk, eggs, skins, etc.)
4. Recommendations on surveillance

Terrestrial Manual

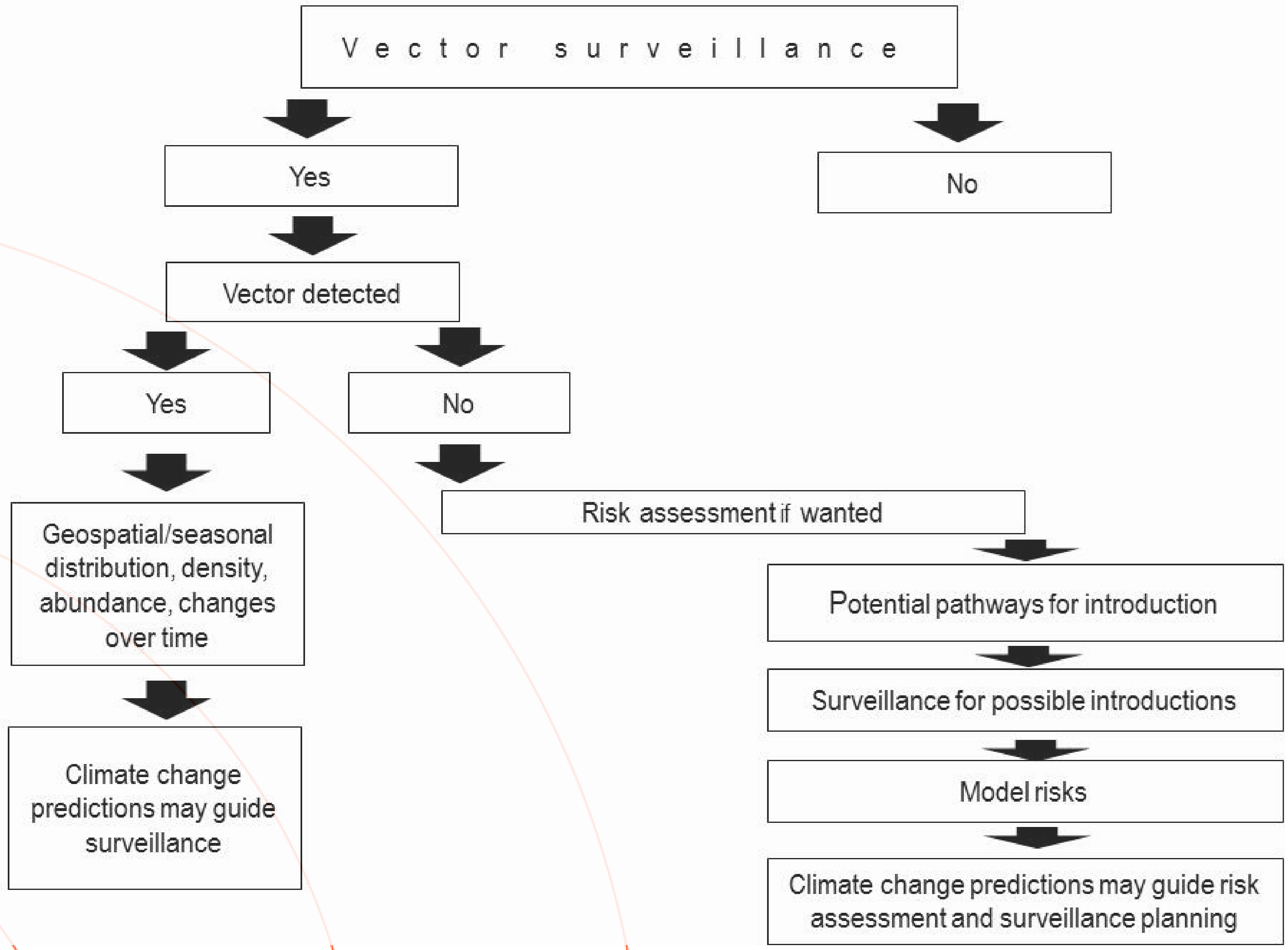
Complementary Chapters – Regularly updated

1. Standards for diagnosis and vaccines
2. Epidemiological information
3. Detailed information on vectors, vector species, etc

Specific considerations for VBD

1. Definition of disease occurrence
    - Detection of the pathogenic agent in an animal (not vector)
2. Animal health Status
    - Vector Surveillance – presence/absence of vector
    - Seasonal Freedom
    - High surveillance area bordering infected country or zone
3. Protection of animals from vectors
    - vector-protected establishment or facility
    - During transport
4. Vector related sanitary measures for trade
    - Free of ticks - treatment
    - Protection from vector attacks during transport/transit

Chapter 1.5.


Vector surveillance
Yes
No
Vector detected
Yes
No
Risk assessment if wanted
Geospatial/seasonal distribution, density, abundance, changes over time
Potential pathways for introduction
Surveillance for possible introductions
Model risks
Climate change predictions may guide surveillance
Climate change predictions may guide risk assessment and surveillance planning

Using Terrestrial Code Standards on Vector Surveillance

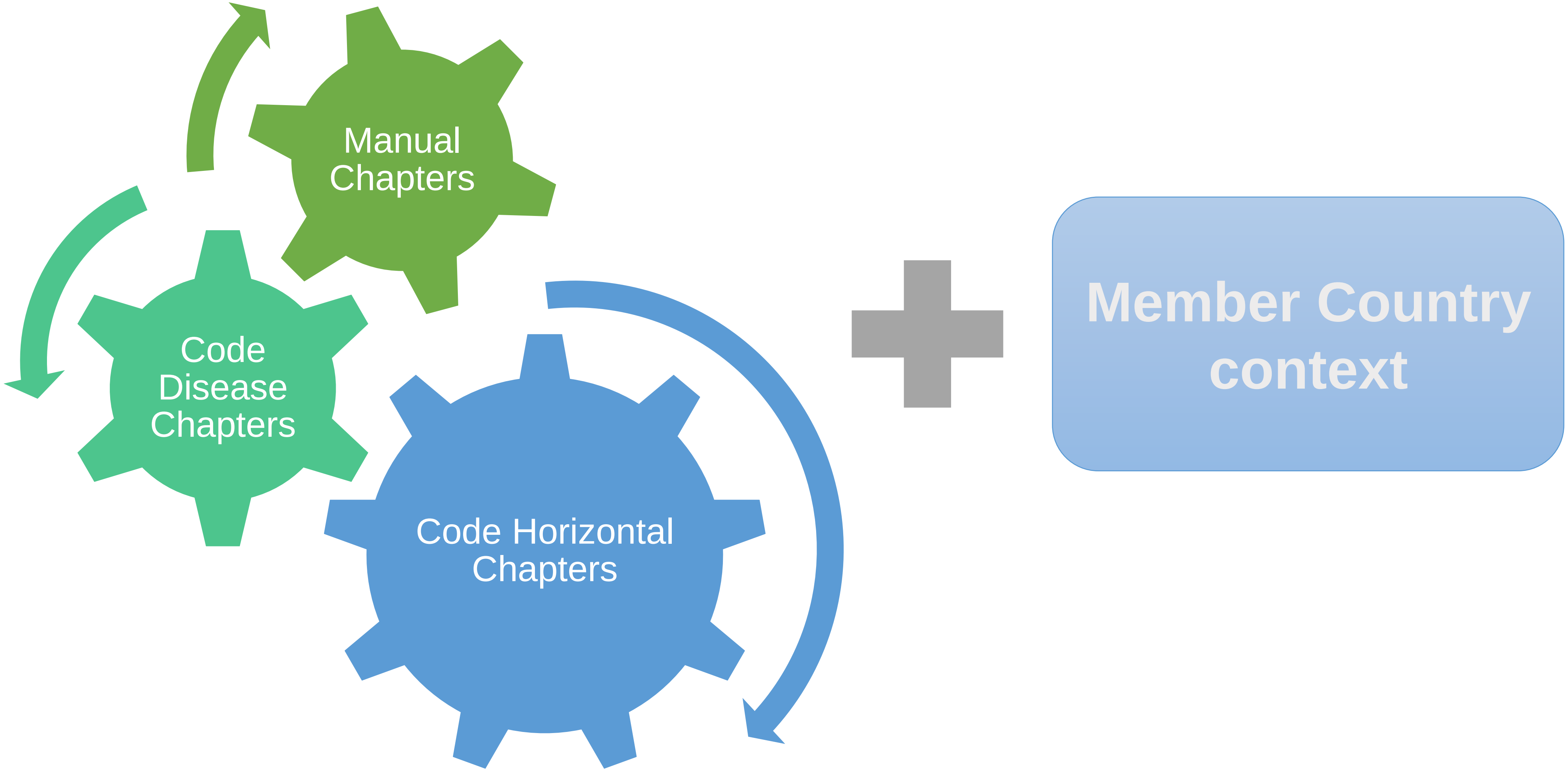
Chapter 1.4. Animal health surveillance
Chapter 1.5. Surveillance for arthropod vectors of animal diseases

Chapter 4.4. Zoning and compartmentalisation
Chapter 4.18. Vaccination
Chapter 4.19. Official control programmes for listed and emerging diseases

Volume II: Disease-specific chapters

Chapter 1.6. Procedures for official recognition of AH status, by WOAH
Chapter 1.7.-1.12. Application for official recognition by WOAH of free status for …

Using the WOAH international standards



Manual Chapters

Code Disease Chapters

Code Horizontal Chapters

Member Country context

Thank you

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World Organisation for Animal Health
Founded as OIE

Organisation mondiale de la santé animale
Fondée en tant qu'OIE

Organización Mundial de Sanidad Animal
Fundada como OIE

WOAH Regional Workshop on Vector Borne diseases in Asia and the Pacific

19-20 September 2024

Updates on recent trends of VBDs Globally and in Asia Pacific reported to WOAH (2023-2024)

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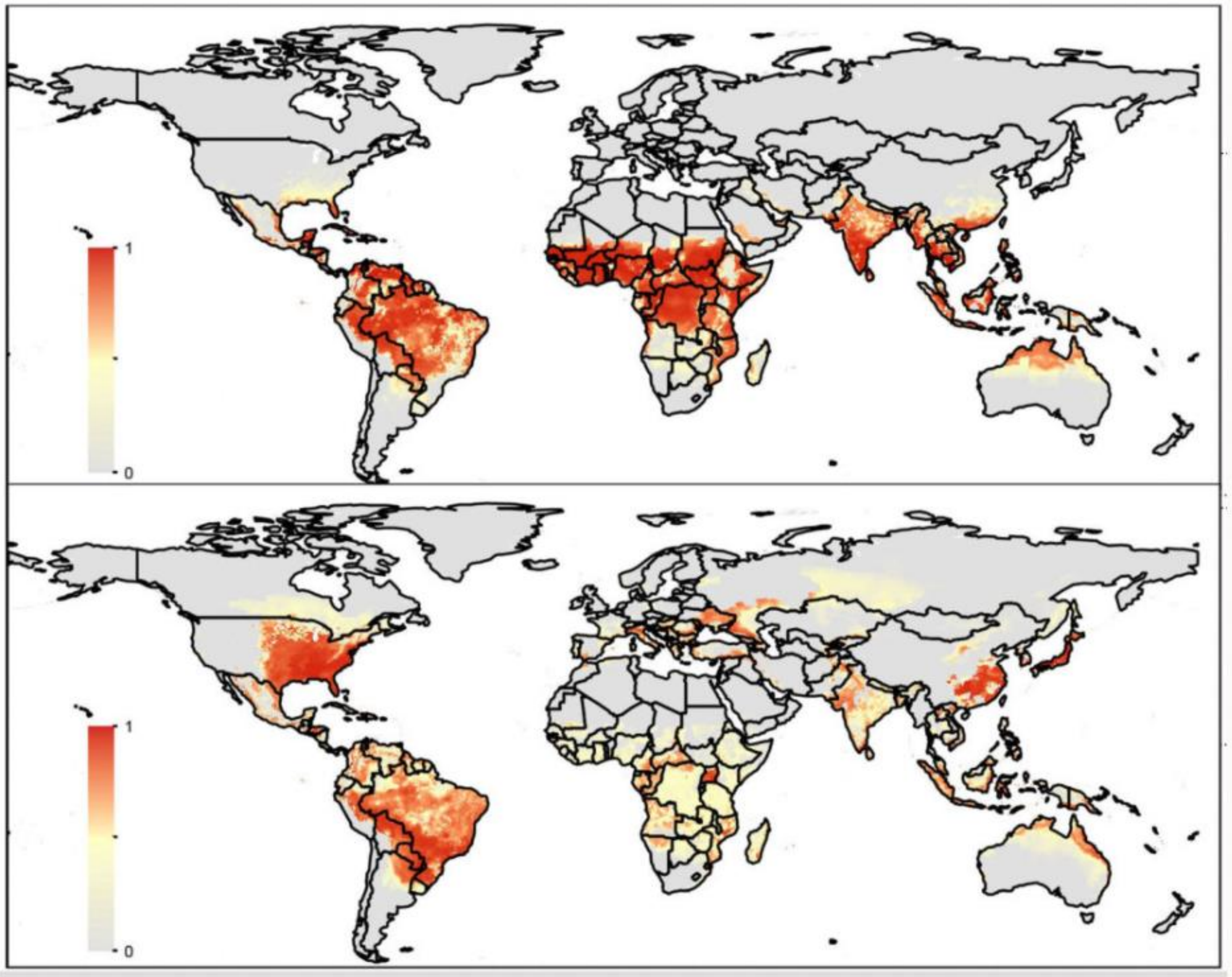
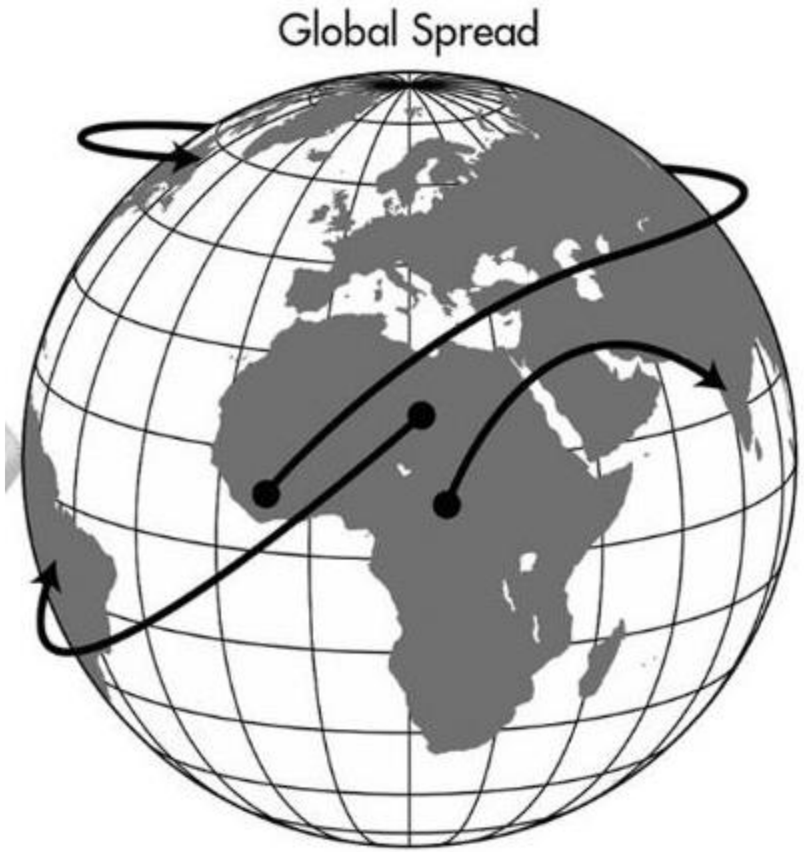
Data Integration Department

Pathogen dynamics in a changing world



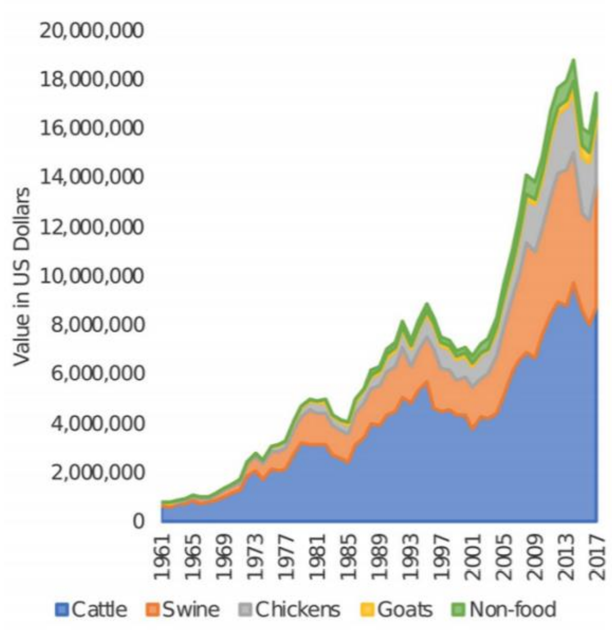
These maps show the predicted global ranges of *Aedes aegypti* (above) and Aedes albopictus (below) in 2050 assuming a 'medium' climate scenario in which greenhouse gas emissions peak in 2080 and then begin to decline. The darker areas have the highest predicted prevalence of mosquitos. MORITZ KRAEMER FOR *NATURE MICROBIOLOGY*

Pathogen dynamics in a changing world



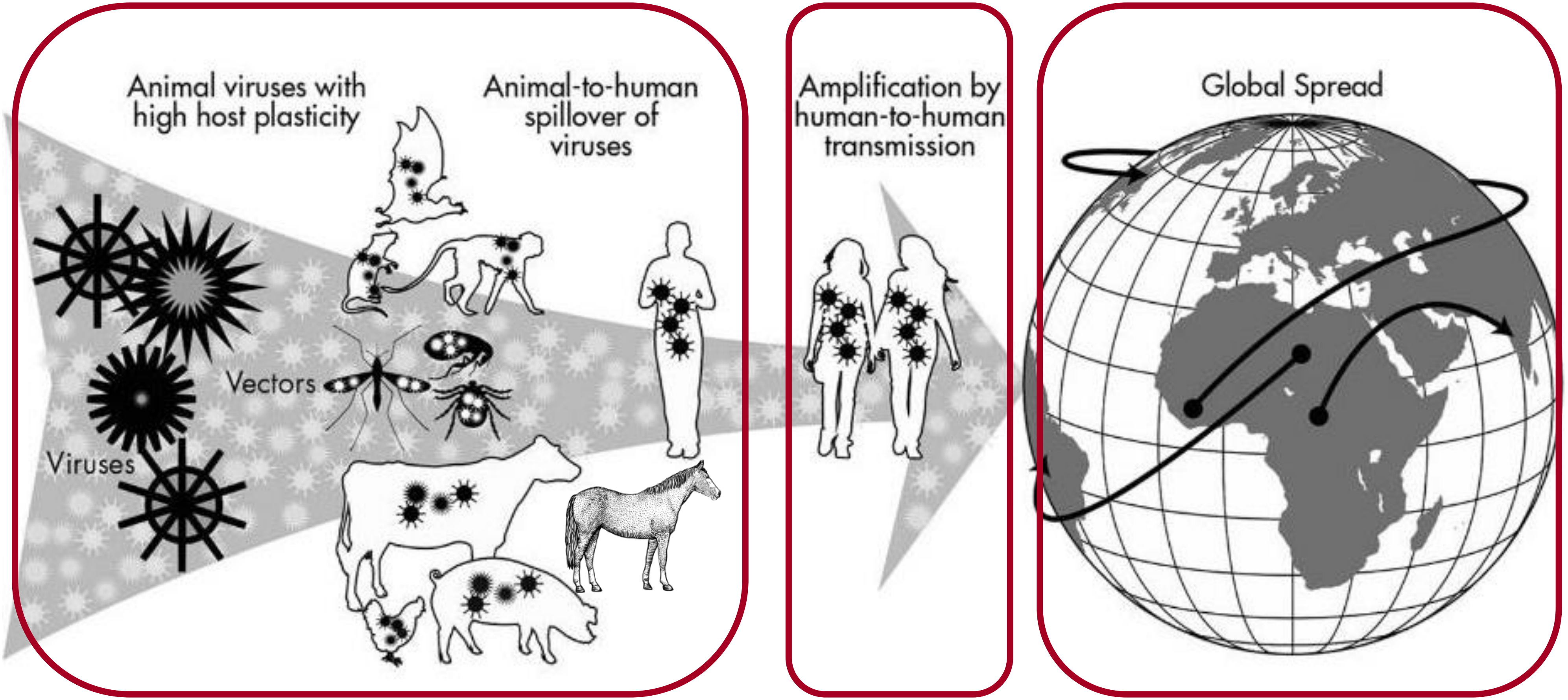
+11 million passengers fly everyday (IATA, 2020)

B. Global trade of live animals



Travoa & Nelson 2020 PloS Pathogens

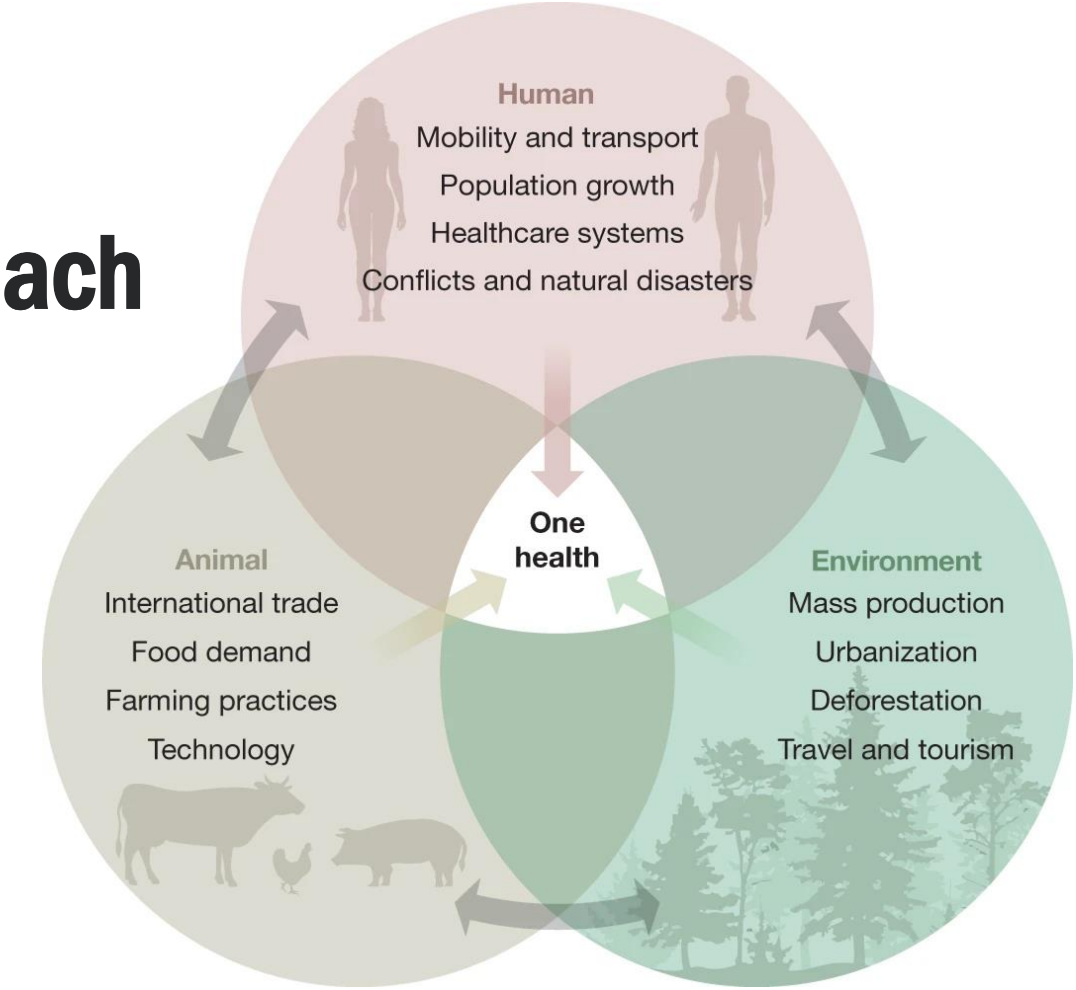
Pathogen dynamics in a changing world



https://www.nature.com/articles/srep14830

Adopting a One Health approach

"Human health and animal health are interdependent and bound to the health of the ecosystems in which they exist."



Human

Mobility and transport

Population growth

Healthcare systems

Conflicts and natural disasters

Animal

International trade

Food demand

Farming practices

Technology

Environment

Mass production

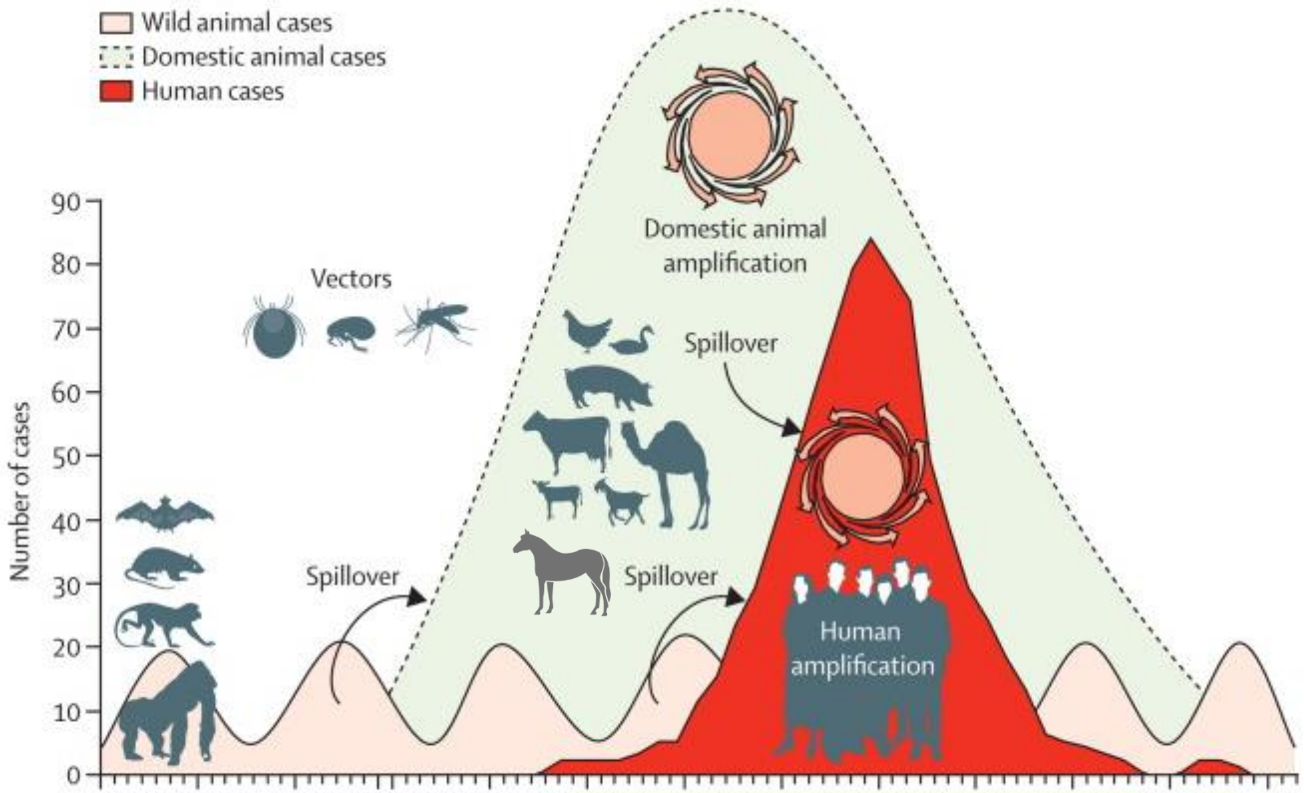
Urbanization

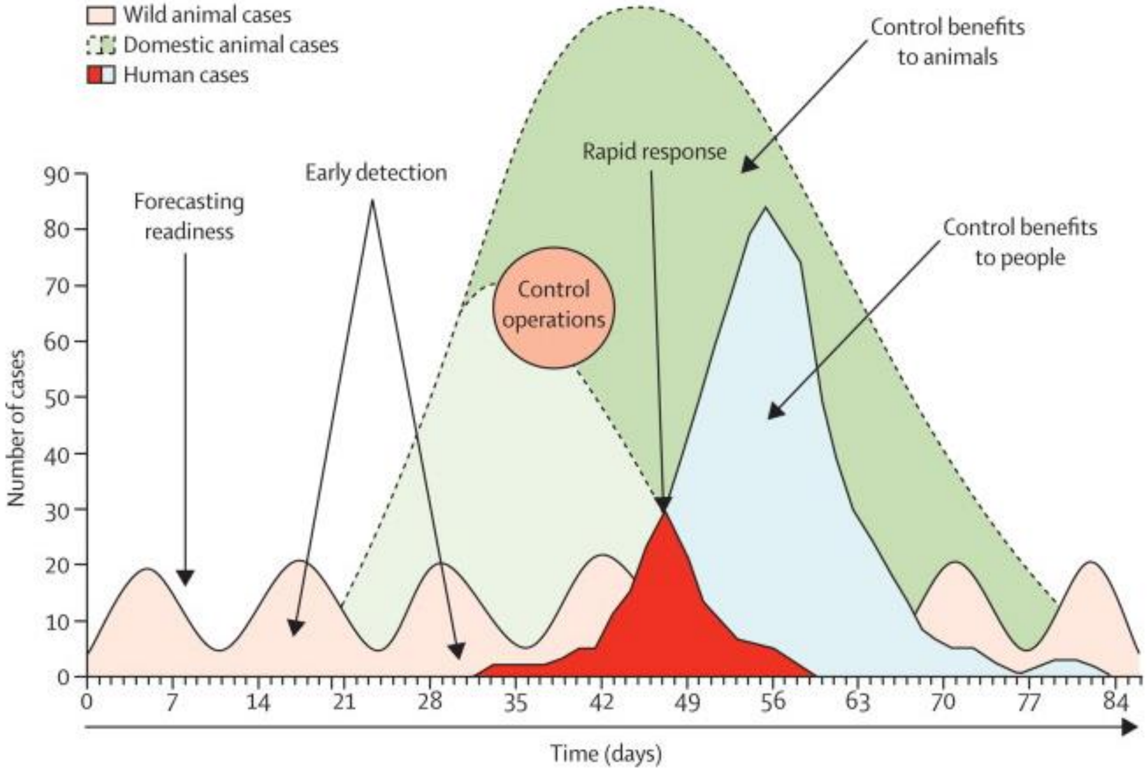
Deforestation

Travel and tourism

One health

Phases of pathogen emergence & surveillance





Relevant epidemiological changes in vector-borne diseases (91GS– Animal Health Situation)

Overview of Vector-Borne Diseases (VBDs)

- **Importance:** VBDs significantly impact both human and animal health globally
- **Climate Change Impact:** Alters vector density, activity periods, and geographical distribution, increasing the risk of VBD spread
- The transmission potential of these diseases is **also influenced by a range of factors**, including socio-economics, health-care capacity and ecology.

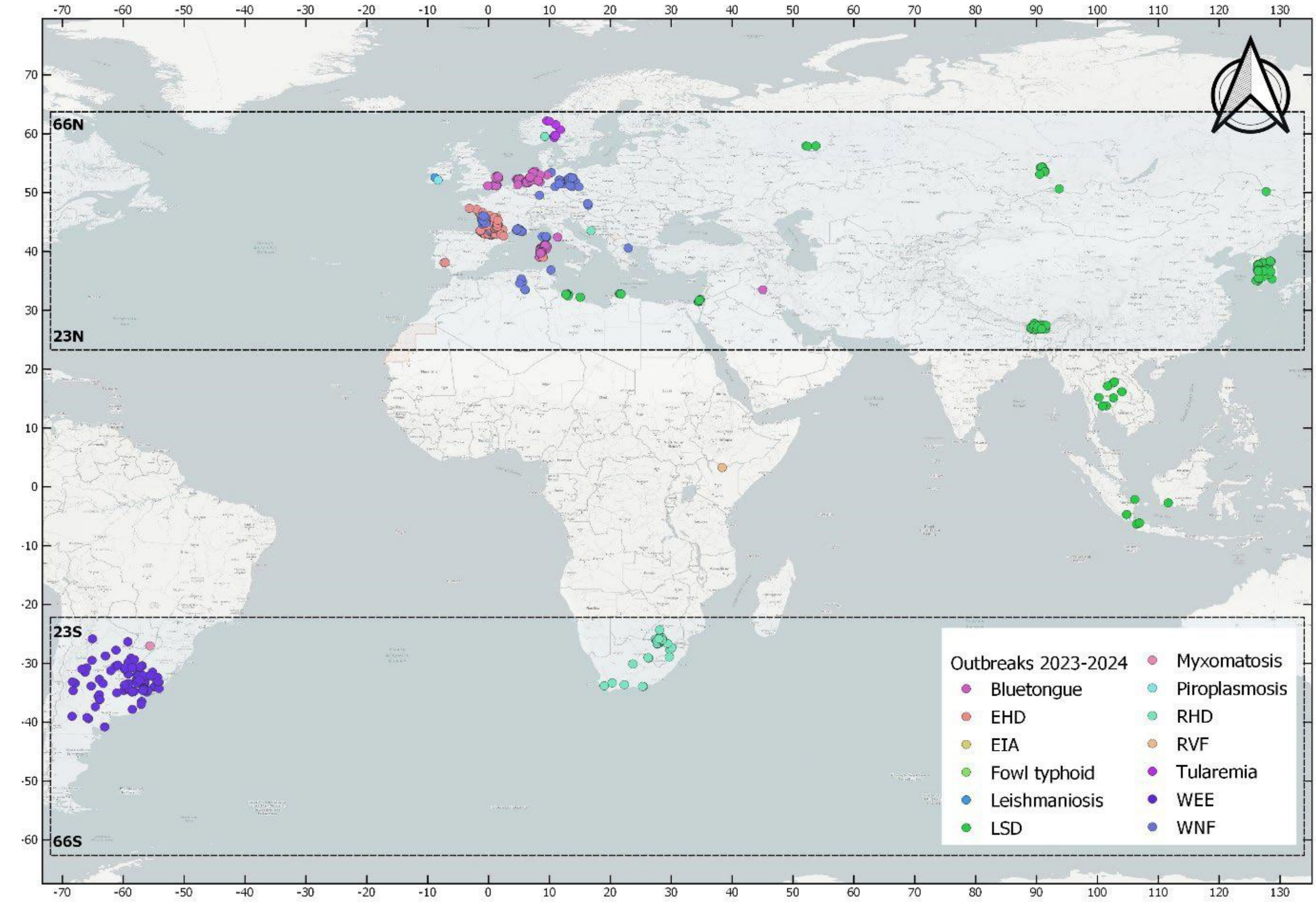
Reporting of VBDs in 2023-2024 -**Key Statistics**:

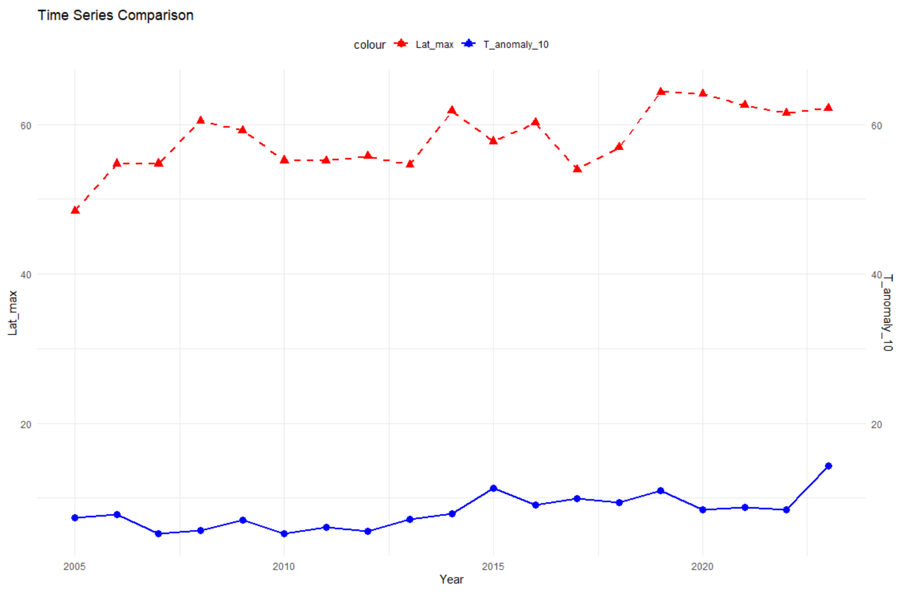
- **Most frequently reported:** West Nile Fever (12 notifications), Bluetongue (8), Lumpy Skin Disease (7), and Equine Infectious Anaemia (6).
- **Geographical Spread:** 28 countries reported 2,422 outbreaks, primarily in the Americas and Europe. Most of the outbreaks were concentrated in the Americas, with a very large event of Western equine encephalomyelitis (Western) (1,461 outbreaks), followed by Europe with 697 outbreaks, in this case reported for eight different VBDs.
- Lumpy skin disease was the most frequently reported VBD in Asia, with 144 outbreaks.

Relevant epidemiological changes in vector-borne diseases (91GS– Animal Health Situation)

- **VBDs and Climate Change- Significant Observations:**
- 99% of VBD outbreaks reported were in temperate regions.
- Increasing trend in the maximum latitude of VBD outbreaks, correlated with rising global temperatures.

Spatial distribution of outbreaks reported to WOAH for ten VBDs through immediate notifications and follow-up reports during 2023 and early 2024 (as of 8 March).The limits of the temperate regions (23.5° and 66.5° N/S of the Equator) are shown on the map:





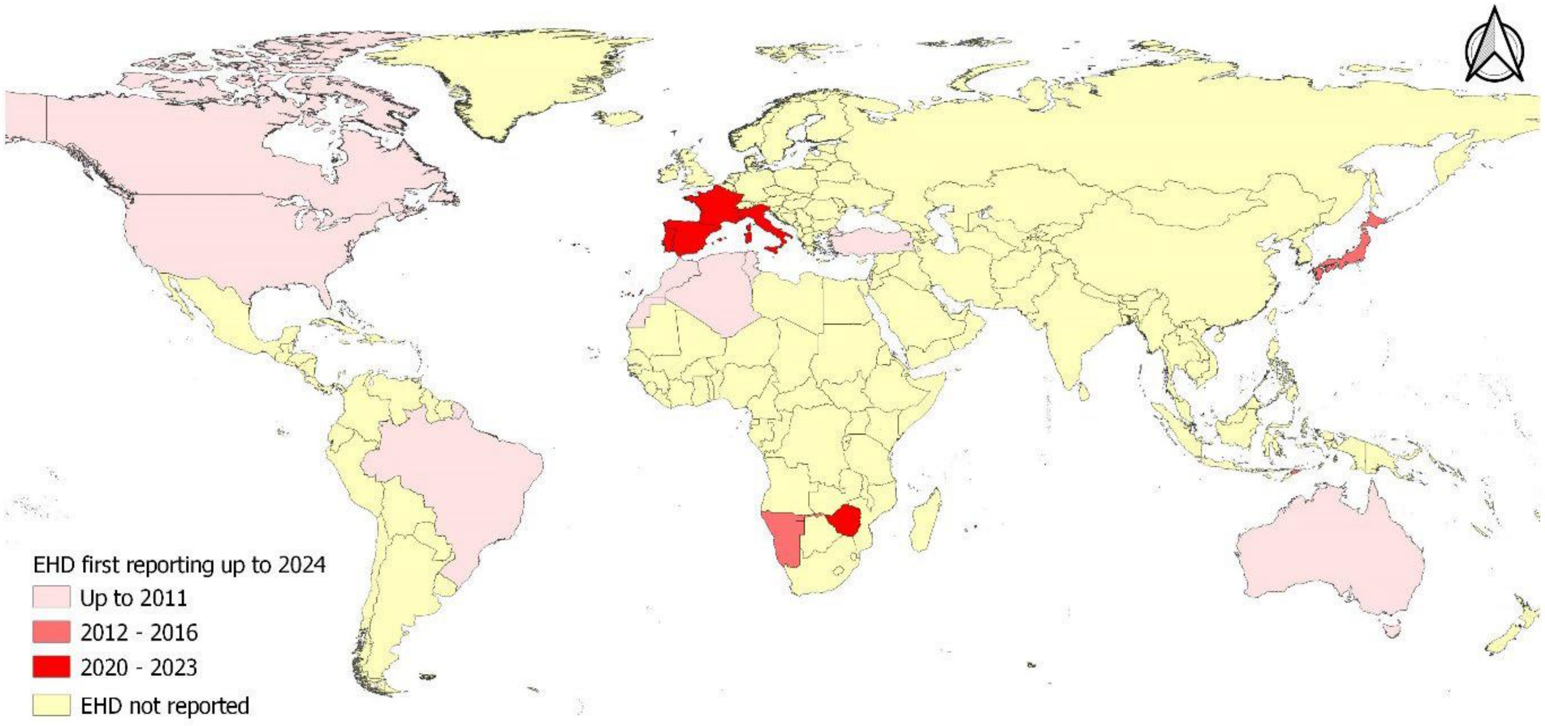
Time series comparison of the maximum annual latitude at which outbreaks were reported and the global annual anomaly temperature detection for the period 2005–2023.

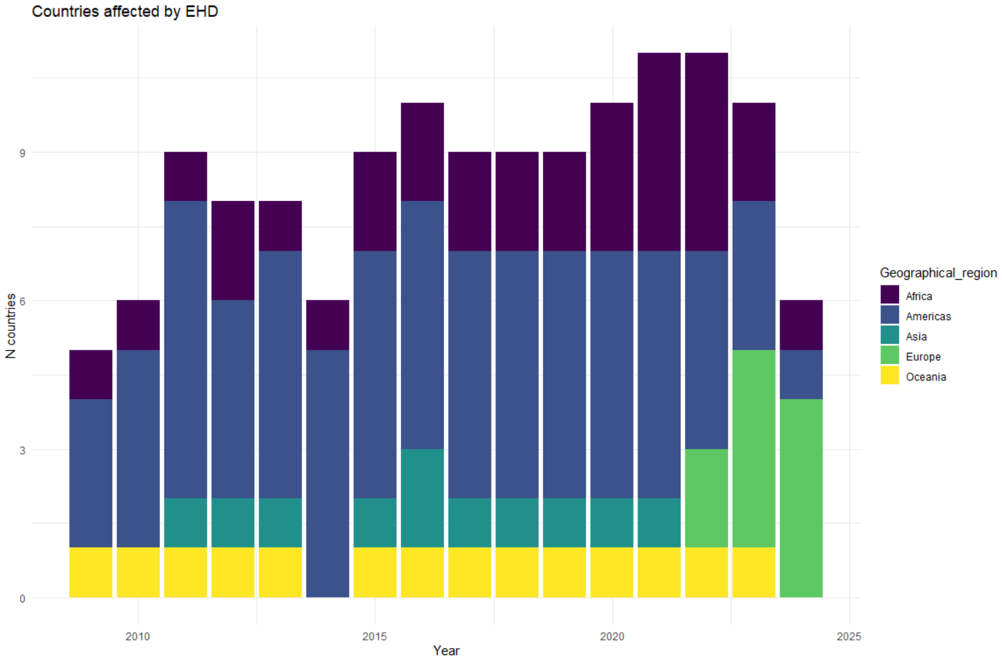
Relevant epidemiological changes in vector-borne diseases (91GS– Animal Health Situation)

Case Study: Epizootic Haemorrhagic Disease (EHD)

- **Spread:** EHD has expanded from North America to new areas, including Europe since 2022. At a global level, 23 countries have reported the presence of the disease since 2009.
- **Recent Developments**: 252 new outbreaks reported in Europe across four countries since 2022.

Global spread of EHD up to 2024. The map categorises countries based on the year of first reporting of the disease:

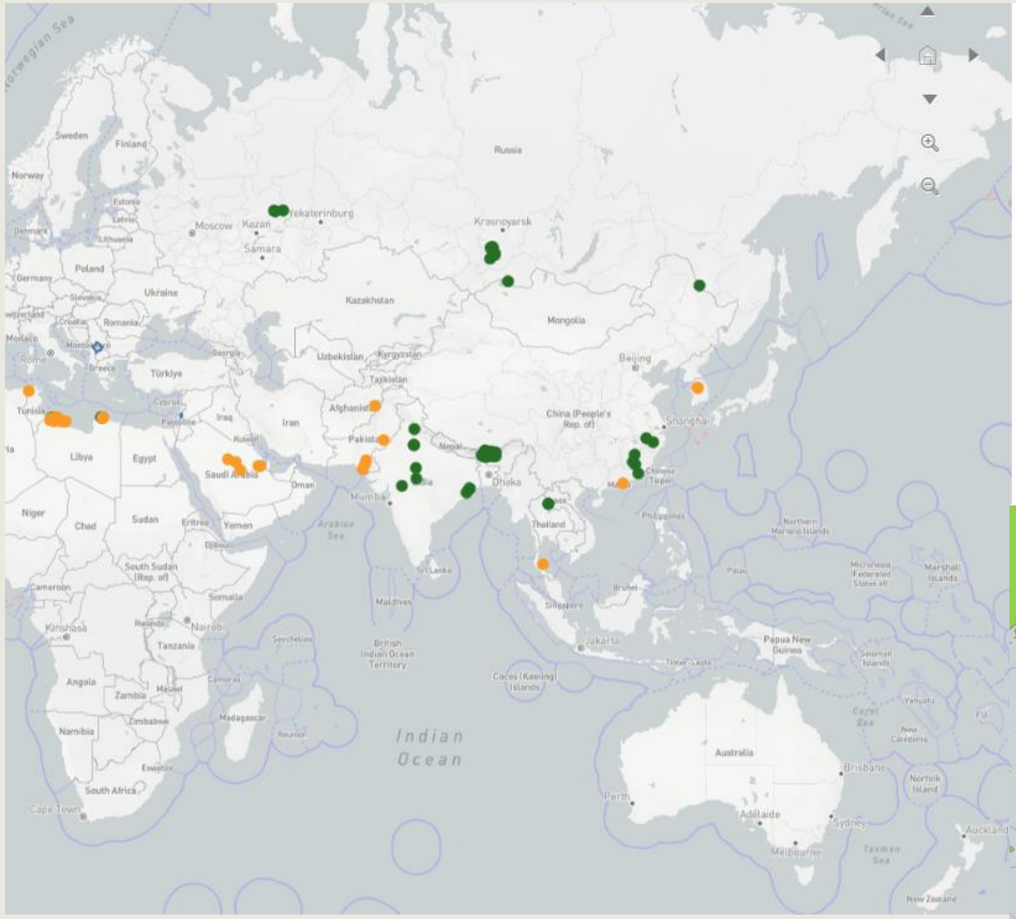




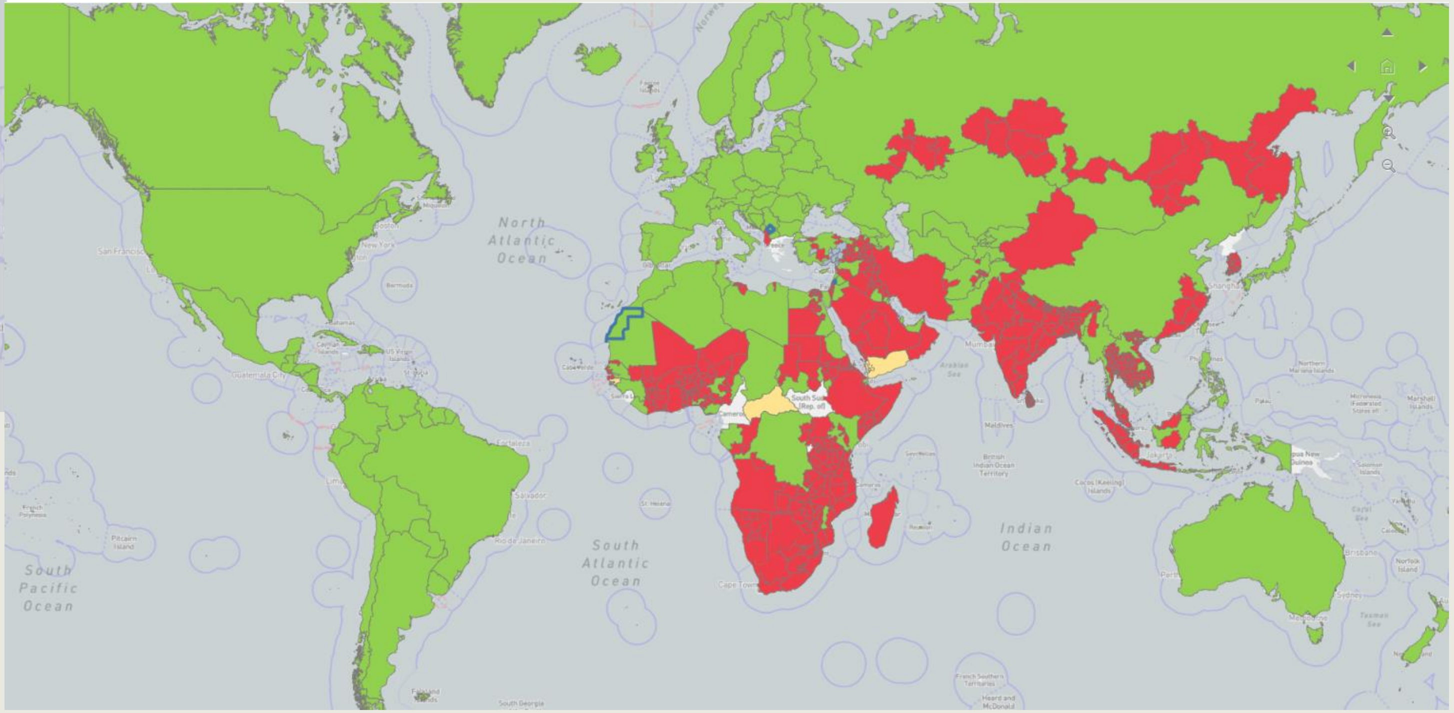
Evolution of countries reporting the presence of EHD during the period 2009–2024 (as of 8 March). Data for the different geographical regions are shown in the bar chart

DISEASE DISTRIBUTION: Lumpy Skin Disease- Data from WAHIS (2019-2024)

- 2060 ⬜ - No data available
- 🟦 9 No information
- 🟩 8 Never reported
- 🟩 7 Absent
- 🟨 6 Suspected limited zones
- 🟨 5 Suspected
- 🟧 4 Inf./Infest. limited zones
- 🟧 3 Inf./Infest.
- 🟥 2 Present limited zones
- 🟥 1 Present



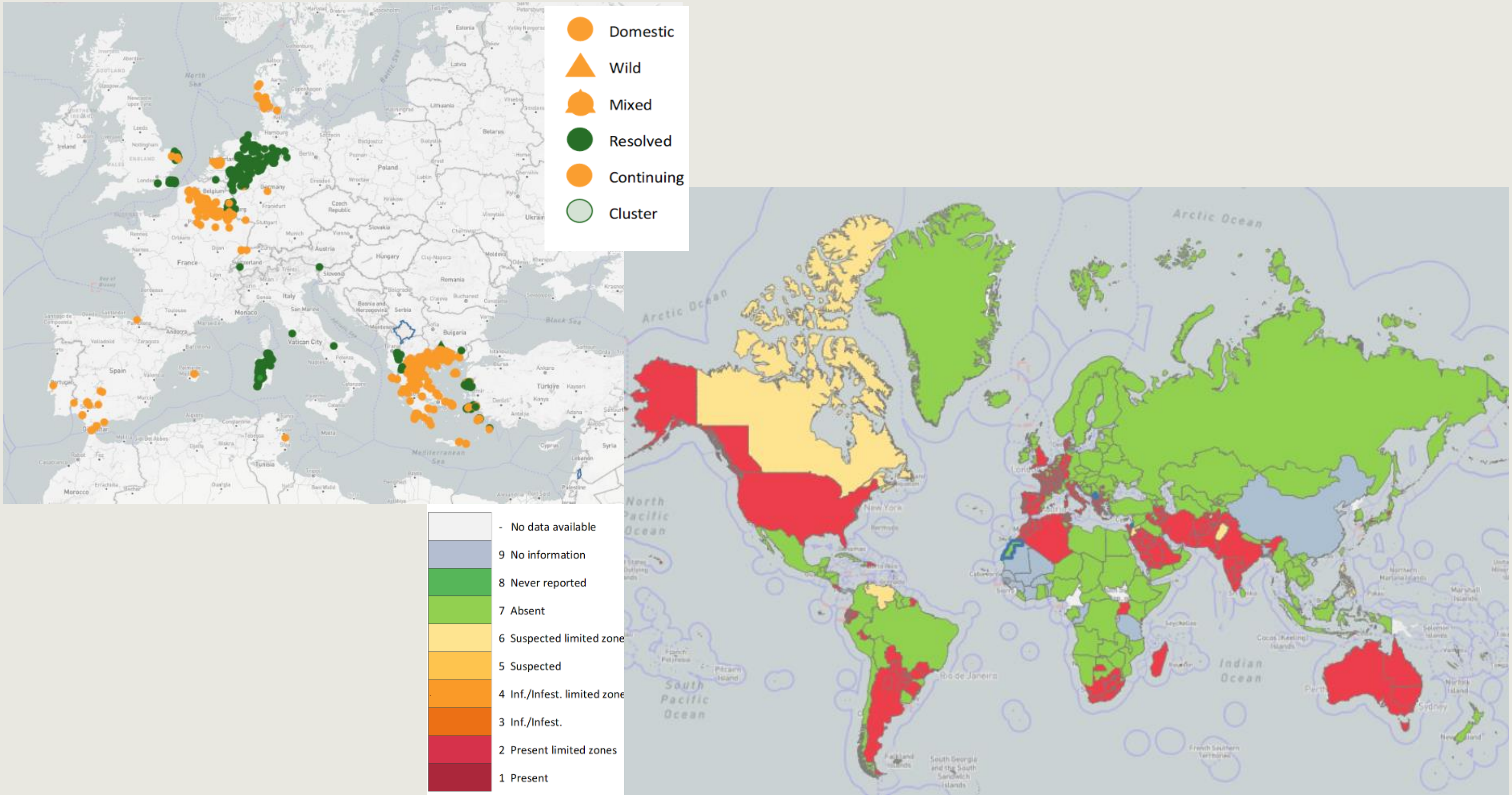
- ● Domestic
- ▲ Wild
- ● Mixed
- ● Resolved
- ● Continuing
- ○ Cluster



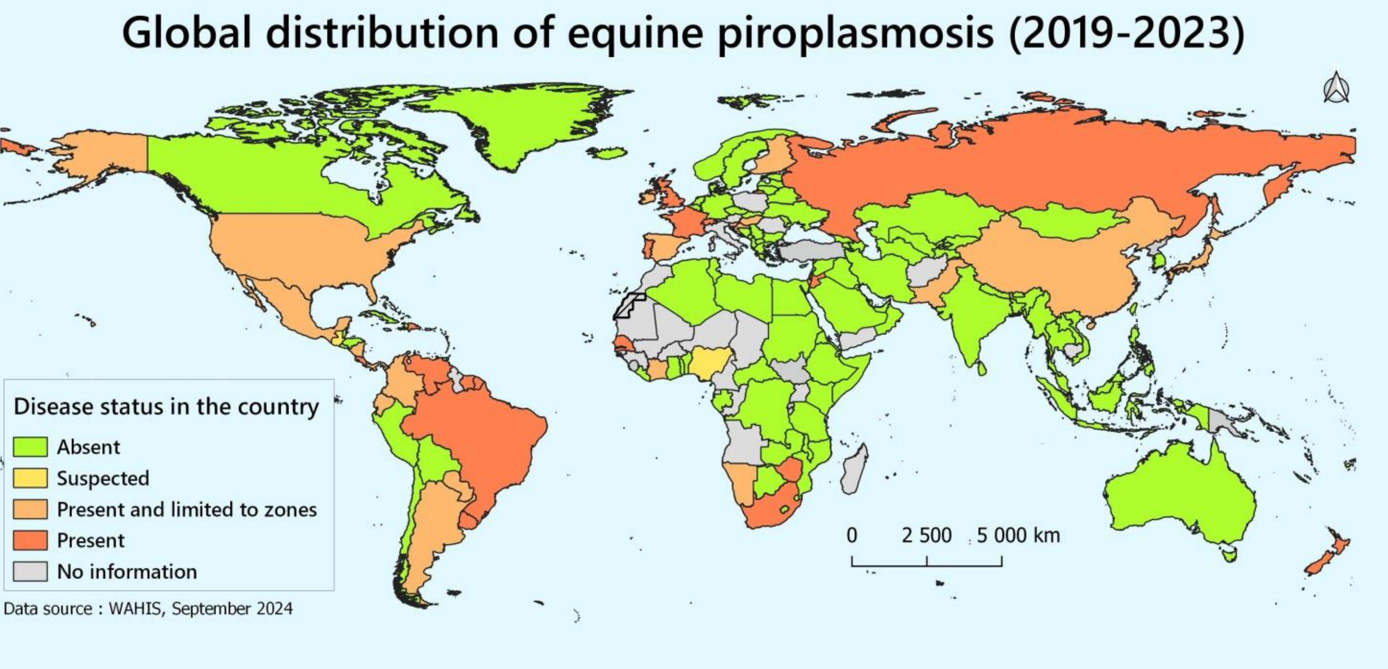
Case Study from the Region: Outbreaks of Japanese Encephalitis (Australia)

- Outbreaks of Japanese encephalitis have been reported in piggeries in Queensland, New South Wales, Victoria and South Australia.
- Climate conditions of above median rainfall and warmer minimum temperature may have been a factor in the event.
- Spillover events into Humans and a case in an Alpaca
- Infection with JE virus in horses were not detected
- Trade restrictions for the movement of horses according to WOAH provisions triggered the revision of the JE Code Chapter

DISEASE DISTRIBUTION: Bluetongue- Data from WAHIS (2019-2024)

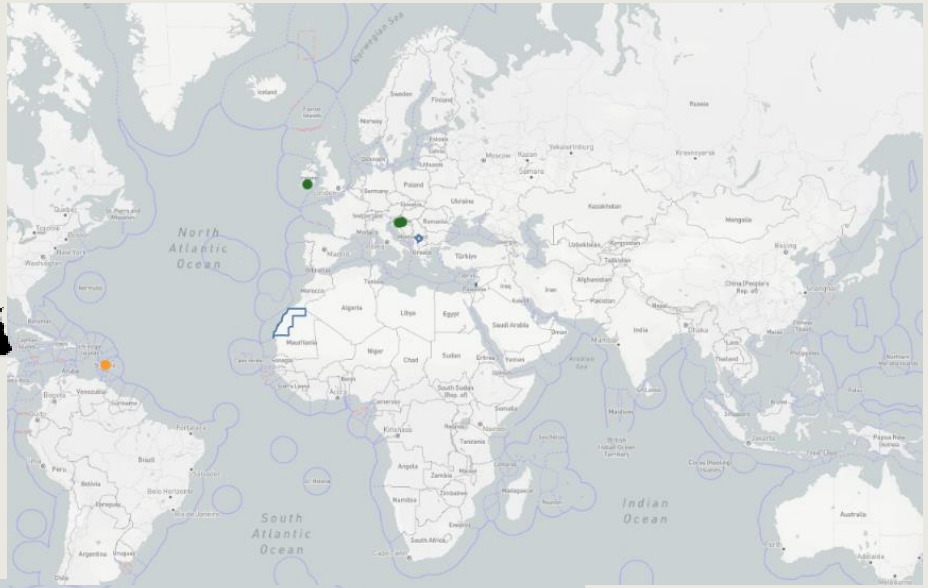


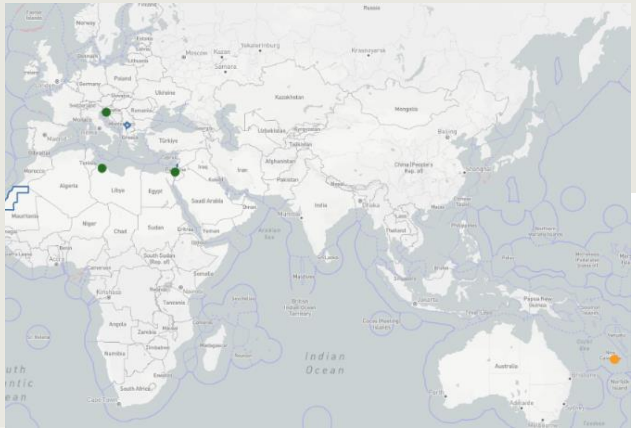
DISEASE DISTRIBUTION: Equine Piroplasmosis & Bovine Babesiosis– Data from [WAHIS]

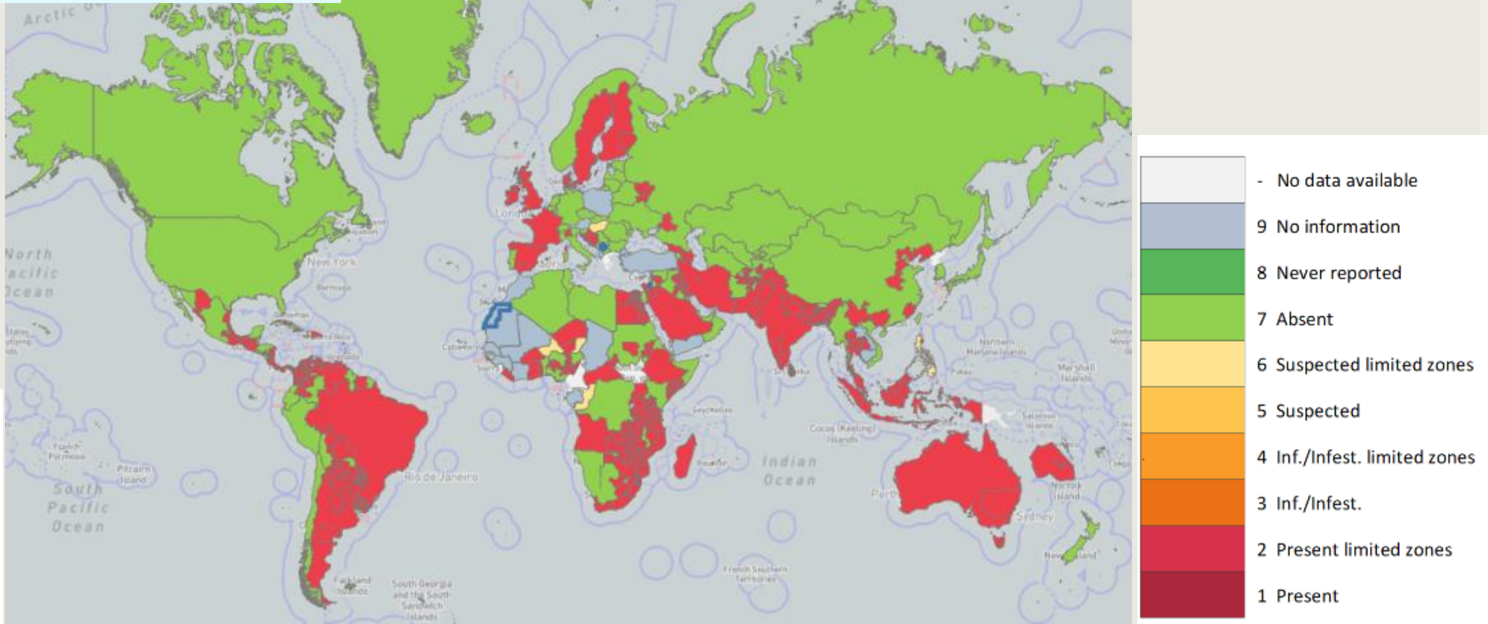


Global distribution of equine piroplasmosis (2019-2023)

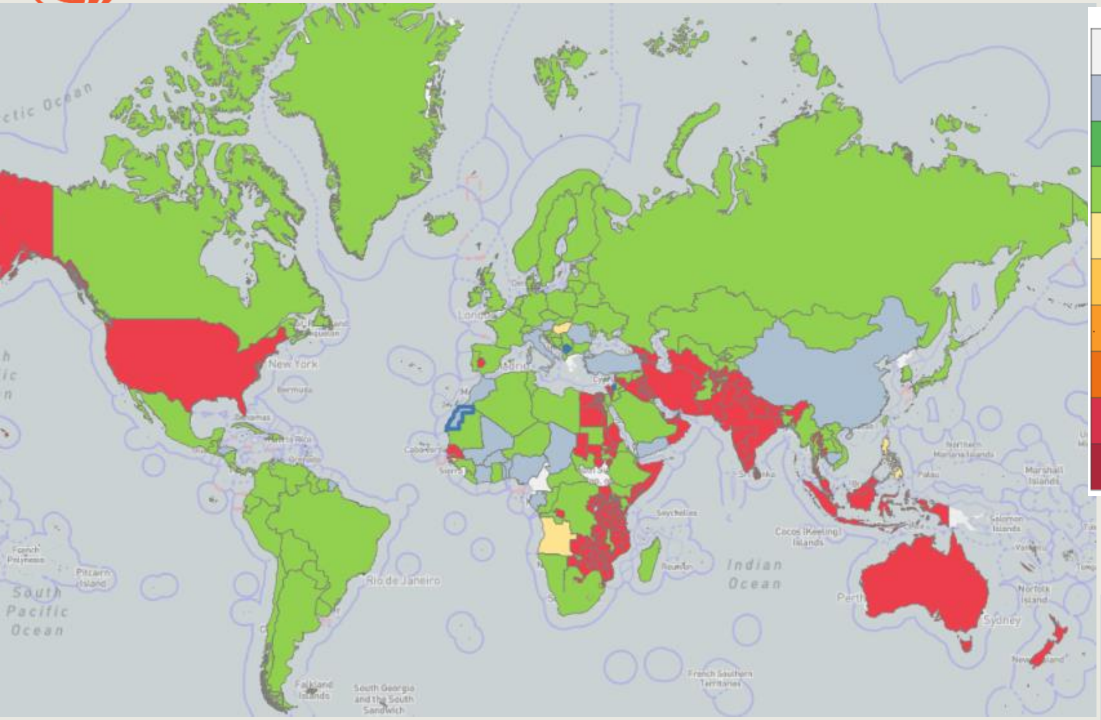
Data source : WAHIS, September 2024

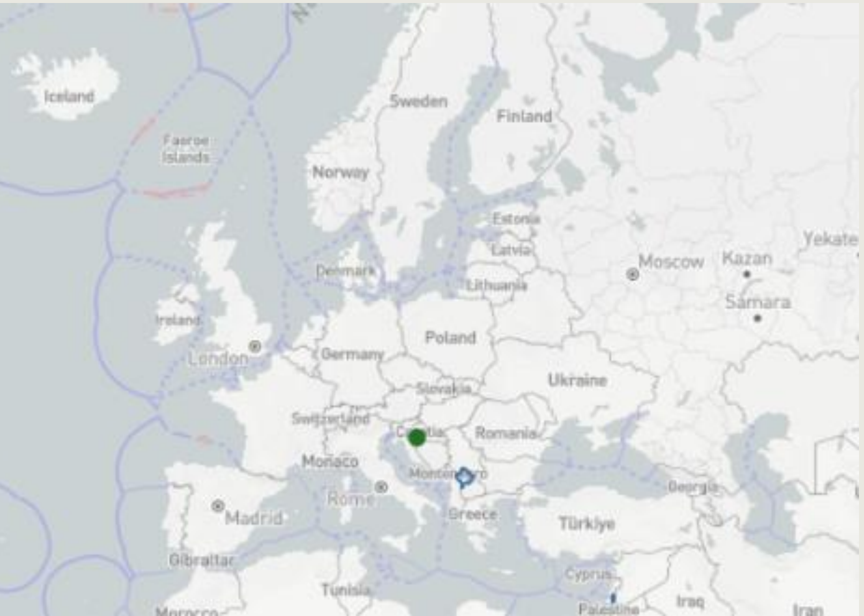


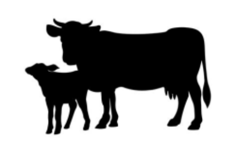




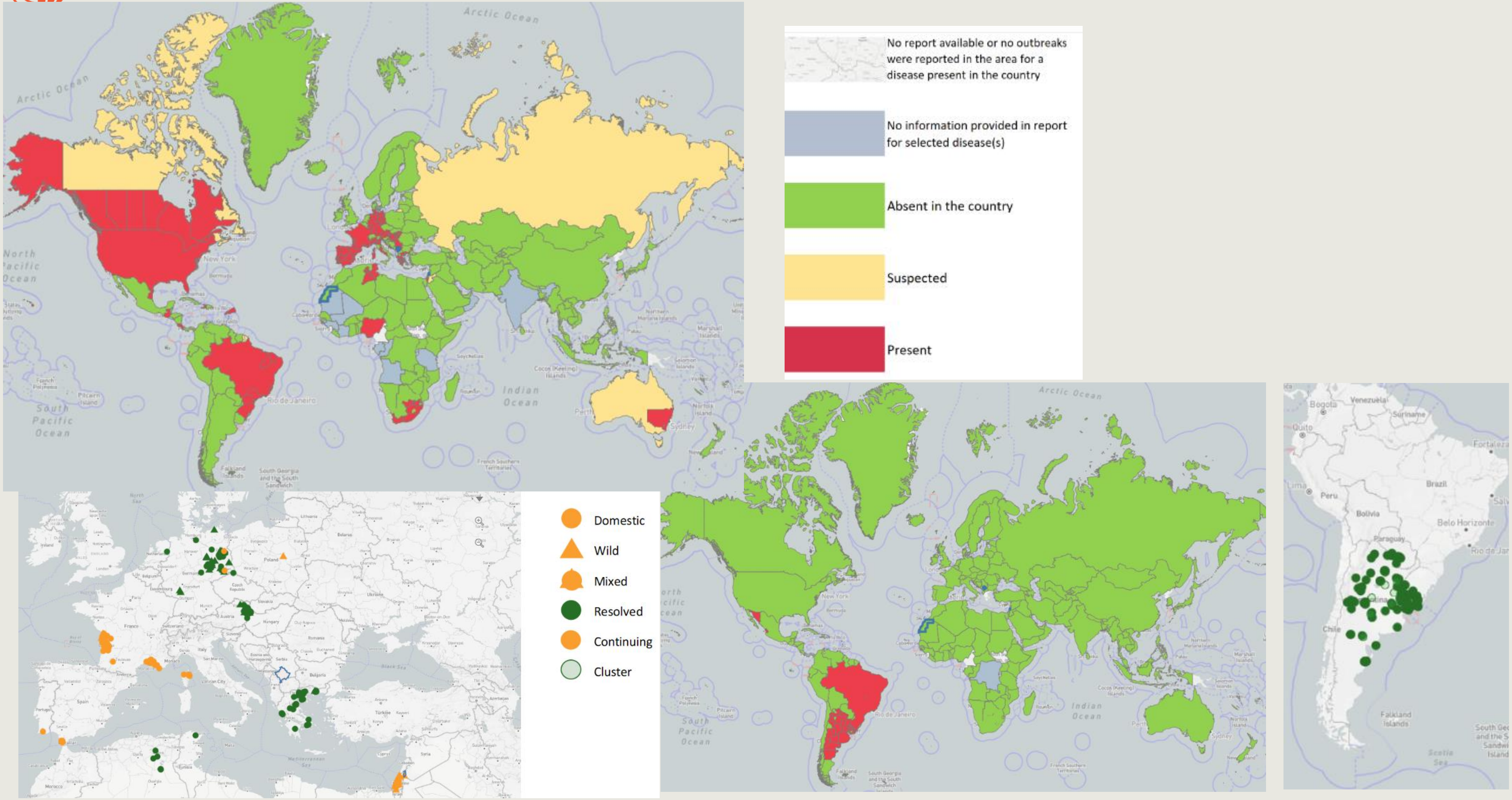
DISEASE DISTRIBUTION: Theileriosis (left above) & Bovine Anaplasmosis (below) – Data from **WAHIS**





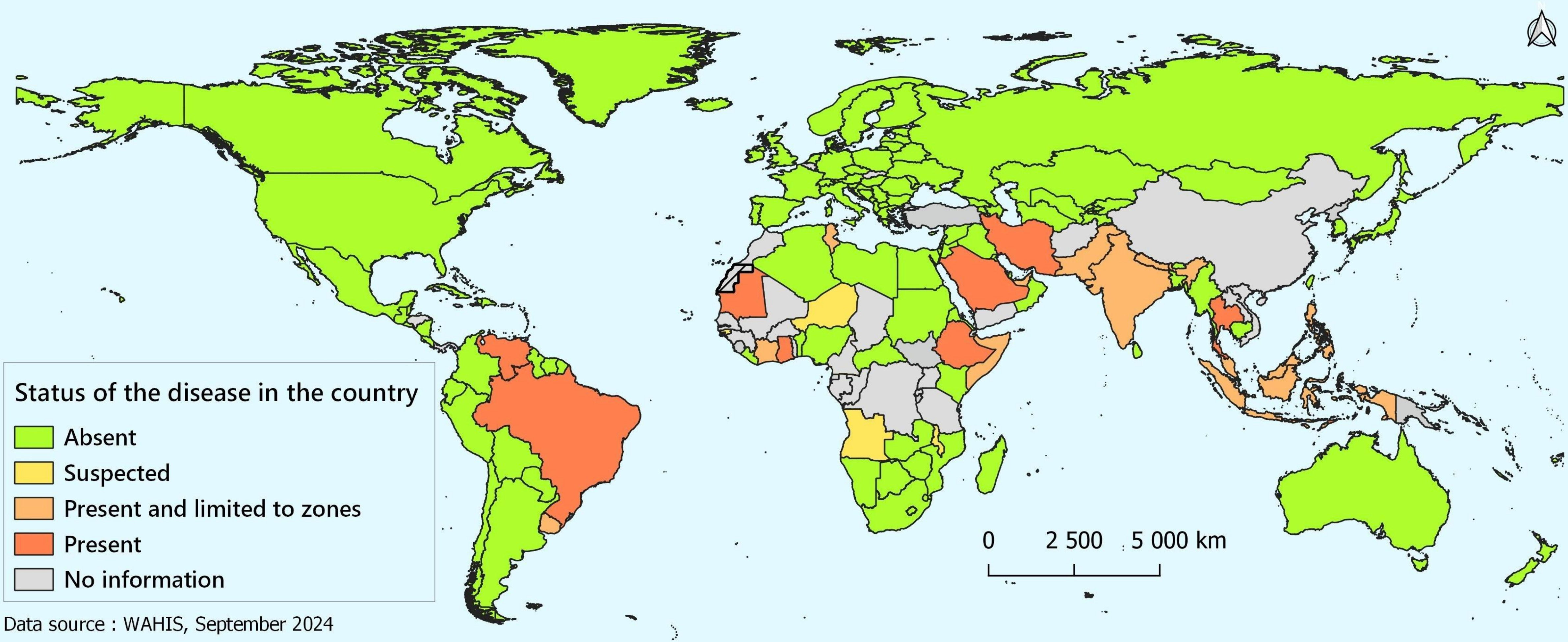


DISEASE DISTRIBUTION: West Nile Fever (left) & Western Equine Encephalomyelitis (right) -WAHIS



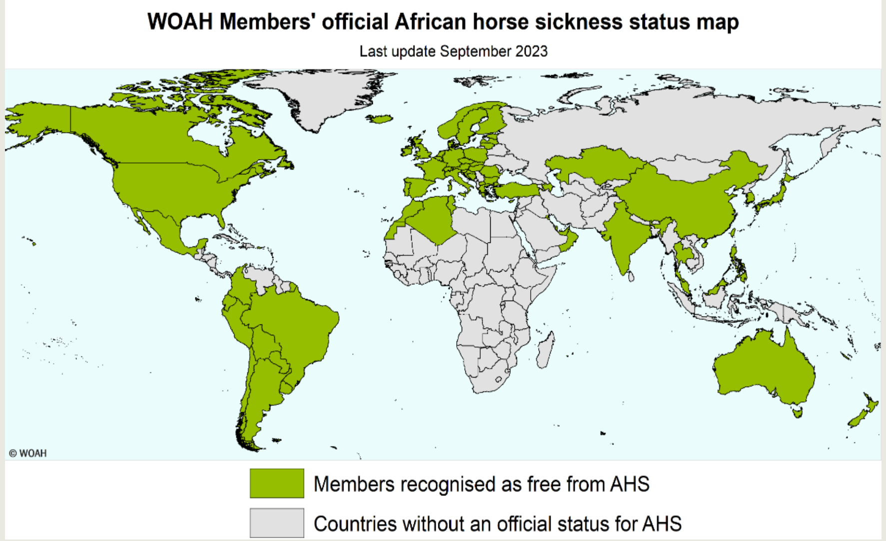
DISEASE DISTRIBUTION - Data from the World Animal Health Information System (WAHIS)

Global distribution of Surra (Trypanosoma evansi) (2019-2023)



Data source : WAHIS, September 2024

DISEASE DISTRIBUTION - Data from the World Animal Health Information System (WAHIS)

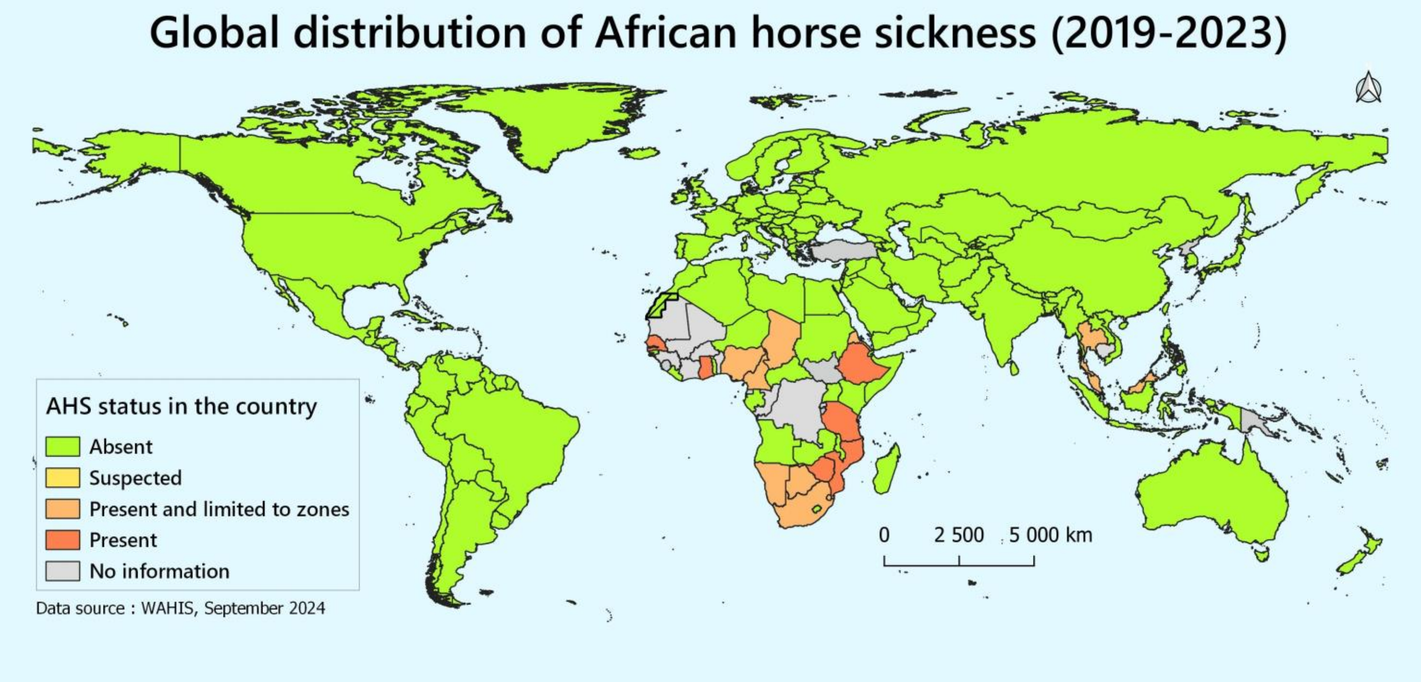


WOAH Members' official African horse sickness status map

Last update September 2023

© WOAH

- 🟩 Members recognised as free from AHS
- ⬜ Countries without an official status for AHS



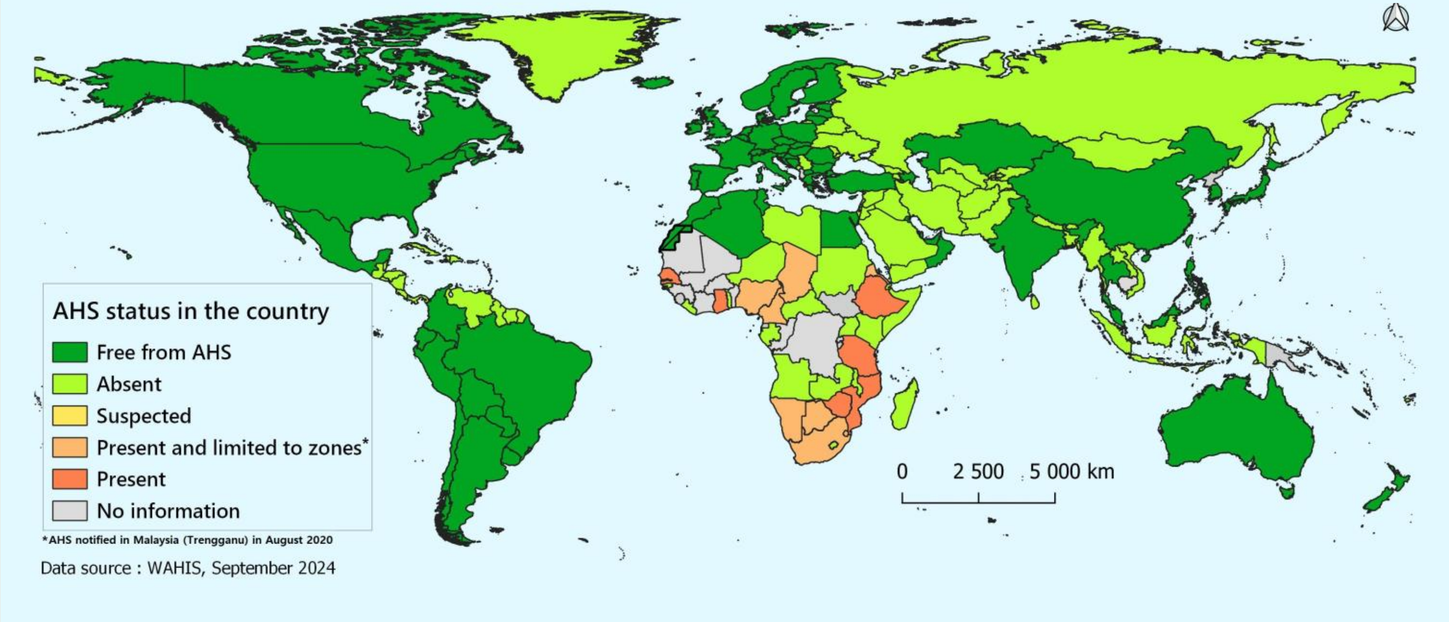
Global distribution of African horse sickness (2019-2023)

AHS status in the country

- 🟩 Absent
- 🟨 Suspected
- 🟧 Present and limited to zones
- 🟥 Present
- ⬜ No information

Data source : WAHIS, September 2024

Global distribution of African horse sickness



AHS status in the country

- 🟩 Free from AHS
- 🟩 Absent
- 🟨 Suspected
- 🟧 Present and limited to zones*
- 🟥 Present
- ⬜ No information

*AHS notified in Malaysia (Trengganu) in August 2020

Data source : WAHIS, September 2024

OIE WORLD ORGANISATION FOR ANIMAL HEALTH
Protecting animals, preserving our future

Certificate¶

African horse sickness status ¶

¶

This is to certify that, following a recommendation of the OIE Scientific Commission for Animal Diseases, the World Assembly of Delegates of the OIE approved on 24 May 2016 the proposal that Kazakhstan be recognised by the OIE as a country free from African horse sickness (AHS) in accordance with the OIE *Terrestrial Animal Health Code* (2015).¶

Key Takeaways:

Climate change is a major driver in the spread of VBDs

- **Expanded Geographical Range**
- **Increased Vector Activity**
- **Unpredictable Outbreaks**
- **Correlation with Global Warming:**

Recommendations

- **Heightened Disease Surveillance**
- **Need for Global Collaboration**
- **Health and Economic Impacts**

Continuous monitoring and adaptive strategies are crucial for effective VBD management.

Thank you

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Regional workshop on Vector Borne Disease
for Asia and the Pacific 2024

NARO 農研機構

Arbovirus infections of livestock animals in Asia:
what we know and don’t know

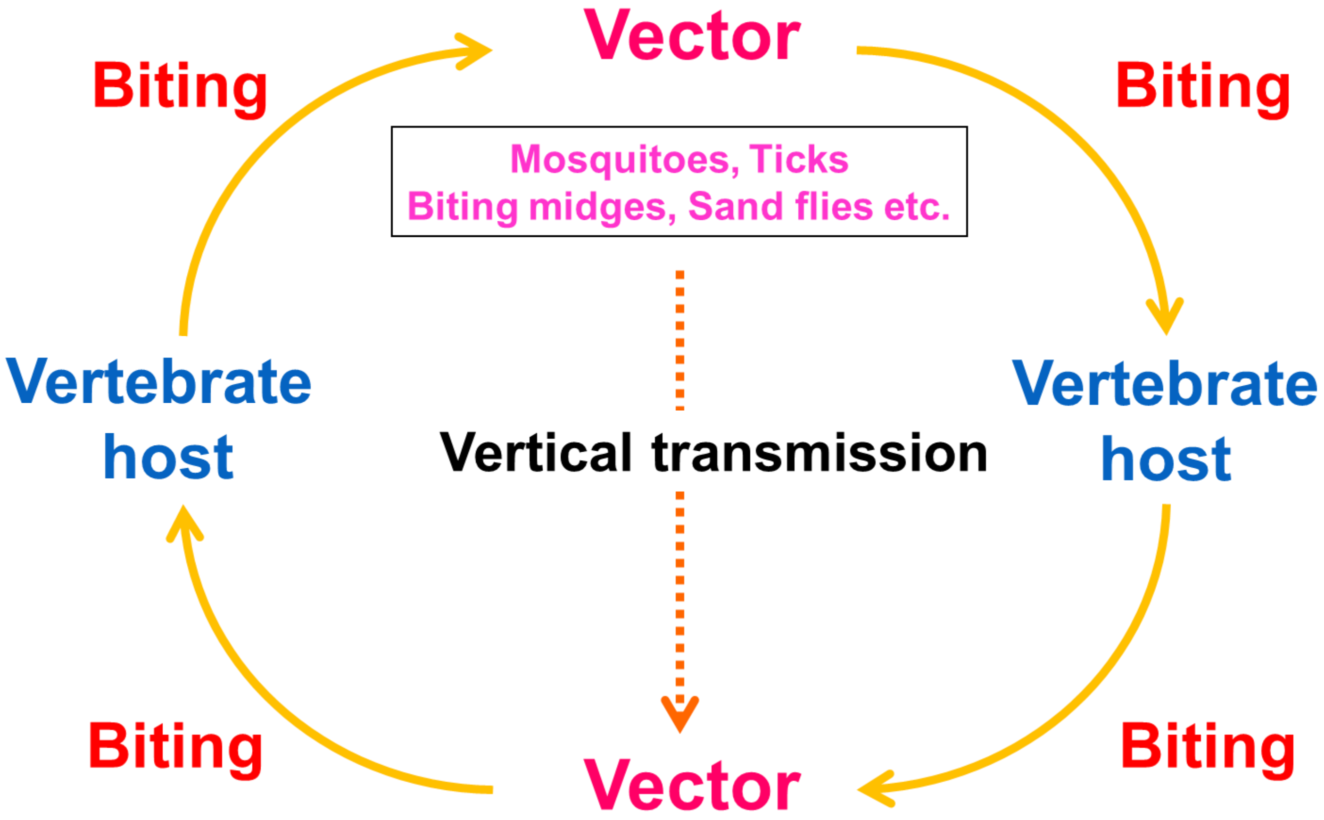
Tohru Yanase

Kagoshima Research Station,
National Institute of Animal Health, NARO,
Japan

NARO

Arbovirus (Arthropod-borne virus)

- Arboviruses are transmitted by arthropod vectors via blood sucking process.
- Arboviruses replicate in both arthropod vectors and vertebrate hosts.
- Arboviruses include many taxonomically different virus groups.



WOAH-listed arbovirus infections in Asia

Infection	Affected animal	Zoonosis	Endemic in Asia	Vector
Bluetongue	ruminants	No	Yes	*Culicoides*
Epizootic hemorrhagic disease	ruminants	No	Yes	*Culicoides*
African horse sickness	horse	No	No	*Culicoides*
Japanese encephalitis	pig, horse	Yes	Yes	mosquitos
Nairobi sheep disease	sheep	No	Yes	ticks
Crimean–Congo hemorrhagic fever	ruminants*	Yes	Yes	ticks
African swine fever	pig	No	Yes	ticks**

* Subclinical in most cases

** Highly contiguous between animals without ticks

- We don’t know the past and present status of the listed arbovirus infections in detail.

Due to

Lack of accurate information of affected animals, epidemiology, etiology and so on…..

Bluetongue (BT):

- Infection with BT virus and affecting ruminants
- High mortality rate in sheep of up to 70%
- Reported sporadic outbreaks in Asia

Epizootic hemorrhagic disease (EHD):

- Infection with EHD virus
- Severe clinical symptoms in white tailed deer and cattle
- Large outbreaks of Ibaraki disease with deglutition disorder in Japan

- BT and EHD viruses have been circulating in Asia.
- Multiple serotypes of these viruses are prevalent.

We don’t know

How many animals are affected by both infections (no good statistical data).

Which serotypes and/or strain has high virulent to domestic animals.

Which vector species principally transmit the viruses in each region.

Not listed, but important arbovirus infections in Asia

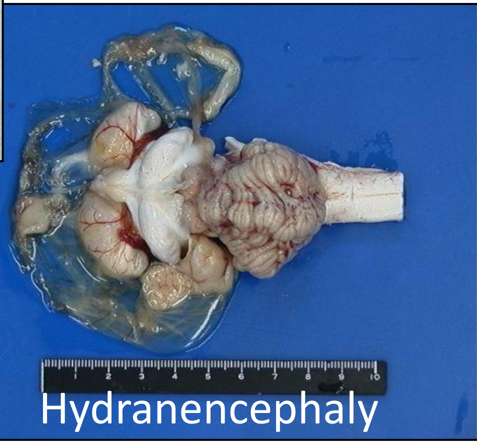
Infection	Affected animal	Manifestations	Vector
Akabane disease	ruminants	abortion, premature birth, congenital malformations	*Culicoides*
Aino virus infection	ruminants	abortion, premature birth, congenital malformations	*Culicoides*
Chuzan disease	cattle	congenital malformations	*Culicoides*
Bovine ephemeral fever	cattle, water buffalo	cessation of lactation in dairy cattle, loss of condition in beef cattle	mosquito or *Culicoides*
Getah	horse, pig	fever, edema, rash (horse) reproductive disorders (pig)	mosquito

- The causative viruses have been isolated/detected in Asian countries/regions.
- These arbovirus infections have impacted livestock industry for many years.

The current status of these arbovirus infections are not shared in regional and global levels.

Akabane disease

Arthrogryposis



Hydranencephaly

Etiological agent:

Akabane virus

Genus: *Orthobunyavirus*

Symptoms:

- Abortion, premature birth, still birth, congenital abnormalities (in utero infection)
- Encephalomyelitis (postnatal infection)

Affected hosts:

Cattle, water buffalo, sheep, goat

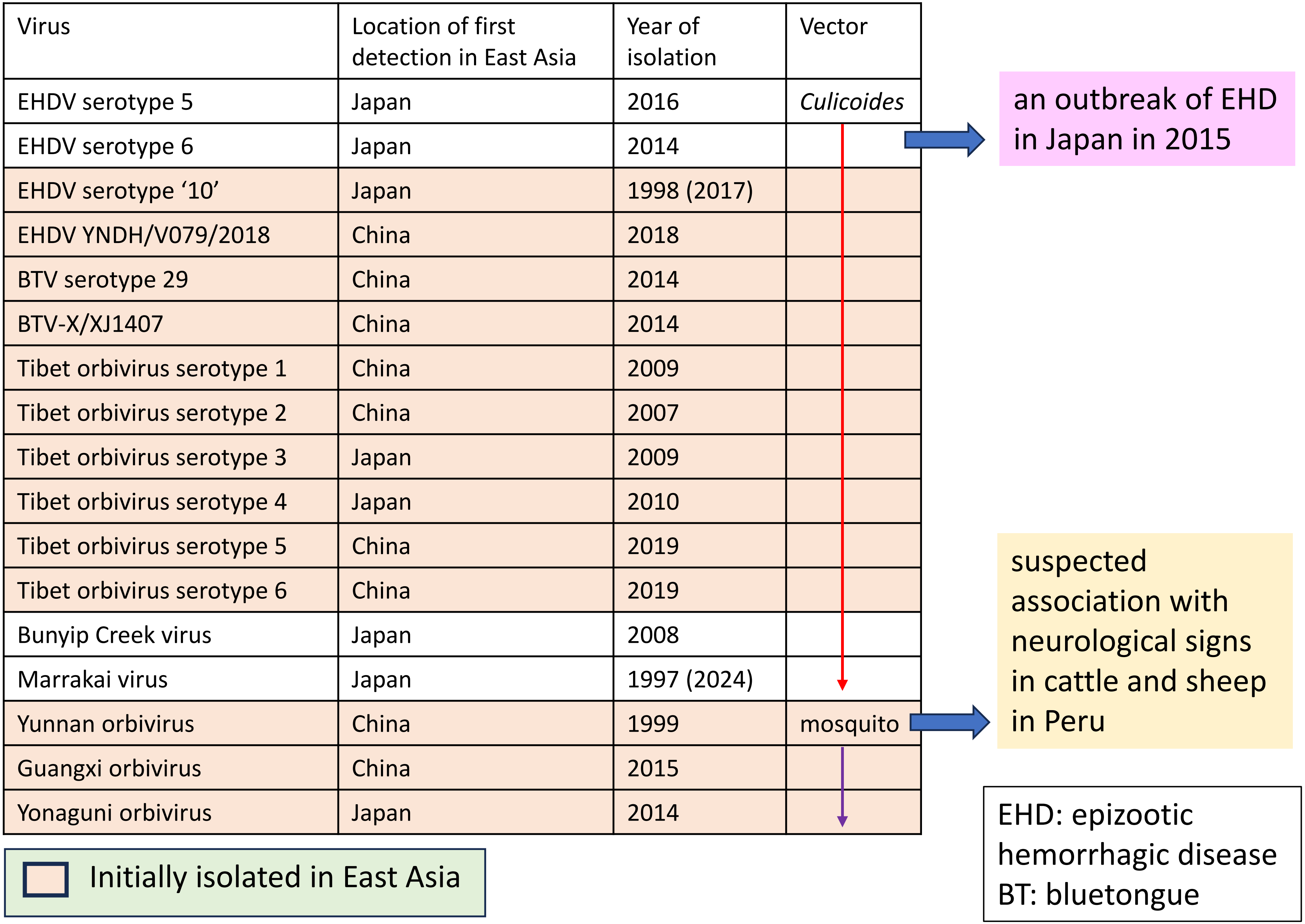
- In the past large outbreak, 42,000 cattle were affected in Japan, indicating Akabane disease has a high potentiality to impact livestock industry.

- Akabane virus is widely distributed in Asia, but there is a few report of affected animals from Asian countries and regions, except Japan.

Arboviruses potentially affecting livestock industry in Asia

Genus	Virus	Affected animal	Manifestations (suspected)	Vector
Orthobunyavirus	Peaton virus	cattle, sheep	abortion, congenital malformations	*Culicoides*
	Shamonda virus	cattle, goat	abortion, congenital malformations	*Culicoides*
	Sathuperi virus	cattle	congenital malformations	*Culicoides*
Orbivirus	D’Aguilar virus	cattle	congenital malformations	*Culicoides*

Orbiviruses recently identified in East Asia



Virus	Location of first detection in East Asia	Year of isolation	Vector
EHDV serotype 5	Japan	2016	*Culicoides*
EHDV serotype 6	Japan	2014	
EHDV serotype '10'	Japan	1998 (2017)	
EHDV YNDH/V079/2018	China	2018	
BTV serotype 29	China	2014	
BTV-X/XJ1407	China	2014	
Tibet orbivirus serotype 1	China	2009	
Tibet orbivirus serotype 2	China	2007	
Tibet orbivirus serotype 3	Japan	2009	
Tibet orbivirus serotype 4	Japan	2010	
Tibet orbivirus serotype 5	China	2019	
Tibet orbivirus serotype 6	China	2019	
Bunyip Creek virus	Japan	2008	
Marrakai virus	Japan	1997 (2024)	
Yunnan orbivirus	China	1999	mosquito
Guangxi orbivirus	China	2015	
Yonaguni orbivirus	Japan	2014	

▨ Initially isolated in East Asia

an outbreak of EHD in Japan in 2015

suspected association with neurological signs in cattle and sheep in Peru

EHD: epizootic hemorrhagic disease
BT: bluetongue

Potential impact of neglected and emerging arboviruses

- It is difficult to assess the impact of neglected and emerging arboviruses

Lack of

Characterization

Diagnostic and detection systems

Epidemiological information

We should be concerned with neglected and emerging arboviruses more!

Mutation

- RNA viruses are characterized by high mutation rates.
- Mutations may change pathogenicity, antigenicity, host range and competency of vectors.

A specific genotype of Akabane virus caused bovine encephalomyelitis by postnatal infection

Porcine reproductive failures associated with Akabane virus were recently reported

Reassortment

- Related segmented viruses exchange genome segments in co-infected cells. The process is called “reassortment”.
- Reassortment may change pathogenicity, antigenicity, host range and competency of vectors, drastically.

Orthobunyavirus
Genome:
three segmented, negative-sense, single-stranded RNA

Akabane virus, Aino virus,
Schmallenberg virus

Orbivirus
Genome:
ten segmented, double-stranded RNA

Bluetongue virus, Chuzan virus,
Epizootic hemorrhagic disease virus

Zoonotic arboviruses

Virus	Manifestations in human	Vector
Batai virus	mild flu-like illness	mosquito
Banna virus	encephalitis	mosquito
Japanese encephalitis virus	encephalitis	mosquito
SFTSV	severe fever with thrombocytopenia syndrome	tick
Crimean–Congo hemorrhagic fever virus	hemorrhagic fever	tick
Kyasanur forest disease virus	hemorrhagic fever	tick
Tick-borne encephalitis virus	encephalitis	tick

- Several mosquito- and tick-borne viruses infect both human and livestock animals.
- Livestock animal may play a role of amplifier for zoonotic arboviruses in some cases.

“Contribution” of livestock animals in transmission cycle of several zoonotic arboviruses remains uncertain.

Global warming

- Global warming may affect distribution, migration, phenology and competence of vectors.

Expansion of distribution range of arboviruses

Changing epidemiology of arbovirus infections

Vector studies are not enough in Asian.

Little information

Principal vectors of each virus in each region

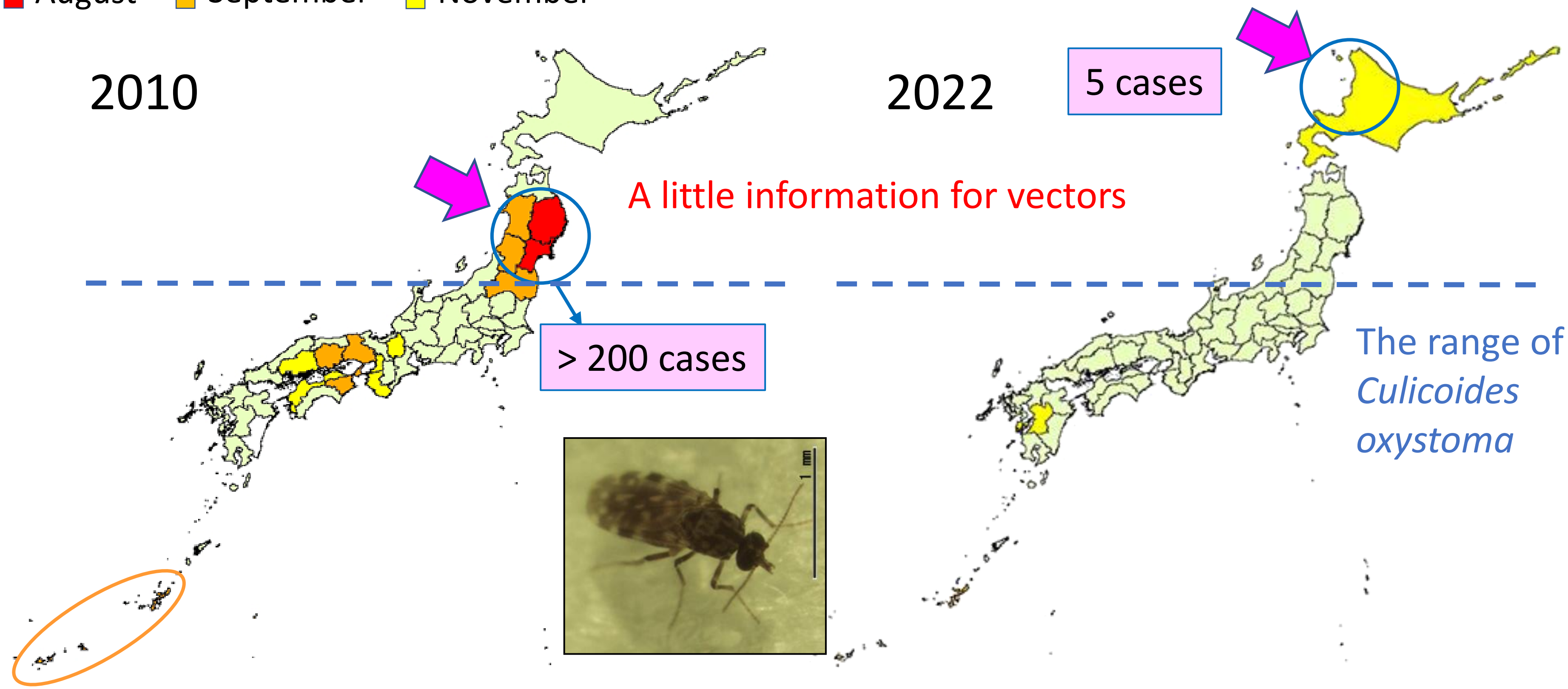
Biology of vector species

Assessment of vector competence by laboratory experiment

Outbreaks of Akabane disease in northern Japan

- Outbreaks of Akabane disease occurred in northern Japan in 2010 and 2022.
- The epizootic regions were out of historical range of known **principal vector species**.

🟥 August 🟧 September 🟨 November



5 cases

A little information for vectors

> 200 cases

The range of *Culicoides oxystoma*

Sero-conversion to Akabane virus in Japan in 2010 and 2022

Essential for future advancement

- Considering the impact of non-listed arbovirus infections (such as Akabane disease and bovine ephemeral fever)
- Risk assessment of neglected and emerging arboviruses
- Collaboration between public health and veterinary regions
- Information sharing with neighboring countries
- Constructing functional reporting systems for arbovirus infections
- Human resources development for arbovirus and vector researches
- Supports from our governments and WOAH

Thank you for your attention!!

Bluetongue virus

Update: Global and Regional and new advances in virus tracking

Dr Stacey Lynch

CSIRO Australian Centre for Disease Preparedness . **WOAH Reference Laboratory for Bluetounge virus**

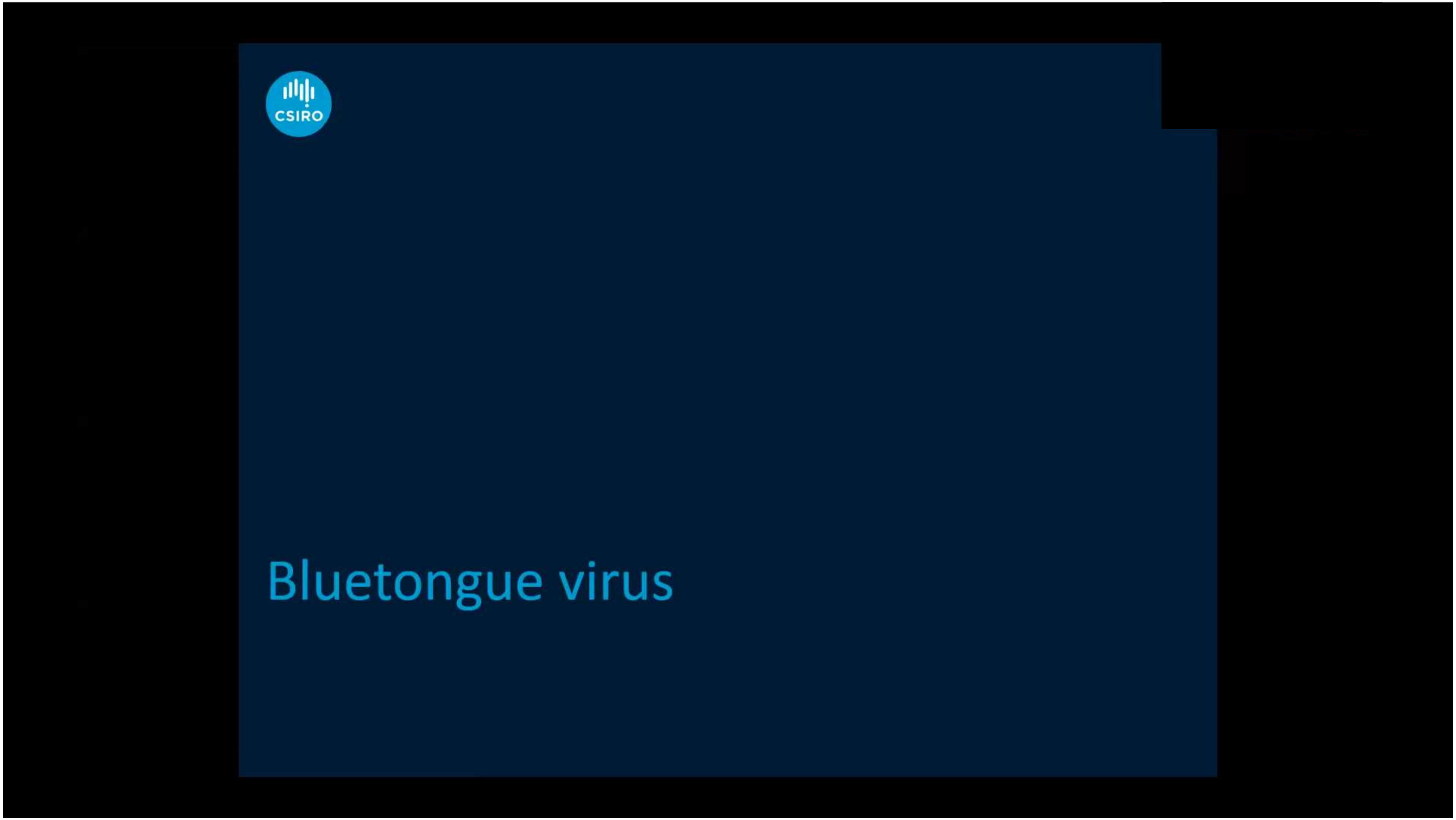
WOAH Regional Workshop on VBDs in Asia and the Pacific | September 2024
Australia's National Science Agency

ACDP provides the highest levels of biocontainment within a purpose built biosecurity infrastructure to help protect Australia's livestock and aquatic industries, as well as people, from emerging infectious disease threats.

WOAH Reference Laboratory for Bluetounge virus : global ecology (esp. regional) inc. molecular epidemiology, improved diagnostics and surveillance strategies to support industry and trade.

- Dr Debbie Eagles, Director ACDP
- Dr Tristian Read, Veterinarian, ACDP

AAHL – Australia's national biocontainment facility



Bluetongue virus

The Disease

- Arbovirus – *Culicoides* midges the primary vector
- A severe viral disease primarily affecting sheep, however infections also occur in cattle, goats and camelids
- WOAH-listed disease – Important implications for trade
- Australia claims freedom from clinical bluetongue disease, however bluetongue virus transmission is common in northern NSW, QLD, NT and WA

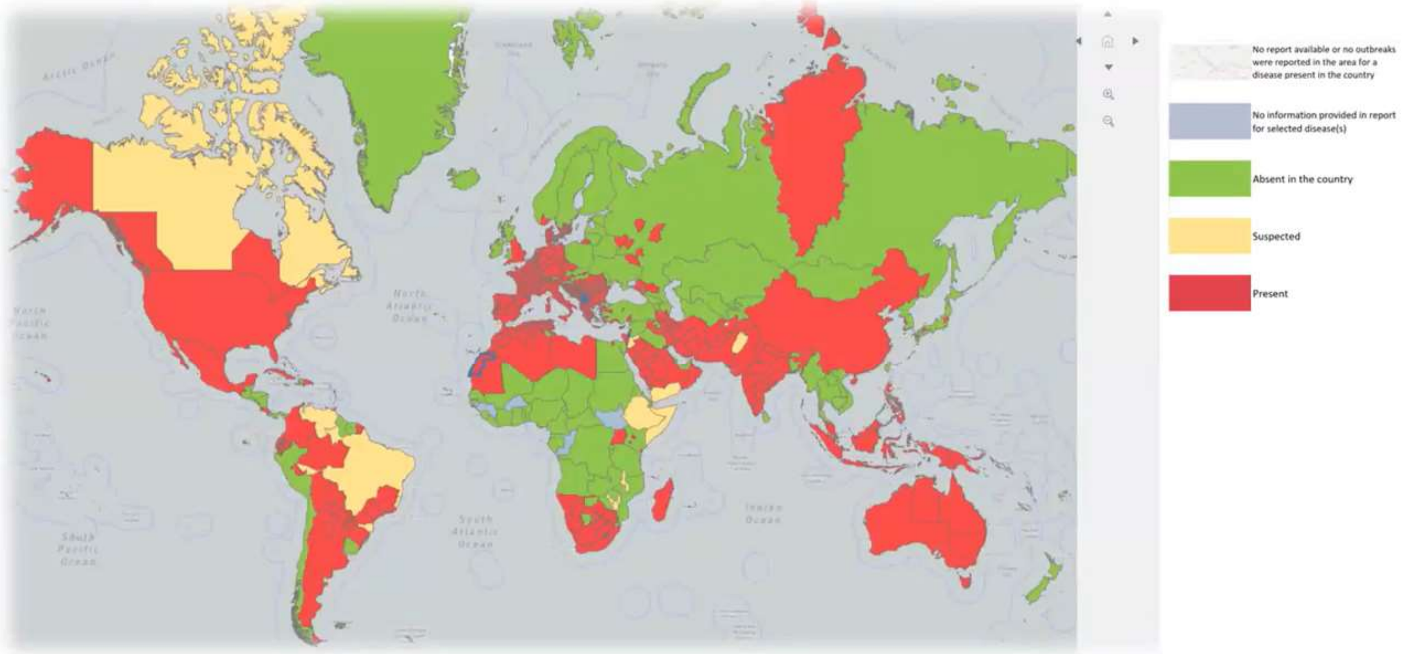
Clinical Signs

- Dependent on **host** (species, breed), **agent** (serotype, strain) and **environment**

- Virus-mediated vascular injury
  - Oedema, hyperaemia, haemorrhage

- Sheep *Morbidity* up to *100% Mortality 0-30%*
  - fever, excessive salivation, depression, dyspnoea, panting
  - clear nasal discharge (later mucopurulent)
  - tongue swollen, cyanotic
  - erosions/ulcerations in mouth

- Cattle, Goats, Camelids *Morbidity < 5% and mortality rare*



Source: WAHIS. Accessed 16-09-24. https://wahis.woah.org/#/dashboards/country-or-disease-dashboard

BTV ecology is changing and the Australian surveillance program

https://www.nvwa.nl/onderwerpen/dierziekten/documenten/dier/dierziekten/overige-dierziekten/publicaties/index

France

- BTV-4 and BTV-8 are considered endemic in France.
- France has recently reported on the emergence of a new strain of BTV-8 that appears to be more pathogenic
- French authorities reporting that current BTV-8 vaccines are effective

Figure 5: Map showing the departments in France affected by the recently emergent strain of BTV-8, dark orange represents the department in which the new strain of BTV-8 was first reported, the lighter orange shows subsequent detections and the red line represents the 50km coastal area where windborne incursion would be likely (This map was created from data published by Platform ESA, sourced at BHVSI-SA, accessed 29 November 2023).

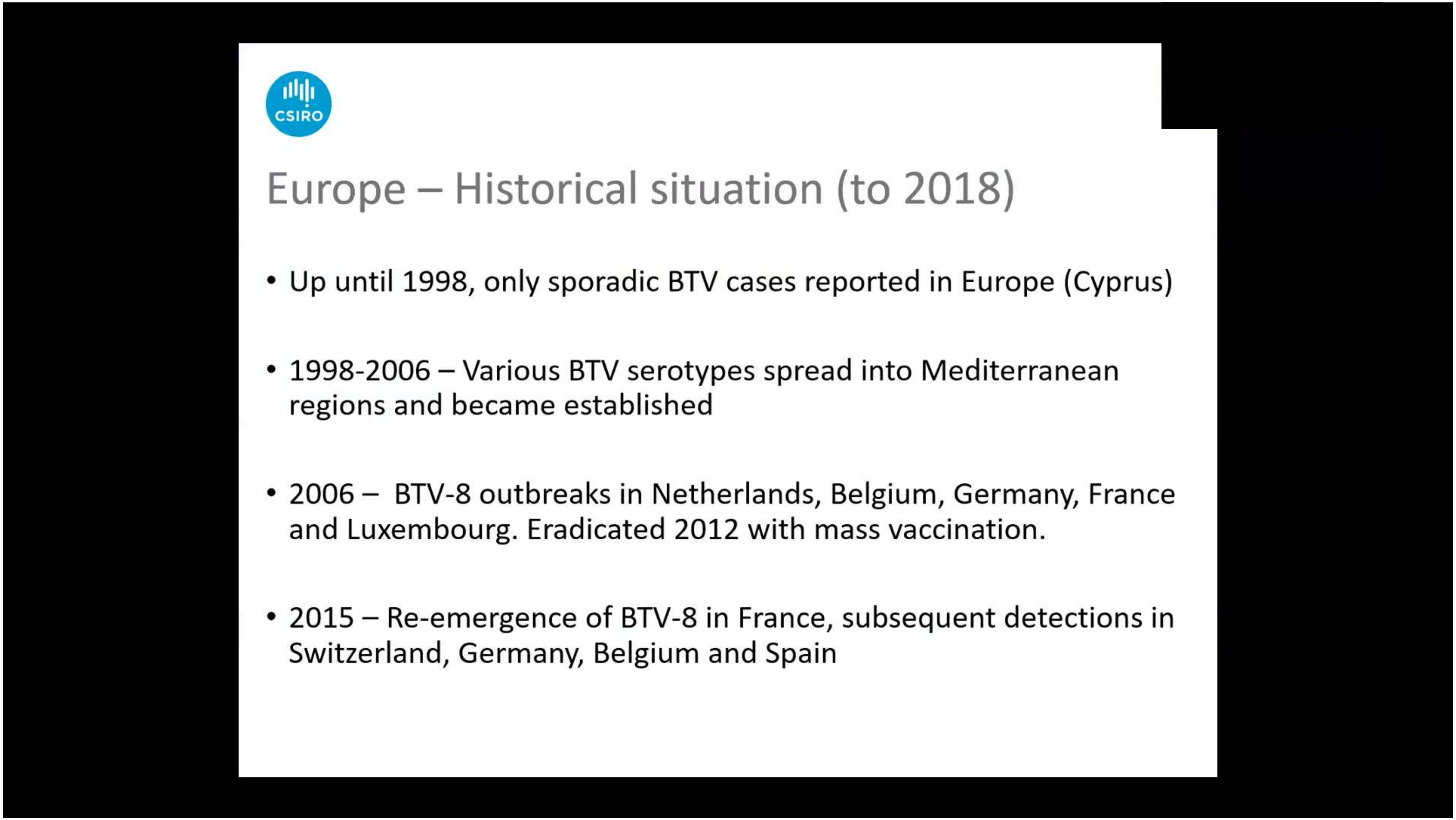
Source: https://www.gov.uk/government/publications/bluetongue-virus-in-europe/29-november-2023-updated-outbreak-assessment-for-bluetongue-virus-in-europe

Spain

- BTV-1 and BTV-4 are endemic, but restricted to certain zones
- November 2023 – Outbreaks of BTV-4 reported in previously free regions of Madrid and Galicia (red dots)

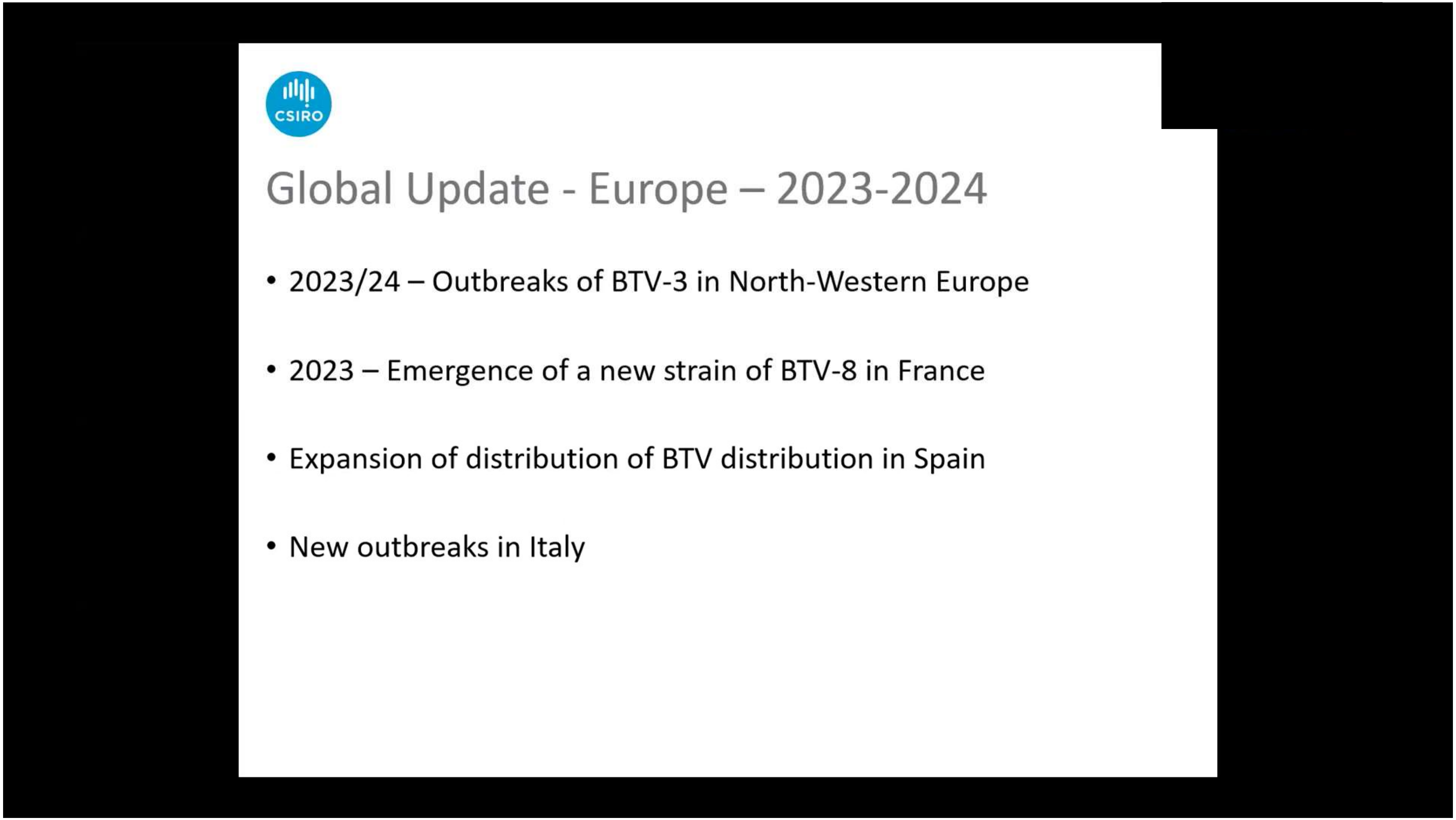
Figure 7: Map showing 5 outbreaks of BTV-4 in Spain (red dots) reported 20 November 2023 by the Spanish Ministry of Agriculture and restriction zones for BTV-4, BTV-1 and unrestricted regions (green) (Source: Spanish Ministry of Agriculture accessed on 29 November 2023).

Source: https://www.gov.uk/government/publications/bluetongue-virus-in-europe/29-november-2023-updated-outbreak-assessment-for-bluetongue-virus-in-europe



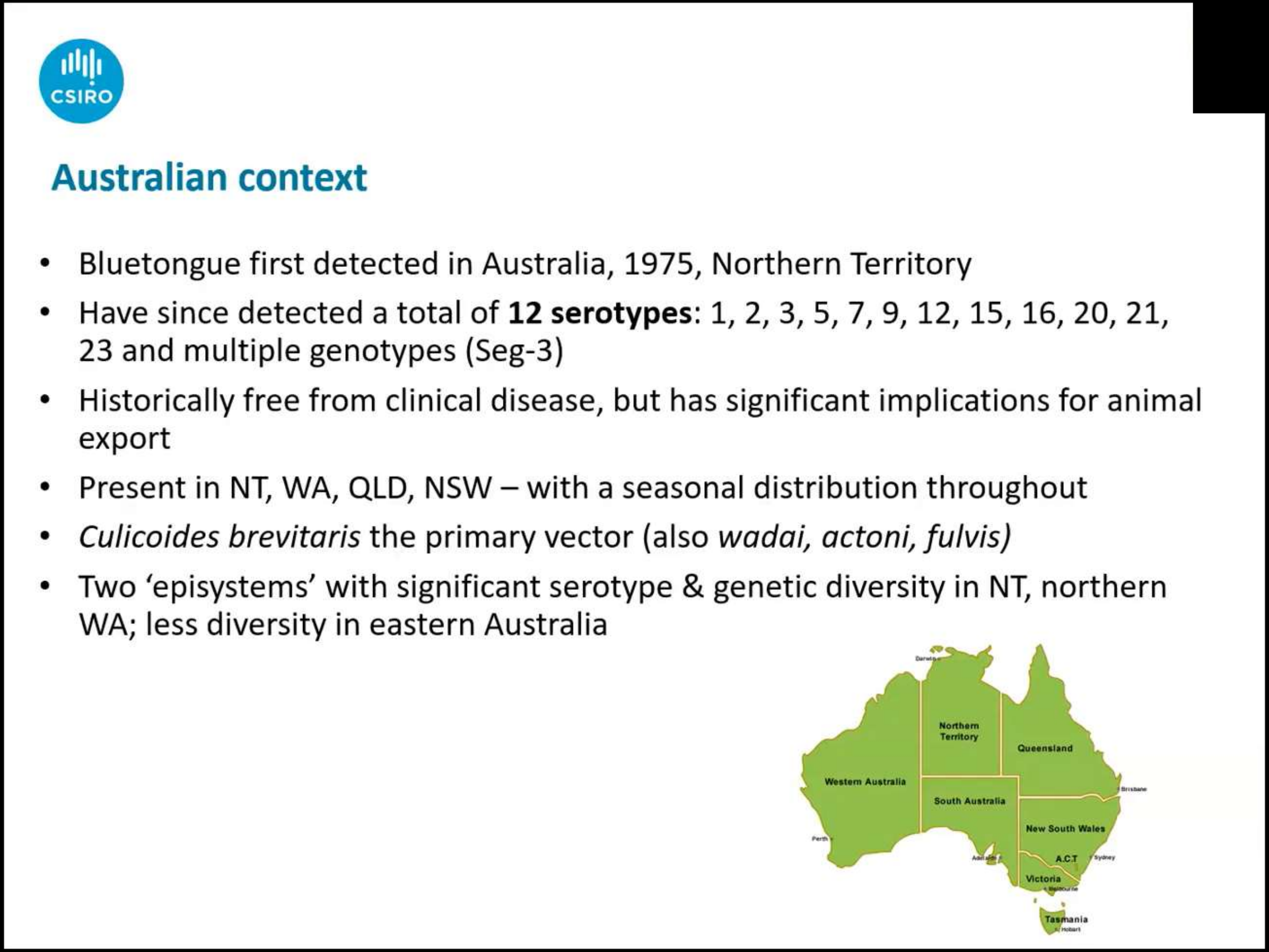
Europe – Historical situation (to 2018)

- Up until 1998, only sporadic BTV cases reported in Europe (Cyprus)
- 1998-2006 – Various BTV serotypes spread into Mediterranean regions and became established
- 2006 – BTV-8 outbreaks in Netherlands, Belgium, Germany, France and Luxembourg. Eradicated 2012 with mass vaccination.
- 2015 – Re-emergence of BTV-8 in France, subsequent detections in Switzerland, Germany, Belgium and Spain



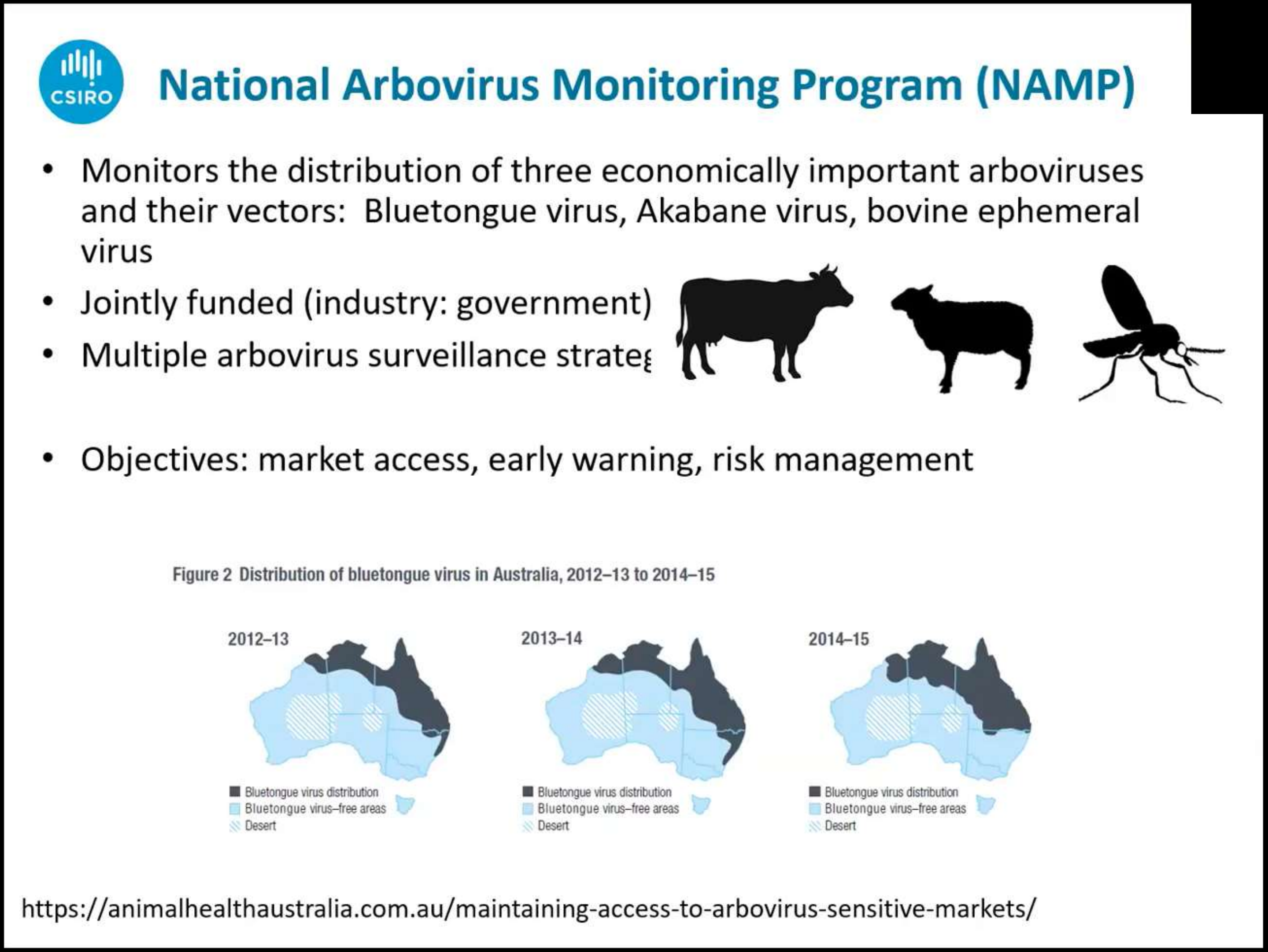
Global Update - Europe – 2023-2024

- 2023/24 – Outbreaks of BTV-3 in North-Western Europe
- 2023 – Emergence of a new strain of BTV-8 in France
- Expansion of distribution of BTV distribution in Spain
- New outbreaks in Italy



Australian context

- Bluetongue first detected in Australia, 1975, Northern Territory
- Have since detected a total of **12 serotypes**: 1, 2, 3, 5, 7, 9, 12, 15, 16, 20, 21, 23 and multiple genotypes (Seg-3)
- Historically free from clinical disease, but has significant implications for animal export
- Present in NT, WA, QLD, NSW – with a seasonal distribution throughout
- *Culicoides brevitaris* the primary vector (also *wadai, actoni, fulvis)*
- Two 'episystems' with significant serotype & genetic diversity in NT, northern WA; less diversity in eastern Australia



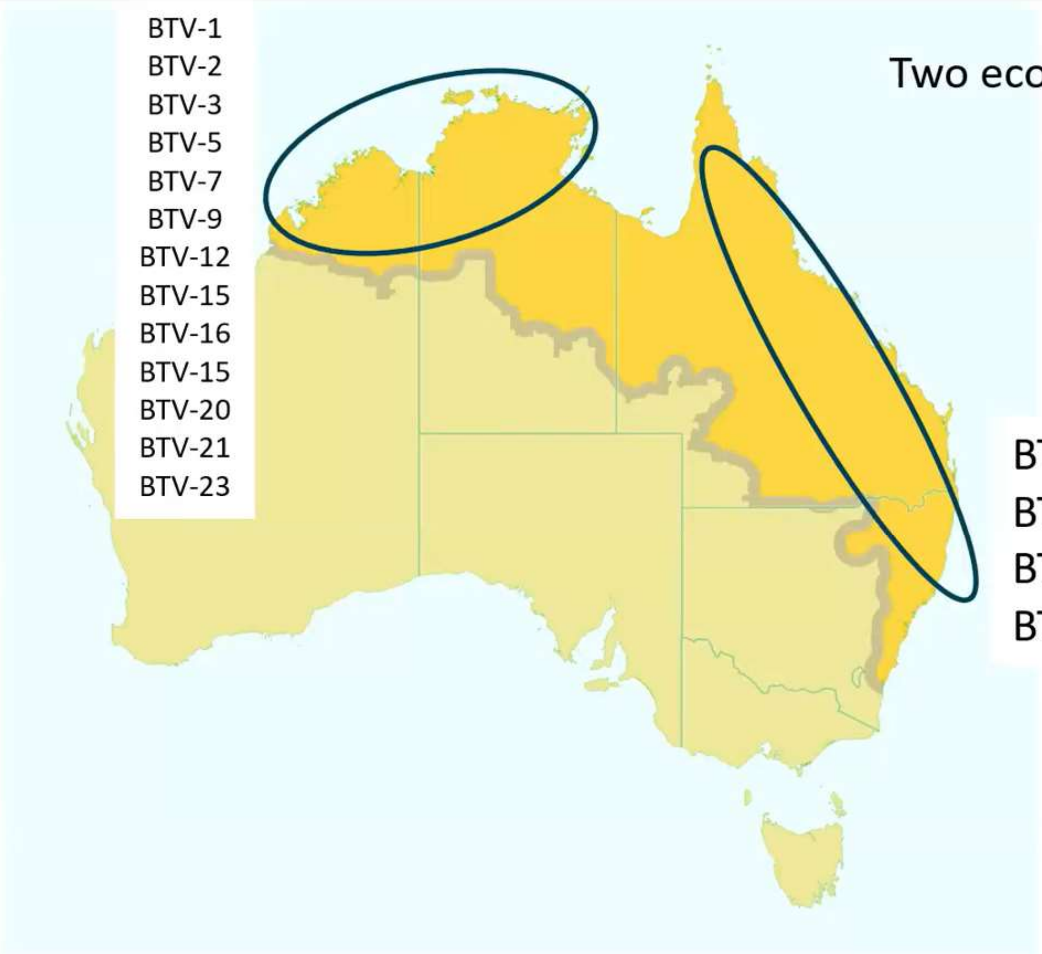
National Arbovirus Monitoring Program (NAMP)

- Monitors the distribution of three economically important arboviruses and their vectors: Bluetongue virus, Akabane virus, bovine ephemeral virus
- Jointly funded (industry: government)
- Multiple arbovirus surveillance strateg
- Objectives: market access, early warning, risk management

Figure 2 Distribution of bluetongue virus in Australia, 2012–13 to 2014–15

https://animalhealthaustralia.com.au/maintaining-access-to-arbovirus-sensitive-markets/

Two ecozon



BTV-1
BTV-2
BTV-3
BTV-5
BTV-7
BTV-9
BTV-12
BTV-15
BTV-16
BTV-15
BTV-20
BTV-21
BTV-23

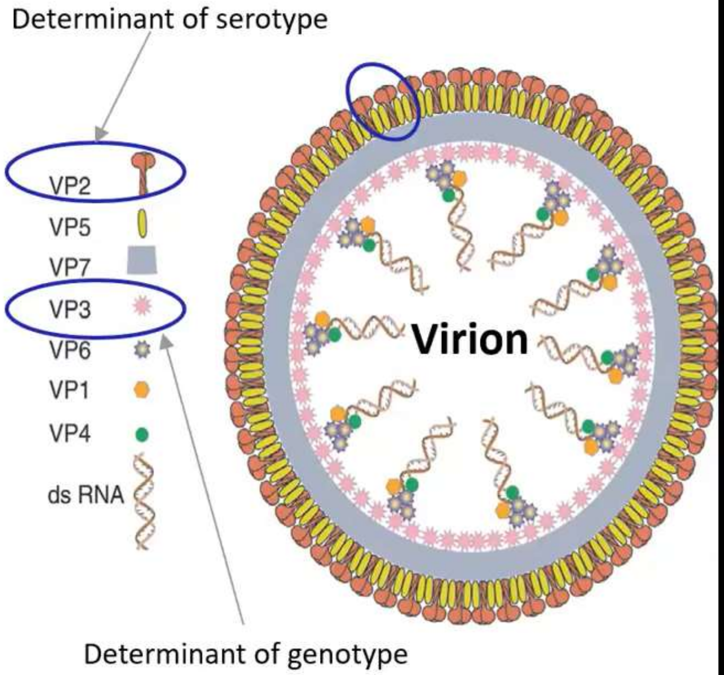
BTV -1
BTV-16
BTV-15
BTV-21

BTV-16 – introduced into NSW in 2017, BTV-15 Intermittent transmissions

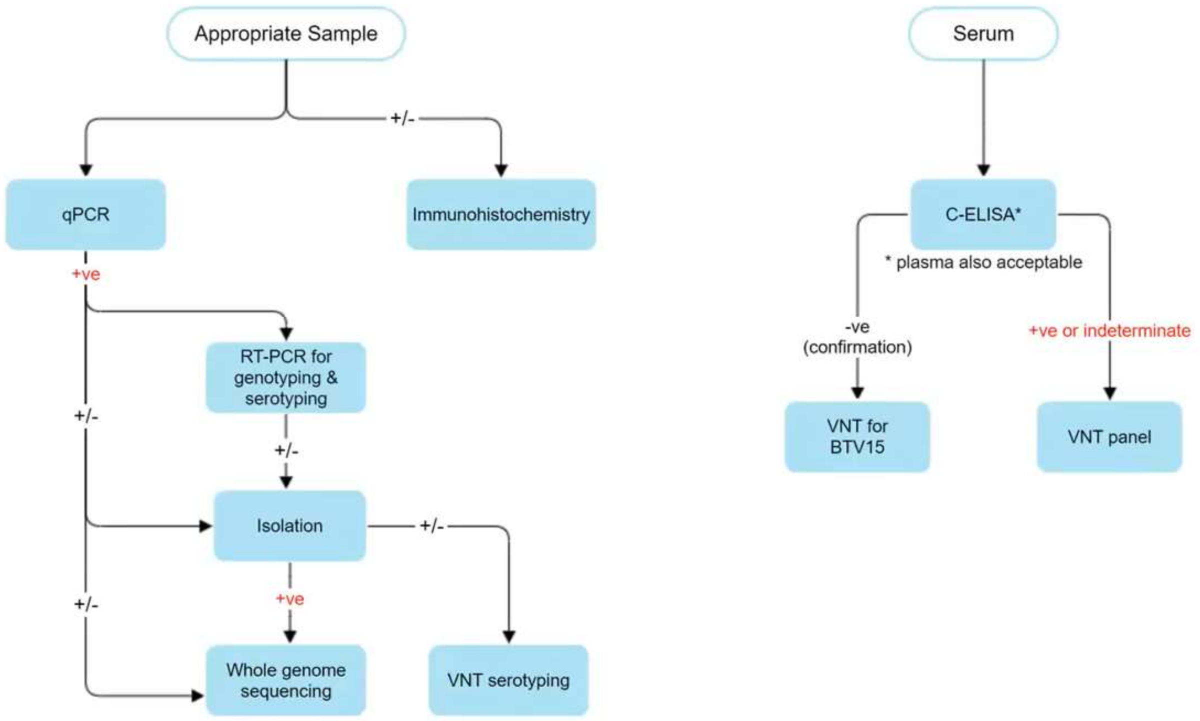
Diagnostic Testing & Advances @ ACDP

The virology

- Family *Reoviridae*; genus *Orbivirus*
  - *Related to African Horse Sickness virus*
- ds RNA segmented genome
- 28^+ serotypes
- **<u>Segmented Genome – 10 distinct segments. Gene reassortment known to occur.</u>**



Bluetongue Virus (BTV) Exclusion



Agent Detection

Appropriate Sample

qPCR

+/-

Immunohistochemistry

+ve

RT-PCR for genotyping & serotyping

+/-

+/-

Isolation

+/-

+ve

+/-

Whole genome sequencing

VNT serotyping

Serology

Serum

C-ELISA*

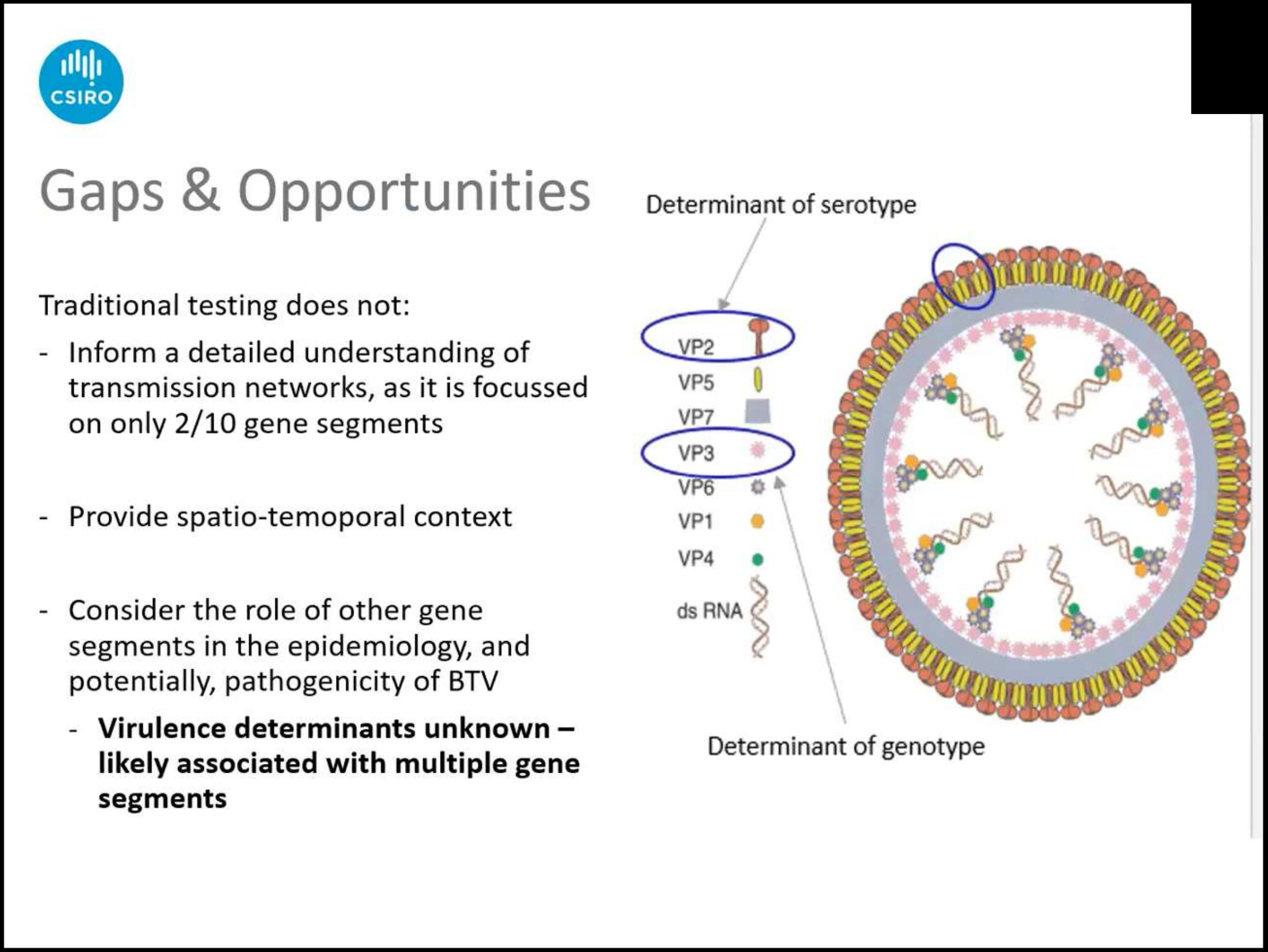
* plasma also acceptable

-ve (confirmation)

+ve or indeterminate

VNT for BTV15

VNT panel



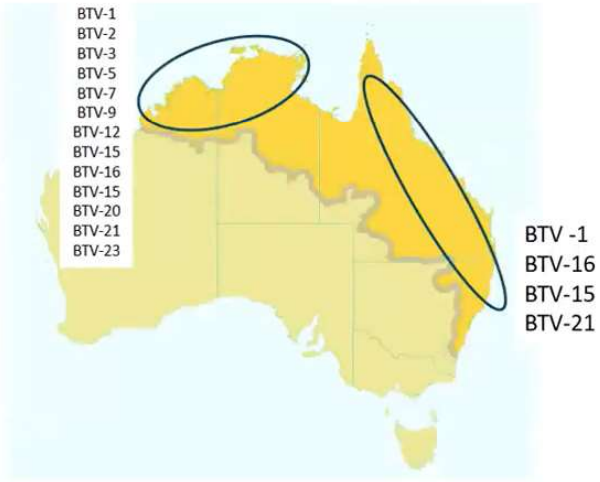
Gaps & Opportunities

Traditional testing does not:

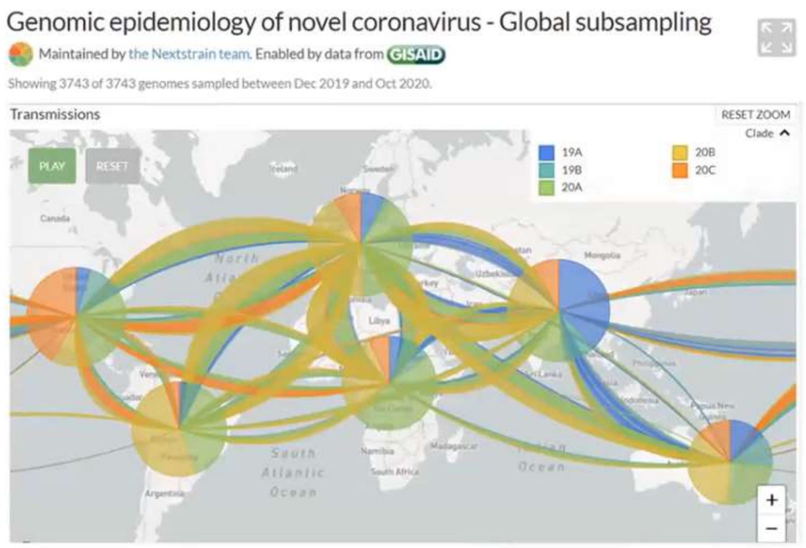
- Inform a detailed understanding of transmission networks, as it is focussed on only 2/10 gene segments
- Provide spatio-temoporal context
- Consider the role of other gene segments in the epidemiology, and potentially, pathogenicity of BTV
  - **Virulence determinants unknown – likely associated with multiple gene segments**

Recent developments at ACDP - genomics

- Developed a model that can perform fine-grained characterization of the genetic relationships between BTV isolates **at the whole genome level**.
    - – To better understand the relationships between isolates
        - Spatio-temporal within Australia and outside of our country boarders
    - – Potential future application to identifying virulence determinants
- Can visualise this information (along with spatiotemporal data) in Nextstrain®



Nextstrain : now being applied for BTV in Australia



Genomic epidemiology of novel coronavirus - Global subsampling

Maintained by the Nextstrain team. Enabled by data from GISAID

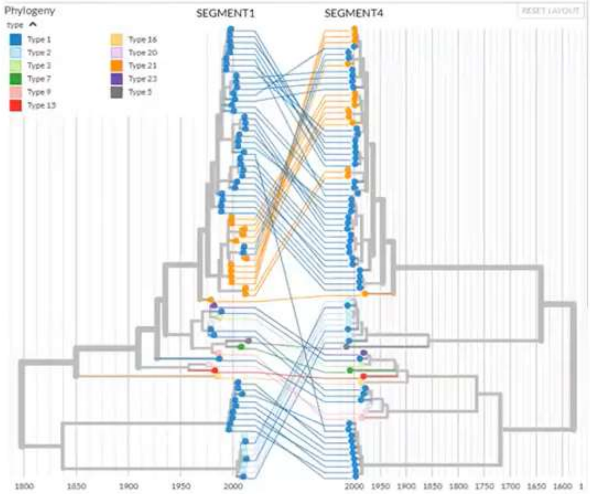
Showing 3743 of 3743 genomes sampled between Dec 2019 and Oct 2020.

Map of possible global transmission pattern of SARS-CoV-2 clades from a subset of GISAID whole genome sequencing data.

Source: Nextstrain

Whole Genome Sequencing and Nextstrain

- Greatly improves our understanding of the molecular epidemiology of BTV
  - Improved understanding of relationships between viruses to **understand changes in virus transmission**
  - Improved ability to detect:
    - **recombination events**
    - **incursion & spread of exotic gene segments**



Thank you

Dr Stacey Lynch
Team Leader, Mammalian Infectious Disease Research

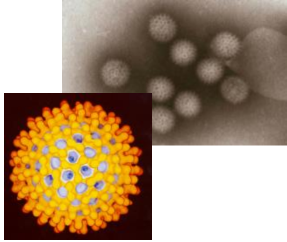
Stacey.Lynch@CSIRO.au

On behalf of the
WOAH Reference Laboratory for Bluetounge virus

Australia's National Science Agency

Maintaining access to arbovirus sensitive markets

https://animalhealthaustralia.com.au/maintaining-access-to-arbovirus-sensitive-markets/



EMERGENCE OH EPIZOOTIC HEMORRHAGIC DISEASE (EHD) IN EUROPE

STEPHAN ZIENTARA

ANSES - DIRECTOR OF ANIMAL HEALTH LABORATORY, FRANCE

EU/WOAH/FAO REFERENCE LAB ON FMD
EU REFERENCE LAB ON EQUINE DISEASES
WOAH REFERENCE LAB ON EHDV

Epizootic Haemorrhagic disease

11 mn

Virology

Disease

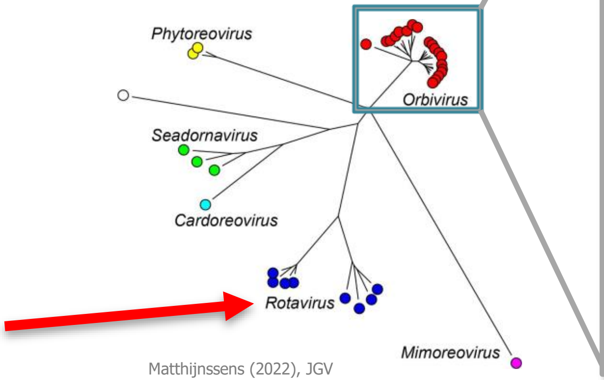
Epidemiology

Diagnosis

Prevention

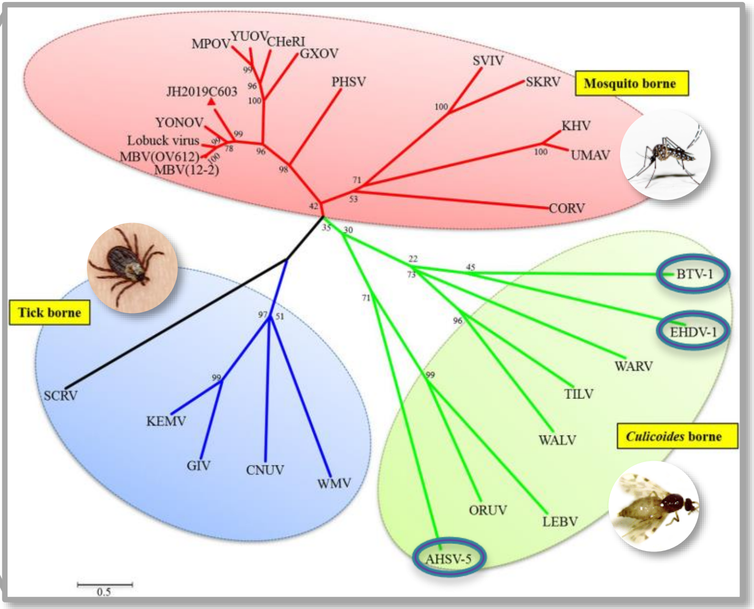
Orbivirus

Family *Sedoreoviridae*



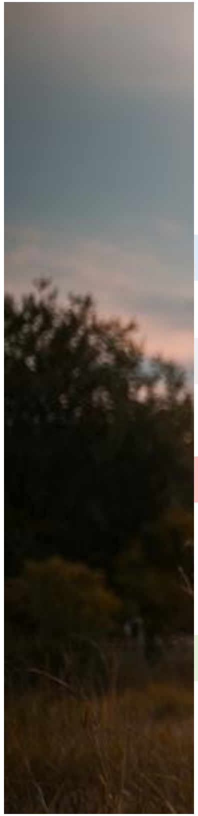
Matthijnssens (2022), JGV

Genus *Orbivirus*: 22 species



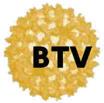
Yang (2021), Virus genes

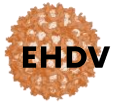
- 3 important diseases
  - ○ **BTV:** Bluetongue virus
  - ○ **EHDV:** Epizootic hemorragic disease virus
  - ○ **AHSV:** African horse sickness virus



Bluetongue (BTV) & Epizootic Hemorrhagic Disease (EHD)

WOAH & European notifiable animal diseases





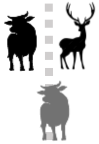
Virus *Sedoreoviridae, Orbivirus*

36 serotypes | 7 serotypes

Host(s)

Susceptible

"Reservoir"



Disease

Bleeding + Inflammation

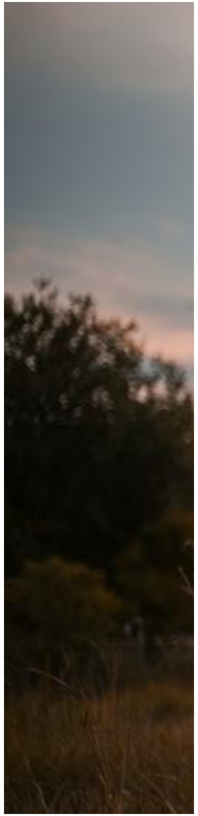
Fever, oedemas, loss of appetite, weakness, excessive salivation, haemorrhages, respiratory distress, ulceration (buccal mucosa, tongue…)

Transmission

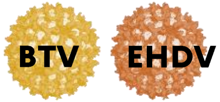
Vector *Culicoides*

Distribution

Enzootic | **Emerging**



Sedoreoviridae, Orbivirus



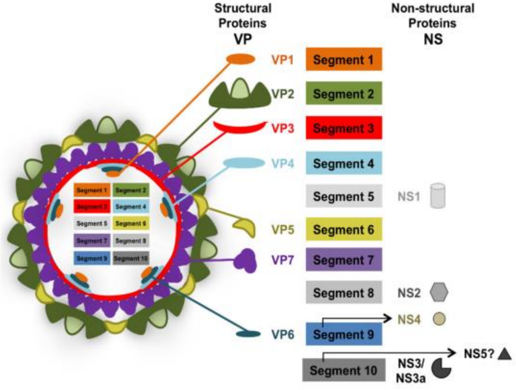


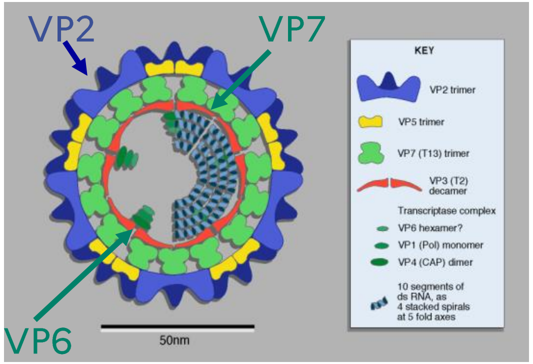
Figure from Rodríguez-Martín *et al.*, 2021

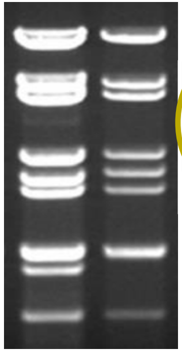
- **Non-enveloped segmented dsRNA+ genome**
- **10 segments ≈ 19,2 kb**
- Conserved sequence at the extremities:
  5′ [GUU(A/U)A(A/U) … AC(A/U)UAC] 3′
- S1 to S8: Monocistronic segment
- S9 & S10: Bicistronic segments
- **Serotyping: Segment 2**

reassortment

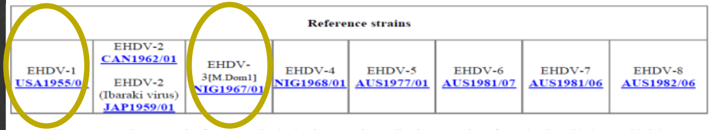
EHDV caused by an Orbivirus

Famille : *Sedoreoviridae*





7 serotypes



Reference strains							
EHDV-1 USA1955/0	EHDV-2 CAN1962/01 EHDV-2 (Ibaraki virus) JAP1959/01	EHDV-3[M.Dom1] NIG1967/01	EHDV-4 NIG1968/01	EHDV-5 AUS1977/01	EHDV-6 AUS1981/07	EHDV-7 AUS1981/06	EHDV-8 AUS1982/06

Table 3: Commonly accepted reference strains in the ds RNA virus collection at Institute for Animal Health (IAH) Pirbright, UK and at the Arthropod-Borne Animal Diseases Research Laboratory (ABADRL), USA.

New serotypes?

South Africa

EHDV-9?

Wright, I. M. 2013: Serological and Genetic Characterisation of Putative New Serotypes of Bluetongue Virus and Epizootic Haemorrhagic Disease Virus Isolated From an Alpaca. North-West University, South Africa

Japan (1998)

EHDV-10?

Contents lists available at ScienceDirect

Infection, Genetics and Evolution

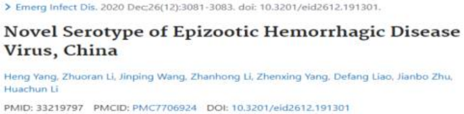
Research paper

Characterization of genome segments 2, 3 and 6 of epizootic hemorrhagic disease virus strains isolated in Japan in 1985–2013: Identification of their serotypes and geographical genetic types

Hiroaki Shirafuji a,*, Tomoko Kato a, Makoto Yamakawa b, Toru Tanaka c, Yutaka Minemori d, Tohru Yanase a

China

EHDV-11 ?



> Emerg Infect Dis. 2020 Dec;26(12):3081-3083. doi: 10.3201/eid2612.191301.

Novel Serotype of Epizootic Hemorrhagic Disease Virus, China

Heng Yang, Zhuoran Li, Jinping Wang, Zhanhong Li, Zhenxing Yang, Defang Liao, Jianbo Zhu, Huachun Li

PMID: 33219797 PMCID: PMC7706924 DOI: 10.3201/eid2612.191301

EHDV Identity card

Family	*Sedoreoviridae*
Genus	Orbivirus (22 species)
Species	*Epizootic hemorrhagic disease virus* (EHDV)
Number of serotypes	7
Genome	dsRNA, 10 segments

Grimes J.M., Burroughs J.N., Gouet P., Diprose J.M., Malby R., Zientara S., Mertens, P.P.C. & Stuart D.I. (1998). The atomic structure of the bluetongue virus core. *Nature*, 395, 470-478.

Although recognised earlier in the south-eastern United States,
EHD was first described after a severe outbreak of the disease in **white-tailed deer** (*Odocoileus virgininianus)* in New Jersey in 1955

Shope R.E., Macnamara L.G. & Mangold R. (1960). – A virus-induced epizootic hemorrhagic disease of the Virginia white-tailed deer (Odocoileus virginianus). J. Experim. Med., 111, 155–170

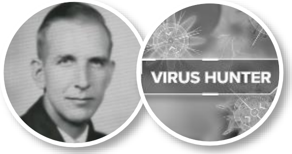
Review

Epizootic haemorrhagic disease N.J. Maclachlan, S. Zientara, G. Savini & P.W. Daniels

Rev. Sci. Tech. Off. Int. Epiz., 2015, 34 (2), 341-351

Richard Edwin Shope

- **Richard Edwin Shope** (1901-1966)

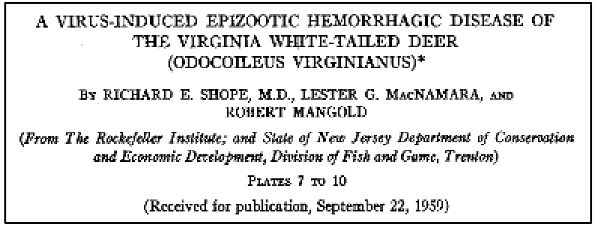


- **1924**: instructor in pharmacology at the University of Iowa, studying **tuberculosis,** and rapidly joined the laboratories of the Rockefeller Institute at **Princeton**.
- **1928**: he left the field of tuberculosis to work on **hog cholera** and thus began a career in the field of virology.
- **1931**: identified swine influenza, together with his mentor Paul A. Lewis.
- **1932: rabbit fibroma.**
- **1933: rabbit papilloma.**

Andrewes C (1979, Nat Acad Sc)

“A new disease of deer”

…but



A VIRUS-INDUCED EPIZOOTIC HEMORRHAGIC DISEASE OF
THE VIRGINIA WHITE-TAILED DEER
(ODOCOILEUS VIRGINIANUS)*

BY RICHARD E. SHOPE, M.D., LESTER G. MACNAMARA, AND
ROBERT MANGOLD

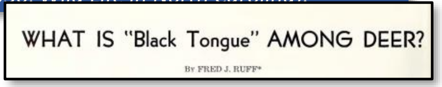
(From The Rockefeller Institute; and State of New Jersey Department of Conservation and Economic Development, Division of Fish and Game, Trenton)

PLATES 7 TO 10

(Received for publication, September 22, 1959)

Shope RE (1960, J Exp Med)

"Among woodsmen and hunters in the South, the disease has long borne the name **"black tongue,"** presumably because one of the characteristics of a deer dead of it was a discolored and swollen tongue which generally protruded from the mouth. **Ruff**…has given a good description of "black tongue" *(Ruff FJ ; 1950. Wild Life in North Carolina).*



WHAT IS "Black Tongue" AMONG DEER?

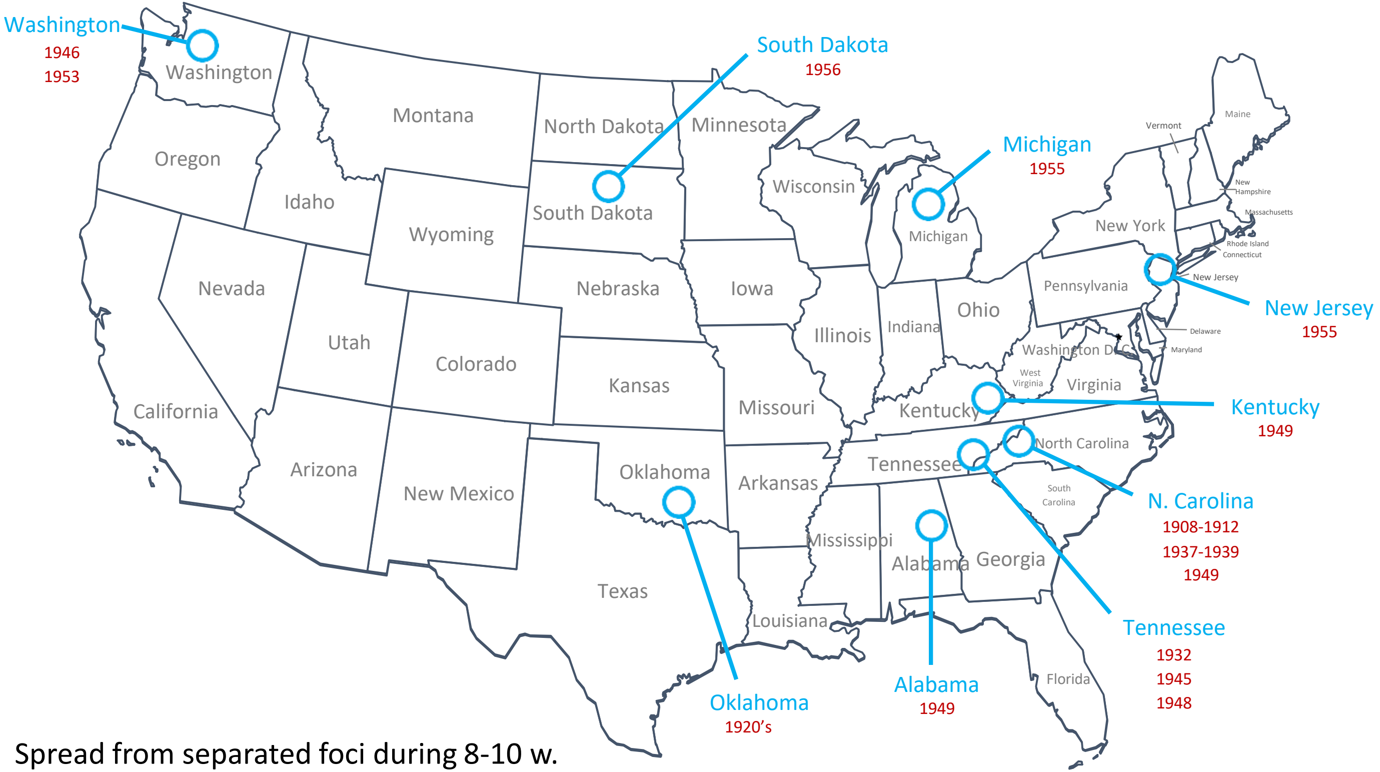
BY FRED J. RUFF*

"we had been in **error** in our belief. Search of the **files** of the **United States Forest Service…** outbreaks of a fatal epizootic disease similar to the one we encountered in New Jersey have occurred in deer in various of the **southeastern states** at irregular intervals **at least since 1890***…"

"However, because this name has confusing connotations… we propose, therefore, to continue to designate the condition as **epizootic hemorrhagic disease of deer (EHD)**."

***Leonard E. Foote** (Wild Life Management Institute; personal communication)

First reported epizootics of EHD



Washington
1946
1953

South Dakota
1956

Michigan
1955

New Jersey
1955

Kentucky
1949

N. Carolina
1908-1912
1937-1939
1949

Tennessee
1932
1945
1948

Alabama
1949

Oklahoma
1920's

Spread from separated foci during 8-10 w.

Late summer/early fall (terminated before winter).

Damien Vitour

Ruff FJ (1950, Wild Life in North Carolina), Shope RE (1960, J Exp Med)

Ibaraki strain EHDV2
Isolated from a cattle in 1959 in Ibaraki, Japan

Virology

Disease

Epidemiology

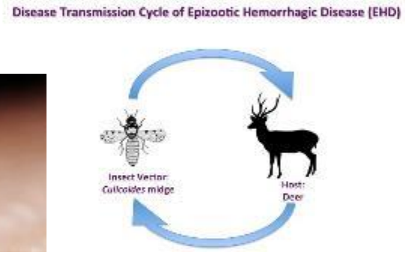
Diagnosis

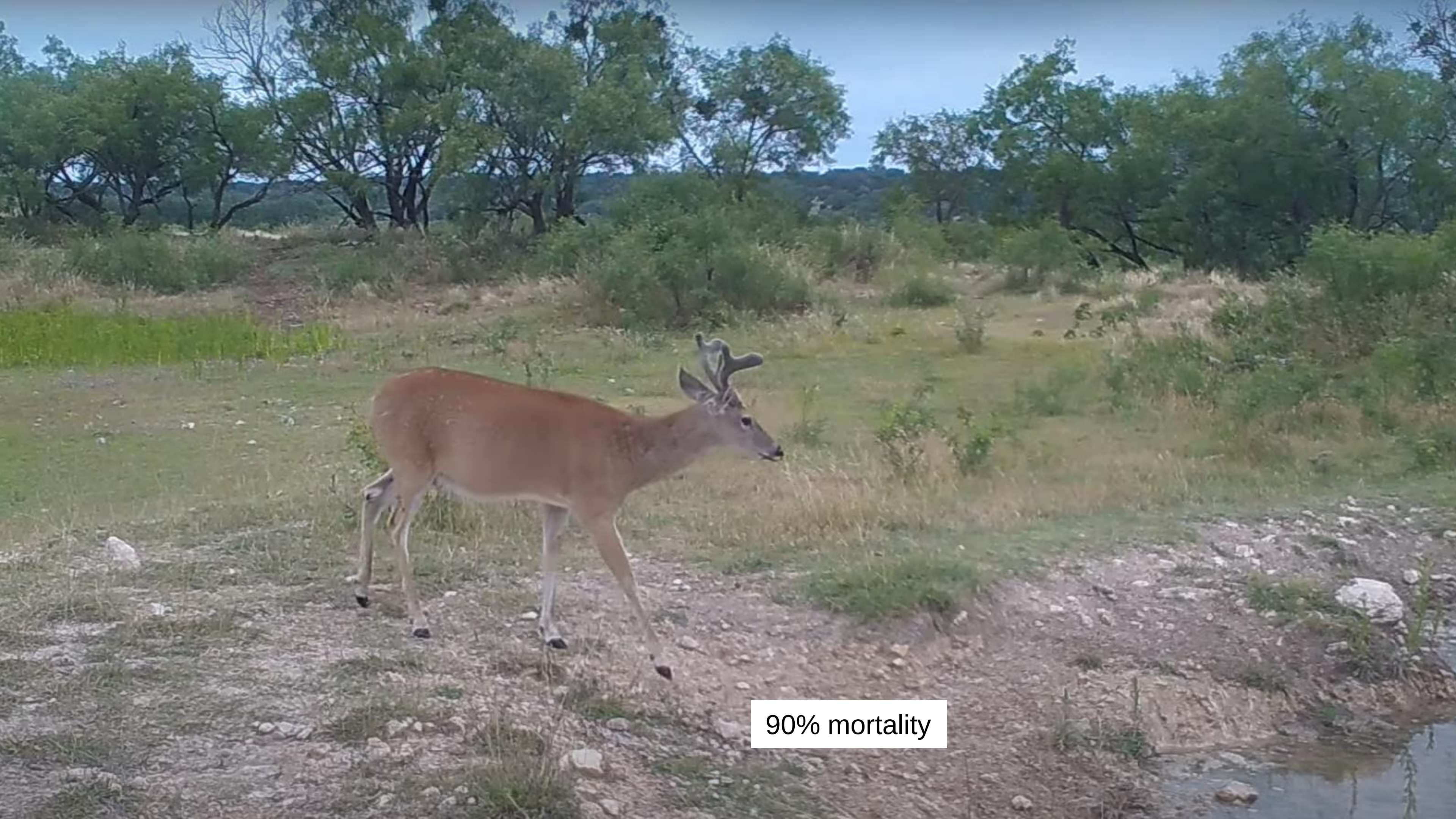
Prevention

Why Epizootic Haemorrhagic Disease of **DEER ?**

Transmission by
Culicoides sonorensis

other species
C. insignis
C. mohave
C. debilipalpis
C. obsoletus
C. scoticus
C. paraensis
C. spinosus
C. stellifer
…





90% mortality

- EHDV serotypes **1, 2, 6, 7 and 8** induce clinical signs in cattle

Epizootic haemorrhagic disease virus (EHDV) mainly infects deer, but sheep and cattle can also be infected.

EHDV added to the WOAH list in **May 2008.**

- Loss of appetite
- Fear of humans lost
- Extensive haemorrhages
- Weakness
- Excessive salivation
- Rapid pulse and respiratory rate
- Fever
- Blue tongue from lack of oxygenated blood
- Breaking of hooves caused by growth interruptions
- Diarrhoea
- Unconciousness
- Death

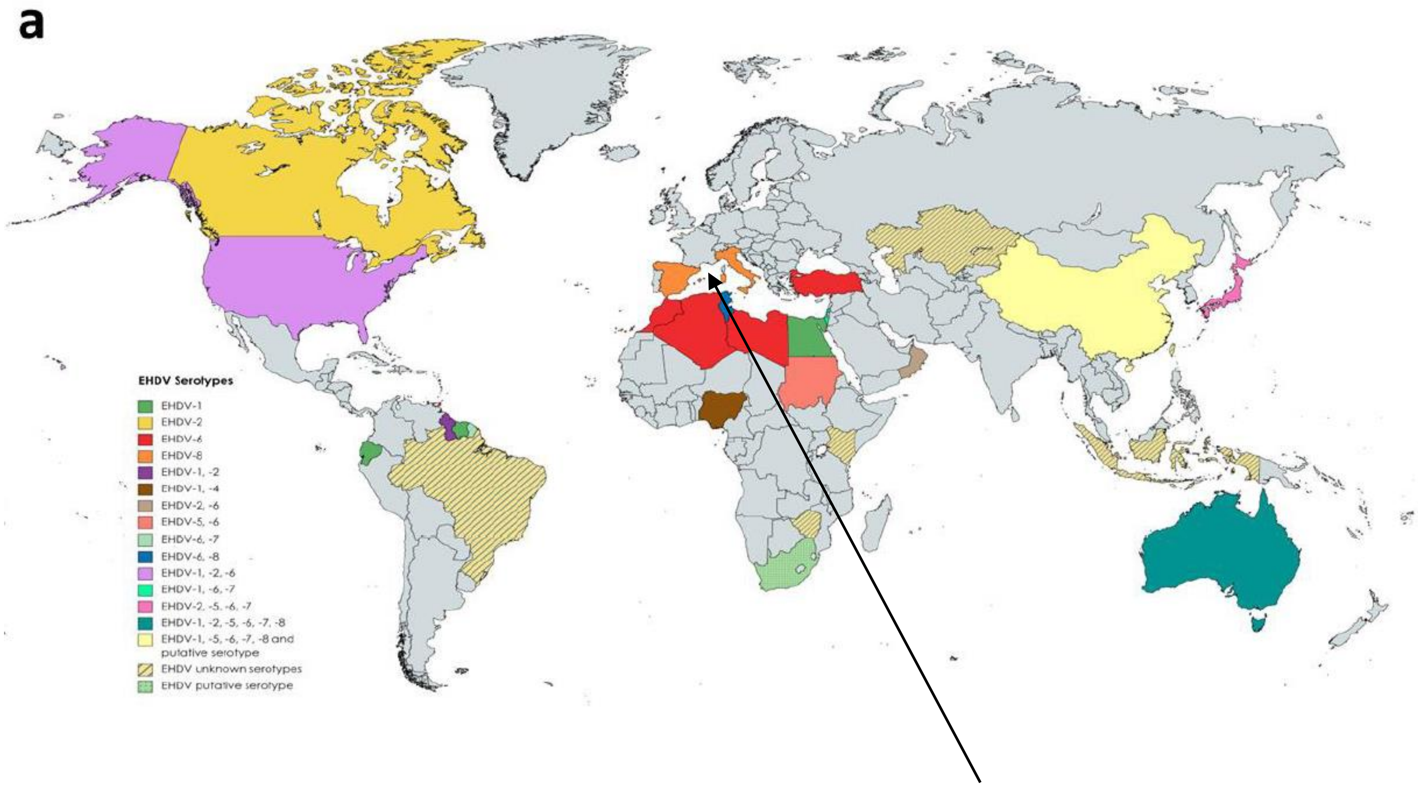
Virology

Disease

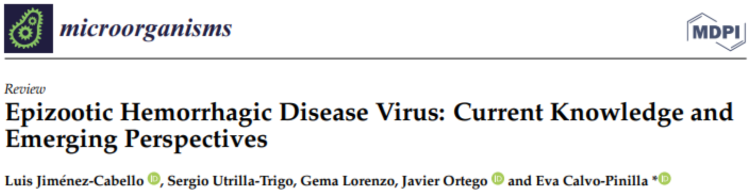
Epidemiology

Diagnosis

Prevention



2022 ; 2023



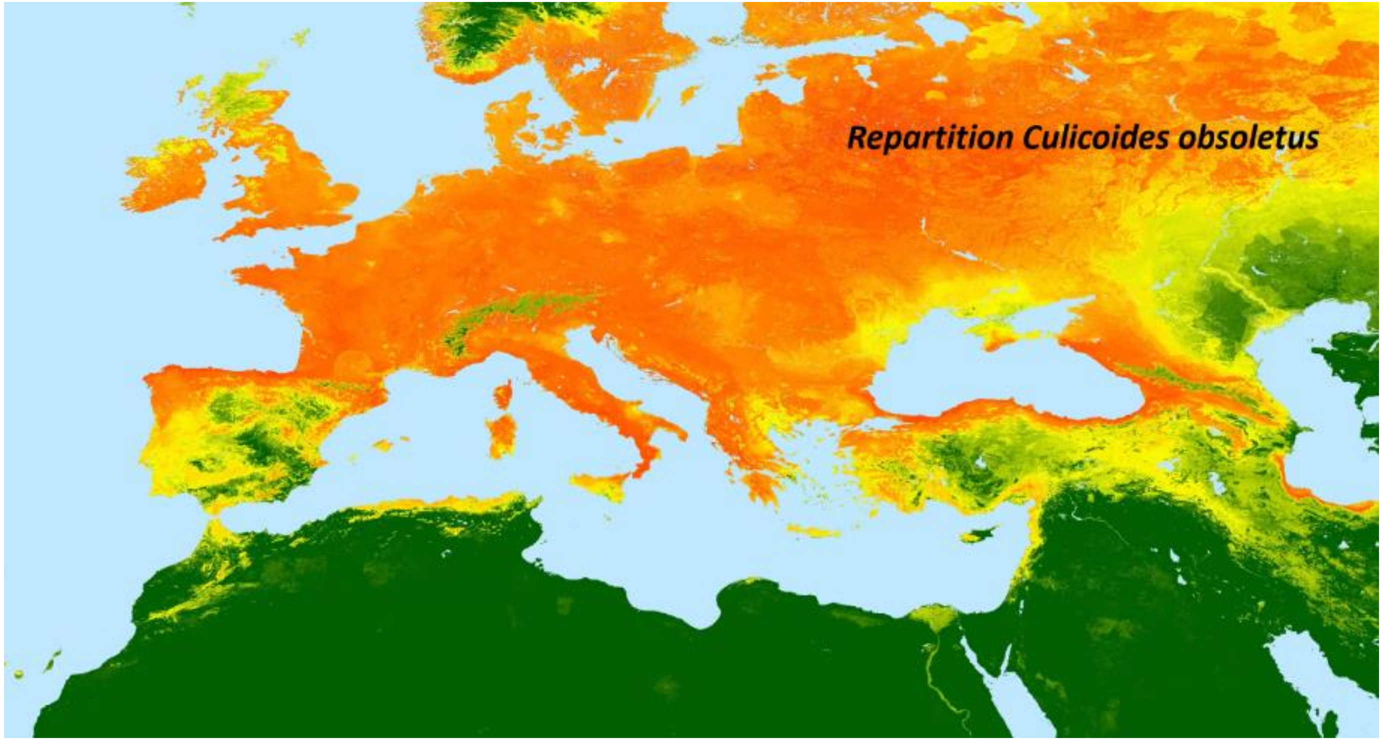
microorganisms

MDPI

Review

Epizootic Hemorrhagic Disease Virus: Current Knowledge and Emerging Perspectives

Luis Jiménez-Cabello, Sergio Utrilla-Trigo, Gema Lorenzo, Javier Ortego and Eva Calvo-Pinilla *



Repartition Culicoides obsoletus

EHDV-8

2021

Epizootic Haemorrhagic Disease virus serotype 8 in Tunisia, 2021

Soufien Sghaier[1], Corinne Sailleau[2], Maurilia Marcacci[3], Sarah Thabet[1], Valentina Curini[3], Thameur Ben Hassine[4], Liana Teodori[3], Ottavio Portanti[3], Salah Hammami[5], Lucija Jurisic[3,6], Massimo Spedicato[3], Lydie Postic[2], Ines Gazani[7], Raja Ben Osman[8], Stephan Zientara[2], Emmanuel Breard[2], Paolo Calistri[3], Juergen A. Richt[9], Edward C. Holmes[10], Giovanni Savini[3], Francesca Di Giallonardo[11], and Alessio Lorusso[3*]

Figure 1. Clinical signs in cattle. (A) Teat erosions, (B) Oral congestion and erosions, (C) Submandibular oedema, conjunctivitis, and lacrimation, (D) Nasal discharge and mucosal erosion.

200 outbreaks

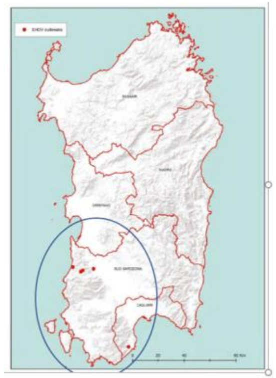
2022

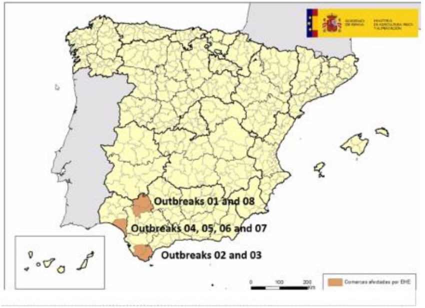
From 28 Octobre 2022

Clinical signs

- Cattle and a deer in Sardinia and Sicily (morbidity rate 5 to 10 %)
- Cattle in Andalusia (morbidity rate 10 to 15 % ; mortality rate <1%)

→ Confirmation EHDV-8





EMERGING INFECTIOUS DISEASES®

EID Journal > Volume 29 > Number 5—May 2023 > Main Article

Volume 29, Number 5—May 2023

Research Letter

Epizootic Hemorrhagic Disease Virus Serotype 8, Italy, 2022

Alessio Lorusso, Stefano Cappai, Federica Loi, Luigia Pinna, Angelo Ruiu, Giantonella Puggioni, Annalisa Guercio, Giuseppa Purpari, Domenico Vicari, Soufien Sghaier, Stephan Zientara, Massimo Spedicato, Salah Hammami, Thameur Ben Hassine, Ottavio Portanti, Emmanuel Breard, Corinne Sailleu, Massimo Ancora, Daria Di Sabatino, Daniela Morelli, Paolo Calistri, and Giovanni Savini

The first infected animal

Alessio Lorusso, IZST

2023

18 September 2023

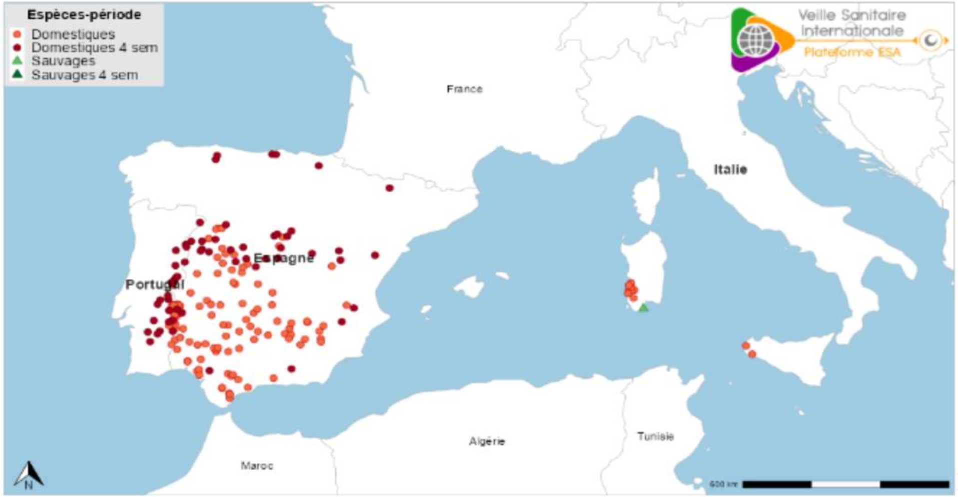
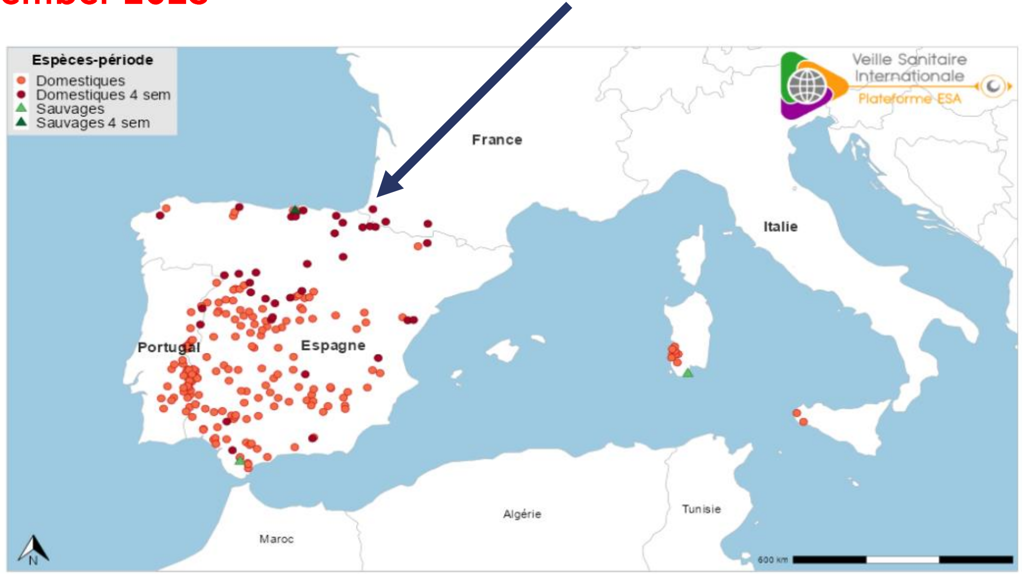


Figure 1. Localisation

September 2023



Hautes-Pyrénées : détection d'un cas de maladie hémorragique épizootique (MHE) dans un élevage bovin

Bovins et ovins sont atteints d'une nouvelle maladie transmise par les cerfs et le chevreuils, via les pucerons. / DDM - CEDRIC MERAVILLES

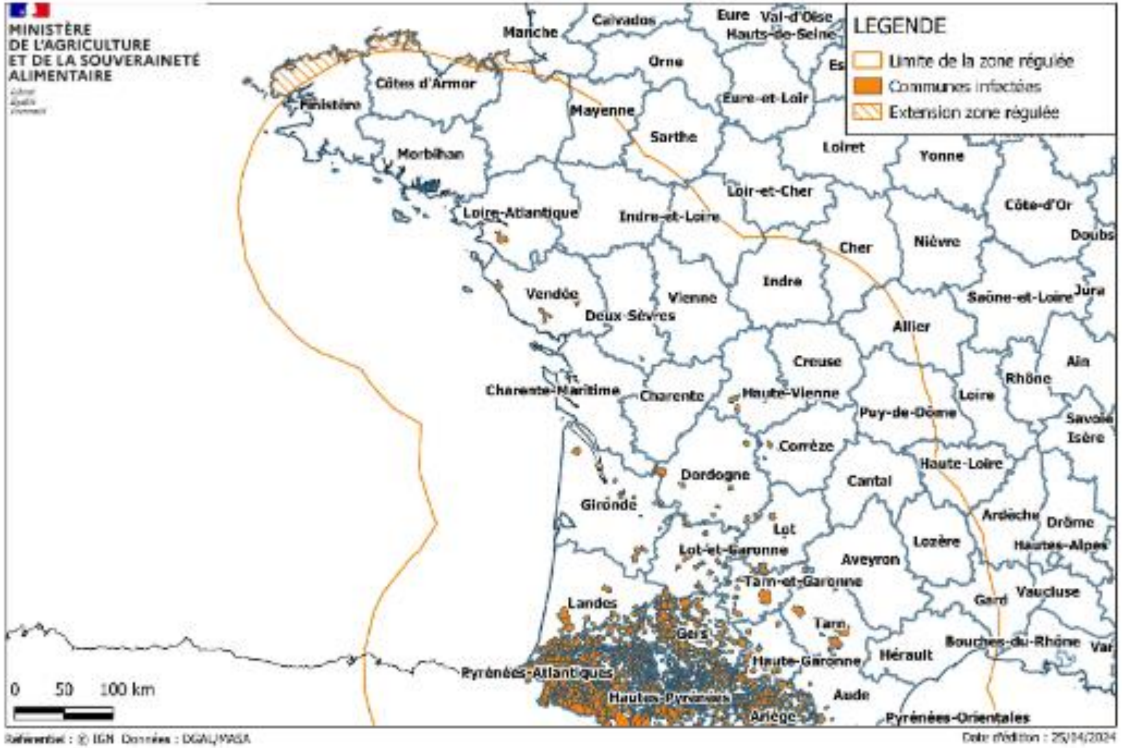
Pyrénées Atlantiques (2), Hautes Pyrénées (1)

18/09/2023

> 4 330 outbreaks

20 infected departments:
09, 11, 19, 24, 31, 32, 33, 40,
46, 44,
47, 64, 65, 81, 82, 85, 87

1 izard
2 deers
1 roe deer



Référentiel : © IGN Données : DGAL/MASA
Date d'édition : 25/04/2024


NIH National Librar
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Search results

Virologie (Montrouge). 2024 Feb 1;28(1):1-2. doi: 10.1684/vir.2024.1035.

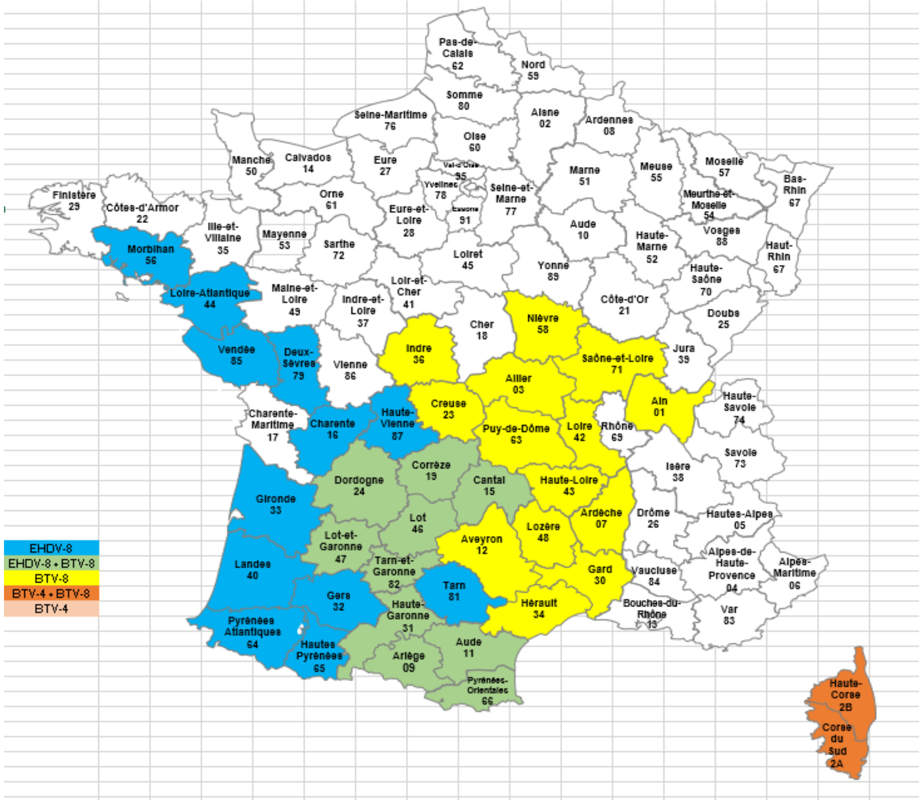
Emergence of Epizootic Hemorrhagic Disease in France in 2023: Impacts and Future Prospects

Stéphan Zientara, Corinne Sailleau, Pascal Dujardin, Emmanuel Bréard, Damien Vitour

Dr Vivien Philis, Lannemezan
Dr Mylène Lemaire-Meyer (LVD09)

Dr Alberto Jorda Blanco (Aude)
Dr Mylène Lemaire-Meyer (LVD09)

29/01/24


Pas-de-Calais 62
Nord 59
Somme 80
Seine-Maritime 76
Aisne 02
Ardennes 08
Oise 60
Manche 50
Calvados 14
Eure 27
Val-d'Oise 95
Marne 51
Meuse 55
Moselle 57
Bas-Rhin 67
Yvelines 78
Seine-et-Marne 77
Meurthe-et-Moselle 54
Finistère 29
Côtes-d'Armor 22
Orne 61
Eure-et-Loire 28
Essonne 91
Aube 10
Vosges 88
Ille-et-Vilaine 35
Mayenne 53
Sarthe 72
Haute-Marne 52
Haut-Rhin 67
Morbihan 56
Loiret 45
Yonne 89
Haute-Saône 70
Loire-Atlantique 44
Maine-et-Loire 49
Indre-et-Loire 37
Loir-et-Cher 41
Côte-d'Or 21
Doubs 25
Nièvre 58
Cher 18
Vendée 85
Deux-Sèvres 79
Vienne 86
Indre 36
Saône-et-Loire 71
Jura 39
Allier 03
Ain 01
Haute-Savoie 74
Charente-Maritime 17
Charente 16
Haute-Vienne 87
Creuse 23
Puy-de-Dôme 63
Loire 42
Rhône 69
Savoie 73
Isère 38
Corrèze 19
Dordogne 24
Cantal 15
Haute-Loire 43
Gironde 33
Lot 46
Ardèche 07
Drôme 26
Hautes-Alpes 05
Lozère 48
Aveyron 12
Lot-et-Garonne 47
Alpes-de-Haute-Provence 04
Alpes-Maritime 06
Landes 40
Tarn-et-Garonne 82
Gard 30
Vaucluse 84
Gers 32
Tarn 81
Hérault 34
Bouches-du-Rhône 13
Var 83
Pyrénées Atlantiques 64
Haute-Garonne 31
Hautes Pyrénées 65
Aude 11
Ariège 09
Pyrénées-Orientales 66
Haute-Corse 2B
Corse du Sud 2A
EHDV-8
EHDV-8 + BTV-8
BTV-8
BTV-4 + BTV-8
BTV-4

2023

EHDV-8
EHDV-8
Italie (9 outbreaks)
Espagne (252 outbreaks)
Portugal (77 outbreaks)
France (4,330 outbreaks)
Europe: > 4,700 outbreaks)

PARIS 2024


PARIS 2024
PARIS 2024
PARIS 2024
PARIS 2024
NON CONTRACTUAL VISUAL

June 2024

Confirmado el primer caso de enfermedad hemorrágica epizoótica de la actual temporada vectorial

El Ministerio de Agricultura, Pesca y Alimentación ha confirmado el primer caso de enfermedad hemorrágica epizoótica en una explotación de bovino de Guadalajara

Vacas libres de enfermedad hemorrágica epizoótica según la última actualización del Gobierno. (Foto: Freepik)

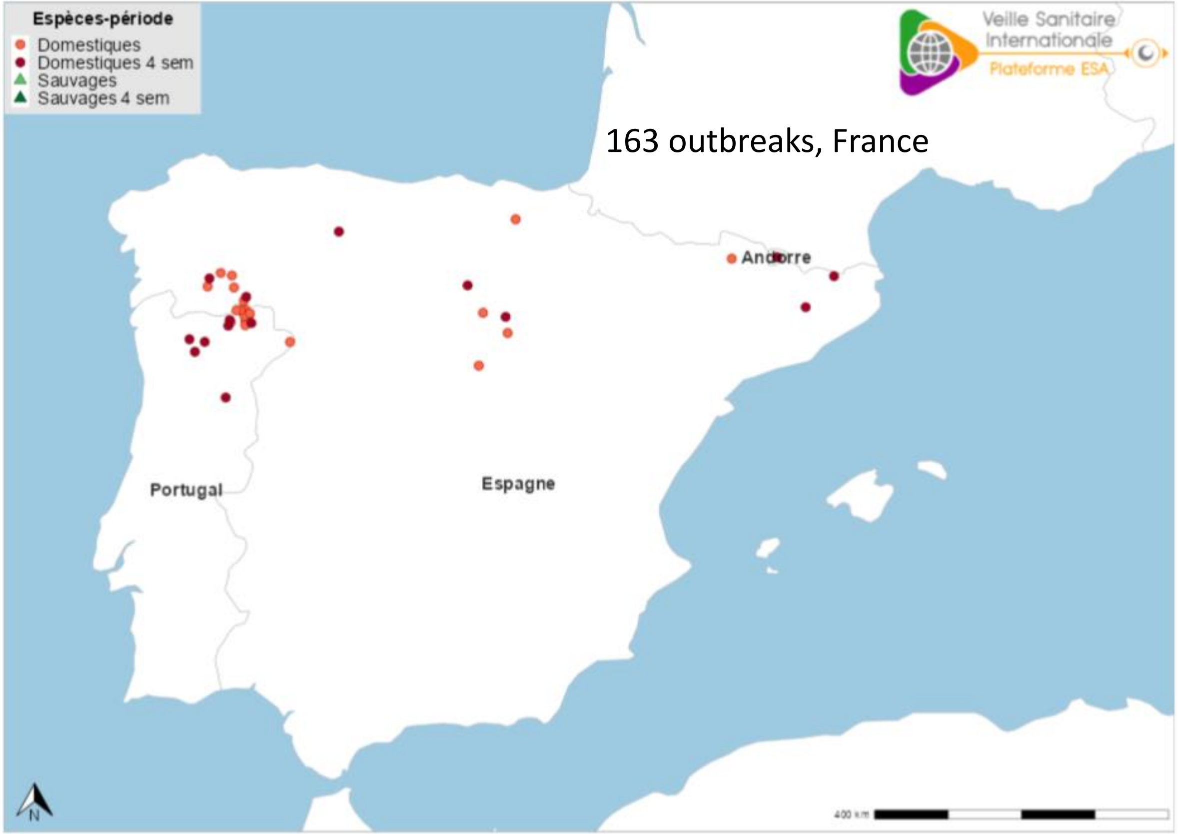
Archivado en:


Nantes
Saint-Nazaire
Angers
Tours
Blois
Parc naturel régional Loire-Anjou-Touraine
Bourges
Nevers
Parc naturel régional du Morvan
Dijon
Besançon
Challans
La Roche-sur-Yon
Les Sables-d'Olonne
Châtellerault
Poitiers
Parc naturel régional de la Brenne
Châteauroux
France
Chalon-sur-Saône
Lausanne
Niort
La Rochelle
Montluçon
Vichy
Mâcon
Roanne
Genève
Annecy
Rochefort
Saintes
Royan
Limoges
Parc naturel régional Périgord-Limousin
Parc naturel régional de Millevaches en Limousin
Clermont-Ferrand
Lyon
Chambéry
Saint-Étienne
Grenoble
Brive-la-Gaillarde
Bordeaux
Bergerac
Valence
Parc national des Écrins
Parc naturel régional de l'Aubrac
Parc naturel régional des Monts d'Ardèche
Parc naturel régional des Landes de Gascogne
Agen
Montauban
Albi
Alès
Parc naturel régional des Grands Causses
Avignon
Mont-de-Marsan
Auch
Toulouse
Montpellier
Aix-en-Provence
Bayonne
Bilbao
Saint-Sébastien
Pau
Lourdes
Carcassonne
Béziers
Marseille
Toulon
Narbonne
Vitoria-Gasteiz
Pampelune
Parc national des Pyrénées
Parc naturel régional des Pyrénées Ariégeoises
Perpignan
Logroño
Andorre
Google

June
EHDV-8

EHD

18 August 2024



163 outbreaks, France

Virology

Disease

Epidemiology

Diagnosis

Prevention

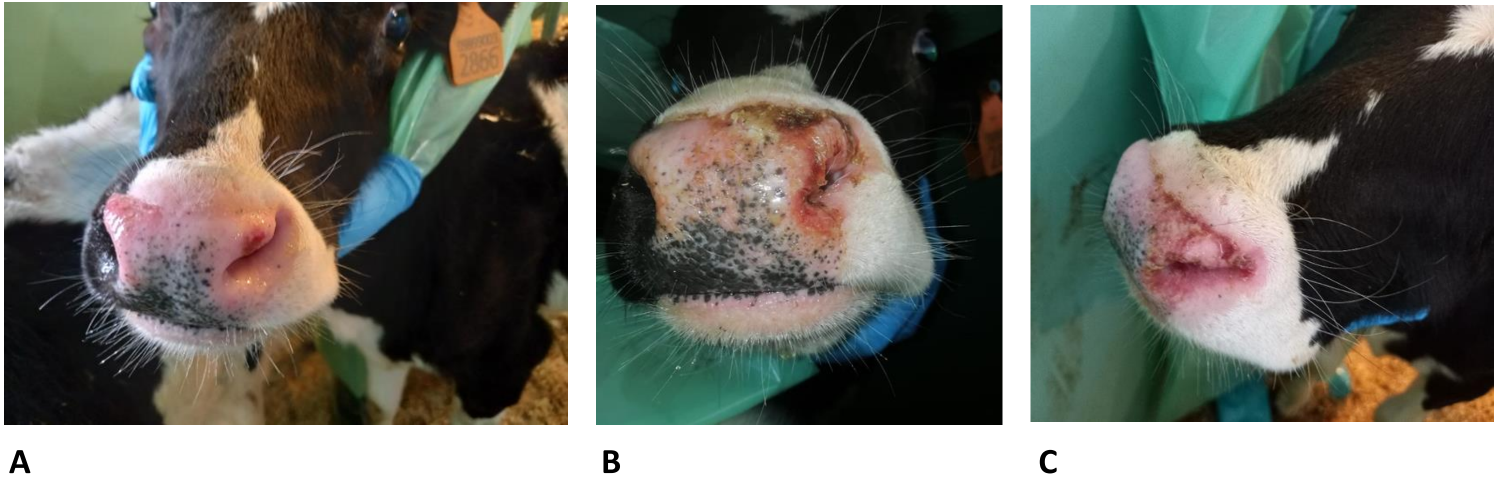
› Vet Ital. 2023 Dec 20. doi: 10.12834/VetIt.3433.23112.1. Online ahead of print.

Experimental infection of cattle, sheep, and goats with the newly emerged epizootic hemorrhagic disease virus serotype 8

Massimo Spedicato [1], Francesca Profeta [1], Sarah Thabet [2], Liana Teodori [1], Alessandra Leone [1], Ottavio Portanti [1], Maura Pisciella [1], Barbara Bonfini [1], Simone Pulsoni [1], Francesca Rosso [1], Emanuela Rossi [1], Paola Ripà [1], Angela De Rosa [1], Eugenia Ciarrocchi [1], Roberta Irelli [1], Antonio Cocco [1], Corinne Sailleu [3], Nicola Ferri [1], Tiziana Di Febo [1], Damien Vitour [3], Emmanuel Breard [3], Daniele Giansante [1], Soufien Sghaier [4], Thameur Ben Hassine [5], Stephan Zientara [3], Romolo Salini [1], Salah Hammami [2], Giovanni Savini [1], Alessio Lorusso [6]

Affiliations + expand

PMID: 38117055 DOI: 10.12834/VetIt.3433.23112.1



6 calves, 4-5 months old, 2 males ; 4 females
Strain EHDV-8, Sardinia 2022, 1 passage BSR cells
2 ml inoculum SC+ 1 ml ID, 6,7 log10 TCID50/ml

3/6: fever
1 calf: clinical signs

Figure 1

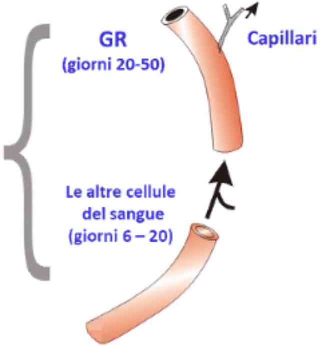
IZS
TERAMO
/
**ISTITUTO
ZOOPROFILATTICO
SPERIMENTALE**
DELL'ABRUZZO
E DEL MOLISE
"G. CAPORALE"

BT≠EHD

Viraemia

BT

- ☐ Cattle
  - ☐ VI: 5-60 dd
  - ☐ RT-PCR: 5-180 dd
- ☐ Sheep
  - ☐ VI: 5-30 dd
  - ☐ RT-PCR: 5-100 dd
- ☐ Goats
  - ☐ VI: 5-30 dd
  - ☐ RT-PCR: 5-100 dd



EHD

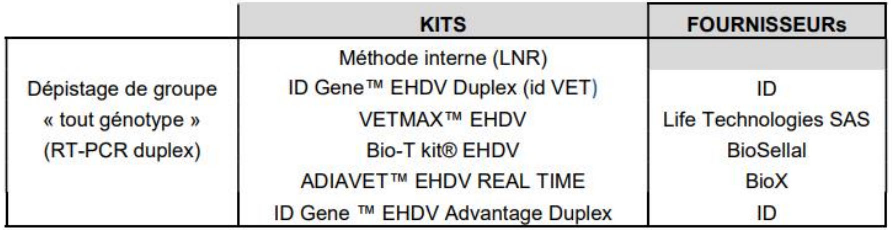
- ☐ Cattle
  - ☐ VI: 7-42 dd (EHDV-8: 2-16 dd)
  - ☐ RT-PCR: 2-180 dd
- ☐ Sheep
  - ☐ VI: 2-7
  - ☐ RT-PCR: 5-100 dd
- ☐ Goats
  - ☐ VI: 0
  - ☐ RT-PCR: 0

G Savini

anses
Laboratoire de santé animale
De Maisons Alfort
LNR Fièvre catarrhale ovine et
MHE

10/04/2024

Validated EHDV PCR



	KITS	FOURNISSEURs
Dépistage de groupe « tout génotype » (RT-PCR duplex)	Méthode interne (LNR)	
	ID Gene™ EHDV Duplex (id VET)	ID
	VETMAX™ EHDV	Life Technologies SAS
	Bio-T kit® EHDV	BioSellal
	ADIAVET™ EHDV REAL TIME	BioX
	ID Gene ™ EHDV Advantage Duplex	ID

Ceva

Ceva Animal Health

Inactivated vaccine EHDV-8

Temporay authorization in France

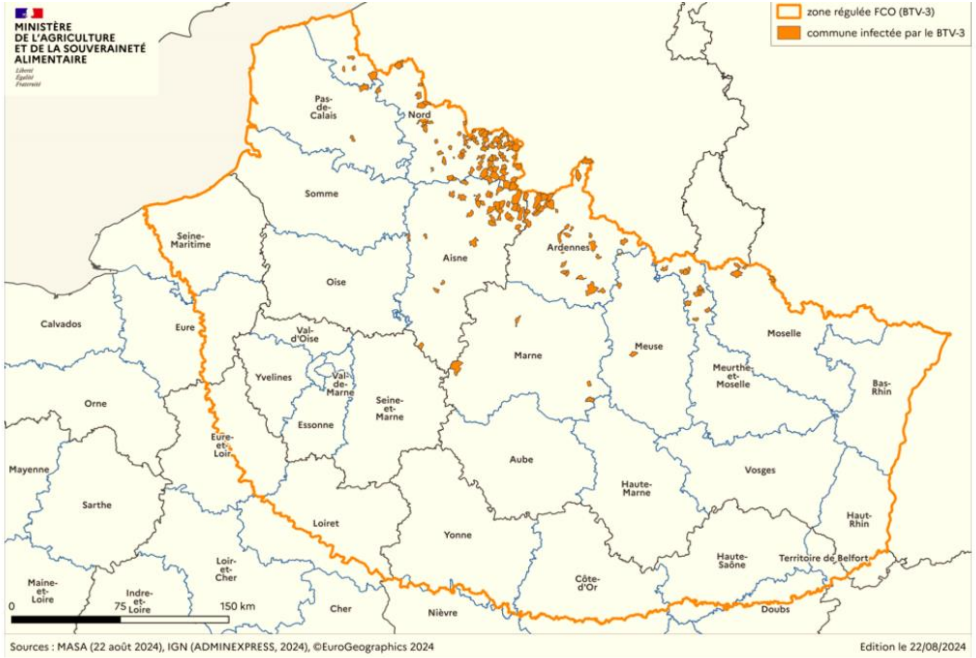
Cattle

2 injections primo-vaccination.

Prevention of viremia (PCR >40) and reduction of clinical signs

- 190 outbreaks

22 August 2024



Sources : MASA (22 août 2024), IGN (ADMINEXPRESS, 2024), ©EuroGeographics 2024

Edition le 22/08/2024

Août 2024

This map includes information on BTV infection
Source: CIR (EU) 2021/620

This map is meant purely as a documentation tool and has no legal effect. The relevant legal acts are published in the Official Journal of the European Union

* This designation is without prejudice to positions on status, and is in line with UNSCR 1244 and the ICJ Opinion on the Kosovo Declaration of Independence.

BTV-3
2,900 outbreaks

BTV-3
> 500 outbreaks

BTV-3
1,885 outbreaks

New strain BTV-8

Acknowledgements

anses

Organisation mondiale de la santé animale
Fondée en tant qu'OIE

Corinne Sailleau

IZS
TERAMO

Giovanni Savini

Alessio Lorusso

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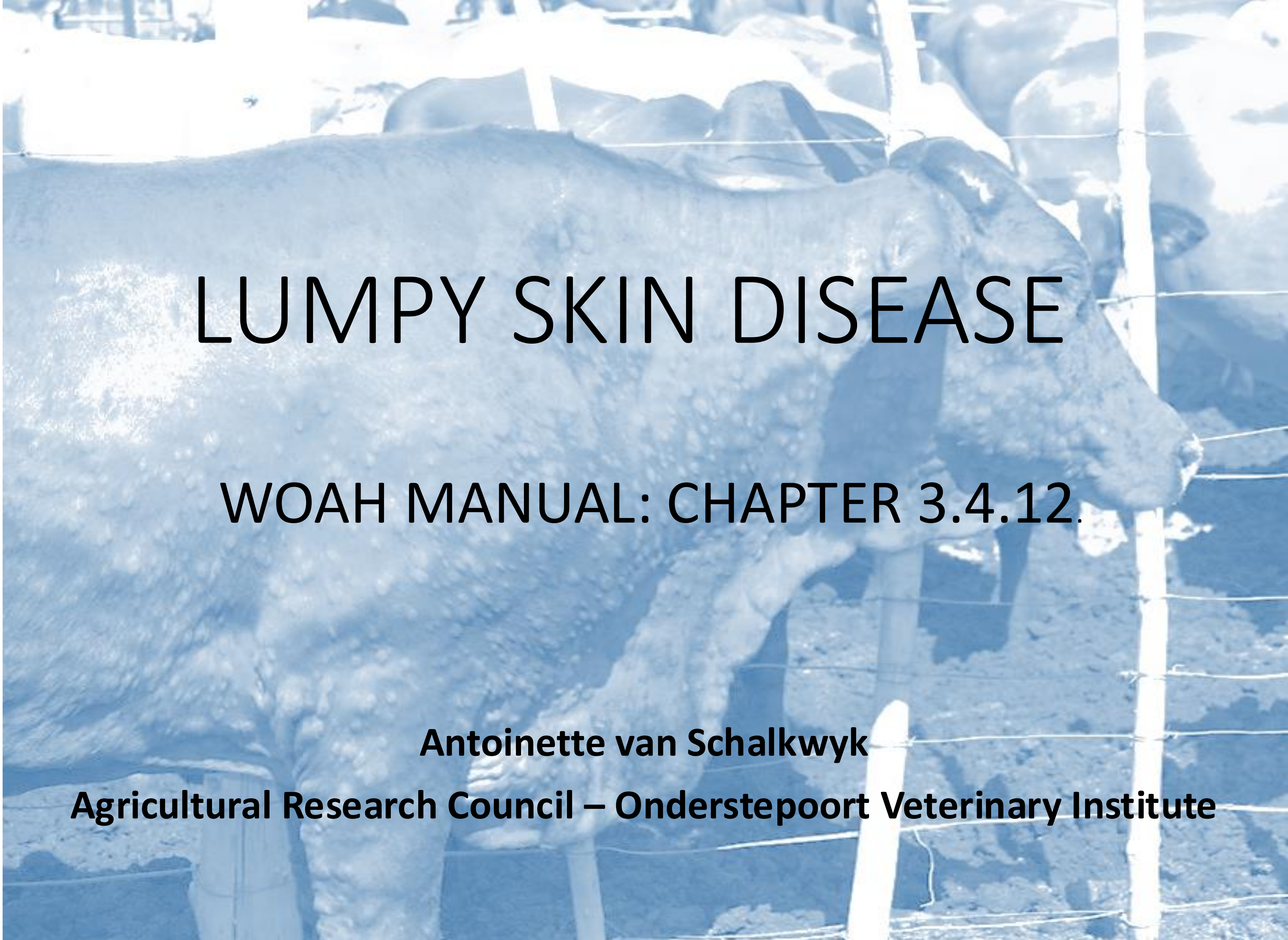
Thank you for your attention

WOAH Regional Workshop
on Vector Borne diseases in
Asia and the Pacific

19-20 September 2024



LUMPY SKIN DISEASE

WOAH MANUAL: CHAPTER 3.4.12.

Antoinette van Schalkwyk

Agricultural Research Council – Onderstepoort Veterinary Institute

Lumpy skin disease: Introduction

Causative agent: [Poxvirus] – {*Capripoxvirus*}
- Lumpy skin disease virus

Type strain: Neethling strain (Western Cape, RSA, 1957)

Ruminants: Cattle and water buffalo.

Wildlife:. Springbok, impala, eland, giraffe, camel, gazelle, oryx, Arabian oryx, banteng and Mainland searow

Notifiable disease: WOAH

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Lumpy skin disease: Transmission

Highly contagious viral infection

Vector-borne, non-zoonotic and transboundary disease

NOT an arbovirus

Require more investigations

Direct contact: Skin nodules, nasal discharge or saliva from infected animals

In-direct: Contaminated food, water and milk

Vertically: Intrauterine route

Long-distance dispersal of LSDV seems to occur via the movement of infected animals

Seasonal patterns indicate that arthropod-borne transmission (Mechanical):
Blood-sucking or biting arthropods:
Stable flies (*Stomoxys calcitrans*), Mosquitoes (*Aedes aegypti*),
Hard ticks (*Rhipicephalus* and *Amblyomma* species)
House fly (*Musca domestica*)

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Lumpy skin disease: Role of wildlife species

In 2022, isolation and characterisation of LSDV from a giraffe in a zoo was reported in Vietnam (Dao et al., 2022).

Namibia: an eland antelope (Taurotragus oryx), which was asymptomatic for LSD, but LSDV DNA isolated (Molini et al., 2021)

India: Farmed camels (Kumar et al., 2023)

India: Free living gazelle (Sundhankar et al., 2023)

This evidence is supported by extensive serosurveys of wildlife in Africa which detected antibodies in very low numbers of samples (Davies, 1982; Hedger and Hamblin, 1983), leading the authors to conclude "wildlife in Africa probably does not play a very important part in the perpetuation and spread of LSDV".

LSDV has spread rapidly in recent years into the Middle East and Asia, and the susceptibility of wildlife species in these regions to LSDV is unknown.

In South Africa:
Springbuck and giraffe - National parks and game reserves

Require more investigations

Lumpy skin disease: Global spread

Zambia: 1929

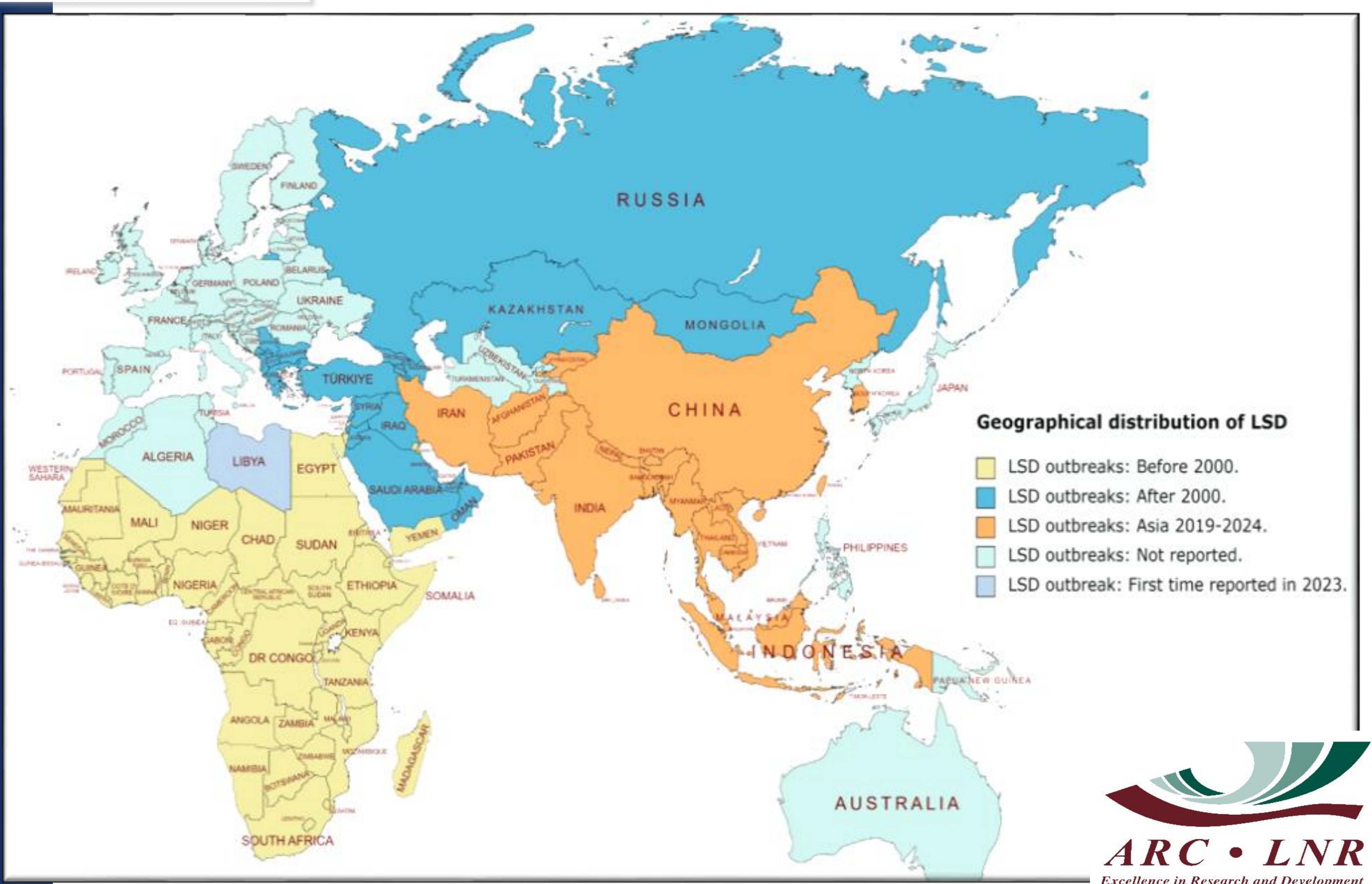
South Africa: 1944

Kenya: 1958

Middle East: 1988 and again in 2006

Europe, Caucus and Russia: 2015

China and India: 2019



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Lumpy skin disease: Epidemiology

Clusters based on Markers

- 🟧 1.2
- 🟩 1.2 -KSGP
- ■ 1.1 & 1.2
- 🟨 1.2 & 2.3
- 🟪 2.5
- 🟩 1.1 & 1.2 & 2.1 & 2.2 & 2.4 & 2.5 & 2.6
- 🟦 No sequence data

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Lumpy skin disease: Phylogenetics

Clusters 1.1 and 1.2

LSDVs representing sequences from both clusters were circulating in Africa in the 1950's.

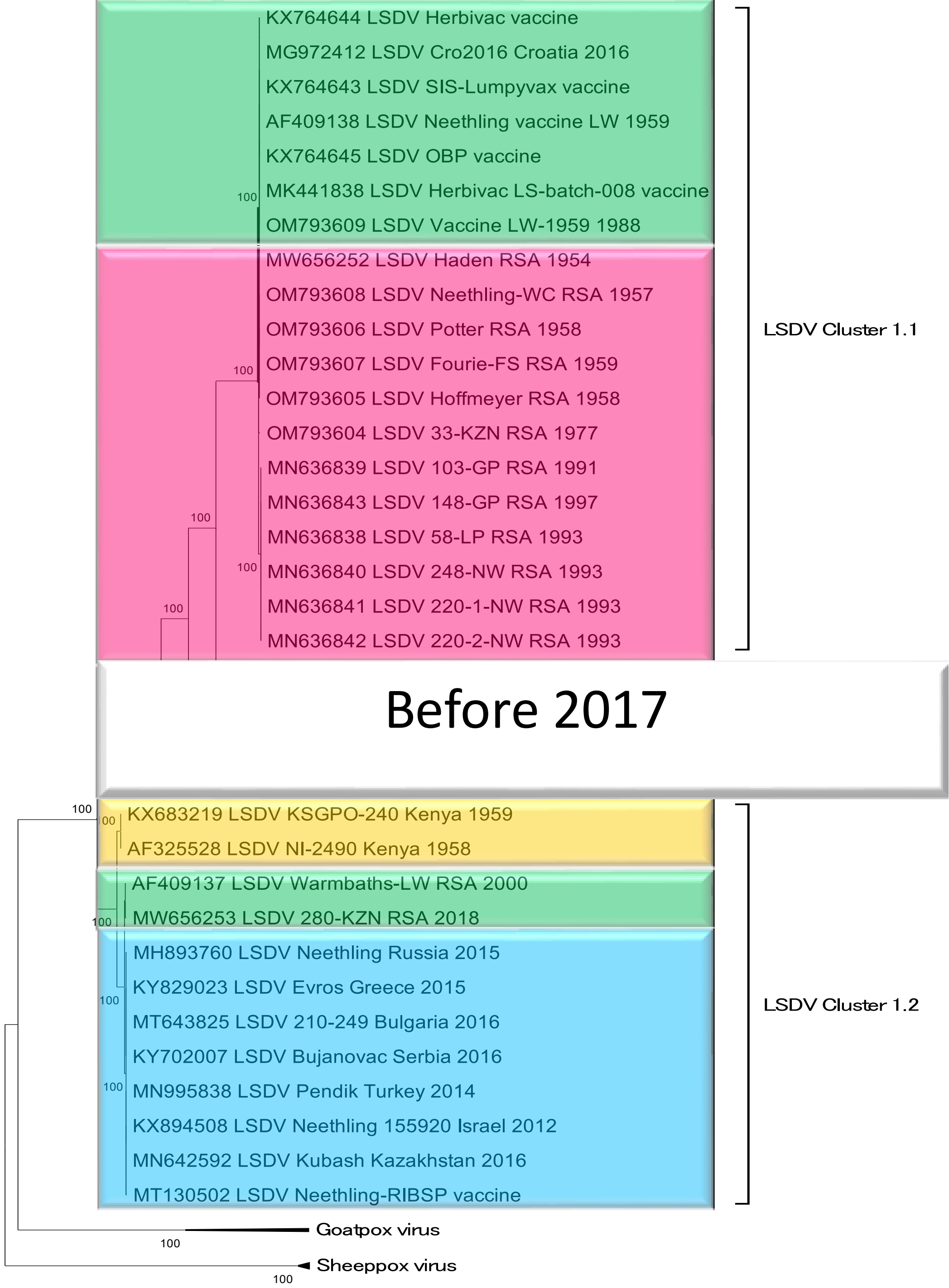
± 2,200 SNPs between cluster 1.1 and 1.2

(Kara et al., 2003; van Schalkwyk et al., 2021)

Majority of the DIVA assays are based on differentiation between cluster 1.1 and 1.2. Thus not suitable to detect the field isolates of cluster 1.1

- ± 1860 SNPs in 114 ORFs
  - 57% Synonymous
  - 26% Non-Synonymous
- ± 330 (15%) IGR

TMRCA: ± 500 years



Before 2017

Lumpy skin disease: Phylogenetics (Cluster 1.1)

Oldest isolate: Haden / 1954
(van Schalkwyk et al., 2021)

Prototype: Neethling-WC / 1957
(Alexander et al., 1957; van Schalkwyk et al., 2022)

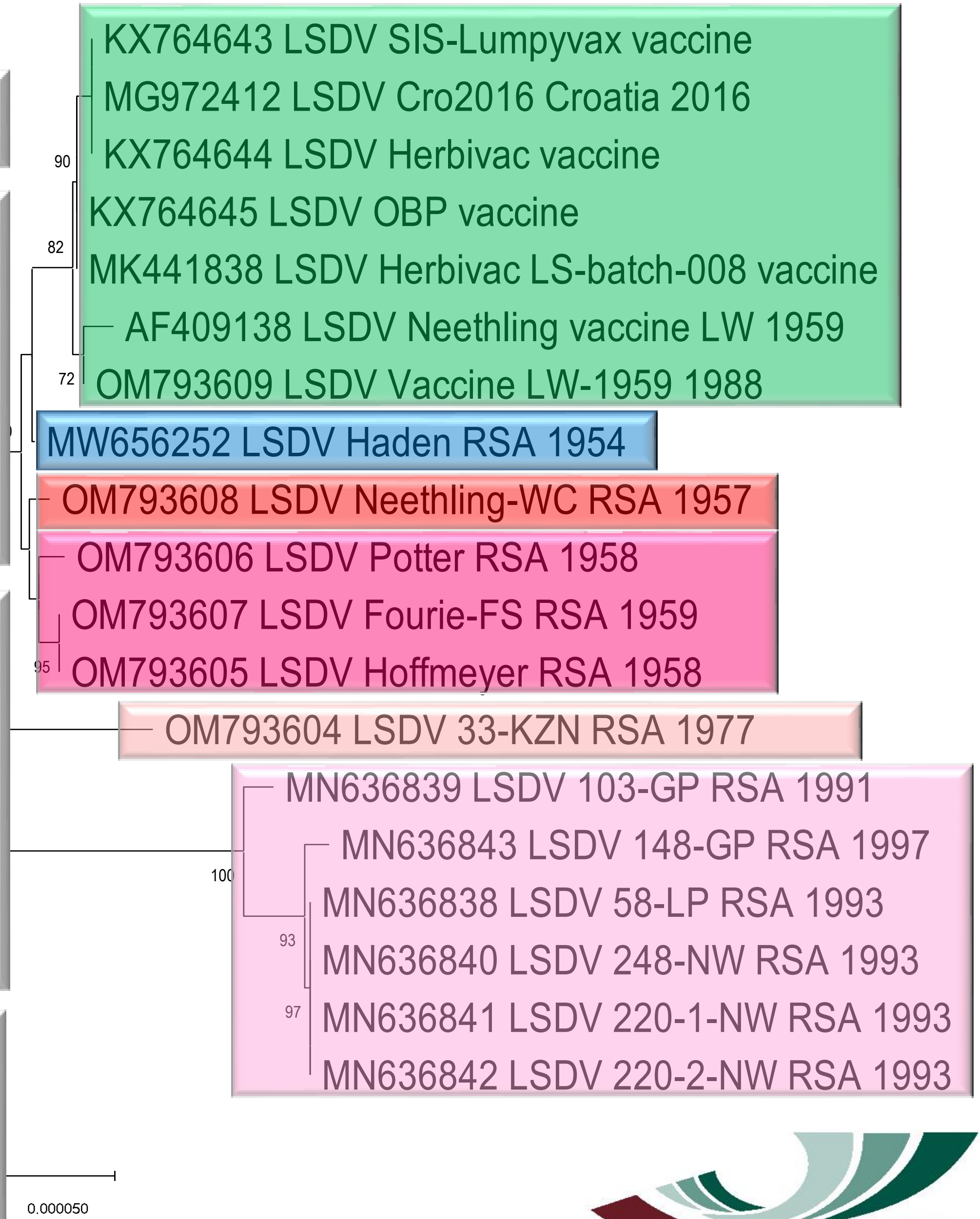
- Vaccine: Neethling-LW1959 (van Rooyen et al., 1959; Kara et al., 2003)
- Vaccine: OBP, Herbivac, SIS-Lumpyvax (Mathijs et al., 2016; Douglass et al., 2019)

Wild type field isolates:
South Africa
1950's, 1970's and 1990's
(van Schalkwyk et al., 2020 and 2022)

Cluster 1.1 - **Attenuation**

Seven SNPs between Neethling-WC/1957 and Neethling-LW1959 vaccine
(van Schalkwyk et al., 2022)

- Non-synonymous:
  - ○ LW028 T135A
  - ○ LW083: K663N
  - ○ LW098: G553S
  - ○ LW098: I625T
- Reading frame:
  - ○ LW086: Termination
    LW131: Termination
    LW134: Termination



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Lumpy skin disease: Phylogenetics (Cluster 1.2)

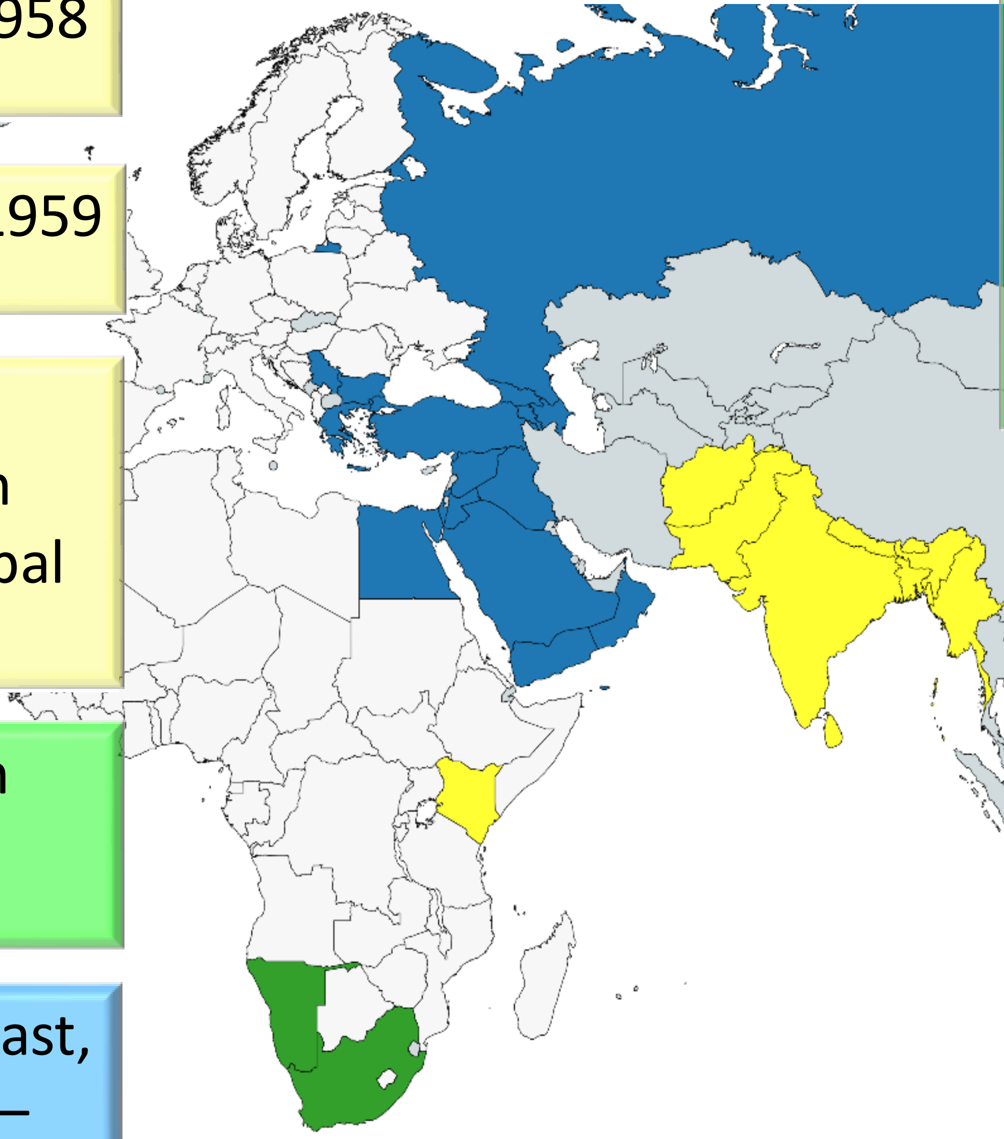
Isolate: 2490/Kenya/1958
(Tulman et al., 2000)

Vaccine: KSGPO-240/1959
(Vandenbussche et al., 2016)

Vaccine: KSGPO-240/1959. Outbreak in Bangladesh, India, Nepal and Pakistan

Isolates from southern Africa 2000 – 2022
(Kara et al., 2003)

Isolates from Middle East, Europe and Asia 2012 – 2016



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Lumpy skin disease

Parental sequences are both vaccines:
- Neethling-LW1959
- KSGPO-240

Recombinants

2.1: Saratov/Russia/2017
(Sprygin et al., 2018)

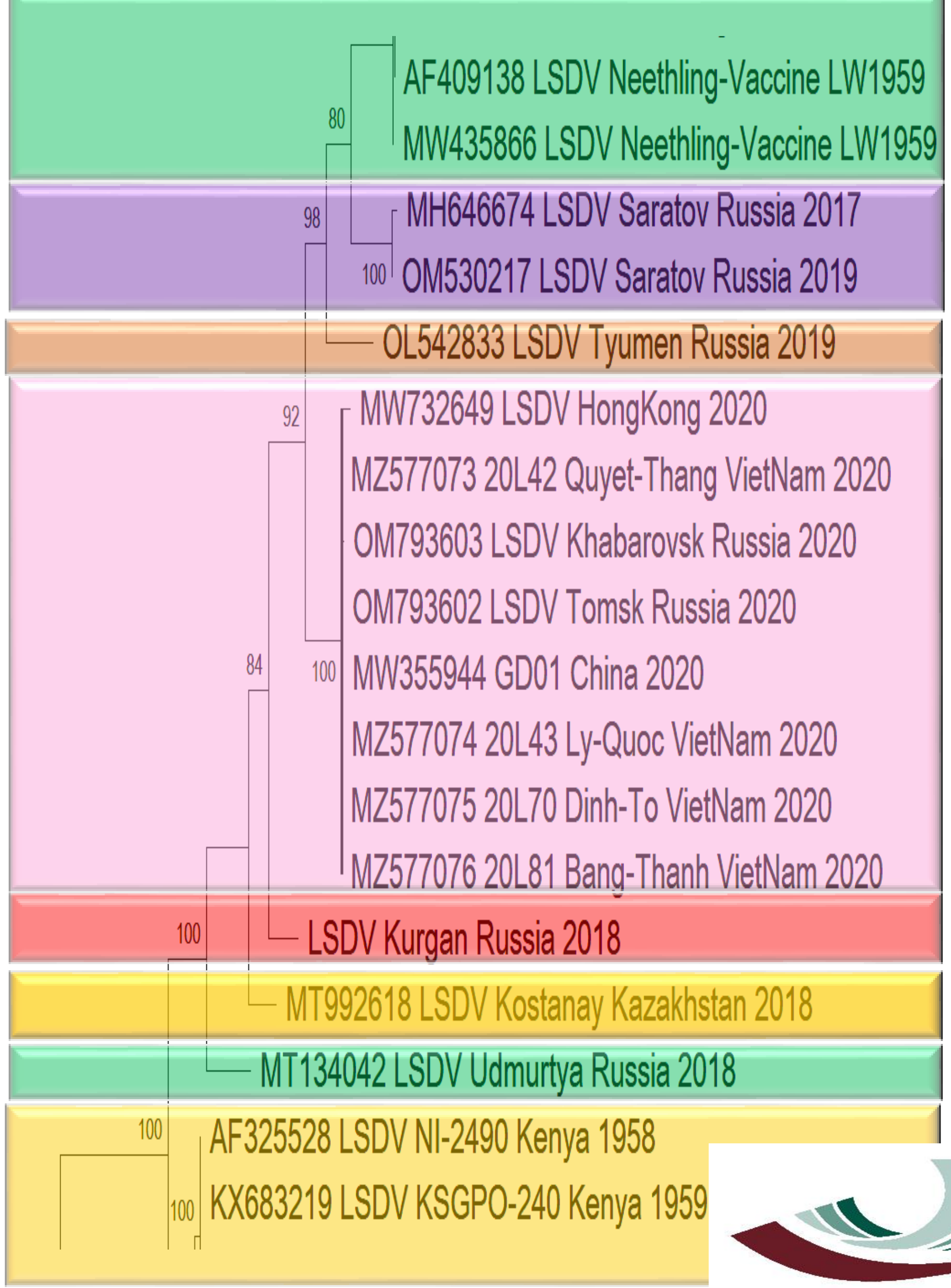
2.2: Udmurtya/Russia/2018
(Sprygin et al., 2018)

2.3: Kostanay/Kazakhstan/2018

2.4: Tyumen/Russia/2019
(Krotova et al., 2022)

2.5: GD01/China/2019
(Ma et al., 2021)

2.6: Kurgan/Russia/2018
(Sprygin et al., 2024)



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Recombinants

The Importance of Quality Control of LSDV Live Attenuated Vaccines for Its Safe Application in the Field

by Andy Haegeman[1,*], Ilse De Leeuw[1], Meruyert Saduakassova[2], Willem Van Campe[3], Laetitia Aerts[4], Wannes Philips[4], Akhmetzhan Sultanov[2], Laurent Mostin[3] and Kris De Clercq[1]

Recombinant LSDV Strains in Asia: Vaccine Spillover or Natural Emergence?

by Frank Vandenbussche[1,†], Elisabeth Mathijs[1,†], Wannes Philips[1], Meruyert Saduakassova[2], Ilse De Leeuw[3], Akhmetzhan Sultanov[2], Andy Haegeman[3] and Kris De Clercq[3,*]

Contaminated LSD vaccine = Neethling, KSPG vaccine and GTPV

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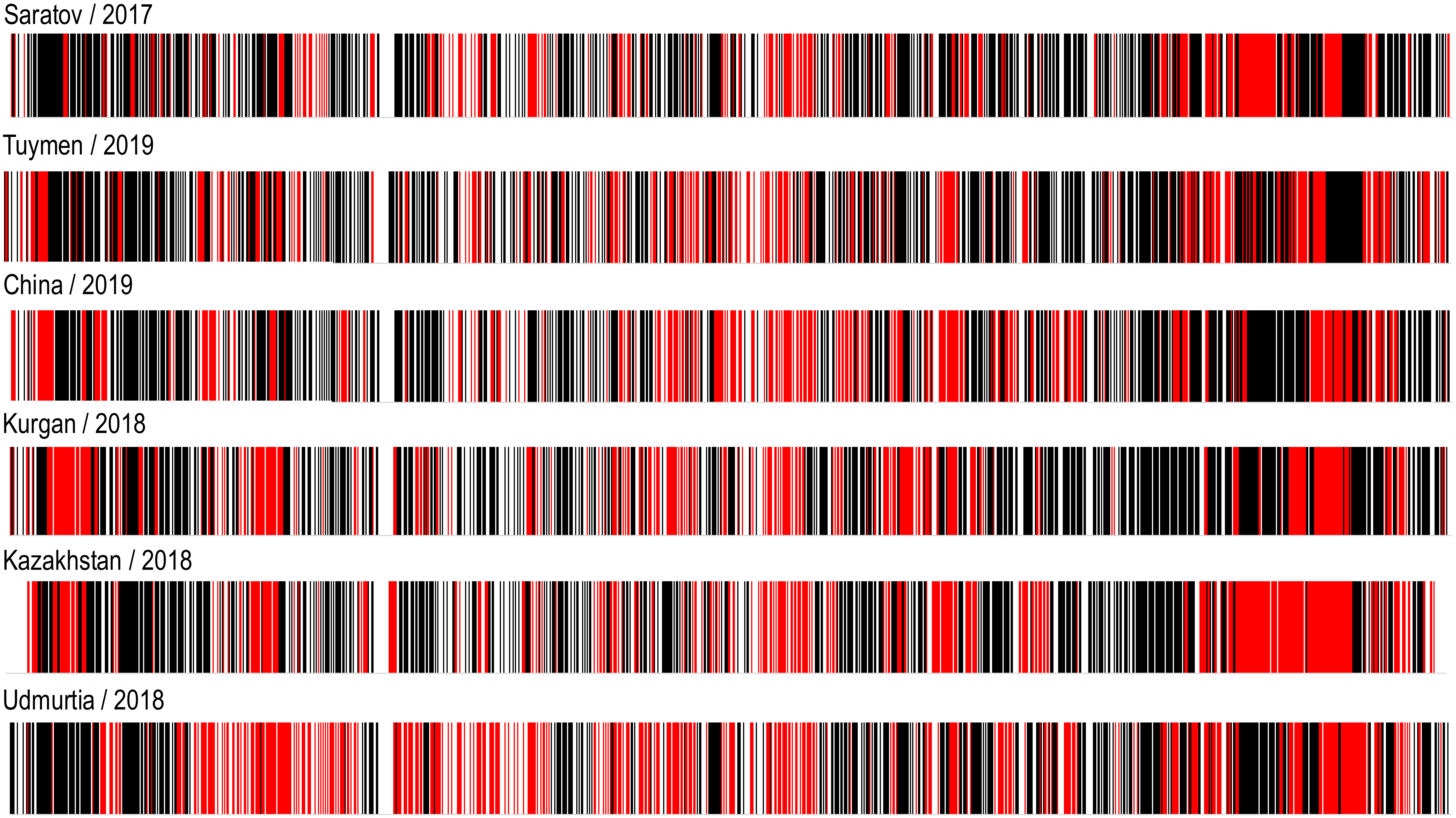

Saratov / 2017
Tuymen / 2019
China / 2019
Kurgan / 2018
Kazakhstan / 2018
Udmurtia / 2018

Lumpy skin disease

Russia: Saratov & Udmurtiya

Non-vector-borne transmission of lumpy skin disease virus

Kononov Aleksandr[1], Byadovskaya Olga[1], Wallace B. David[2,3], Prutnikov Pavel[1], Pestova Yana[1], Kononova Svetlana[1], Nesterov Alexander[1], Rusaleev Vladimir[1], Lozovoy Dmitriy[1] & Sprygin Alexander[1]✉

A lumpy skin disease virus which underwent a recombination event demonstrates more aggressive growth in primary cells and cattle than the classical field isolate

Svetlana Kononova[1] | Aleksandr Kononov[1] | Irina Shumilova[1] | Olga Byadovskaya[1] | Alexander Nesterov[1] | Pavel Prutnikov[1] | Shawn Babiuk[2] | Alexander Sprygin[1]

Experimentally controlled study indicates that the naturally occurring recombinant vaccine-like lumpy skin disease strain Udmurtiya/2019, detected during freezing winter in northern latitudes, is transmitted *via* indirect contact

Alexander Nesterov[1], Ali Mazloum[1], Olga Byadovskaya[1], Irina Shumilova[1], Antoinette Van Schalkwyk[2,3], Alena Krotova[1], Vladimir Kirpichenko[4], Irina Donnik[5], Ilya Chvala[1] and Alexander Sprygin[1*]

Overwintering of recombinant lumpy skin disease virus in northern latitudes, Russia

Irina Shumilova[1] | Alena Krotova[1] | Alexander Nesterov[1] | Olga Byadovskaya[1] | Antoinette van Schalkwyk[2] | Alexander Sprygin[1]

Recombinants: Novel phenotypes
- Transmission
- Overwintering
- Aggressive growth

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Lumpy skin disease: Phylogenetics

Phylogenetic analysis shows the majority of LSDV strains group into two monophyletic clusters (cluster 1.1 and 1.2) (Biswas et al., 2020; Van Schalkwyk et al., 2021).

Cluster 1.1:
Neethling Prototype strain and vaccine

Cluster 1.1 consists of LSDV Neethling vaccine strains that are based on the LSDV/Neethling/WC-1957 type-strain (Kara et al., 2003; Van Rooyen et al., 1959; van Schalkwyk et al., 2020) and historic wild-type strains from South Africa.

Cluster 1.2:
KSGP and "wild type"

Cluster 1.2 consists of wild-type strains from southern Africa, Kenya, the northern hemisphere, and the Kenyan KSGP O-240 commercial vaccine.

Cluster 2.1 -2.6:
Six unique recombinant strains

In addition to these two clusters, there have recently been recombinant LSDV strains isolated from clinical cases of LSD in the field in Russia and central Asia (Flannery *et al.,* 2021; Sprygin *et al.,* 2018; 2020; Wang *et al.,* 2021). These recombinant viruses show unique patterns of accessory gene alleles, consisting of sections of both wild-type and "vaccine" LSDV strains.

Lumpy skin disease: Laboratory confirmation

- Laboratory confirmation:

- “Gold standard” serological test: serum/virus neutralization test (SNT/VNT).

Not all animals either naturally infected or vaccinated develop LSDV neutralizing antibodies.

- Enzyme-linked immunosorbent assay (ELISA) by IDVet (France).
- Conventional and Real-Time Polymerase chain reaction (PCR) assays.
- Virus isolation on cell culture (Skin nodules).

Lumpy skin disease: WOAH Manual: B. DIAGNOSTIC TECHNIQUES

Key:

+++ = recommended for this purpose

++ recommended but has limitations

+ = suitable in very limited circumstances

– = not appropriate for this purpose

Method	Purpose					
	Population freedom from infection	Individual animal freedom from infection prior to movement	Contribute to eradication policies	Confirmation of clinical cases	Prevalence of infection – surveillance	Immune status in individual animals or populations post-vaccination
	Detection of the agent					
Virus isolation	+	++	+	+++	+	–
PCR	++	+++	++	+++	+	–
Transmission electron microscopy	–	–	–	+	–	–
	Detection of immune response					
VNT	++	++	++	++	++	++
IFAT	+	+	+	+	+	+
ELISA	++	++	++	++	++	++

PCR = polymerase chain reaction; VNT = virus neutralisation test;

IFAT = indirect fluorescent antibody test; ELISA = enzyme-linked immunosorbent assay

Lumpy skin disease: Molecular test to differentiate vaccine and wild-type LSDV

DIVA: **D**ifferentiation of **I**nfected from **V**accinated **A**nimals

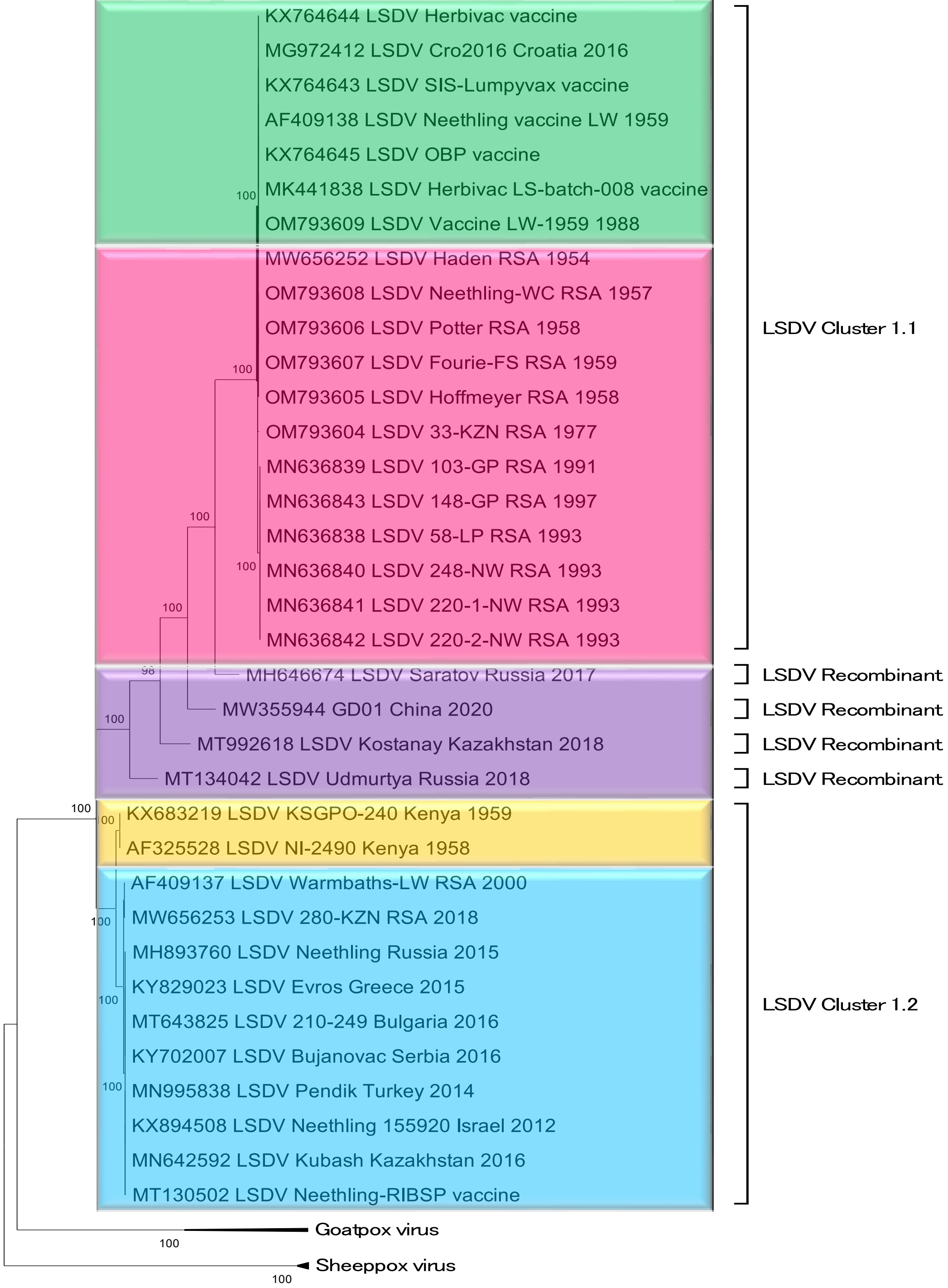
CAN **differentiate** between cluster 1.1 and 1.2.

CAN NOT differentiate between vaccine and wild type isolates within Cluster 1.1

CAN NOT differentiate between vaccines and novel recombinant strains (Cluster 2.1 – 2.5)

Quantitative real-time PCR assays have been designed to differentiate the “Neethling response” caused by vaccination with a Neethling-based LSDV strains and wild-type LSDV strains from cluster 1.2 (Agianniotaki et al., 2017; Pestova et al., 2018; Vidanovic et al., 2016).

However, they cannot distinguish between a LSDV Neethling vaccine strain and the novel recombinant LSDV strains recently isolated from disease outbreaks in Asia (Byadovskaya et al., 2021; Flannery et al., 2021). These DIVA assays are also not capable of discriminating between LSDV Neethling vaccine strains and recently characterised (historic) wild-type viruses from South Africa belonging within cluster 1.1 (Van Schalkwyk et al., 2020; 2021).



Lumpy skin disease: New Markers

Kumar et al., 2023

HRM-based gap-qRT-PCR: 801bp in terminal repeat region (ITR)

- Vaccine: (Lumpi-ProVac^{Ind}) vs. Wild type: (LSDV/2019/India/Ranchi)

Haegeman et al., 2023

Duplex qRT-PCR: LW133 and LW144

- Vaccine (Neethling) vs. Wild type: Cluster 1.2 vs. Recombinant (Cluster 2.5)

Krotova et al., 2023

PCR and Sanger sequencing: 705bp in ORF LW134

- Vaccines (Neethling and KSGPO) vs. Wild type Cluster 1.2 vs. Recombinant (Cluster 2.1, 2.2, 2.3, 2.4 and 2.5)

Lumpy skin disease: New Diagnostic tests

Nan et al., 2023	Triplex real-time PCR: • LSDV vs GTPV vs SPPV
Liao et al., 2023	CRISPR-Cas12a: • LSDV vs GTPV vs SPPV
Nandi et al., 2023	Isothermal PCR: 27bp in ORF LW126 • Vaccines (GTPV) vs. Wild type Cluster 1.2-KSGPO
Abdalhamed et al., 2022	Gold nanoparticle – lateral flow test
Sthitmatee et al., 2023	In-house ELISA using whole virus (LSD/THA/CMU/21/05)

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Lumpy skin disease: WOAH Manual: C. REQUIREMENTS FOR VACCINES

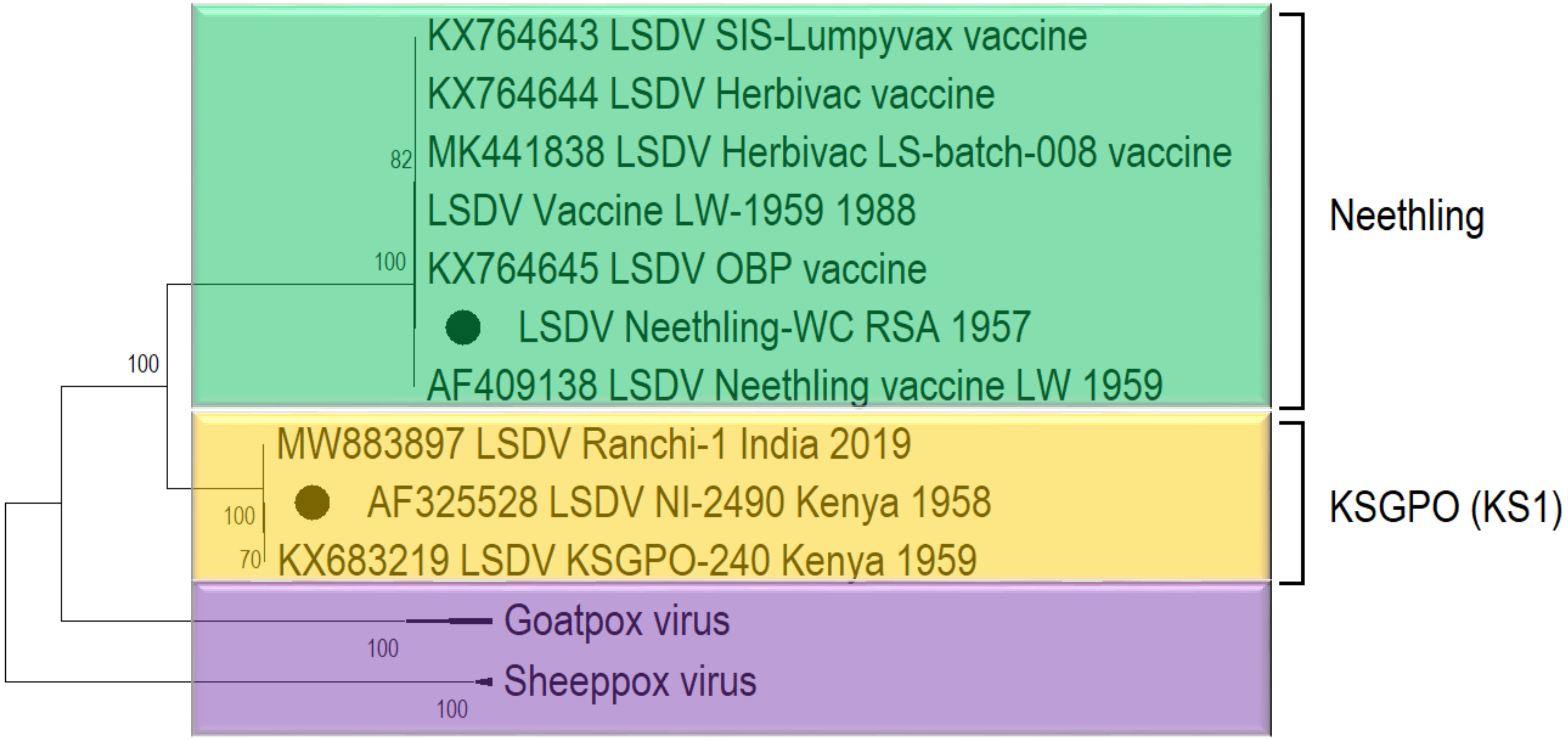
NO DIVA

Homologous vaccines:
Attenuated LSDV
(Neethling and KSGPO)

Heterologous vaccines:
Goatpox (Gorgan /
Uttarkashi)
Sheeppox (NISHKI)

Haegeman et al., 2023;
Hamdi et al., 2020;
Wolf et al., 2022

DIVA



Homologous inactivated vaccines: Safe, regular boosters; <1 year immunity

New vaccines: vector-, subunit, mRNA vaccines

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Lumpy skin disease: Available vaccines

Manufacturer	Product Name and Virus Strain	Target Species	Titre, Dose, Administration
Onderstepoort Biological Products (OBP) South Africa	Lumpy Skin Disease (LSD Neethling strain)	Vaccine for Cattle	$10^{3.5}$TCID$_{50}$/dose 2 ml SC
Intervet (Pty) South Africa/MSD Animal Health	Lumpyvax™ (LSD SIS Neethling strain)	Vaccine for Cattle	$10^{4.0}$TCID$_{50}$/dose 2 ml SC
MCI Santé Animale Morocco	Bovivax-LSD™ (LSD Kenya strain)	Vaccine for Cattle	$10^{3.5}$TCID$_{50}$/dose 2 ml SC
Jordan Bio-Industries Center (JOVAC) Jordan	LumpyShield-N™ (LSD Neethling strain)	Vaccine for Cattle	$10^{4.0}$TCID$_{50}$/dose 2 ml SC
Jordan Bio-Industries Center (JOVAC) Jordan	Caprivac™ (Gorgan GTP strain)	Vaccine for Cattle	
Middle East for Vaccines (MEVAC) Egypt	MEVAC LSD (LSD Neethling strain)	Vaccine for Cattle	$10^{3.5}$TCID$_{50}$/dose 2 ml SC
National Veterinary Institute (NVI) Ethiopia	Lumpy Skin Disease vaccine (LSD Neethling strain)	Vaccine for Cattle	$10^{3.0}$TCID$_{50}$/dose 2 ml SC
Kenya Veterinary Vaccines Production Institute (KEVEVAPI)	Lumpivax™ (LSD Neethling strain)	Vaccine for Cattle	Not known TCID$_{50}$/dose 2 ml SC
Pendik Veterinary Control Institute/ Ministry of Agriculture, Turkey	Penpox-M™ Live SPPV (Bakirköy SPPV strain)	Vaccine for Cattle	$10^{2.5}$TCID$_{50}$/dose 2 ml SC
Vetal Company Turkey	Poxvac™ (Bakirköy SPPV strain)	Vaccine for Sheep and Cattle	$10^{2.5}$TCID$_{50}$/dose 2 ml SC
	Lumpyvac™ (LSD Neethling strain)	Vaccine for Cattle	$10^{3.5}$TCID$_{50}$/dose 2 ml SC
Dollvet Turkey	Poxdoll™ (Bakirköy SPPV strain)	Vaccine for Sheep, goats and Cattle	$10^{2.5}$TCID$_{50}$/dose 2 ml SC
	LSD-NDOLL (LSD Neethling strain)	Vaccine for Cattle	$10^{3.5}$TCID$_{50}$/dose 2 ml SC
FGBI-Federal Centre for Animal Health Russia	Sheep Pox Cultyral Dry™(Arriah (NISHKI) SPPV strain)	Vaccine for Sheep and Cattle	Not known TCID$_{50}$/dose
ABIC, Israel	RM 65 Sheeppox (Yugoslavia RM65)	Vaccine for Sheep and Cattle	

Tuppurainen et al., 2021

Lumpy skin disease: Vaccine testing (literature study by Pravesh Kara)

Breed Age Gender	Construct / Vaccine Dose Route & Volume	Number of animals	Fever (%)	Start of fever (Ave Days)	Inoculation site reaction (%)	>1 nodule (%)	Clinical reaction [other than fever] (%)	Shedding (PCR) (%)	Nodule (PCR) (%)	Viremia (PCR / VI) (%)	VNT 1 (%)	VNT 2 (%)	ELISA (%)	IPMA (%)	iFIT / IFAT (%)	Reference
Holstein - Friesen 6 months Male	LSD Neethling OBP [1.4x10^7 TCID$_{50}$] SC Route: 2ml	5	0/5 (0%)	N/A	1/5 (20%)	0/5 (0%)	1/5 (20%)	Nd	0/1 (0%)	PCR 0/5 VI 0/5	0/5 (0%)	nd	nd	nd	nd	Kara et al., 2018
Holstein 6 months Male	LSD Neethling OBP [1x$10^{3.5}$ TCID$_{50}$] SC Route: 2ml	7	6/7 (86%)	1 dpv (4.2 days)	0/7 (0%)	0/7 (0%)	0/7 (0%)	Nd	0/7 (0%)	0/7 (0%)	1/7 (14%)	3/7 (43%)	nd	7/7 (100%)	nd	Haegeman et al., 2021a
	LSD Neethling Lumpyvax [1x104 TCID50] SC Route	7	7/7 (100%)	1 dpv (10.3days)	0/7 (0%)	0/7 (0%)	0/7 (0%)	Nd	0/7 (0%)	0/7 (0%)	1/7 (14%)	4/7 (57%)	nd	5/7 (72%)	nd	
	LSD Neethling HerbivacLS [1x102.5 TCID50] SC Route	7	4/7 (57%)	1 dpv (3 days)	0/7 (0%)	3/7 (43%)	3/7 (43%)	nd	3/7 (43%)	4/7 (57%)	3/7 (43%)	5/7 (71%)	nd	6/7 (86%)	nd	
	LSD Neethling (O variant) MCI [1x103 TCID50] SC Route	7	4/7 (57%)	1 dpv (3.8 days)	3/7 (43%)	2/7 (29%)	3/7 (43%)	nd	2/7 (29%)	2/7 (29%)	4/7 (57%)	3/7 (43%)	nd	7/7 (100%)	nd	
	LSD KSGP Kenyavac [1x102.5 TCID50] SC Route	7	5/7 (71%)	1 dpv (6.8 days)	0/7 (0%)	0/7 (0%)	0/7 (0%)	nd	0/7 (0%)	0/7 (0%)	0/7 (0%)	2/7 (29%)	nd	5/7 (72%)	nd	
Holstein-cross 4-6 months	LSD Neethling (LSD_Nt) [1x104 TCID$_{50}$] SC Route: 2ml	15	7/15 (47%)	2 dpv (2 days)	0/15 (0%)	1/15 (7%)	1/15 (7%)	1/15 (7%)	1/15 (7%)	nd	7/15 (47%)	nd	nd	nd	nd	Bamouh et al., 2021
	LSD Neethling (LSD_Nt) [1x105 TCID$_{50}$] SC Route: 2ml	30	13/30 (43%)	NI (4.3 days)	2/30 (7%)	2/30 (7%)	2/30 (7%)	2/30 (7%)	2/30 (7%)	nd	23/30 (73%)	nd	nd	nd	nd	
	LSD KSGP O-240 [1x104 TCID50] SC Route: 2ml	12	5/12 (42%)	NI (5.6 days)	0/12 (0%)	0/12 (0%)	0/12 (0%)	0/12 (0%)	0/12 (0%)	nd	12/12 (100%)	nd	nd	nd	nd	
	LSD KSGP O-240 [1x105 TCID50] SC Route: 2ml	12	9/12 (75%)	NI (3.8 days)	1/12 (8%)	3/12 (25%)	3/12 (25%)	3/12 (25%)	3/12 (25%)	nd	12/12 (100%)	nd	nd	nd	nd	
Morocco (Zebu) 6-8 months	LSD Neethling OBP 1x104 TCID50 SC Route	15	1/15 (7%)	1 dpv (1 day only)	0/15 (0%)	0/15 (0%)	0/15 (0%)	0/15 (0%)	0/15 (0%)	nd	7/15 (47%)	nd	nd	nd	nd	Hamdi et al., 2020
Holstein-Friesen 9-10 months	LSD Neethling (Nt_hd) [1x107 TCID50] IV Route: 3ml & SC Route: 1ml	6	0/6 (0%)	N/A	2/6 (33%)	0/6 (0%)	0/6 (0%)	2/6 (33%)	0/6 (0%)	4/6 (67%)	4/6 (67%)	nd	5/6 (83%)	nd	6/6 (100%)	Moller et al., 2019
Holstein-Friesen 4-6 months	LSD Neethling HerbivacLS [1x102.5 TCID50] SC Route: 2ml	6	3/6 (50%)	5-6 dpv. (4-6 days)	5/6 (83%)	0/6 (0%)	5/6 (83%)	0/6 (0%)	nd	4/6 (67%)	5/6 (83%)	nd	5/6 (83%)	nd	nd	Wolff et al., 2020
Borana (Zebu) 12 -24 months	LSD Neethling (NVI, Ethiopia) [1x104.5 TCID50] SC Route	5	0/5 (0%)	N/A	0/5 (0%)	0/5 (0%)	0/5 (0%)	nd	nd	nd	nd	nd	nd	nd	0/5 (0%)	Gari et al., 2015
	LSD Neethling (NVI, Ethiopia) [1x103.5 TCID50] SC Route	5	0/5 (0%)	N/A	0/5 (0%)	0/5 (0%)	0/5 (0%)	nd	nd	nd	nd	nd	nd	nd	0/5 (0%)	
	LSD KSGP O-180 [1x104.5 TCID50 SC Route	5	0/5 (0%)	N/A	0/5 (0%)	0/5 (0%)	0/5 (0%)	nd	nd	nd	nd	nd	nd	nd	0/5 (0%)	
	LSD KSGP O-180 [1x103.5 TCID50 SC Route	5	0/5 (0%)	N/A	0/5 (0%)	0/5 (0%)	0/5 (0%)	nd	nd	nd	nd	nd	nd	nd	0/5 (0%)	
Dexter 11-16 months Male	LSD Neethling OBP [1x103.5 TCID50] SC Route: Vaccination 1	6	0/6 (0%)	N/A	0/6 (0%)	0/6 (0%)	0/6 (0%)	nd	nd	0/6 (0%)	0/6 (0%)	nd	nd	nd	nd	Osuagwuh et al., 2007
	LSD Neethling OBP [1x103.5 TCID50] SC Route: Repeat Vaccination 21 dpv	6	0/6 (0%)	N/A	0/6 (0%)	0/6 (0%)	0/6 (0%)	nd	nd	0/6 (0%)	4/6 (67%)	nd	nd	nd	nd	
Holstein 6 months Male	LSD Lumpivax (KEVEVAPI, Kenya) [Dose: NI] SC Route: 2ml	7	7/7 (100%)	NI	7/7 (100%)	2/7 (29%)	7/7 (100%)	nd	3/3 (100%)	1/7 (14%)	nd	nd	1/7 (14%)	7/7 (100%)	nd	Haegeman et al., 2021b
Breed: NI 6-9 months Male	LSD Lumpi-ProVac Ind [1x103.5 TCID50] Route: NI	8	3/8 (37.5%)	NI	0/8 (0%)	0/8 (0%)	Viremia 5/8 (62.5%) 3dpv only	0/8 (0%)	0/8 (0%)	PCR 5/8 (62.5%) 3dpv only	7/8 (87.5%)	nd	nd	nd	nd	Kumar et al., 2022

Not all animals naturally infected or vaccinated develop neutralizing antibodies against LSDV

or

they develop low levels of antibodies undetectable by current serological assays

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Lumpy skin disease: South Africa

Endemic since 1945
Annual outbreaks – Summer months

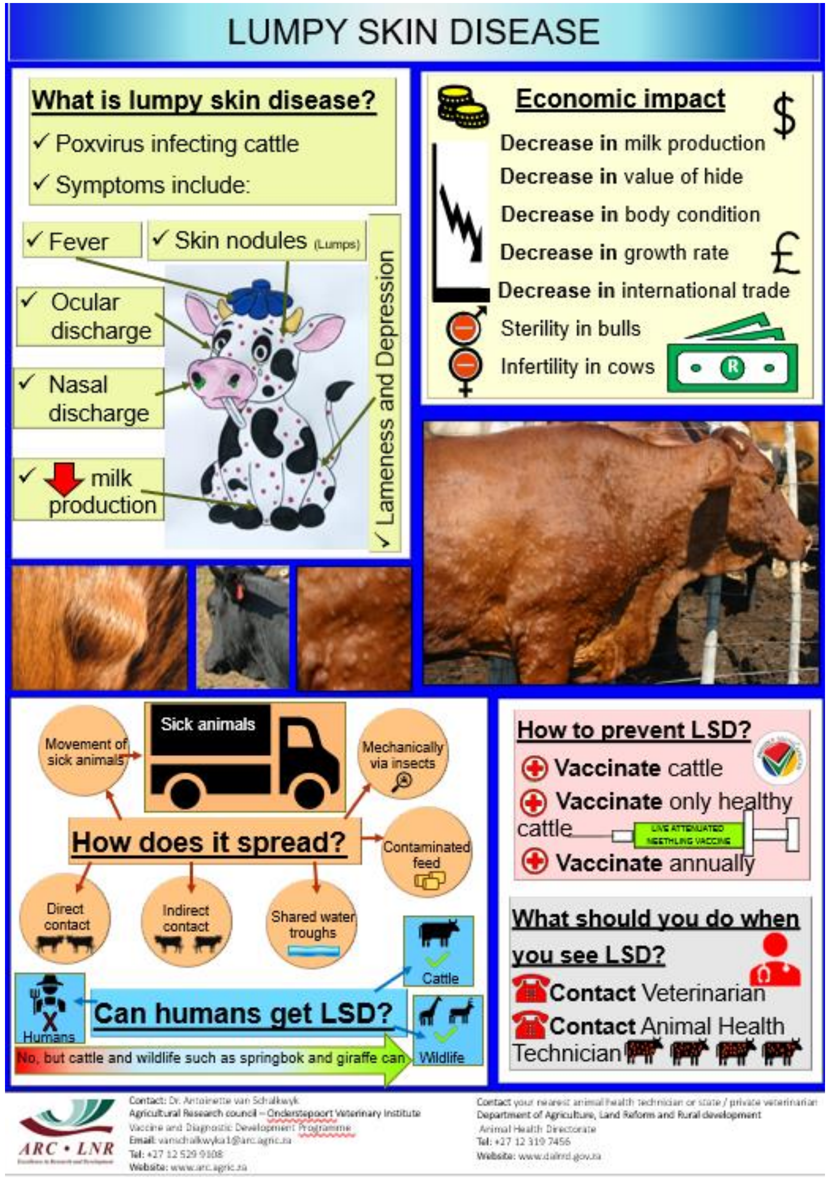
Diagnostic – Laboratory confirmation

- Molecular: Realtime PCR
- Serology: VNT
- Serology: IDVet ELISA
- Complete genome sequencing

Vaccination: Live attenuate Neethling vaccine:

- OBP vaccine Onderstepoort Biological Products, South Africa
- Herbivac - Deltamune, South Africa
- Lumpyvax - MSD Animal Health, South Africa
- Annual vaccination - encourage

Education and information: 5 Languages



LUMPY SKIN DISEASE

What is lumpy skin disease?
✓ Poxvirus infecting cattle
✓ Symptoms include:

✓ Fever
✓ Skin nodules (Lumps)
✓ Ocular discharge
✓ Nasal discharge
✓ milk production
✓ Lameness and Depression

Economic impact
Decrease in milk production
Decrease in value of hide
Decrease in body condition
Decrease in growth rate
Decrease in international trade
Sterility in bulls
Infertility in cows

How does it spread?

Can humans get LSD?
No, but cattle and wildlife such as springbok and giraffe can

How to prevent LSD?
Vaccinate cattle
Vaccinate only healthy cattle
Vaccinate annually

What should you do when you see LSD?
Contact Veterinarian
Contact Animal Health Technician

Contact: Dr. Antoinette van Schalkwyk
Agricultural Research council – Onderstepoort Veterinary Institute
Vaccine and Diagnostic Development Programme
Email: vanschalkwyka1@arc.agric.za
Tel: +27 12 529 9108
Website: www.arc.agric.za

Contact your nearest animal health technician or state / private veterinarian
Department of Agriculture, Land Reform and Rural development
Animal Health Directorate
Tel: +27 12 319 7456
Website: www.dalrrd.gov.za

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Excellence in Research and Development

Questions?

Antoinette van Schalkwyk
Agricultural Research Council – Onderstepoort Veterinary Institute

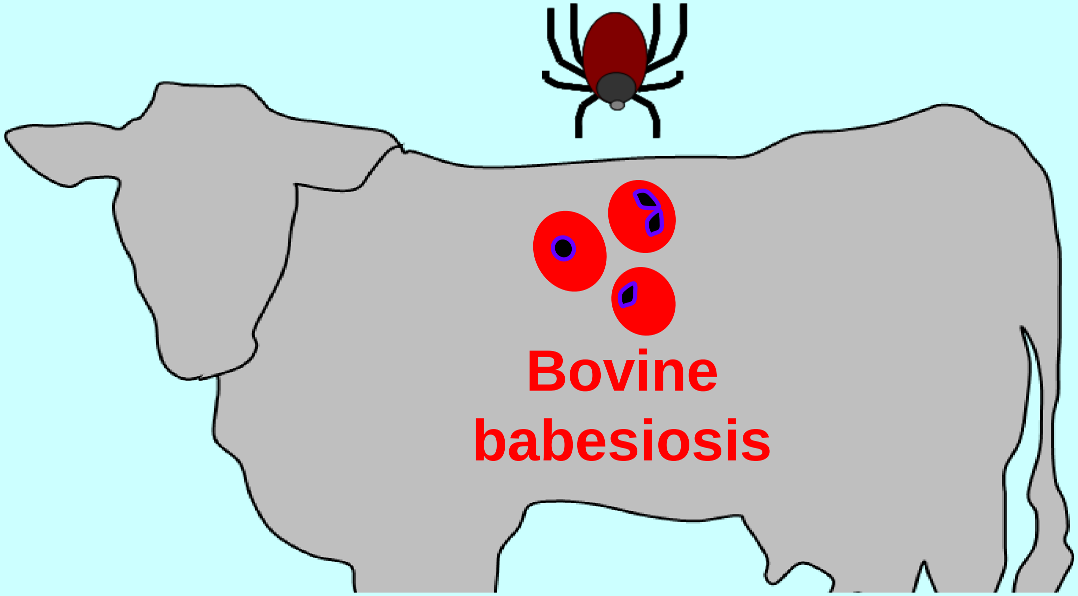
vanschalkwyka1@arc.agric.za

Updates on bovine babesiosis
-distribution and diagnosis-

Thillaiampalam Sivakumar

National Research Center for Protozoan Diseases
Obihiro University of Agriculture and Veterinary Medicine, Japan

Bovine babesiosis and its economic importance



Infected ticks

Bovine babesiosis

Production loss

Death

Treatment → Economic loss

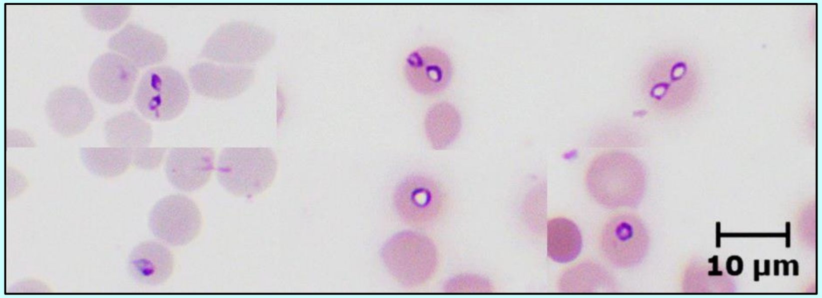
Tick control

Impaired trade

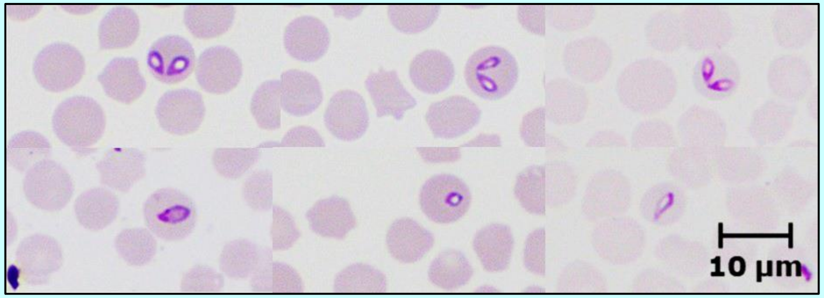
Control of bovine babesiosis is important.

Babesia species capable of causing clinical bovine babesiosis

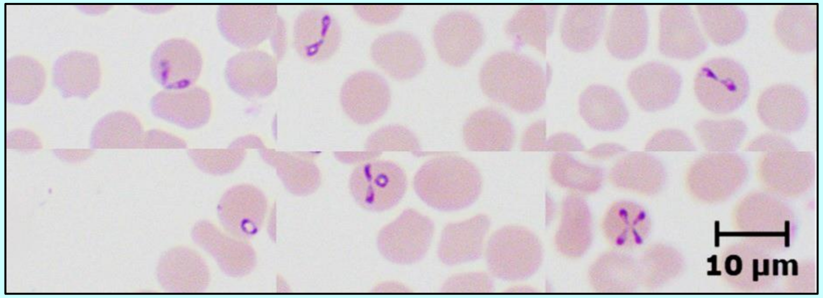
Babesia bovis



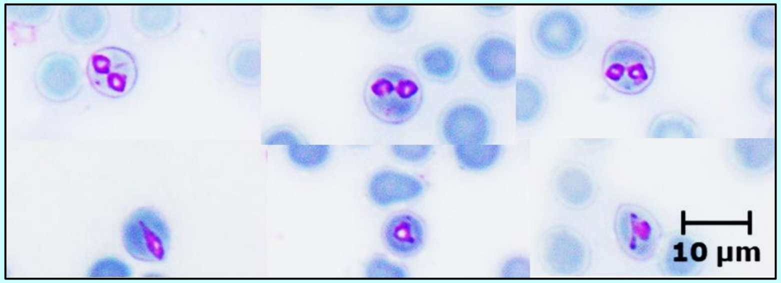
Babesia bigemina

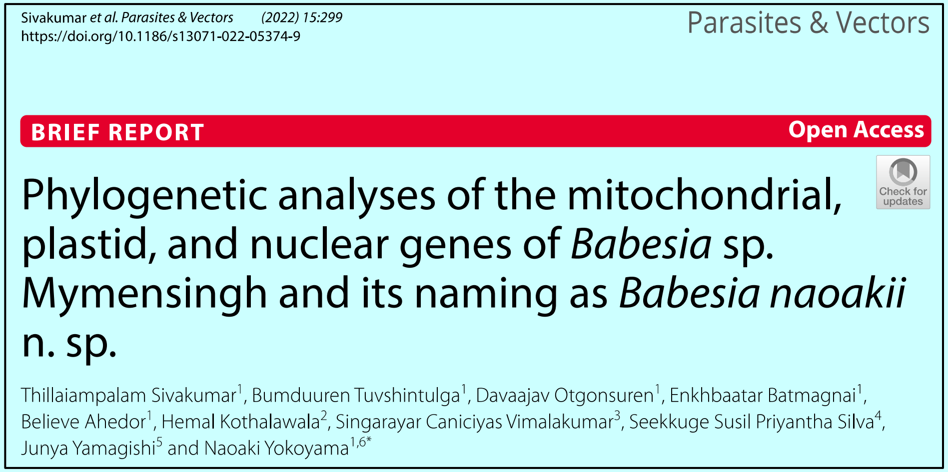


Babesia divergens



Babesia naoakii - a new species that can cause clinical bovine babesiosis





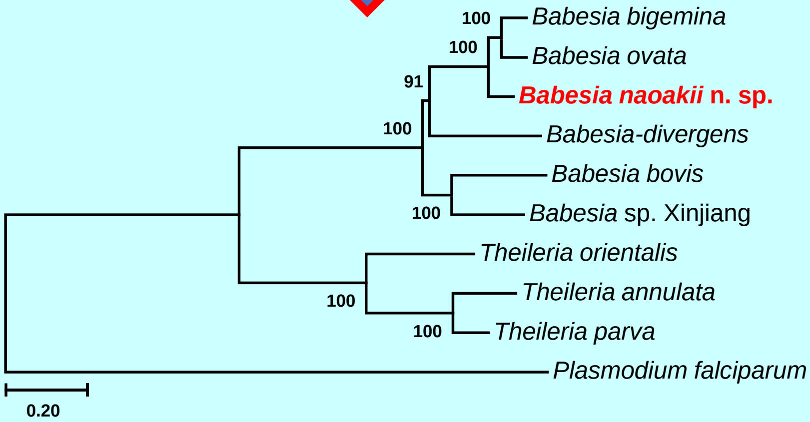
Sivakumar *et al. Parasites & Vectors* (2022) 15:299
https://doi.org/10.1186/s13071-022-05374-9

Parasites & Vectors

BRIEF REPORT **Open Access**

Phylogenetic analyses of the mitochondrial, plastid, and nuclear genes of *Babesia* sp. Mymensingh and its naming as *Babesia naoakii* n. sp.

Thillaiampalam Sivakumar[1], Bumduuren Tuvshintulga[1], Davaajav Otgonsuren[1], Enkhbaatar Batmagnai[1], Believe Ahedor[1], Hemal Kothalawala[2], Singarayar Caniciyas Vimalakumar[3], Seekkuge Susil Priyantha Silva[4], Junya Yamagishi[5] and Naoaki Yokoyama[1,6*]



Tick vectors of bovine *Babesia* species

B. bovis

Rhipicephalus microplus

R. annulatus

R. geigyi

B. bigemina

R. microplus

R. decoloratus

R. annulatus

R. geigyi

R. evertsi

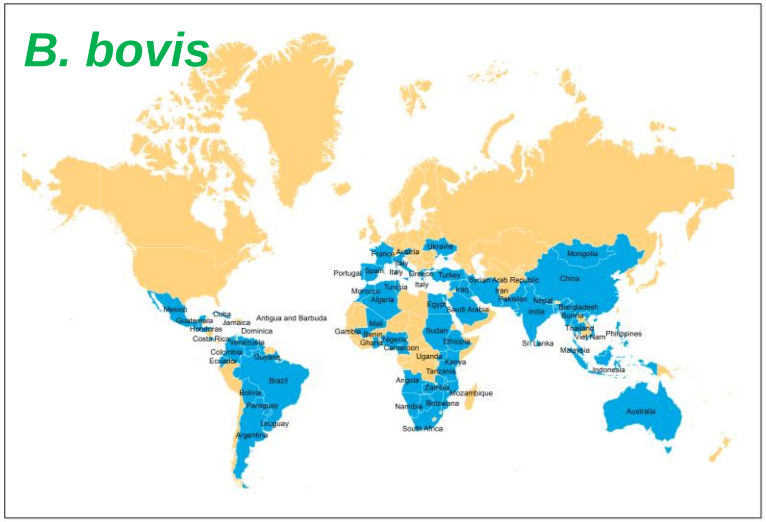
B. divergens

Ixodes ricinus

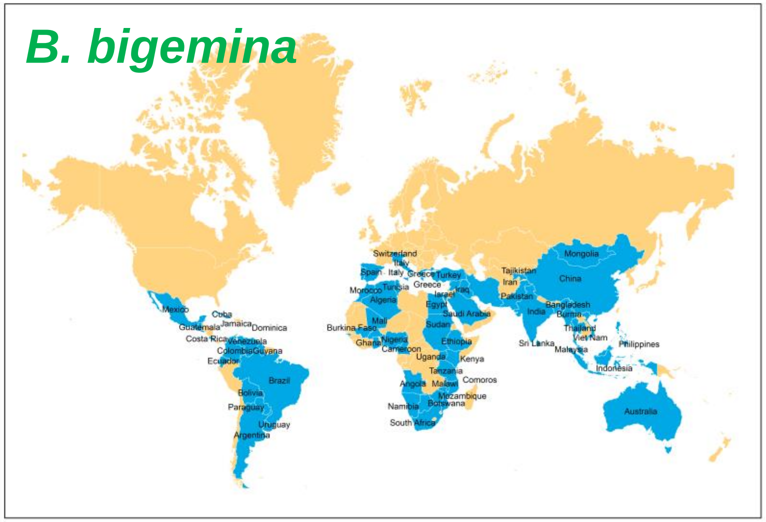
B. naoakii

Undetermined

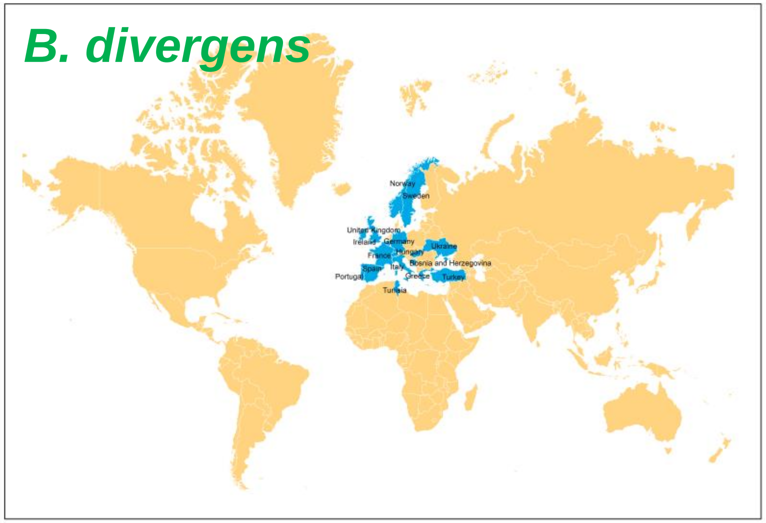
Global distribution of bovine *Babesia* species



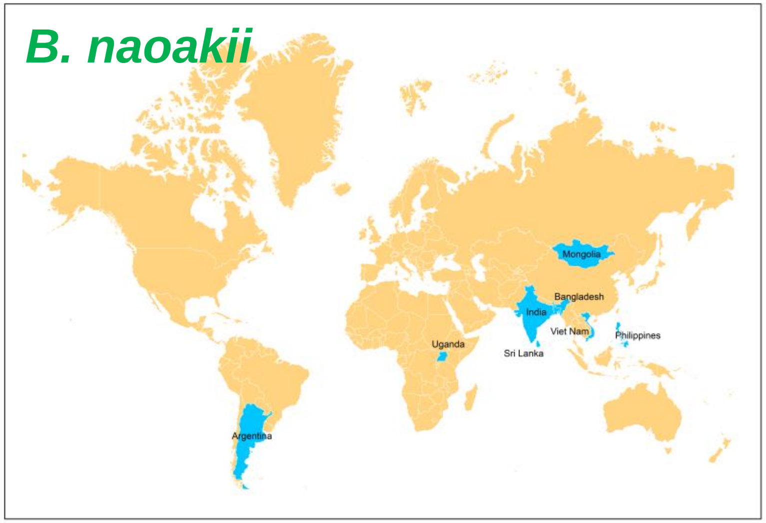
B. bovis



B. bigemina



B. divergens

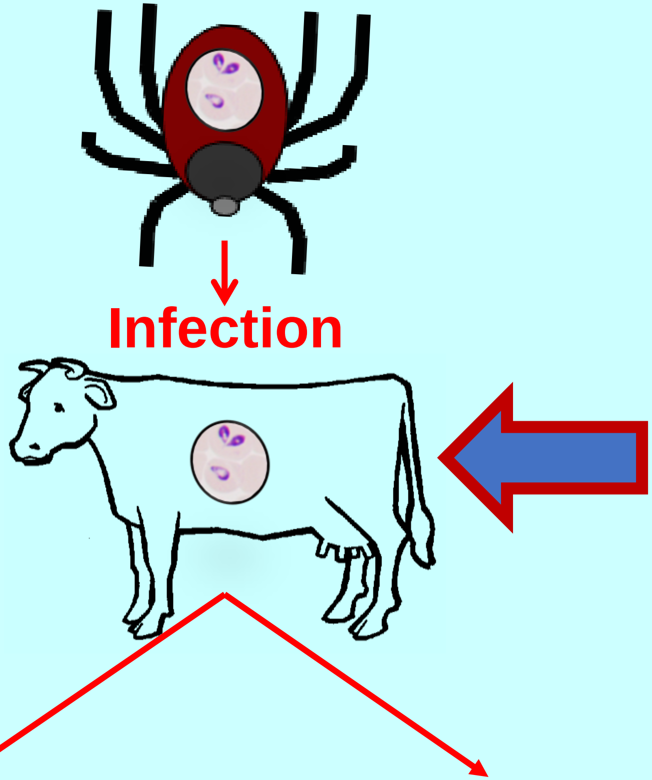


B. naoakii

Diagnosis of bovine babesiosis

1. Risk factors
2. Clinical diagnosis
3. Parasitological diagnosis
4. Molecular diagnosis

Risk factors for clinical bovine babesiosis



Infection

Asymptomatic
No clinical signs

Symptomatic
Clinical disease

1. Age
Calves are resistant

2. Acquired immunity
Acquired immunity protects cattle.

↑

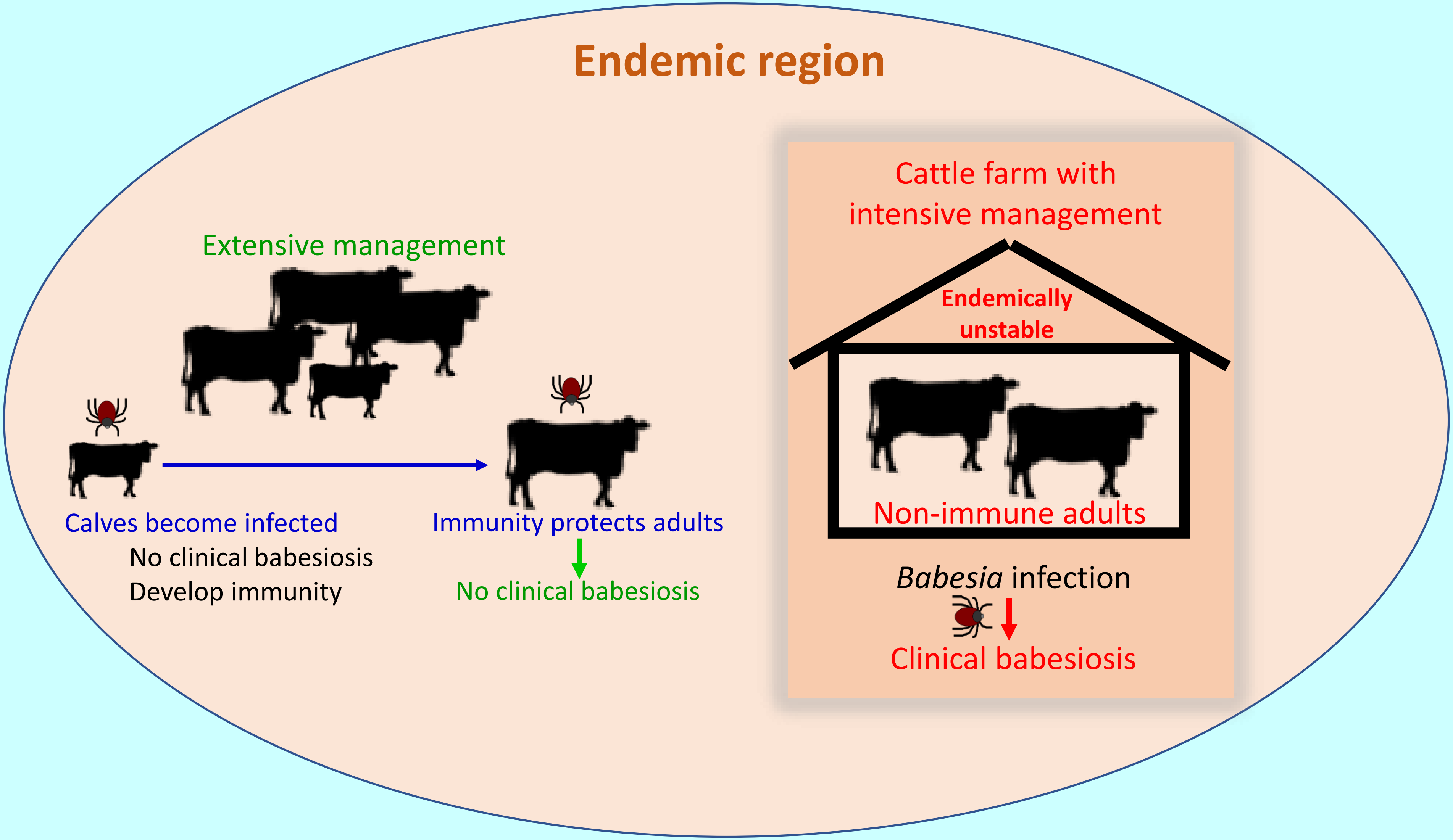
3. Management practices
Cattle managed extensively are more likely to develop immunity.

↓

4. Endemic stability
No or sporadic cases

5. Cattle breed
Bos indicus is resistant, but not *Bos taurus*.

Clinical bovine babesiosis in endemic countries
Scenario 1: endemic instability



Endemic region

Extensive management

Calves become infected

No clinical babesiosis

Develop immunity

Immunity protects adults

No clinical babesiosis

Cattle farm with intensive management

Endemically unstable

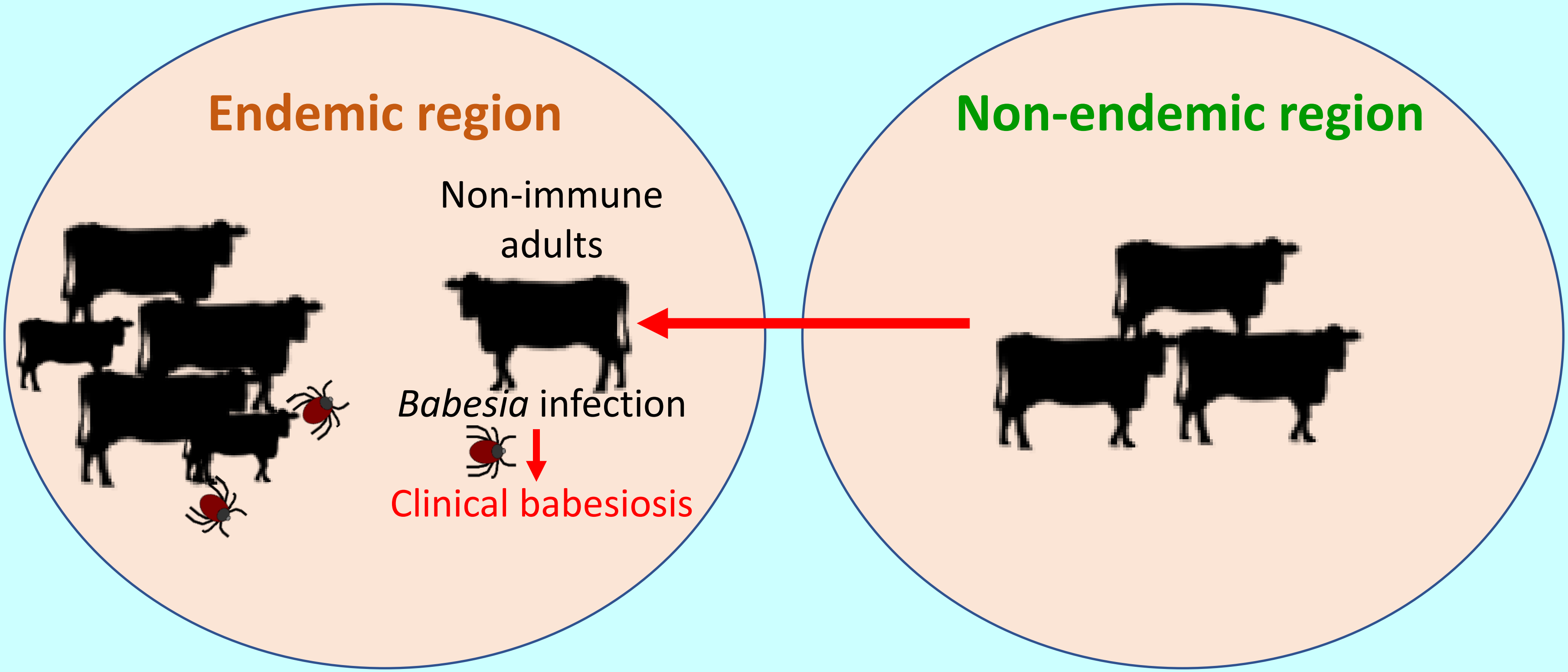
Non-immune adults

Babesia infection

Clinical babesiosis

Clinical bovine babesiosis in endemic countries

Scenario 2: Introduction of naïve cattle



Endemic region

Non-endemic region

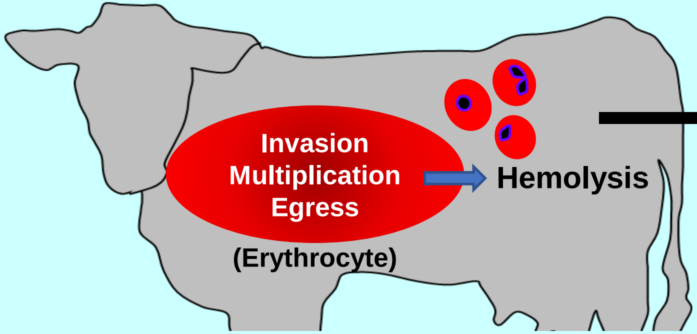
Non-immune adults

Babesia infection

Clinical babesiosis

Clinical diagnosis

Intravascular hemolysis



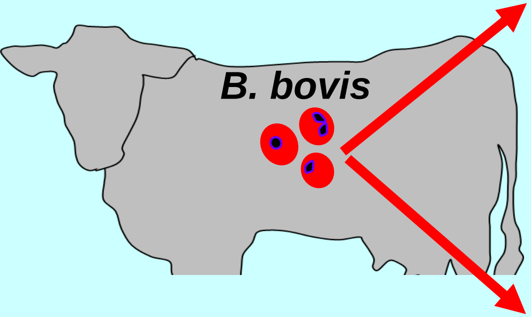
B. bovis
B. bigemina
B. divergens
B. naoakii

High fever
Anemia
Jaundice

Hemoglobinuria

Hypoxia

Bovine babesiosis caused by *B. bovis*



Overproduction of cytokines (Immunodisease)

Sequestration of RBCs in capillaries

Vasodilation → **Hypotension**

Endothelial damage → **Coagulation disorders**

Increased vascular Permeability → **Oedema**

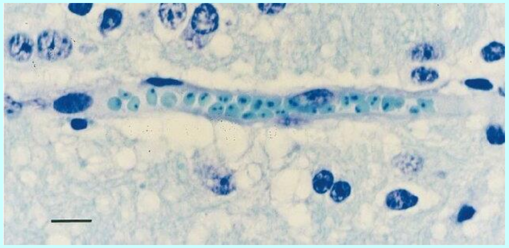
Infiltration of neutrophils

Tissue damage in brain and lungs

Cerebral babesiosis

Respiratory distress syndrome

Infected RBC
(Suarez et al., 2019)



Sequestrated RBCs in brain capillaries
(Nevils et al., 2000)

Parasitological diagnosis

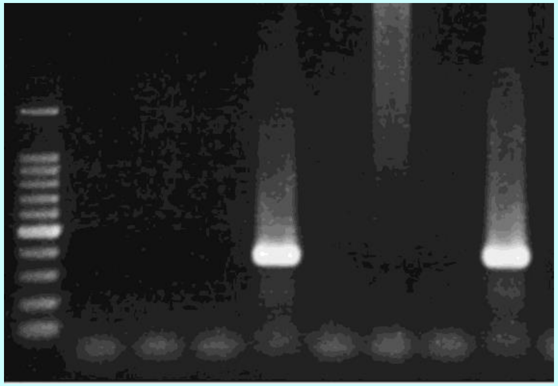
Capillary blood → Thin smears → Staining → Microscopy

Characteristics	***B. bovis***	***B. divergens***	***B. bigemina***	***B. naoakii***
Size (μm)	Small 1–1.5 × 0.5–1.0	Small 1–1.5 × 0.5–1.0	Large 3–3.5 × 1–1.5	Large 2.3–3 × 1.6–2.2
Location in RBC	Central	Rim	Entire RBC	Entire RBC
Angle between paired merozoites	Obtuse	Obtuse	Acute	Obtuse
Parasitemia in acute infection	Low (<1%)	High	High	High

Molecular diagnosis

Blood → DNA → PCR → Electrophoresis

***Babesia* species**	**Target**
B. bovis	RAP-1, cytochrome b
B. bigemina	AMA-1, RAP-1, cytochrome b
B. naoakii	AMA-1



Specific and sensitive

Early diagnosis is important.

A survey of clinical bovine babesiosis in Sri Lanka

No.	Breed	Age	RBC indices			*Babesia* spp.	Treatment	Prognosis
			HGB	HCT	RBC			
1	Jersey	4	ND	ND	ND	*Bbo* + *Bbi*	Diminazene	Recovered
2	Friesian	3	8.4	22.6	5.65	*Bbi*	Diminazene	Recovered
3	Jersey	4	9.6	27.6	5.94	*Bbi*	Diminazene	Recovered
4	Friesian	4	6.8	19.6	3.94	*Bna*	Diminazene	Recovered
5	**Jersey**	5	**2.8**	**7.9**	**1.38**	*Bbo* + *Bbi*	Diminazene	**Died**
6	Jersey	4	8.7	24	5.59	*Bbo* + *Bbi*	Diminazene	Recovered
7	Jersey	4	9.4	25.7	5.51	*Bbo* + *Bbi*	Diminazene	Recovered
8	Jersey	5	ND	ND	ND	*Bbo* + *Bbi* + *Bna*	Diminazene	Recovered
9	Jersey	4	6.8	21.9	3.88	*Bbo*	Diminazene	Recovered
10	Jersey	5	6.7	21.5	3.5	*Bbi*	Diminazene	Recovered
11	**Jersey**	6	**2.83**	**10.6**	**2.22**	*Bbi*	Diminazene	**Died**
12	**Jersey**	3	**4.8**	**13.3**	**3.03**	*Bbo* + *Bbi*	Diminazene	**Died**
13	Jersey	6	ND	ND	ND	*Bbo* + *Bbi*	Diminazene	Recovered

ND, Not done; *Bbo*, *B. bovis*; *Bbi*, *B. bigemina*, *Bna*, *B. naoakii*

(HGB: g/dl, HCT: %, RBC: × 10^6/μl)

Cattle with severe anemia died.

Treatment and prevention

Treatment

Therapeutic dose and route of administration

Drug	**Dose**	**Route**
Diminazene aceturate	3.5 mg/kg	Intramuscular
Imidocarb	1.2 mg/kg	Subcutaneous

Prevention

Tick control

Vaccination with live-attenuated *B. bovis* and *B. bigemina* strains

Summary

1. Causative *Babesia*

B. bovis*, *B. bigemina*, *B. naoakii*, and *B. divergens

2. Lifecycle and transmission

Transmitted to cattle by specific tick vectors

3. Pathogenesis and clinical signs

Hemolytic anemia, cerebral babesiosis, and immunodisease

4. Risk factors

Age, acquired immunity, grazing management, endemic status, and breed

5. Diagnosis

Clinical, parasitological, and molecular diagnosis

6. Treatment

Chemotherapy and supportive therapy

7. Prevention

Tick control, vaccination, and chemoprophylaxis

Contact us

Dr. Thillaiampalam Sivakumar
sivavets@gmail.com

WOAH Reference Laboratory
for Bovine Babesiosis

Reference Centre
World Organisation
for Animal Health
Founded as OIE

Dr. Naoaki Yokoyama
yokoyama@obihiro.ac.jp

Visit our website for further details

https://www.obihiro.ac.jp/facility/protozoa/en/woah-reference-centres

Distribution, surveillance and diagnosis of JEV in animals

Dong-Kun Yang/ WOAH expert for JE

2024. 9. 19

World Organisation
for Animal Health
Founded as OIE

Distribution of JE in human in Asia and Pacific region

From CDC

Arbovirus	Number of countries	Population (% of global population)	Estimated death per year	Chronic case per year
JEV	24	3,706,910,037 (57)	3,500 to 15,000	7,350 to 22,500

- Map of countries in Asia and Pacific region where JEV has been identified
- JEV has the biggest population in endemic countries among vector borne diseases

Why is JE important in animals ?

- Since the first case of JEV infection was reported in 1871, JEV infections have been reported in human and animals.
- **Public health impact**: JE is a significant public health concern, especially in Asia and the Western Pacific regions, where it causes thousands of cases and deaths annually.
- **Neurological damage**: JE can lead to severe neurological damage, including encephalitis, seizures, and long-term cognitive and motor impairments. Approximately 20-30% of those who develop encephalitis die, and 30-50% of survivors suffer from permanent neurological sequelae.
- **Lack of specific treatment**: There is no specific antiviral treatment for JE.
- **Economic burden**: The disease imposes a significant economic burden on affected families and healthcare systems due to the high costs of medical care and long-term rehabilitation for survivors.
- **Preventable disease**: JE is preventable through effective vaccination programs and mosquito control measures.

Characteristics of *Cx. tritaeniorhynchus*, *Cx. orientalis* transmitting JEV 3 or 5

Culex tritaeniorhynchus

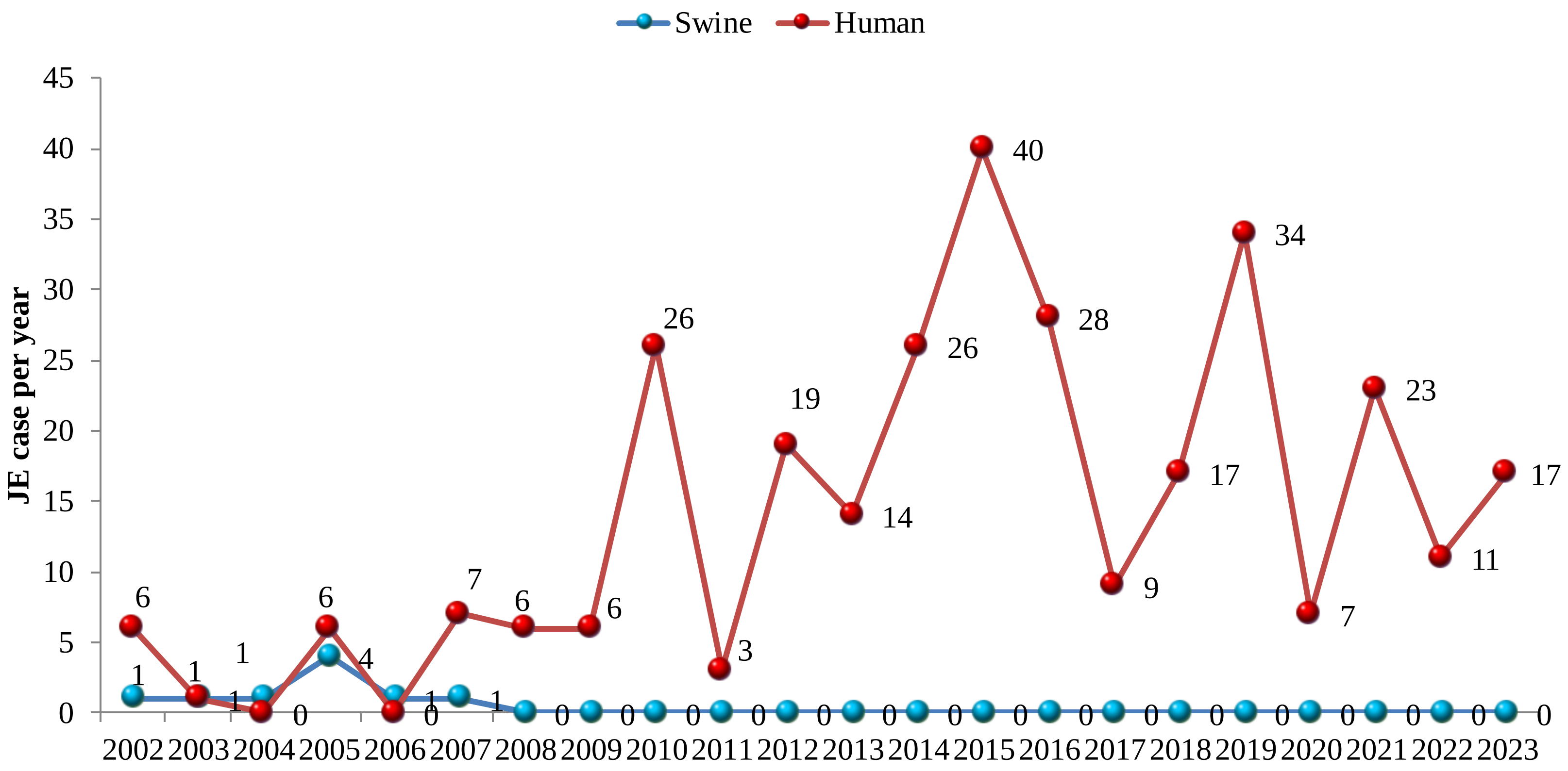
Culex orientalis

The *Cx. tritaeniorhynchus and Cx. orientalis* are associated with transmission of JEV genotype 3 and 5 respectively.

Habitat preference: *Culex orientalis* is commonly found in rice paddies, marshes, and other stagnant water bodies. These environments provide ideal breeding grounds for the mosquito, facilitating its role as a vector for JE.

Feeding behavior: This mosquito species is primarily zoophilic, meaning it prefers to feed on animals rather than humans. However, it can still bite humans, especially when animal hosts are scarce.

JE cases in human and swine in South Korea since 2002



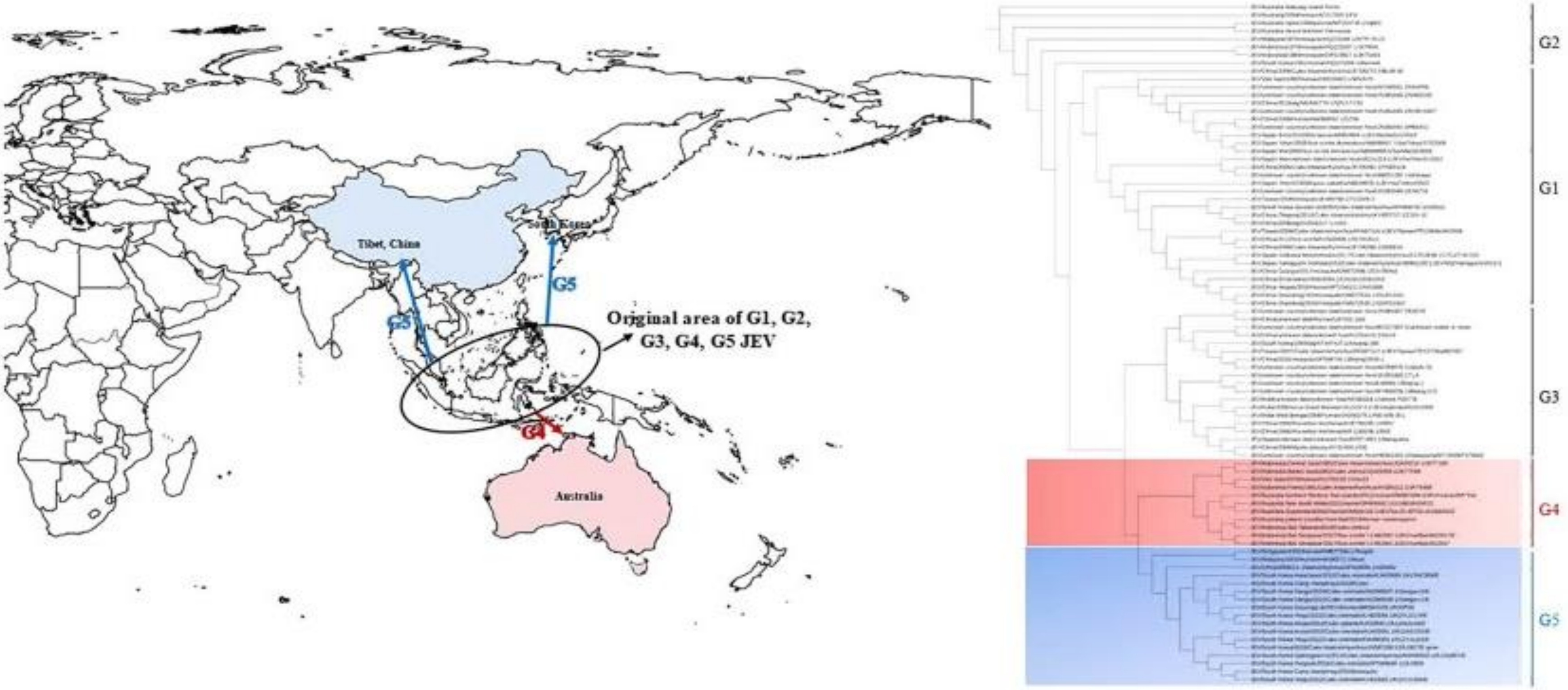
There has been no JEV infection in swine since 2008.

But. 17 JE cases occurred in human in 2023.

JEV genotype 5 has been identified in human since 2010.

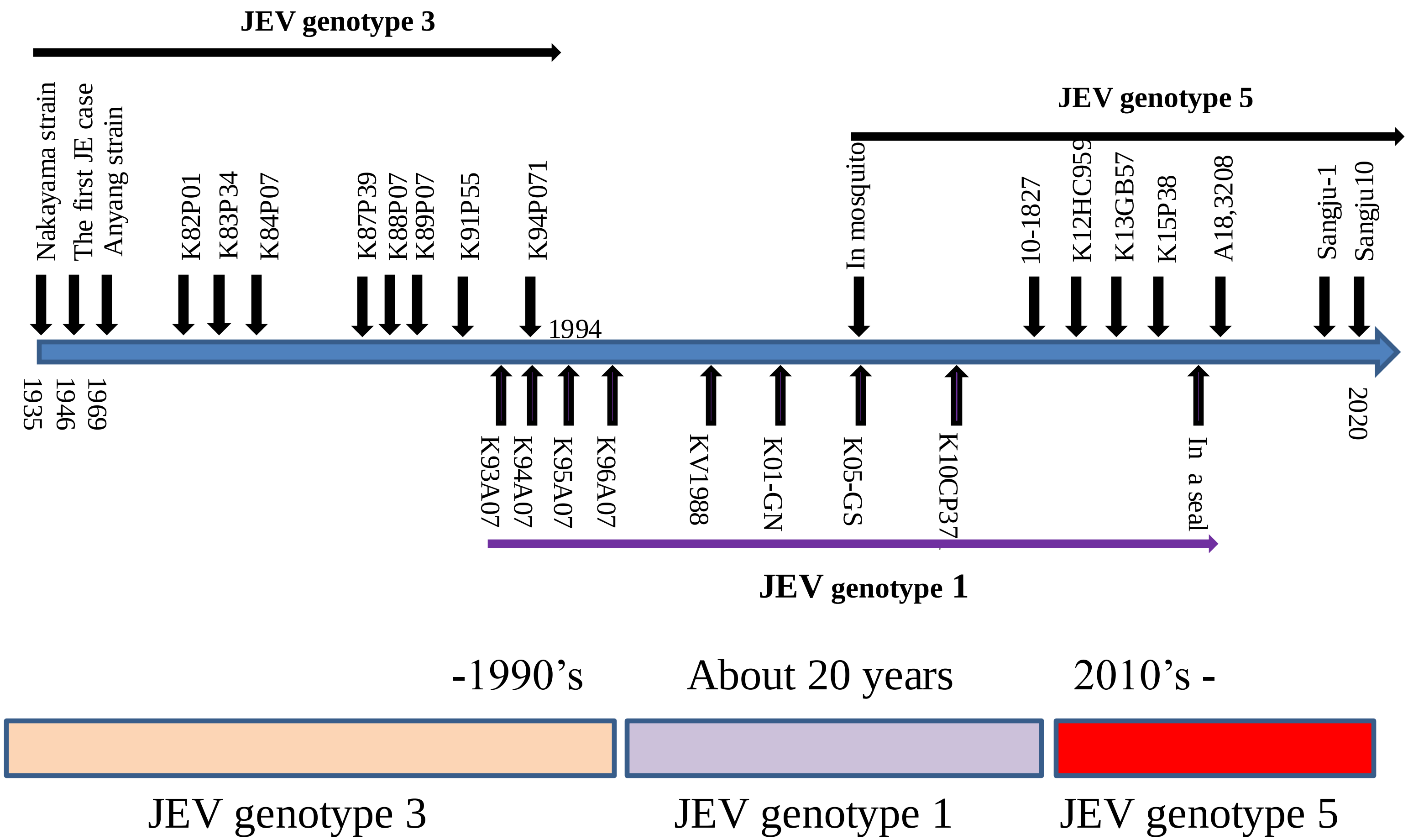
JE vaccine belonging to JEV 3 has been used for Korean and animals.

Distribution of JEV genotype in Asia in 2022



From 2009, the hidden genotype 5 suddenly emerged from the Tibetan region of China and from South Korea in East Asia.
Similarly, **in 2022** the long silent genotype 4 of JEV emerged in Australia.

JEV genotype shift is occurring in Korea



The detecting and monitoring the JEV carried by mosquitoes in the natural environment are effective method that can help to predict whether JE genotype strains have the potential to cause human infection or not.

JEV infection was identified in a seal residing in a zoo

A seal resided in a wild zoo located in Southern region of Korea was commissioned to APQA in 2017. The seal died of heartworm and JEV infection.

The JEV was classified into JEV genotype 1 based on the nucleotide sequence analysis.

Why do we conduct serological survey for JEV?

- **Early detection of antigen**: Serological tests help in the early detection of JEV in animal populations, which is crucial for monitoring and controlling potential outbreaks. This early detection allows for timely interventions to prevent the spread of the virus to humans and other animals.
- **Understanding transmission dynamics**: This information is vital for identifying key reservoir hosts and vectors, such as pigs and mosquitoes, which play significant roles in the virus's life cycle.
- **Evaluating vaccination programs**: Serological testing is essential for assessing the effectiveness of vaccination programs in animals. By measuring antibody levels, researchers can determine the immunstatus of animal populations and make informed decisions about the need for booster vaccinations or other preventive measures.

Considerations before serological test

[Pig & Horse]

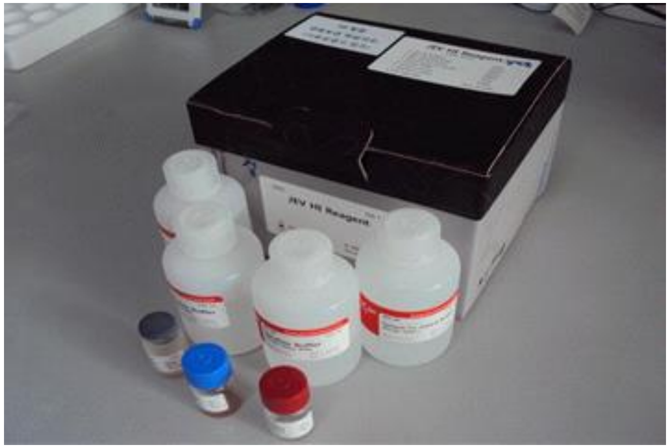
1. Vaccination (Live-attenuated vaccine)
   - Vaccination policy to sow population in Korea
   - Vaccination to racehorse population
2. Maternal antibodies
3. Another flavivirus infection?

[Other animals]

[Solution]

1. Vaccination or maternal antibodies : Sampling paired sera
2. Other *flavivirus* infection : Cross neutralization test
   - e.g. JEV ⟷ WNV(exotic) : difference above 4 fold dilution

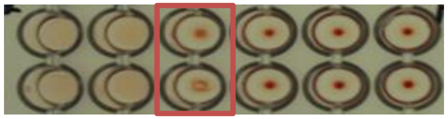
How to conduct HI test



The commercial HI kit for JEV

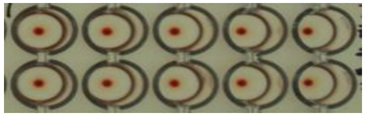
Goose red blood cells packed 100%

Virus Back titration



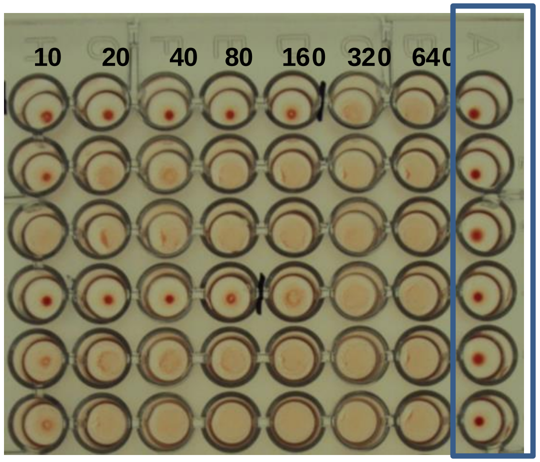
4-8HA unit is O.K.

RBC Control



Sample no.

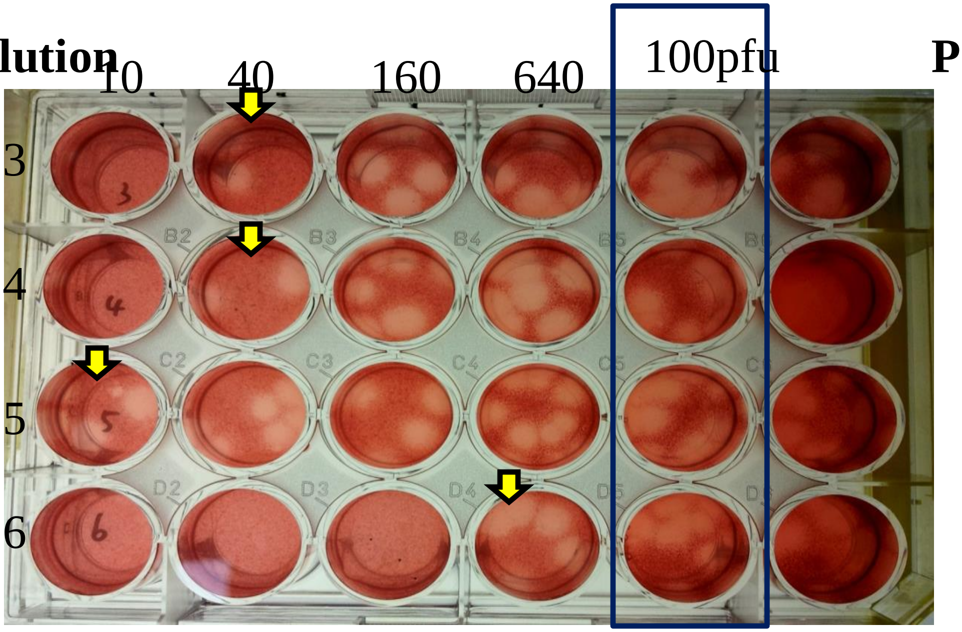
RBC control



Sample no.	HI titer
1	160
2	10
3	<10
4	80
5	<10
6	<10

The commercial HI kit for the detection of JEV antibodies is available for animals.

Example of PRNT to detect JEV antibodies



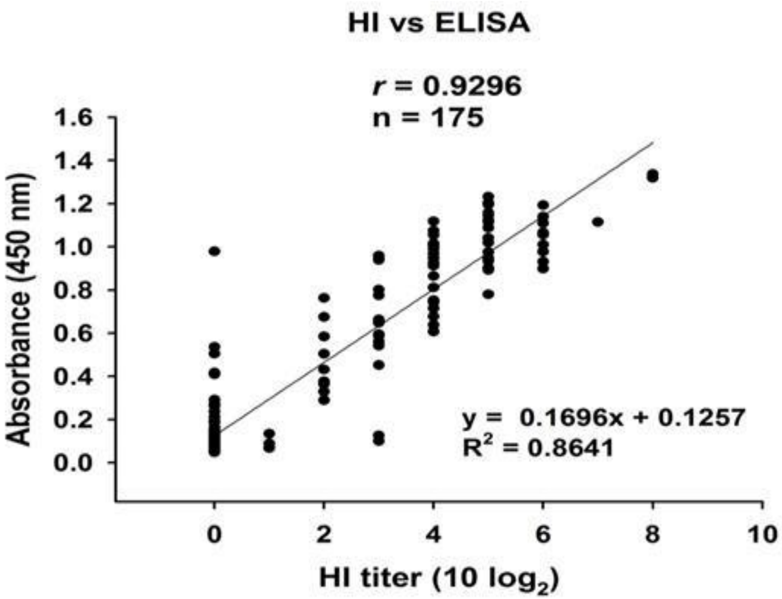
Serum dilution	10	40	160	640	100pfu	**PRNT$_{90}$ Titer**
Sample no.3						**40**
Sample no.4						**40**
Sample no.5						**<10**
Sample no.6						**160**

- The principle of plaque assay is to differentiate accumulated dead cells by virus infection from surrounding surviving cells.

  - PRNT $_{90}$ means 90% of JEVs were inhibited by antibody within serum.

- There are some limitations of PRNT in testing large numbers of sera.

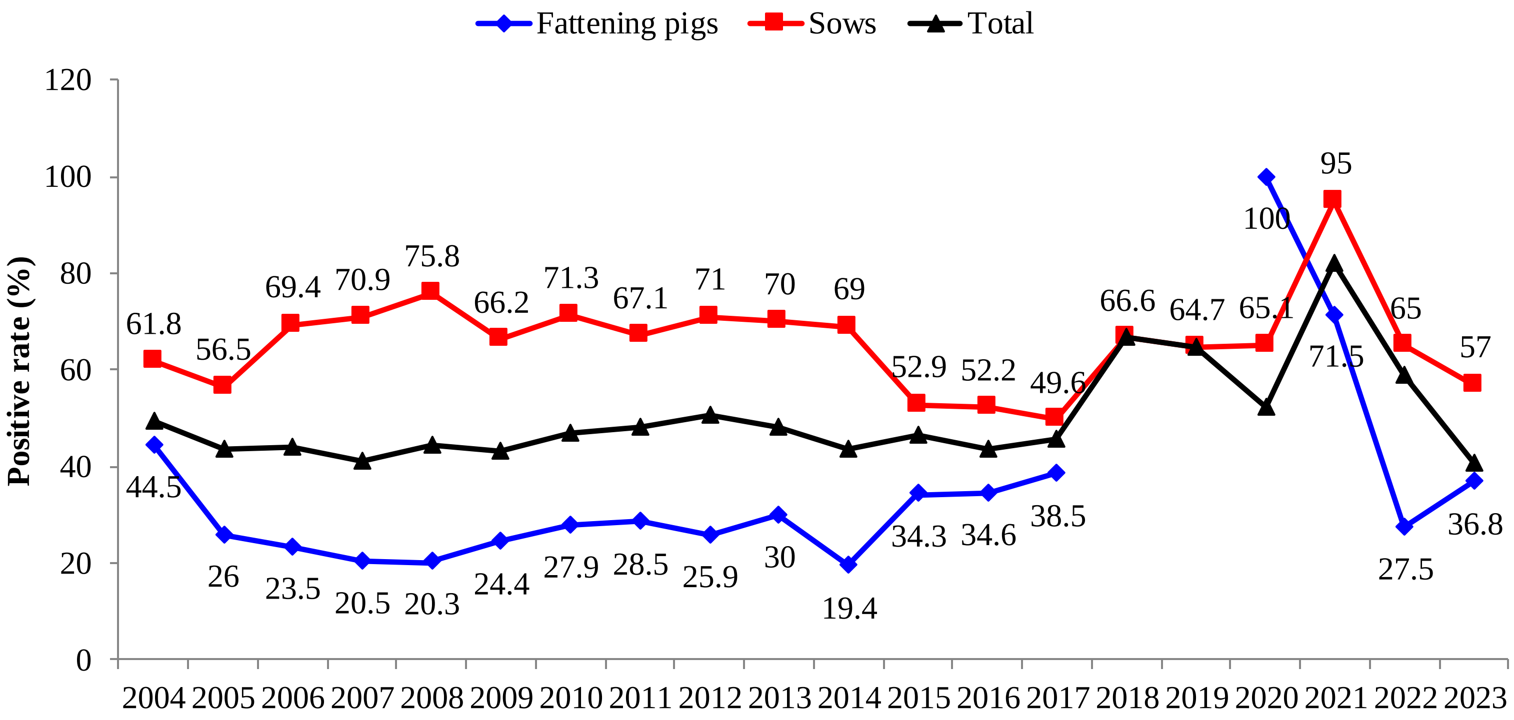
Correlation between ELISA and HI test



N=175 sera		No. of samples with HI	
		Positive	Negative
ELISA	positive	71	8
	Negative	6	90
	Sum	77	98
	Sensitivity	92.2%	
	Specificity		91.8%
	Accuracy	92.0%	

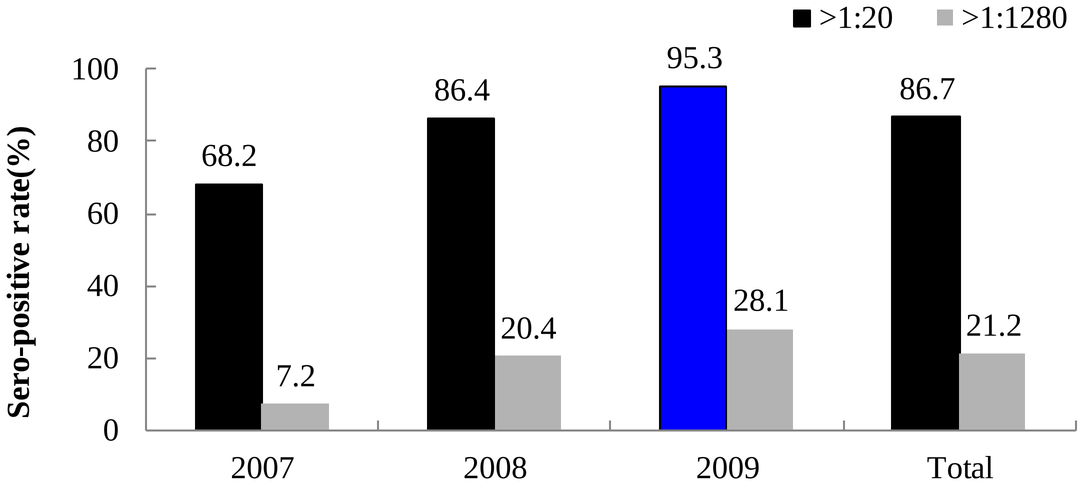
- These results suggest that I-ELISA is useful for sero-surveillance of JEV in swine.

Sero-surveillance of JEV in pigs since 2004



- Sera obtained from 5,000 to 8,000 pigs each year have been checked by HI or ELISA test since 2004.
- HI and ELISA tests have been used to measure JEV antibodies in pig sera since 2017.
- If all sows on a pig farm are negative for JEV, vaccination is recommended.

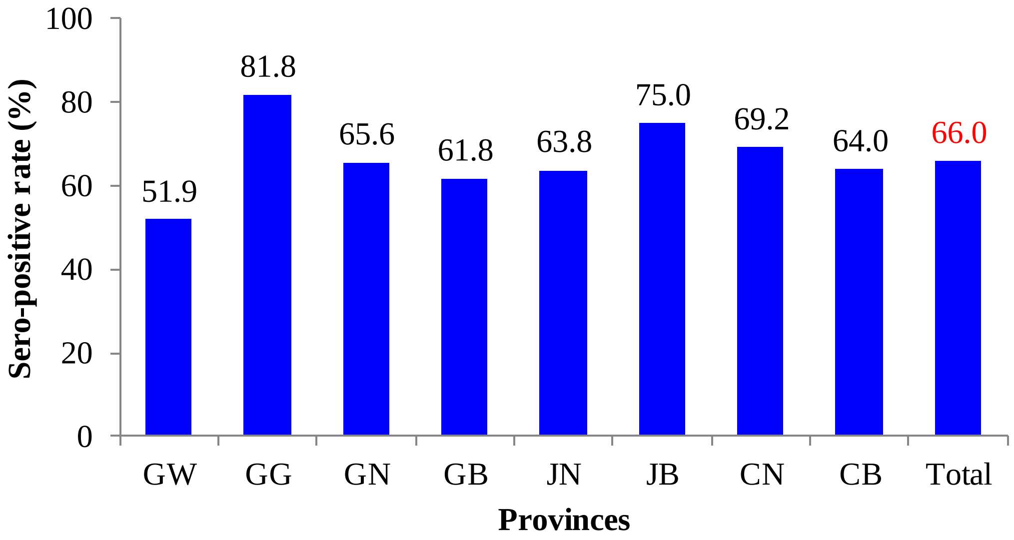
Sero-surveillance of JEV in wild birds captured in South Korea



- Blood samples were collected from 1,316 wild birds including migratory birds in 16 sites of 6 provinces.
- Of the 1,316 serum samples tested, 1,141 sera (86.7%) were positive for JEV.

- Migrating birds are believed to be one of the factors responsible for transmitting the JEV.
- When the chicken is sero-positive against JEV, it means the widespread presence of JEV.

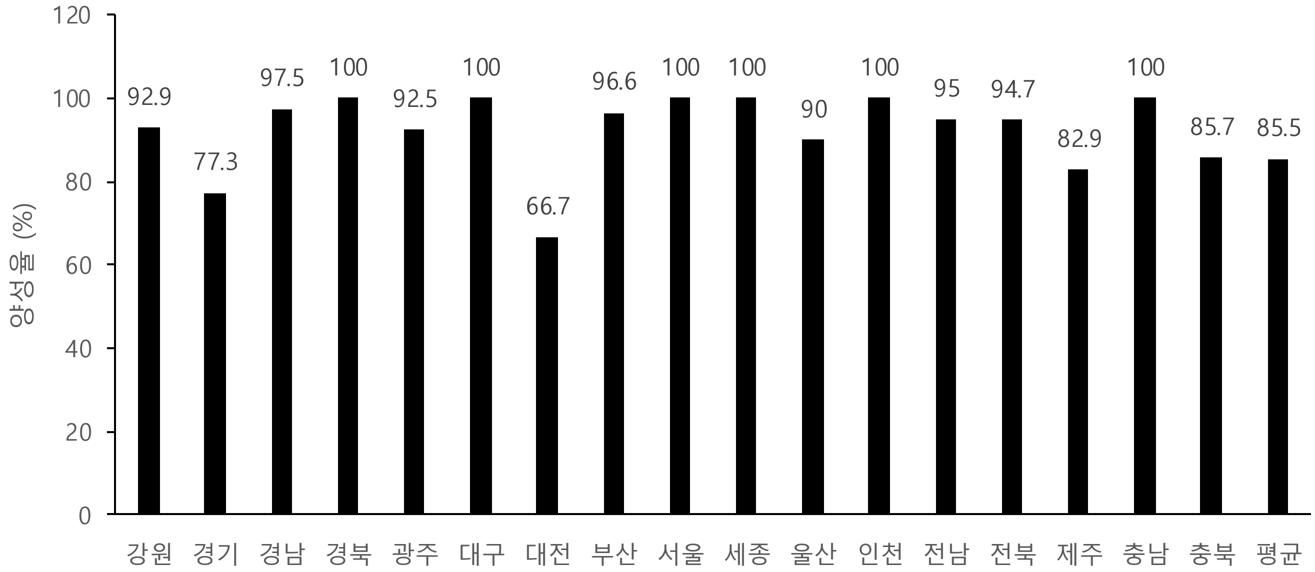
Sero-surveillance of JEV in wild boars in South Korea



- The results showed that 66.0% (190/288) of wild boars in Korea had neutralizing antibodies against JEV.

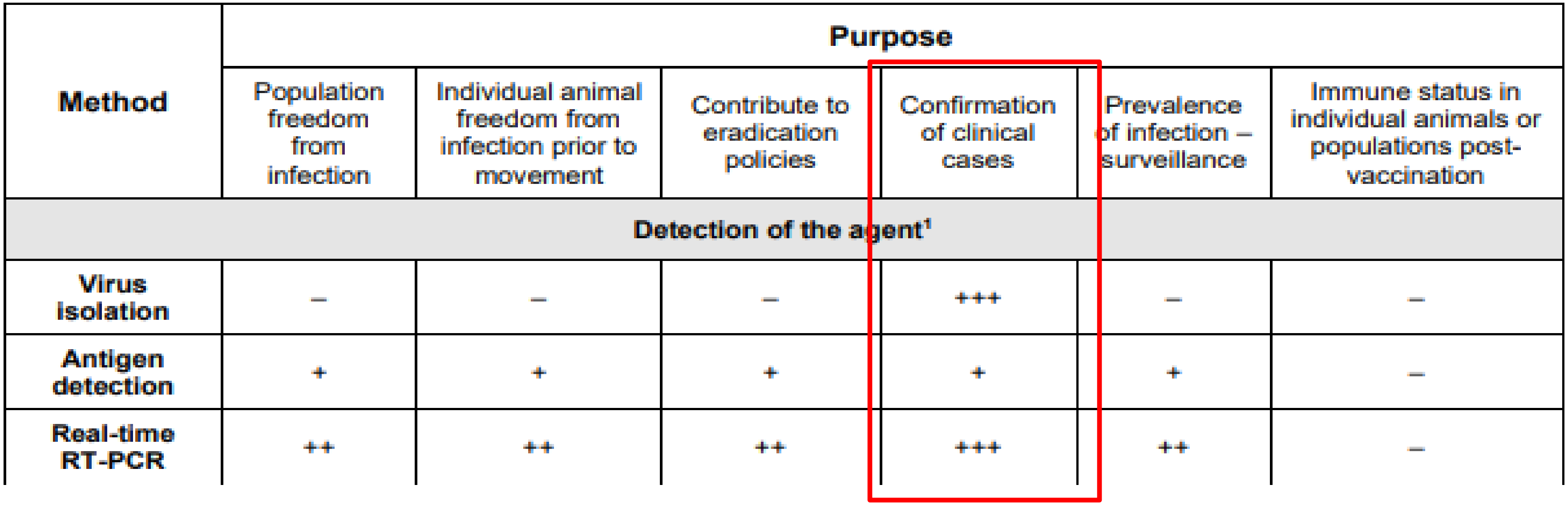
- Wild boars are amplifying hosts of the JEV and are believed to be one of transmitters.

Sero-surveillance of JEV in horse sera



- Of the 1,331 horse sera collected in 2023, 85.5% were positive for JEV.
- As a result of analyzing regional distribution, the number of horses in Daejeon was the lowest at 66.7%.
- The JEV antibodies in horse are an immune response following vaccination and JEV vaccine is recommended for antibody-negative horses.

Overview of diagnosis of JEV antigen in animals



Method	Purpose					
	Population freedom from infection	Individual animal freedom from infection prior to movement	Contribute to eradication policies	Confirmation of clinical cases	Prevalence of infection – surveillance	Immune status in individual animals or populations post-vaccination
Detection of the agent[1]						
Virus isolation	–	–	–	+++	–	–
Antigen detection	+	+	+	+	+	–
Real-time RT-PCR	++	++	++	+++	++	–

- Diagnostic test methods including virus isolation, real time RT-PCR, mouse inoculation have been used to detect JEV antigens.

Diagnosis of JE in pigs and horses

- Most JE infection in sows manifests as a reproductive disease to reach 50–70% abortions in sows, subclinical in horses.

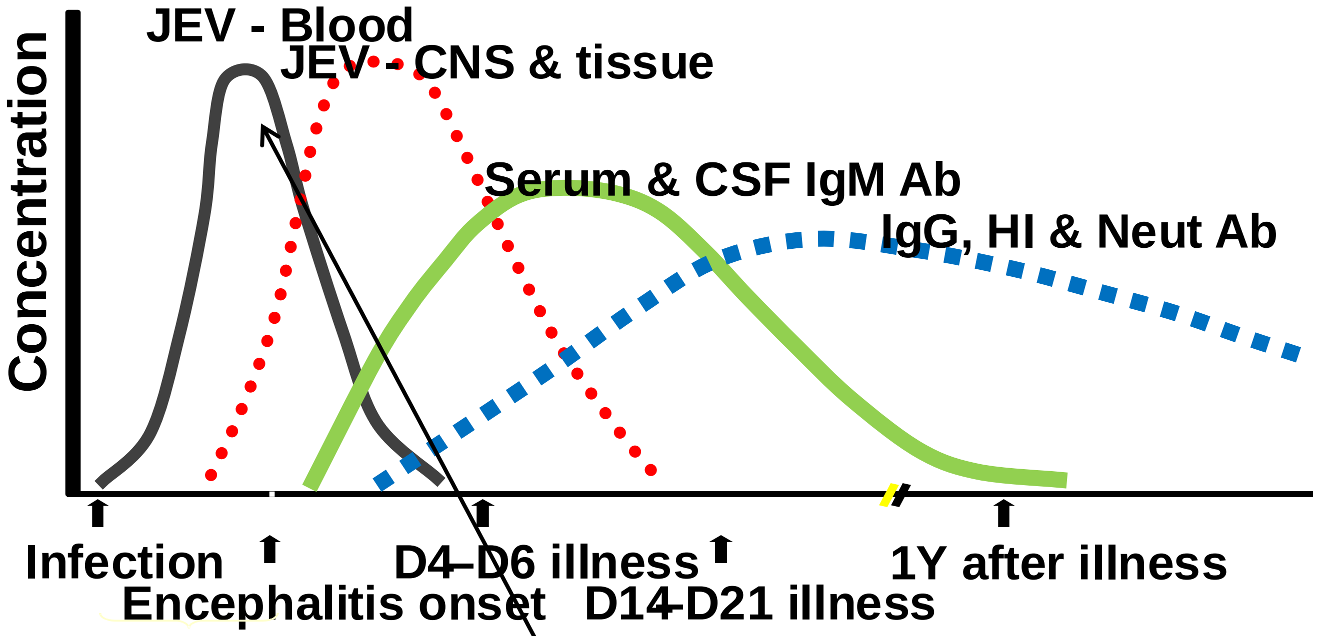
☐ Stillbirths or mummified fetuses; usually at term

- Live born piglets most often demonstrate neurologic signs of tremors and convulsions and may die soon after birth.

☐ Mild febrile disease or subclinical disease in non-pregnant females
☐ Natural infection results in long lasting immunity
☐ Mortality rate is near zero in adult swine
☐ Identification of JEV on brain or spinal cord in horse

- Under 70-day old fetus: JEV antigen has to be identified with VI, or RT-PCR.
- Over 70-day old fetus: JEV antibody on thoracic fluid should be checked.

Host response to JE infection



Virus strain	Route	ID. of pig	Post inoculation days					
			2	4	6	8	15	22
KV1899-37P	IM*	1	-/-	-/-	-/-	-/-	-/-	-/-
		2	-/-	-/-	-/-	-/-	-/-	-/-
		3	+/+	-/-	-/-	-/-	-/-	-/-
		4	+/+	-/-	-/-	-/-	-/-	-/-
Control	-	1	-/-	-/-	-/-	-/-	-/-	-/-

+/+: Positive results in both virus isolation and real-time RT-PCR.

Because of short period of viremia, the timing of virus detection must be considered.

Diagnostic procedure to detect JE antigen in suspected samples

- Cerebro-spinal fluid, brain tissue, aborted fetus, plasma, Mosquito etc

Antigen preparation(10% homogenization etc) and extraction of RNA

One step RT-PCR or real time RT-PCR
(Target : E or NS gene)

Negative

The End

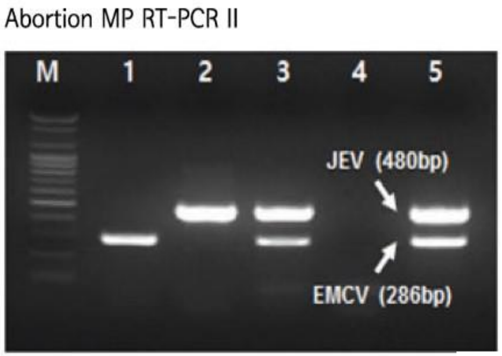
Positive

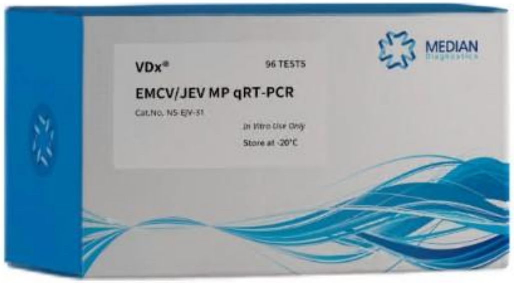
sequencing

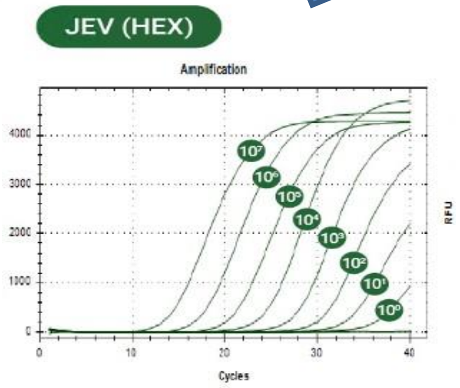
Virus Isolation from sample material
in C6/36, BHK-21, and Vero cells

Characterization
(IFA, EM, Inoculation in suckling mouse, HA etc)

Multiplex RT-PCR and real time RT-PCR kit to detect JEV



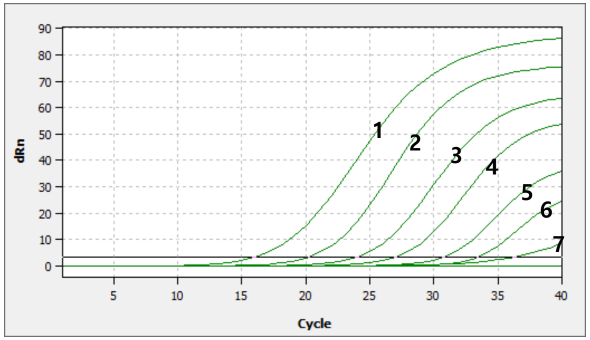




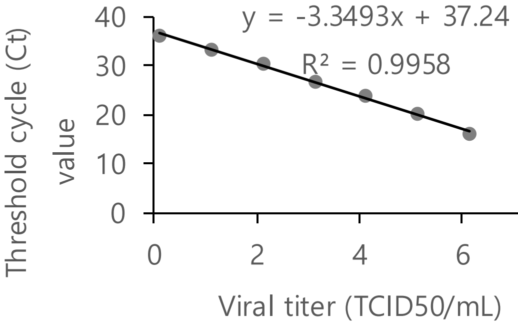
- Conventional RT-PCR kits for the detection of JEV in brain, fetal fluid and sera have been commercialized.
- Real time RT-PCR kit is also available to detect JEV in samples.

Example of application of real time RT-PCR kit to JEV genotypes

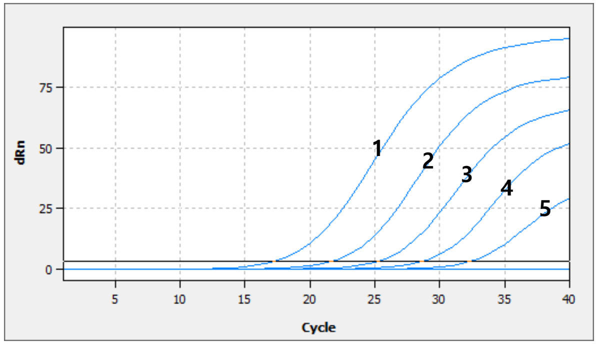
JEV G1



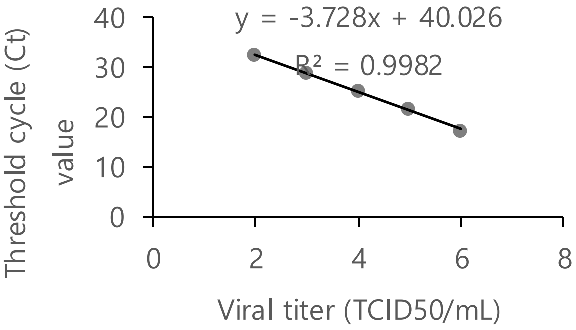
1.18 TCID$_{50}$/mL



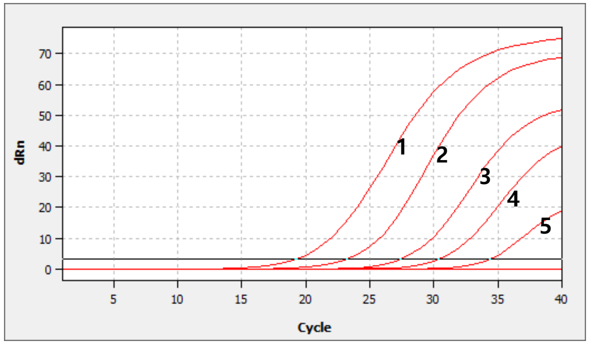
JEV G3



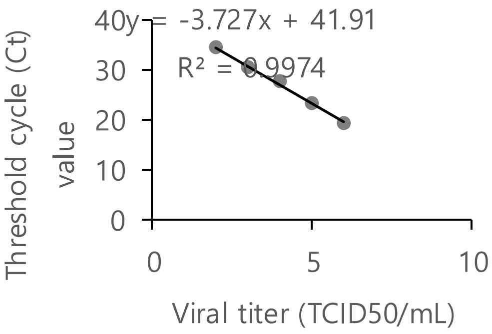
6.48 TCID$_{50}$/mL



JEV G5

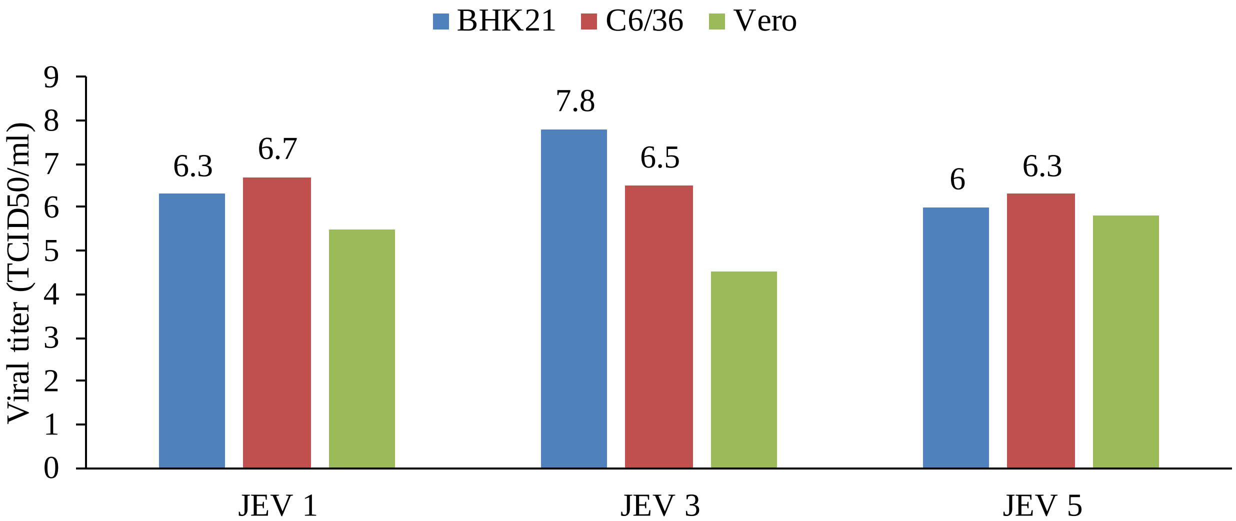


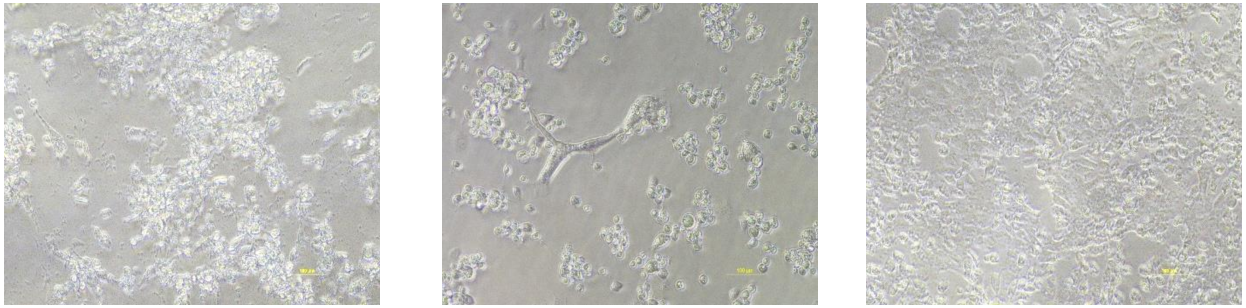
20.77 TCID$_{50}$/mL



- The real time RT-PCR kit detected three genotypes of JEV and showed the lowest detection limit to JEV genotype 1 of 1.18 TCID$_{50}$/ml.

Proliferation ability of JEVs in 3 types of cells





- JEV has different proliferative abilities depending on the cells.
- BHK-21 and C6/36 cells are suitable for isolating JEV.
- C6/36 cells should be culture at 28 degrees.

Mouse inoculation test to detect JEV

- **The 3-5 day old nursing mice** inoculated with JEV showed paralysis, signs of nerve system and died within 7 days post inoculation.

- **Four-week old mice** inoculated with JEV via intracranial route died of neurologic disease. The most susceptible five mouse species to the JEV are C3J/He, DBA/2, C57BL/6, Balb/c, ICR.

How to control JE in animals

- **Vaccination**: Implementing vaccination programs for animals, especially pigs, can significantly reduce the spread of JEV. Vaccines help build immunity in animal populations, preventing the virus from amplifying and spreading.
- **Mosquito control**: Reducing mosquito populations through environmental management, such as eliminating standing water where mosquitoes breed, and using insecticides can help control the primary vectors of JEV.
- **Active surveillance**: Regular surveillance and monitoring of animal populations for signs of JEV can help in early detection and prompt response to outbreaks. This includes serological testing to identify infected animals.
- **Public awareness and education**: Educating farmers and animal handlers about the importance of mosquito control, vaccination, and early detection measures can enhance the effectiveness of control programs. Awareness campaigns can also promote the adoption of best practices to prevent the spread of JEV.

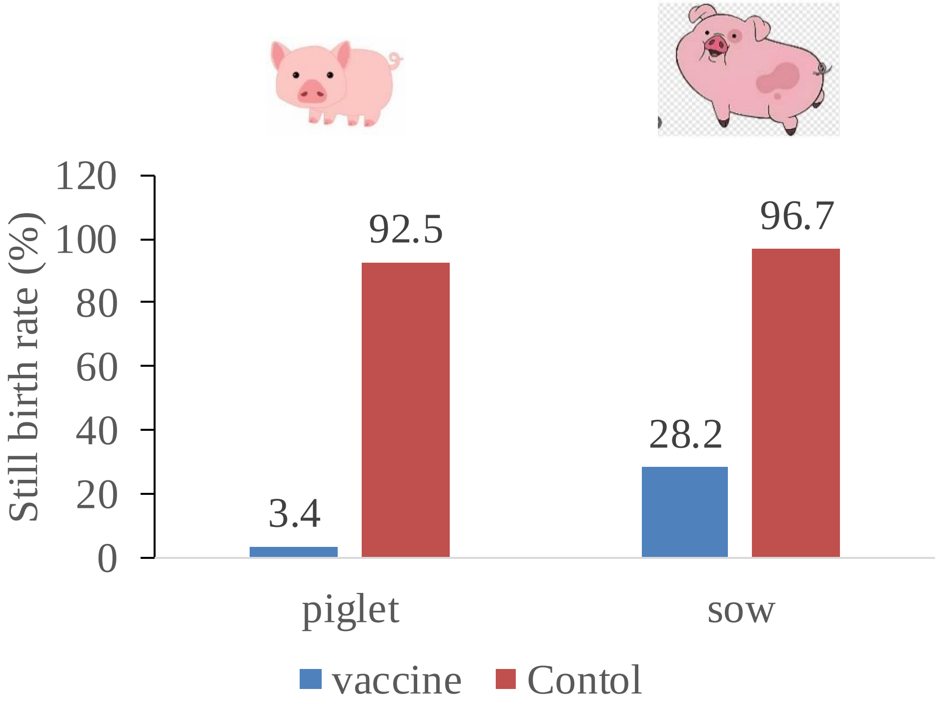
JEV vaccination and vector control

- Vaccination is the most effective preventive method for animals.
- Minimizing exposure of animals to mosquitoes using nets is possible.

Type	Virus strain	Culture method	For use in	Genotype
Inactivated JE	Nakayama	Chicken embryos	Horse/pigs	3
Inactivated JE	Beijing	-	Horse/pigs	3
Live JE	AT	Hamster kidney cell	Pigs	3
Live JE	M	Hmlu-1	Pigs	3
Live JE	Anyang300	Duck primary cell	Pigs	3
Live JE	SA-14-14-2	BHK-21 cells	human and Pigs	3
Live JE	M-17	Porcine kidney cell	Pigs	3

- Vectors can be controlled by using insecticides in rice fields, growing larvivorous fish and mosquitofish.

Example of JEV vaccine application on pig farms



- In total, 3,790 sows were inoculated with JEV vaccine in three provinces in 1975.
- The stillbirth rate in sows inoculated with JEV vaccine was reduced rapidly.
- But sows that were not treated with JEV vaccine showed high still birth rates (92.5 to 96.7%).

Summary

- **Continuous cooperation and efforts** are needed to improve human and animal health.
- **Strengthen the monitoring of JEV gene changes:** it is essential to enhance methods for detecting and monitoring JEV genotypes in the natural environment. In Europe and Africa, JEV infections were reported.
- **Enhanced surveillance for early detection**: as mosquito activity is expanding due to climate change, active surveillance into JEV is required in Asian countries.
- **Vaccination**: continuous vaccination of pigs and horses is recommended to prevent JEV infection in animals.
- **Development of new JE vaccine**: the JEV 3 vaccine has the protection rate against JEV 1 ranging from 92% to 97%.

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West Nile Fever

WOAH Regional Workshop on Vector Borne diseases in Asia and the Pacific

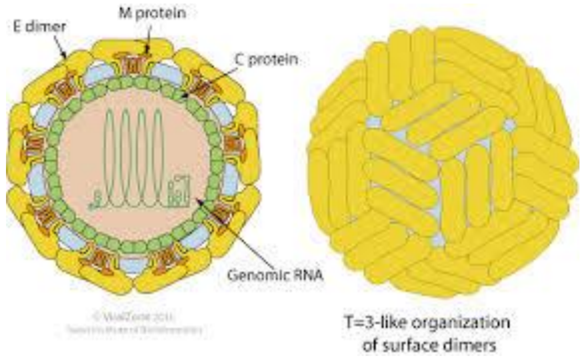
Federica Monaco
f.monaco@izs.it
Istituto Zooprofilattico Sperimentale
dell'Abruzzo e del Molise "G. Caporale"
WOAH Reference laboratory for WNF

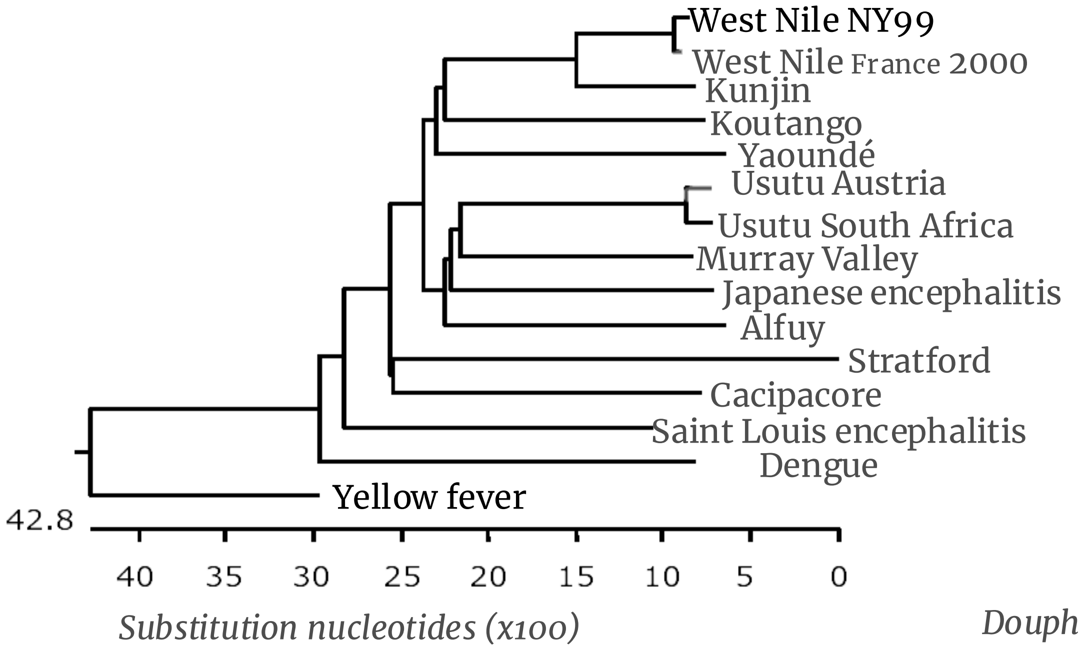
Tokyo, 19th September 2024

West Nile virus

West Nile virus (WNV) is a mosquito-borne virus belonging to the genus *Flavivirus* in the *Flaviviridae* family capable of infecting a wide range of species

Serologically, West Nile virus is a member of the Japanese encephalitis serocomplex





Douphin, 2006

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West Nile virus

WNV is among the most
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has been
Africa, E
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Several V
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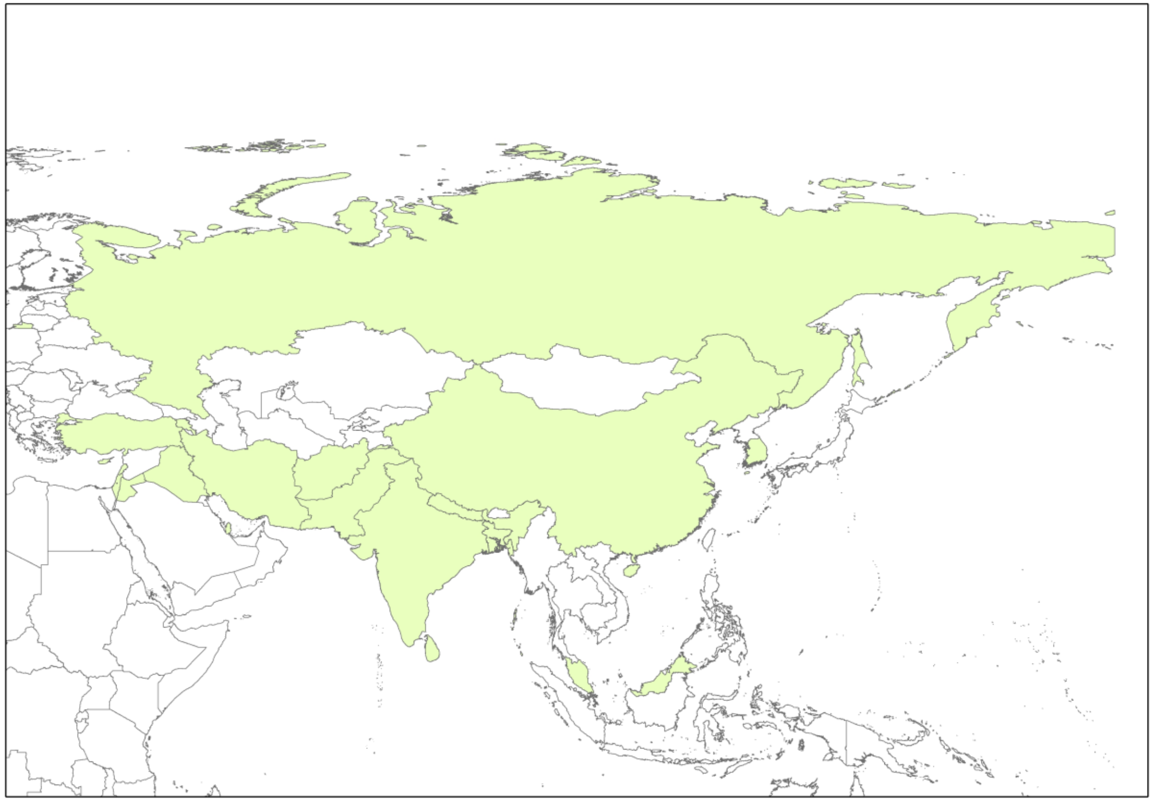
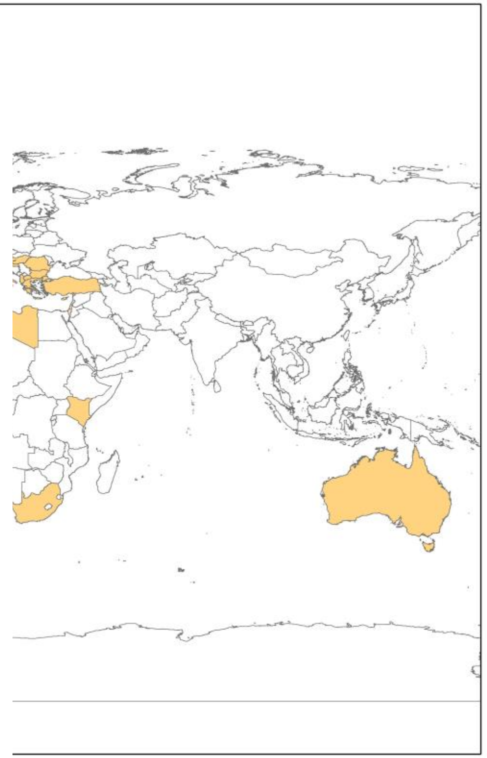
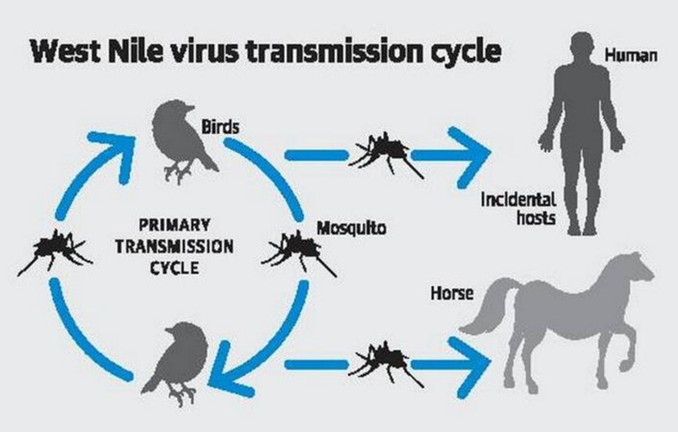




ata source: WAHID and ECDC
(2019-2024)

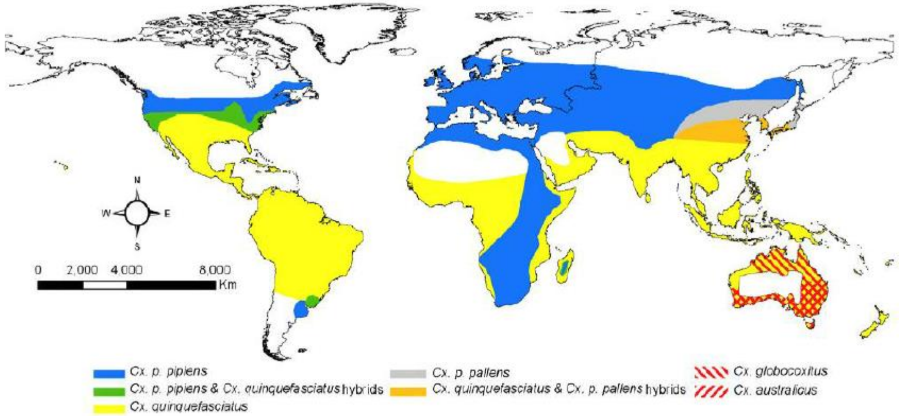
West Nile virus

WNV is maintained in nature by enzootic cycle between **adult ornithophilic mosquitoes** in mainly belonging to the **Culex,** genera and several bird species

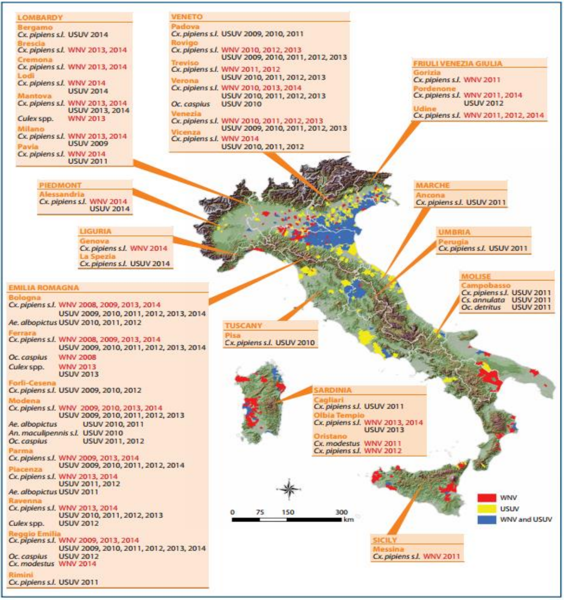


WNV is predominantly vectored worldwide by members of the **Culex pipiens complex**

Horses and **humans** are considered dead end hosts of the virus and do not contribute to the transmission cycle



Global distribution of *Cx. pipiens* complex mosquitoes. Geographic range for *Cx. p. pipiens* includes both forms (*pipiens and molestus*). *Cx. australicus* and *Cx. globocoxitus* are restricted to Australia.
(Ciota and Kramer 2013)



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Symptoms in human

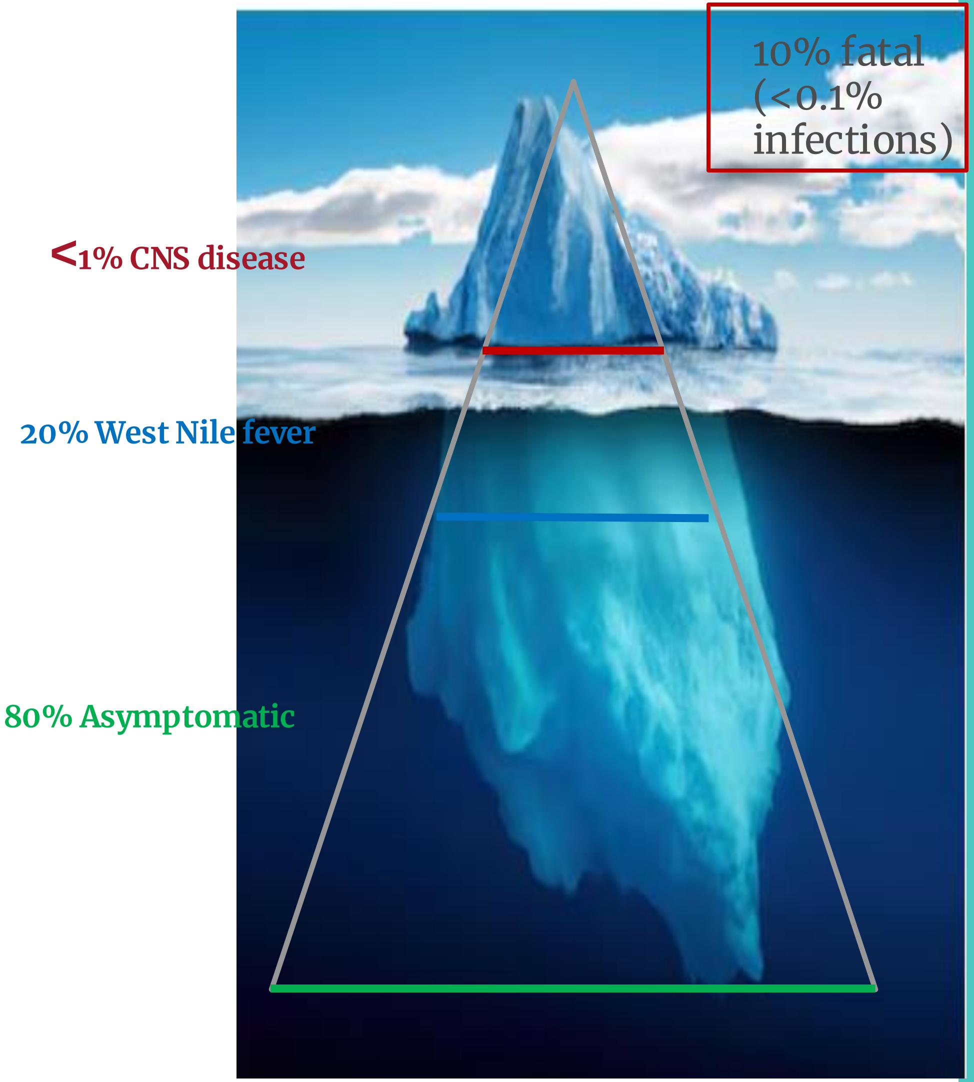
The incubation period is 2-14 days

80% of human infections have no symptoms

About 20% of WNV infections in humans may cause West Nile fever (WNF),

Less than 1% may cause West Nile neuroinvasive disease (WNND) that affects the nervous system.

1 WNND → 150 infections



Symptoms in horses

The incubation period is 3-15 days

The infection usually is asymptomatic (>70%) or with mild symptoms like fever, weakness, myalgia (20%):

1-10% of infected horses has the neuroinvasive form

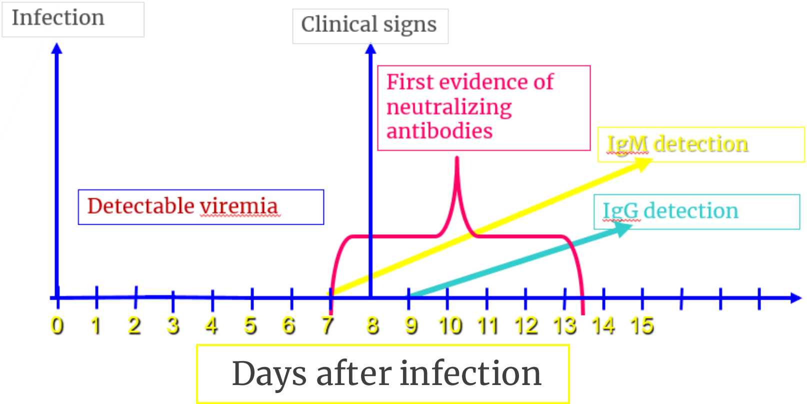
- virus in the CNS (spinal cord, hindbrain, midbrain)

The fatality rate in horses can reach 57-60%

- In USA (2000) was 38.3%
- In Italy was 42% (1998), 15.6% (2008) 24.3% (2009)

Viremia precedes the clinical manifestations of disease

Rarely, horses are symptomatic AND viremic



Bunning et al., 2002

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Serum, blood, tissue, mosquitoes

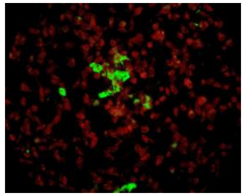
Real time RT-PCR (OIE, 2018)

NEG

STOP

POS

IV (C6/36, Vero, BHK21, RK13)



Identification (IF or RT-PCR)

WGS
(Diagne, 2023)

Ct threshold

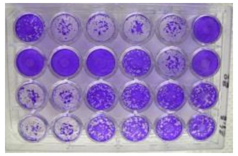
WGS
(Diagne, 2023)

Serum

ELISA IgG & IgM

POS

PRNT/VN



(OIE, 2018)

WND
Usutu
TBE …

NEG

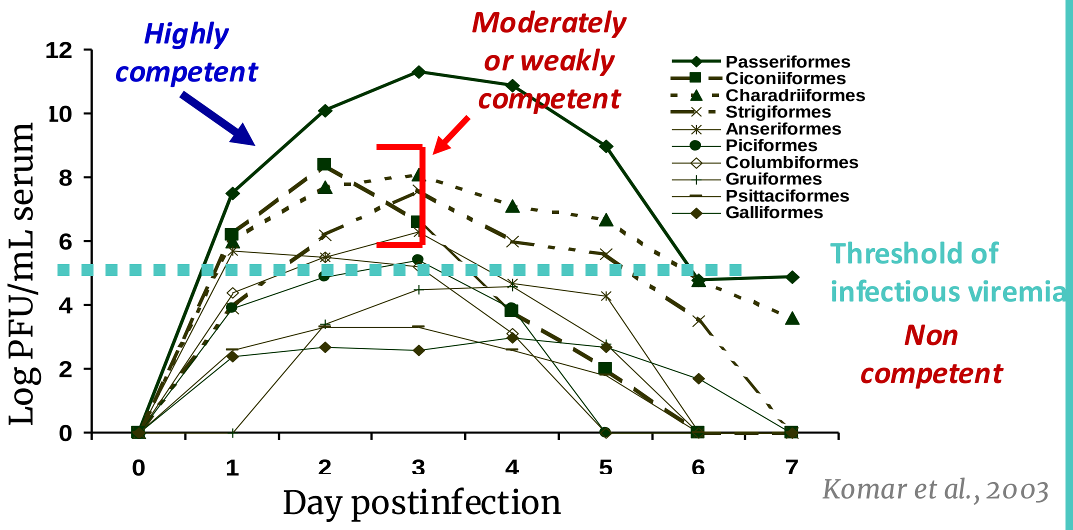
STOP

Birds

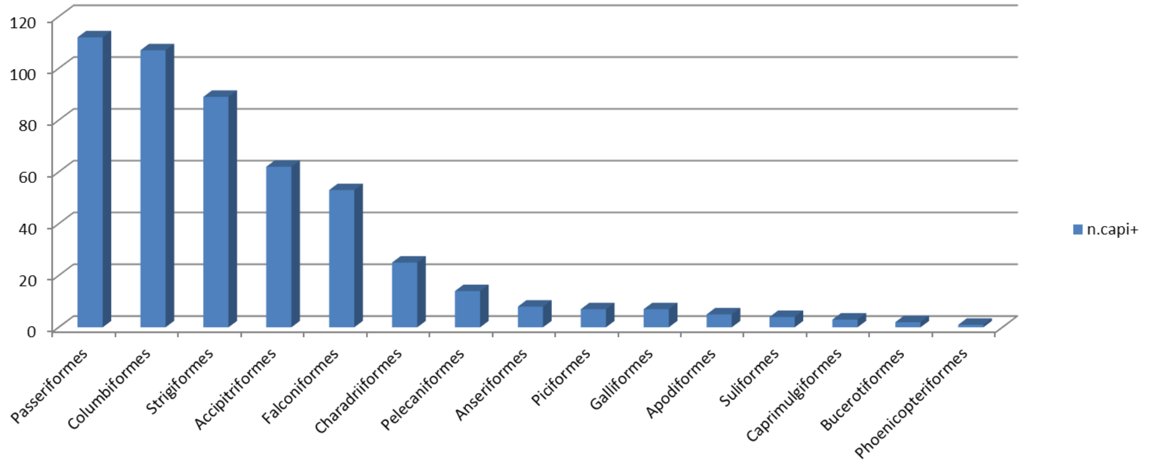
Over **300 species** of birds have been identified as viable WNV hosts

There is significant variability in **viremia levels** and **disease**

Clinical signs following WNV infection is uncommon and related to bird **species** (birds of prey) and **viral strain**



Komar et al., 2003



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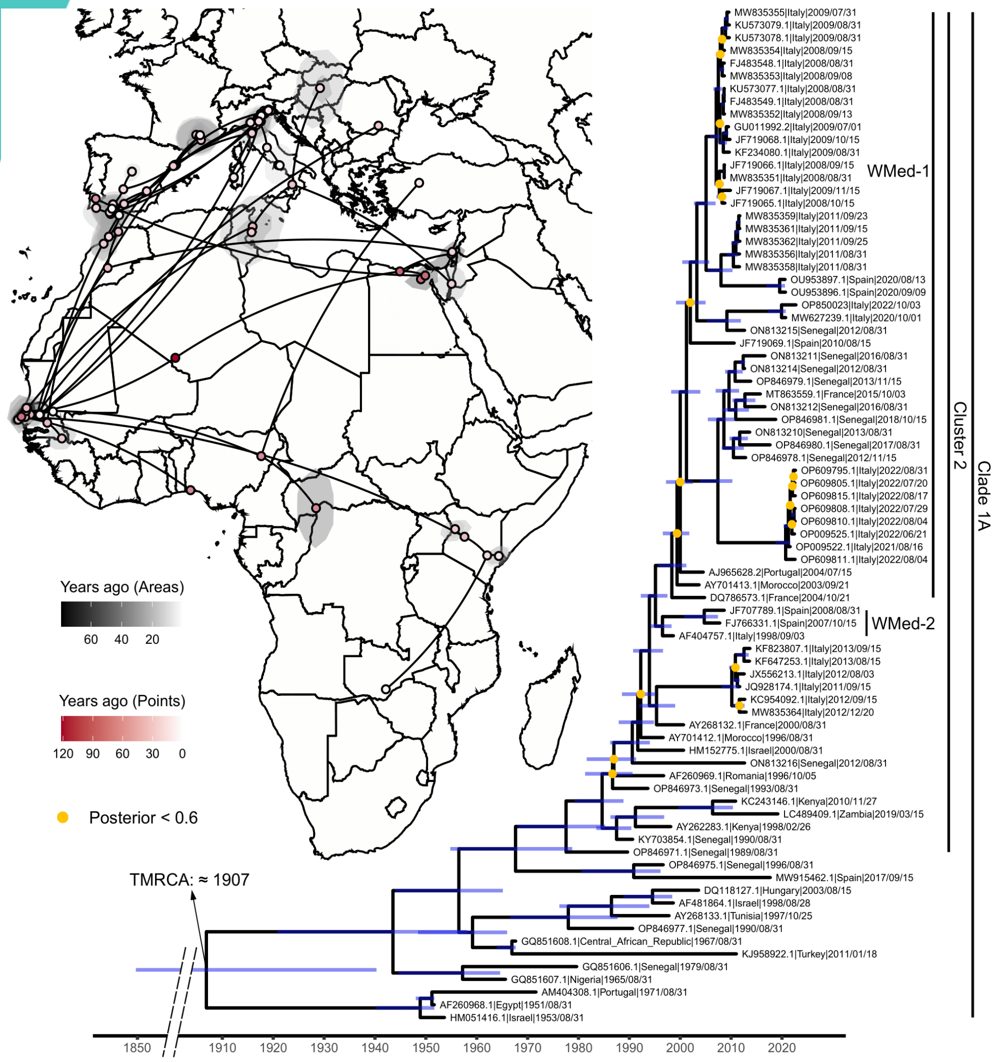
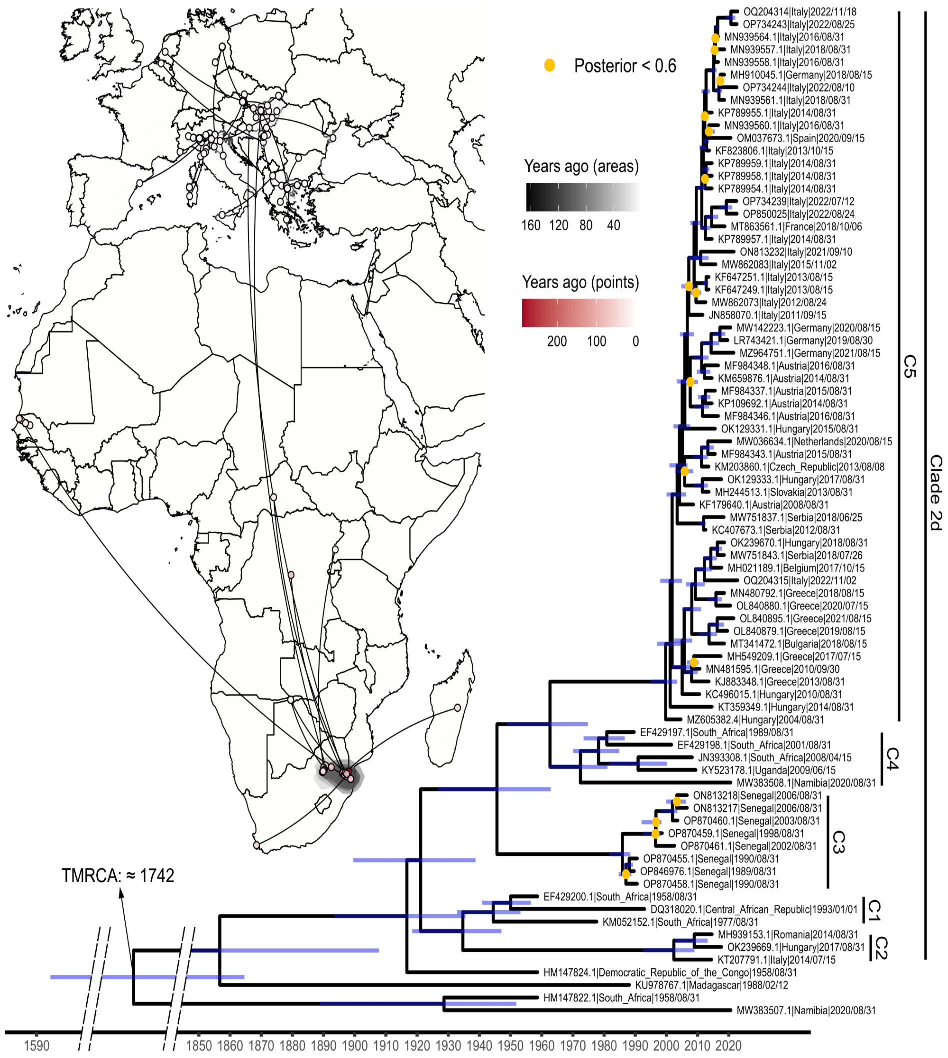
WNV L1



WNV L2

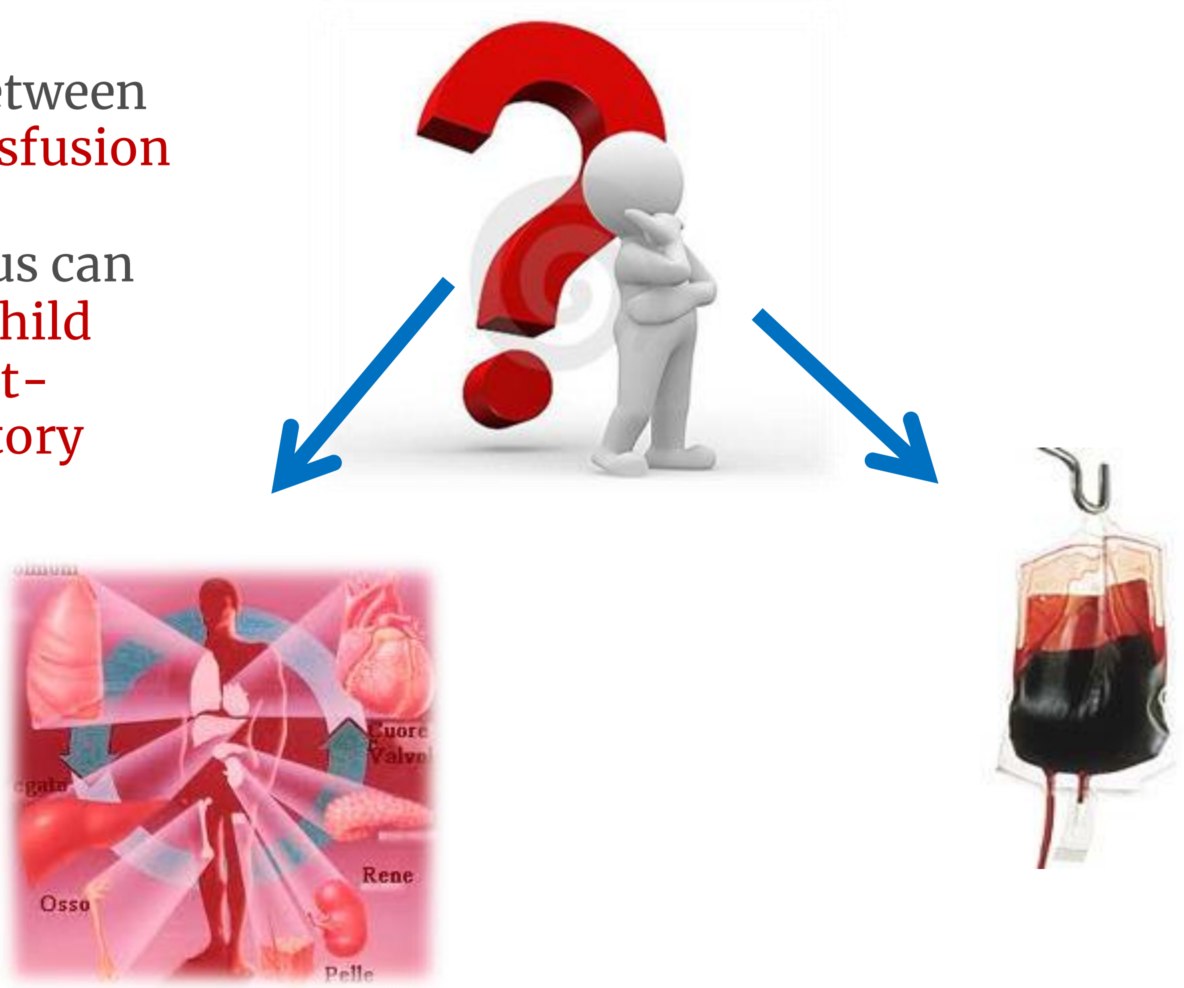


Mencattelli et al., 2023

Transmission - SoHO

The virus can also spread between humans through blood transfusion and organ transplant.

Other ways in which the virus can spread are from mother to child during pregnancy and breast-feeding and through laboratory exposure



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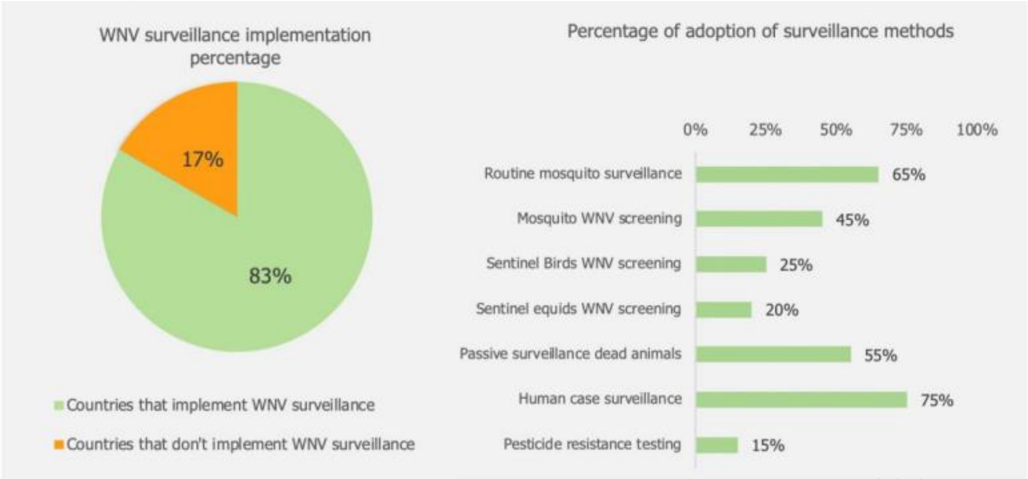
Importance of veterinary surveillance

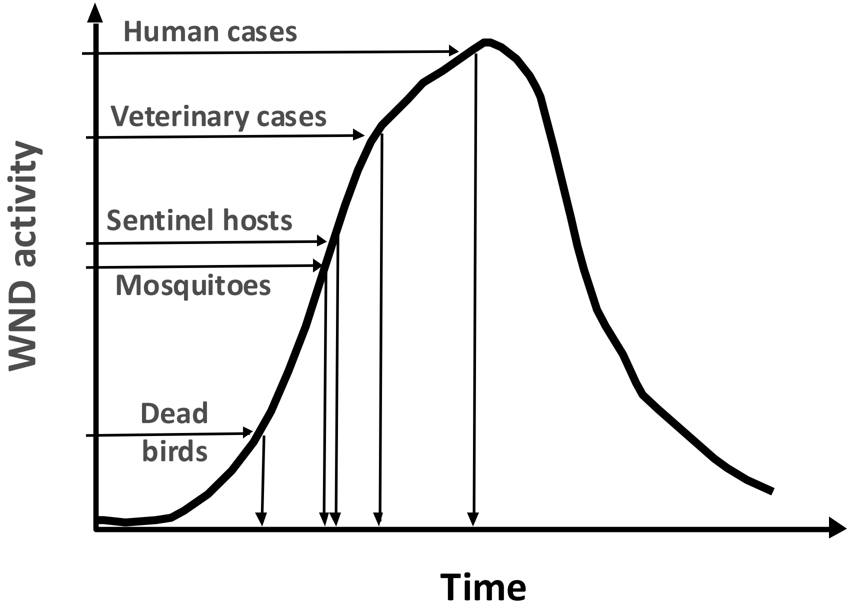
Early detection of WNV circulation for rapid risk assessment and adoption of appropriate preventive measures in **public health.**

Surveillance of WNV circulation requires a multidisciplinary effort

- complexity of the epidemiological cycle



ECDC, 2020



Entomological and veterinary surveillance are keys:

- to assess the associated human health risk
- to trigger a more timely and effective control of the disease in humans

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WNV surveillance: the Italian model

High transmission risk area

Territories (Provinces NUT-3) where WNV is circulating or has circulated in at least one of the 5 years before as well as the surrounding areas

Low transmission risk area

Territories (Provinces NUT-3) where WNV has never been/rarely reported, which have eco-climatic condition favorable to viral circulation

Minimum transmission risk area

Territories (Provinces NUT-3) where WNV has never been reported and where eco-climatic conditions are not suitable to WNV circulation

WNV surveillance: the Italian model

Veterinary surveillance is focused on the following components:

- ✓ Surveillance of resident birds of target species (**Magpie, Carrion Crow and Eurasian jay**) in **High** and **Low risk** areas
  - ✓ alternatively in Low risk areas surveillance can be conducted on rural or open air poultry rearing units.
- ✓ Entomological surveillance. **High** and **Low risk** areas (1 trap/20X20 km)
- ✓ Horses clinical surveillance. **(whole country)**
- ✓ Wild bird mortality surveillance **(whole country)**

To guarantee harmonization and representativeness of the data collected within active surveillance each province (NUT-3) is divided in units of 1200-1600 km2 and activities referred to each unit.

WN infection clinical suspicion/ surveillance activities within National Plan

T E R A M O

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Official veterinarian

- coordinated on a regional level
- implemented surveillance activities
- collect each type of species (bird, horse, mosquitoes)
- notify suspected in SIMAN
- Send samples to IIZZSS
- notify confirmed outbreaks in SIMAN

IIZZSS

- at regional level
- tested each type of samples/species (bird, horse, mosquitoes)
- In case of positivity, send the samples to CESME

CESME

- At national level
- Confirms suspected specimens
- Verify the correctness of notifications in SIMAN
- Communicate the outbreak to the Ministry of Health
- Communicate the outbreak to National Italian blood Centre and National Italian transplant Centre
- Report the outbreaks to international bodies
- Divulgate the epidemiological situation to general public


Sistema Informativo Veterinario

Ministero della Salute

14:00. Il portale osserva il seguente orario di servizio: dal Lunedì al S

Trapianti
Centro Nazionale Trapianti

CENTRO NAZIONALE SANGUE
Istituto Superiore di Sanità

European Commission

efsa
European Food Safety Authority

World Organisation for Animal Health
Founded as OIE

ecdc


Sorveglianza integrata del West Nile e Usutu virus

Bollettino N. 1 del 28 giugno 2018
RISULTATI NAZIONALI

1. In Evidenza
2. Sorveglianza umana
3. Sorveglianza equidi
4. Sorveglianza uccelli bersaglio
5. Sorveglianza uccelli selvatici
6. Sorveglianza entomologica
7. Sorveglianza avicoli e altre specie animali
8. Sorveglianza Usutu
9. Piano nazionale integrato di sorveglianza e risposta ai virus West Nile e Usutu – 2018

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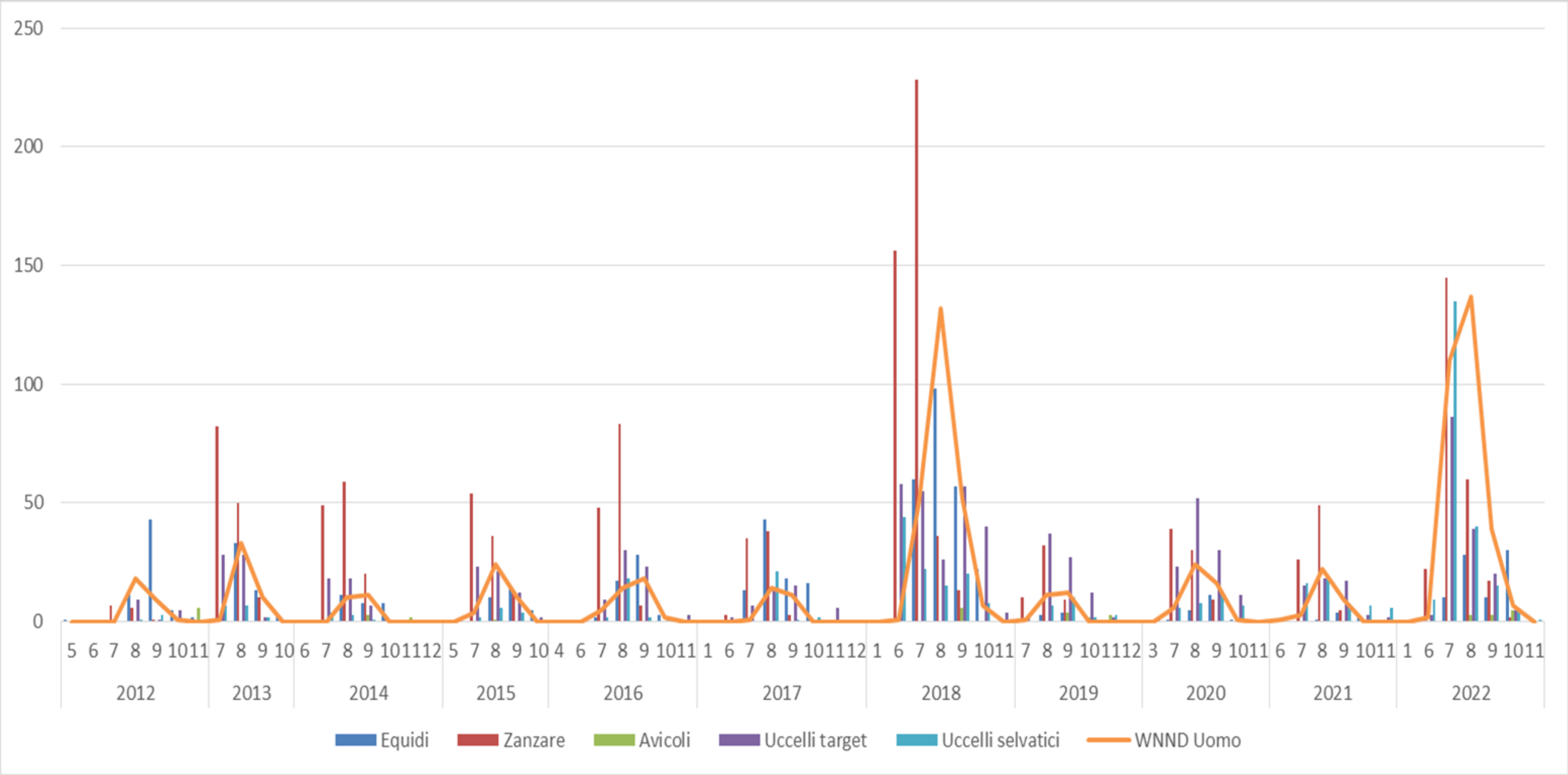
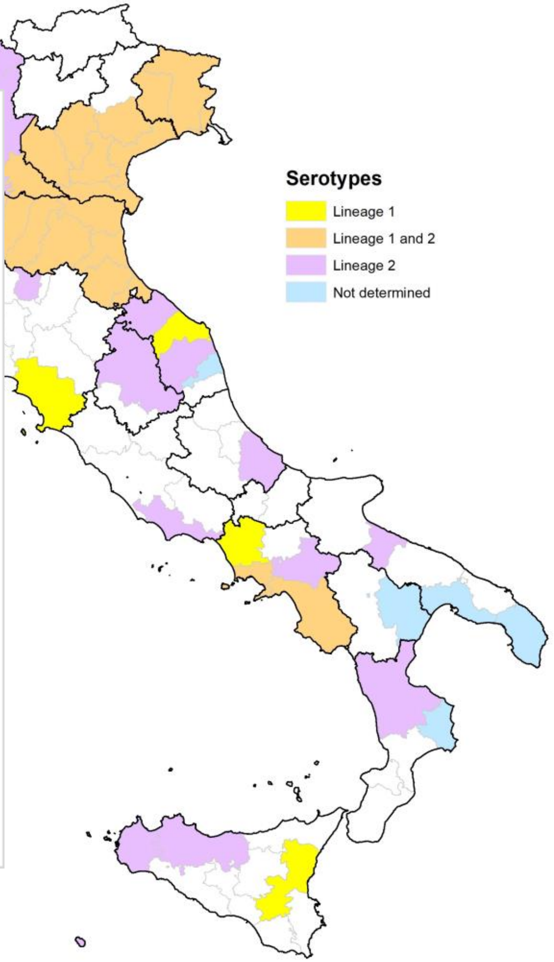
WNV numbers: the results of 2024 surveillance





91 wild birds
134 mosquito pools

Updated to 4 Semptember

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AIDEO: AI and EO as Innovative Methods for Monitoring West Nile Virus Spread

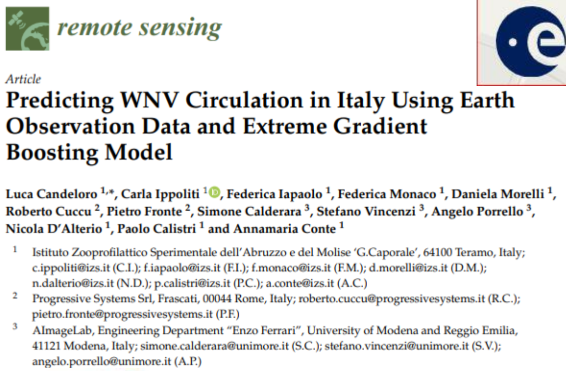
aideo

The recent and massive availability of **Earth Observation (EO)** data and the continuous development of innovative **Artificial Intelligence (AI) methods** can be of great help

- to **automatically identify patterns** in big datasets
- to **make highly accurate predictions**
- to **define intervention priorities** within national diseases surveillance plans

www.aideo.eu
https://eo4society.esa.int/projects/aideo/

Funded by esa


remote sensing

Article

Predicting WNV Circulation in Italy Using Earth Observation Data and Extreme Gradient Boosting Model

Luca Candeloro [1,*], Carla Ippoliti [1], Federica Iapaolo [1], Federica Monaco [1], Daniela Morelli [1], Roberto Cuccu [2], Pietro Fronte [2], Simone Calderara [3], Stefano Vincenzi [3], Angelo Porrello [3], Nicola D'Alterio [1], Paolo Calistri [1] and Annamaria Conte [1]

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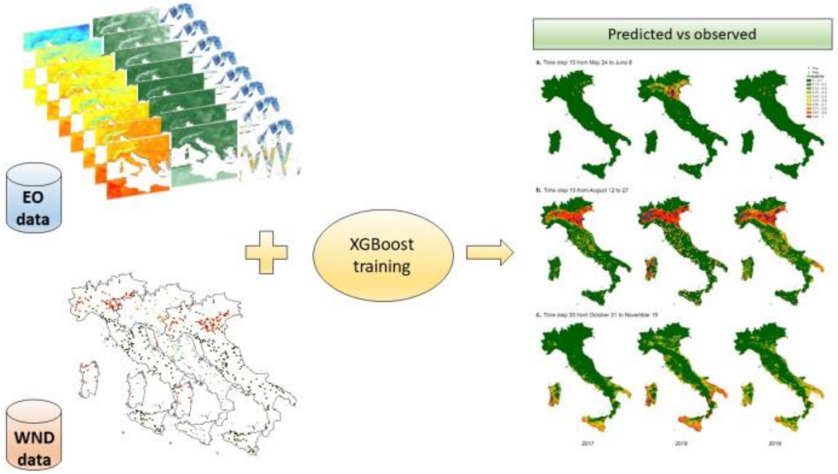
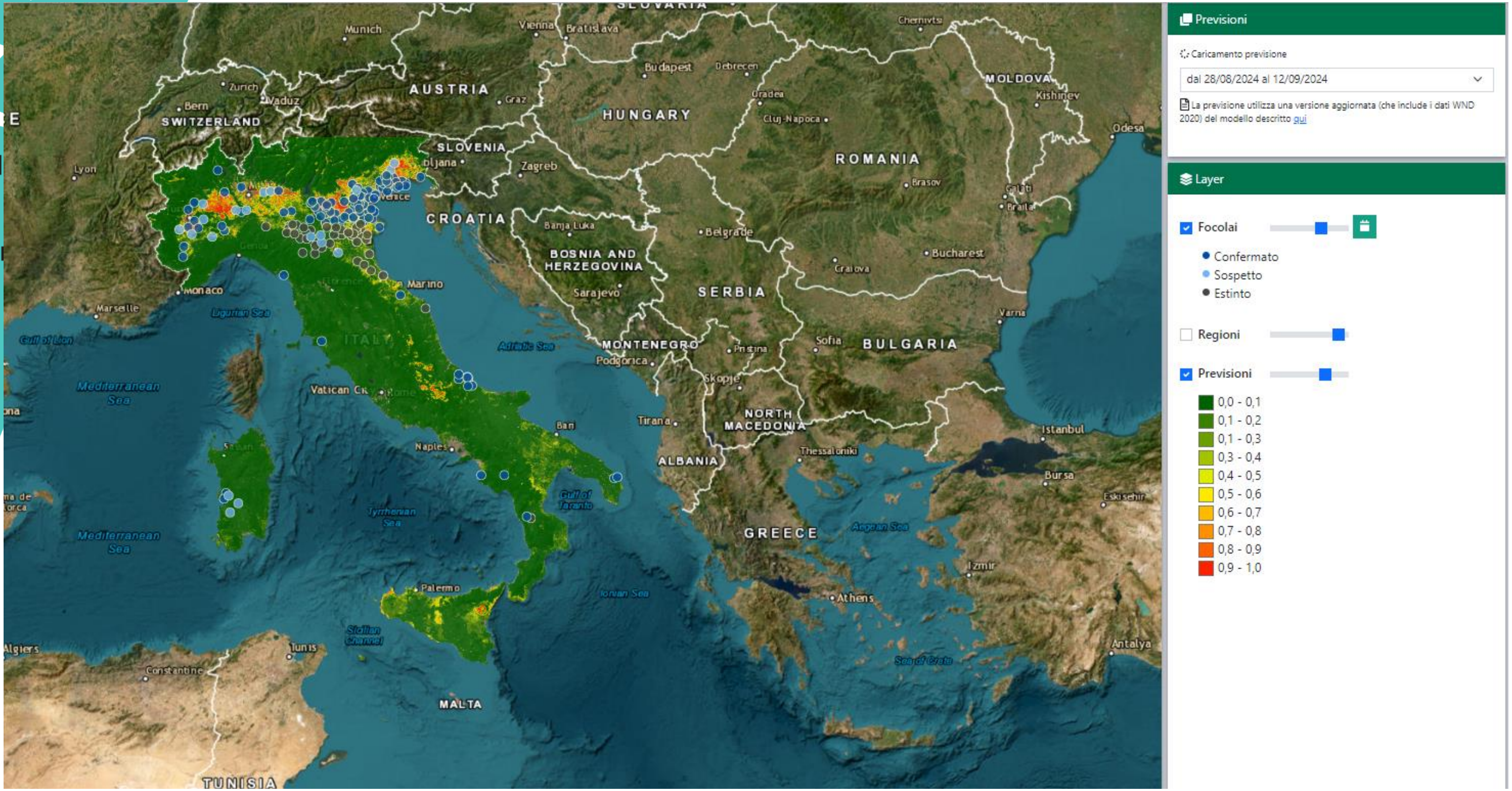
[3] AImageLab, Engineering Department "Enzo Ferrari", University of Modena and Reggio Emilia, 41121 Modena, Italy; simone.calderara@unimore.it (S.C.); stefano.vincenzi@unimore.it (S.V.); angelo.porrello@unimore.it (A.P.)



TERAM

ISTITUTO
ZOOPROFILATTI
SPERIMENTALE
DELL'ABRUZZO
E DEL MOLISE
“G. CAPORALE”



Previsioni

Caricamento previsione

dal 28/08/2024 al 12/09/2024

La previsione utilizza una versione aggiornata (che include i dati WND 2020) del modello descritto qui

Layer

☑ Focolai
- ● Confermato
- ● Sospetto
- ● Estinto

☐ Regioni

☑ Previsioni

🟩	0,0 - 0,1
🟩	0,1 - 0,2
🟩	0,1 - 0,3
🟩	0,3 - 0,4
🟨	0,4 - 0,5
🟨	0,5 - 0,6
🟧	0,6 - 0,7
🟧	0,7 - 0,8
🟧	0,8 - 0,9
🟥	0,9 - 1,0

https://mapserver.izs.it/gis_wn_predictions/#

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E DEL MOLISE
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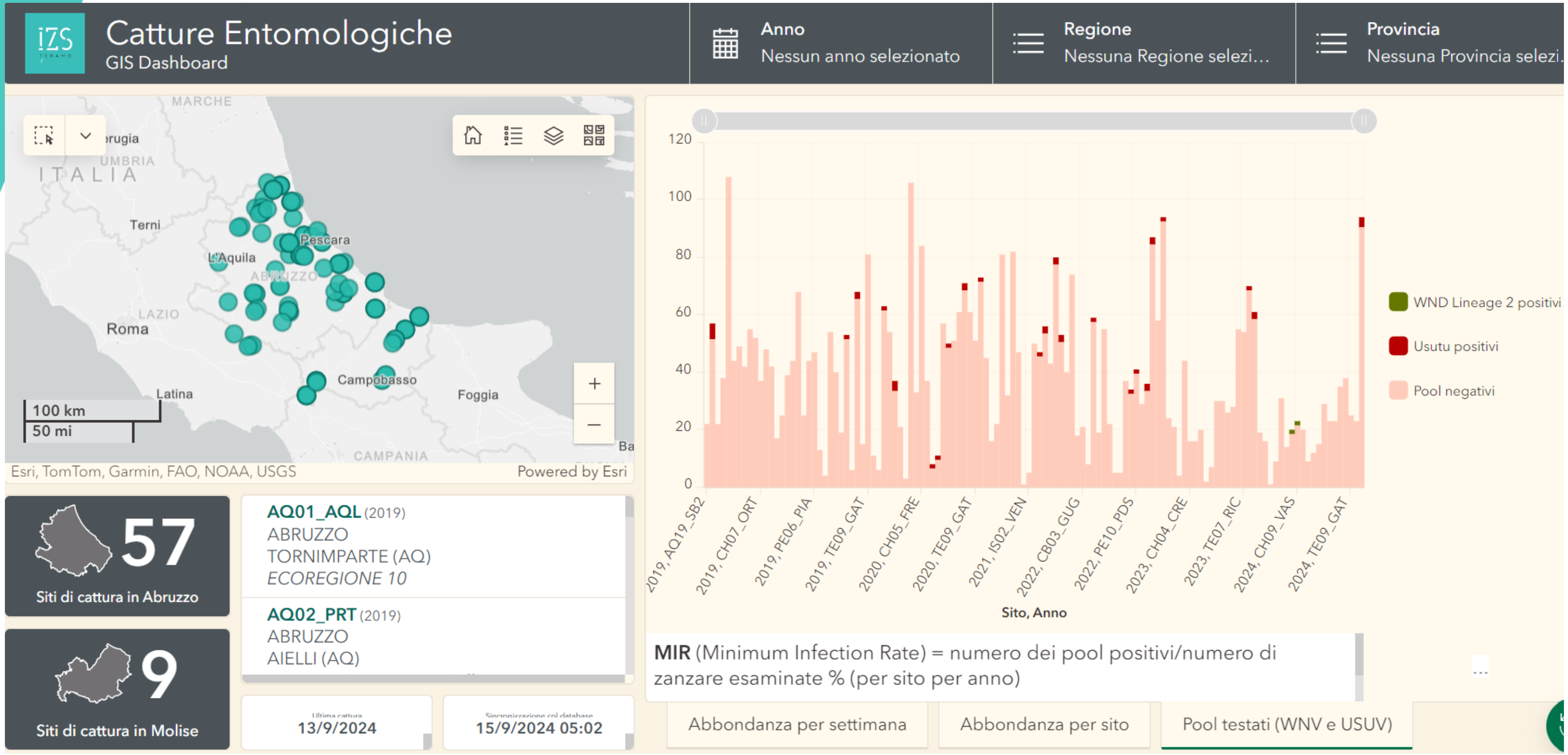
Mosquitoes dashboard



Catture Entomologiche
GIS Dashboard

Anno
Nessun anno selezionato

Regione
Nessuna Regione selezi...

Provincia
Nessuna Provincia selezi.

57
Siti di cattura in Abruzzo

9
Siti di cattura in Molise

AQ01_AQL (2019)
ABRUZZO
TORNIMPARTE (AQ)
ECOREGIONE 10

AQ02_PRT (2019)
ABRUZZO
AIELLI (AQ)

Ultima cattura
13/9/2024

Sincronizzazione col database
15/9/2024 05:02

MIR (Minimum Infection Rate) = numero dei pool positivi/numero di zanzare esaminate % (per sito per anno)

Abbondanza per settimana | Abbondanza per sito | Pool testati (WNV e USUV)

https://www.arcgis.com/apps/dashboards/282dbe6c42264e9aba37bef5524367b1

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SPERIMENTALE**
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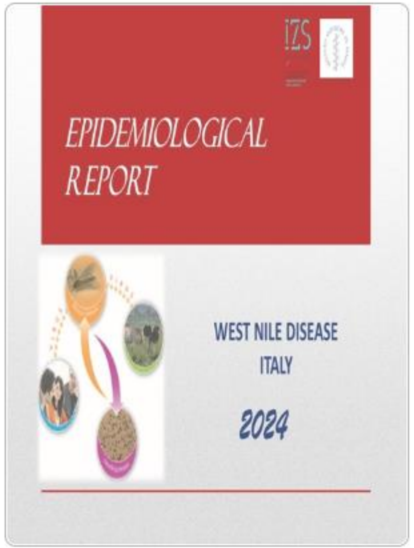
Reports


EPIDEMIOLOGICAL REPORT

WEST NILE DISEASE
ITALY

2024


EPIDEMIOLOGICAL REPORT

WEST NILE DISEASE
IN EUROPE AND
MEDITERRANEAN BASIN

2023

https://westnile.izs.it/j6_wnd/home_en


IZS
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Raccolta

Integrated surveillance of West Nile and Usutu virus

These annual reports summarize the results of West Nile virus and the Usutu virus surveillance activities in Italy

1 2023

2 2022

3 2021

4 2020

5 2019

6 2018

https://storymaps.arcgis.com/collections/b506660247024 41dac792d0cb3aee32c

TERAMO

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DELL'ABRUZZO
E DEL MOLISE
"G. CAPORALE"

References

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- ✓ Candeloro et al. Predicting WNV circulation in Italy using Earth Observation data and extreme gradient boosting model. Remote Sensing (2020) 12 (18), 3064.
- ✓ Ciota and Kramer.Vector-virus interactions and transmission dynamics of West Nile virus. Viruses. 2013 Dec 9;5(12):3021-47. doi: 10.3390/v5123021
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- ✓ Diagne et al. Novel Amplicon-Based Sequencing Approach to West Nile Virus. Viruses. 2023 May 27;15(6):1261. doi: 10.3390/v15061261.
- ✓ European Centre for Disease Prevention and Control. Vector control practices and strategies against West Nile virus. Stockholm: ECDC; 2020.
- ✓ Komar et al. Experimental infection of North American birds with the New York 1999 strain of West Nile virus. Emerg. Infect. Dis., 9 (2003), pp.311-322.
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- ✓ CDC. Species of dead birds in which West Nile virus has been detected, United States, 1999–2016.
- ✓ https://www.cdc.gov/west-nile-virus/media/files/Bird_species_West_Nile_virus_U.S..pdf

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WOAH Regional Workshop on Vector Borne diseases in Asia and the Pacific 19-20 September 2024

WOAH Reference Laboratory
for Leishmaniasis

Reference Centre
World Organisation
for Animal Health
Founded as OIE

Leishmaniasis

Fabrizio Vitale

Direttore Area Biologia Molecolare
Responsabile Centro di Referenza Nazionale Leishmaniosi (CRENAL)
WOAH Leishmania Reference Lab. Expert
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+393357895724

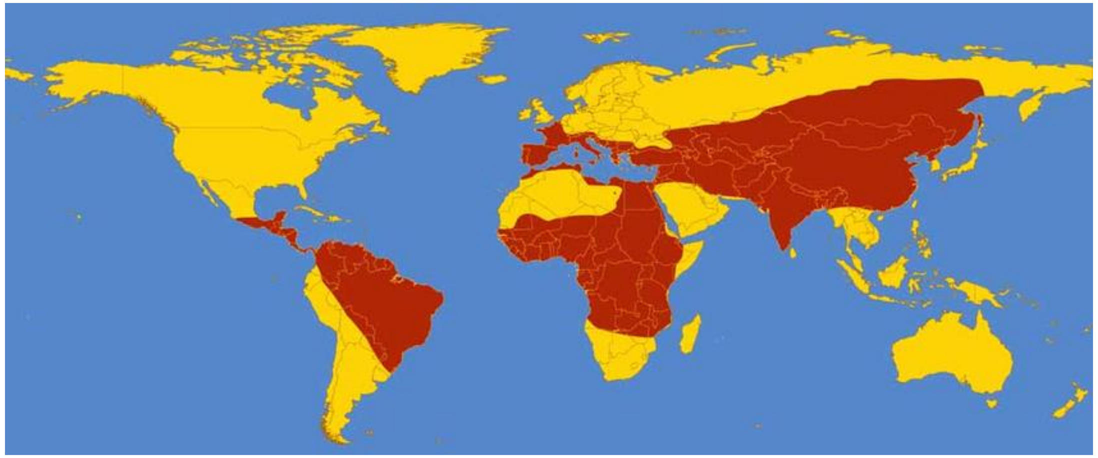
C.Re.Na.L. - Centro di Referenza Nazionale per le Leishmaniosi

What are we talking about?

The leishmaniases are a group of diseases caused by the protozoa parasite Leishmania.

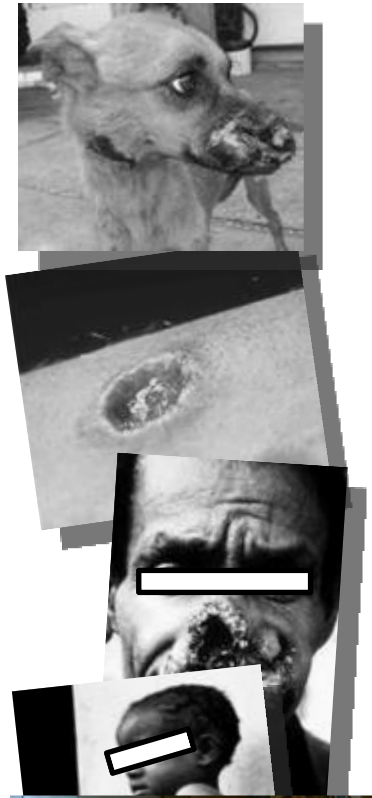
The diseases mainly affects poor people in Africa, Asia and Latin America, and is associated with malnutrition, population displacement, poor housing, weak immune system and lack of resources.

Out of 200 countries and territories reporting to WHO, 99 countries and territories are endemic for leishmaniasis in 2022. This includes 71 countries that are endemic for both VL and CL, 9 countries that are endemic for VL only and 19 countries that are endemic for CL only.



https://www.researchgate.net/publication/228638177_Trypanosomatids_Odd_Organisms_Devastating_Diseases#:~:text=Trypanosomatids%3A%20Odd%20Organisms,4(1)

But also dogs, cats, humans and many others...



[redacted]

[redacted]

Why dogs, cats and many others?

Of the various Leishmania species most are zoonotic, so a zoonotic disease (zoonosis) is one that "jumps" from an animal to a human. These animals are known as "reservoir hosts" and play an important role in the transmission of Leishmania infection and are able to keep the pathogen that causes the disease, alive, over time, in an ecosystem.

MEMENTO

An excellent reservois should:

- Offers optimal conditions for the reproduction and perpetuation of the microorganism.
- Being keep in touch with humans by sandflies;
- Be receptive to the pathogen;
- Be available for carriers;
- Offer the main food resource for sandflies and share the same habitat.

It is evident that the dog is an example of a good reservoir for Leishmania

But...

Is the dog more likely to be a "victim" rather than a reservois?

Thus... Why do the programs of mass killing of dogs (conducted in various parts of the w
on several occasions, in Brazil) fail to control human visceral leishmaniasi

Why dogs, cats and many others?

The fatal nature of canine disease suggests that this species is a recent host in evolutionary terms (Campino, 2002).

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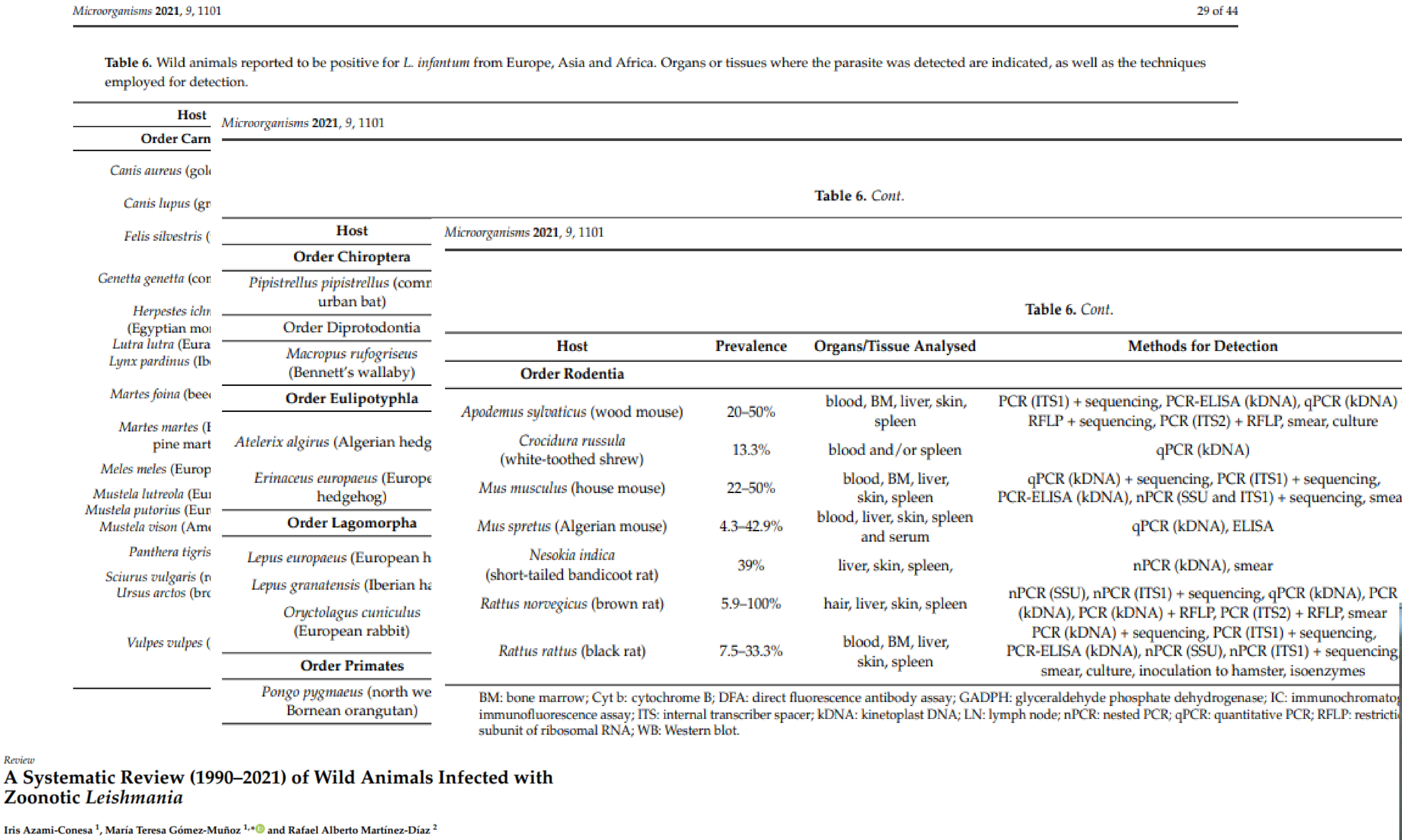


Microorganisms **2021**, 9, 1101 — 29 of 44

Table 6. Wild animals reported to be positive for *L. infantum* from Europe, Asia and Africa. Organs or tissues where the parasite was detected are indicated, as well as the techniques employed for detection.

Host
Order Carn
Canis aureus (gol
Canis lupus (gr
Felis silvestris (
Genetta genetta (cor
Herpestes ichr (Egyptian mo
Lutra lutra (Eura
Lynx pardinus (Ib
Martes foina (bee
Martes martes (I pine mart
Meles meles (Europ
Mustela lutreola (Eu
Mustela putorius (Eur
Mustela vison (Am
Panthera tigris
Sciurus vulgaris (r
Ursus arctos (br
Vulpes vulpes (

Microorganisms **2021**, 9, 1101 — 30 of 44

Table 6. *Cont.*

Host
Order Chiroptera
Pipistrellus pipistrellus (comn urban bat)
Order Diprotodontia
Macropus rufogriseus (Bennett's wallaby)
Order Eulipotyphla
Atelerix algirus (Algerian hedg
Erinaceus europaeus (Europe hedgehog)
Order Lagomorpha
Lepus europaeus (European h
Lepus granatensis (Iberian ha
Oryctolagus cuniculus (European rabbit)
Order Primates
Pongo pygmaeus (north we Bornean orangutan)

Microorganisms **2021**, 9, 1101 — 31 of 44

Table 6. *Cont.*

Host	Prevalence	Organs/Tissue Analysed	Methods for Detection	Country	References
Order Rodentia					
Apodemus sylvaticus (wood mouse)	20–50%	blood, BM, liver, skin, spleen	PCR (ITS1) + sequencing, PCR-ELISA (kDNA), qPCR (kDNA) + RFLP + sequencing, PCR (ITS2) + RFLP, smear, culture	Spain	[128,129,159]
Crocidura russula (white-toothed shrew)	13.3%	blood and/or spleen	qPCR (kDNA)	Spain	[160]
Mus musculus (house mouse)	22–50%	blood, BM, liver, skin, spleen	qPCR (kDNA) + sequencing, PCR (ITS1) + sequencing, PCR-ELISA (kDNA), nPCR (SSU and ITS1) + sequencing, smear	Morocco, Portugal and Spain	[162,163]
Mus spretus (Algerian mouse)	4.3–42.9%	blood, liver, skin, spleen and serum	qPCR (kDNA), ELISA	Spain	[137,160]
Nesokia indica (short-tailed bandicoot rat)	39%	liver, skin, spleen,	nPCR (kDNA), smear	Iran	[162]
Rattus norvegicus (brown rat)	5.9–100%	hair, liver, skin, spleen	nPCR (SSU), nPCR (ITS1) + sequencing, qPCR (kDNA), PCR (kDNA), PCR (kDNA) + RFLP, PCR (ITS2) + RFLP, smear	Greece, Morocco,	[129,131,162,
Rattus rattus (black rat)	7.5–33.3%	blood, BM, liver, skin, spleen	PCR (kDNA) + sequencing, PCR (ITS1) + sequencing, PCR-ELISA (kDNA), nPCR (SSU), nPCR (ITS1) + sequencing smear, culture, inoculation to hamster, isoenzymes		

BM: bone marrow; Cyt b: cytochrome B; DFA: direct fluorescence antibody assay; GADPH: glyceraldehyde phosphate dehydrogenase; IC: immunochromato immunofluorescence assay; ITS: internal transcriber spacer; kDNA: kinetoplast DNA; LN: lymph node; nPCR: nested PCR; qPCR: quantitative PCR; RFLP: restricti subunit of ribosomal RNA; WB: Western blot.

Review

A Systematic Review (1990–2021) of Wild Animals Infected with Zoonotic *Leishmania*

Iris Azami-Conesa [1], María Teresa Gómez-Muñoz [1,*] and Rafael Alberto Martínez-Díaz [2]

That's all? Vectors (sandflies)

Over 1000 species of sandflies are known but less than 50 are credited with the transmission of Leishmanias.

The vector typically:

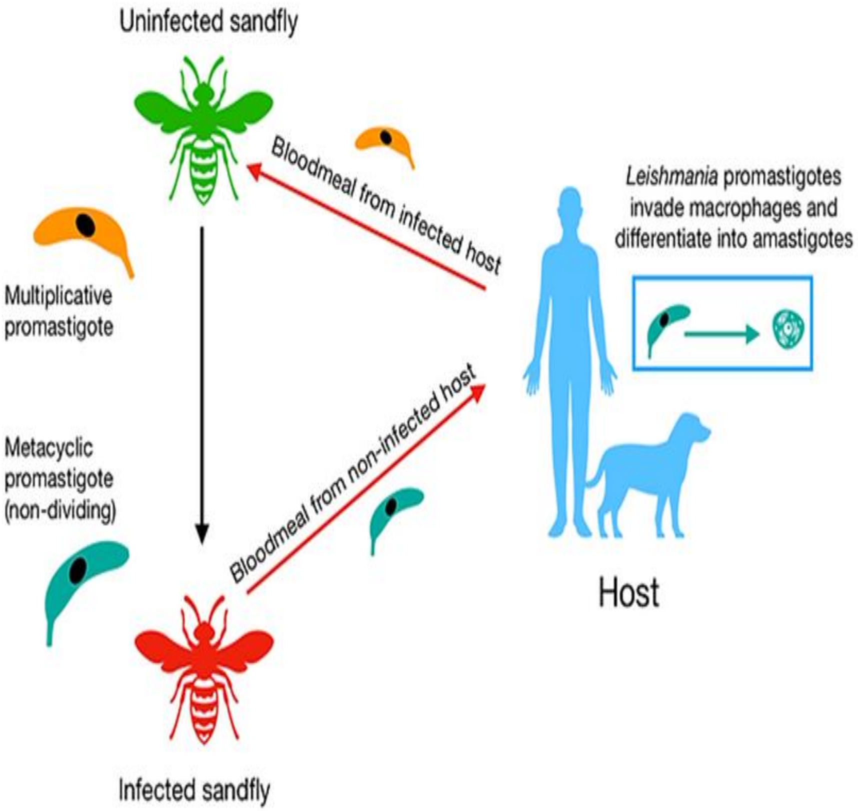
She is female

Performs the blood meal in the evening/night hours

It has a seasonality (warm-temperate temperatures)

It remains a few hundred meters from the place of birth

The larvae of sandflies are "terrestrial"



Wild environments

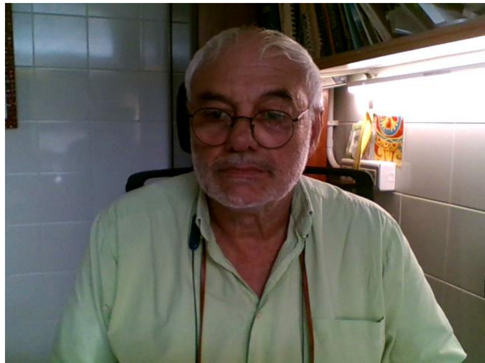
- Ant nests
- Land turtle nests
- Drainage ditches
- Bird nests
- Termite mounds
- Rodent burrows
- Caves
- Shaft recesses
- Forest Floor
- Under and between boulders
- Roots of large trees
- Soil at the base of trees
- Soil under overhanging boulders

Peri-domestic environments

- Animal dens
- Animal shelters
- Chicken coops
- Soil debris and cracks
- Rotting manure heaps
- Earth at the base of old walls
- Under the stones

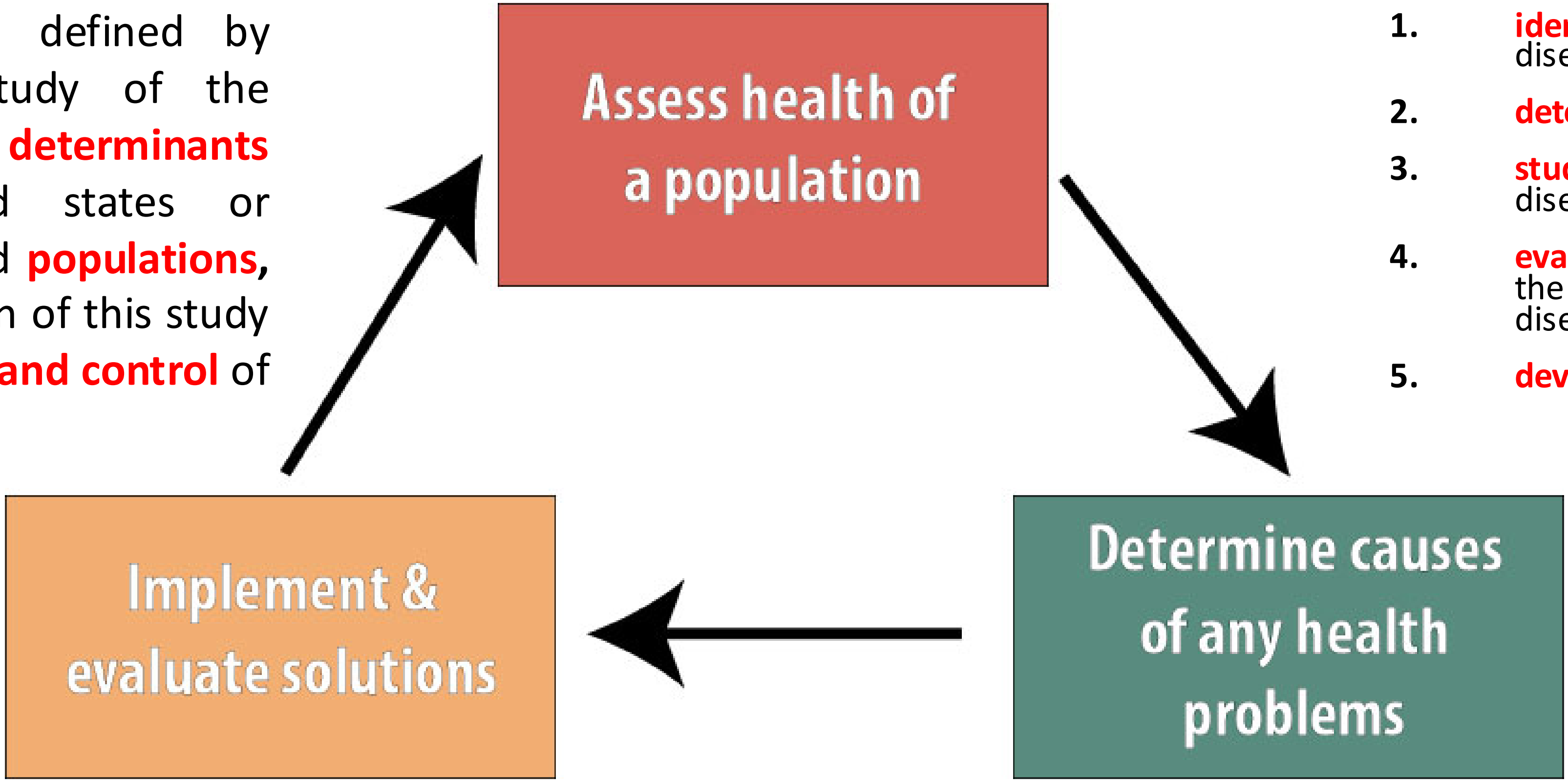
Domestic

- Basements and cellars
- Abandoned houses
- Cracks in floors and walls



Surveillance strategy: focus on Leishmaniasis

Epidemiology, as defined by Last, is "the study of the **distribution** and **determinants** of health-related states or events in specified **populations**, and the application of this study to the **prevention and control** of health problems".



Assess health of a population

Determine causes of any health problems

Implement & evaluate solutions

1. **identify** the etiology or cause of disease.
2. **determine** the extent of disease.
3. **study** the progression of the disease.
4. **evaluate** preventive and therapeutic measures for a disease or condition.
5. **develop** public health policy.

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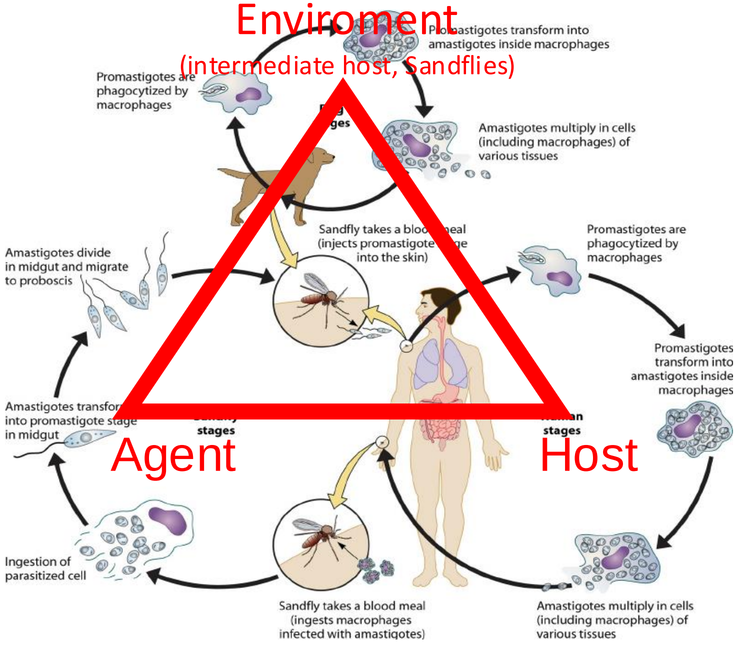
Assess health of
a population

1. **identify** the etiology or cause of disease.

The interaction between living beings, which share the same environment, should be considered as a single dynamic system, in which the health of each component is inevitably interconnected and dependent on the others.



Killick-Kendrick R. Phlebotomine vectors of the leishmaniases: a review. Med Vet Entomol. 1990;4(1):1-24

- *L. aethiopica*
- *L. amazonensis*
- *L. arabica*
- *L. archibaldi*
- *L. aristedesi*
- *L. (Viannia) braziliensis*
- *L. chagasi*
- *L. (Viannia) colombiensis*
- *L. deanei*
- *L. donovani*
- *L. enriettii*
- *L. equatorensis*
- *L. forattinii*
- *L. garnhami*
- *L. gerbili*
- *L. (Viannia) guyanensis*
- *L. herreri*
- *L. hertigi*
- *L. infantum*
- *L. killicki*
- *L. (Viannia) lainsoni*
- *L. major*
- *L. mexicana*
- *L. (Viannia) naiffi*
- *L. (Viannia) panamensis*
- *L. (Viannia) peruviana*
- *L. (Viannia) pifanoi*
- *L. (Viannia) shawi*
- *L. tarentolae*
- *L. tropica*
- *L. turanica*
- *L.venezuelensis*

Distribution range of sandflies according to biogeographical zones

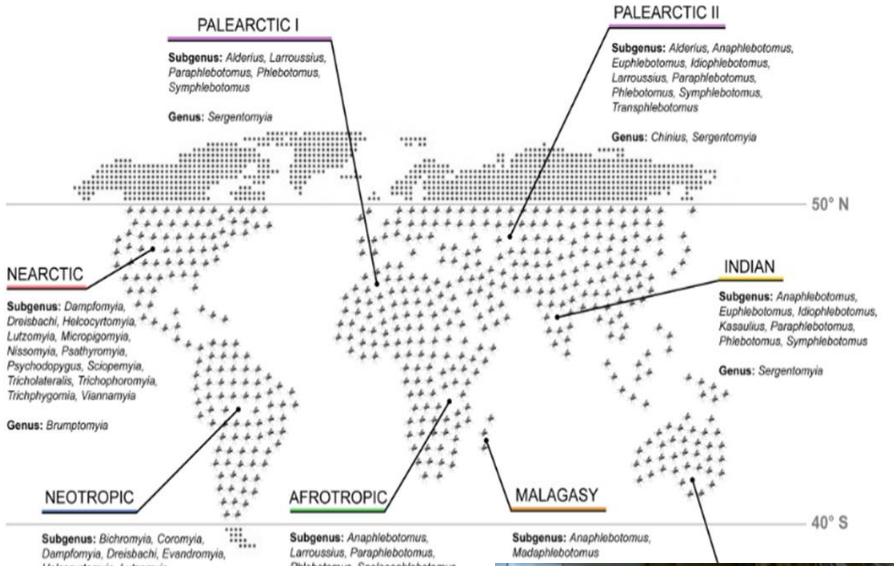


Fig. 1 Sand fly distribution map by genera/subspecies. Sand flies have a global dist
gray horizontal lines), excluding New Zealand and the Pacific islands. In the map, t
classification based on a conservative approach) are listed based on their presence i
Neotropic (dark blue), Afrotropic (green), Malagasy (orange), Australia (light blue)

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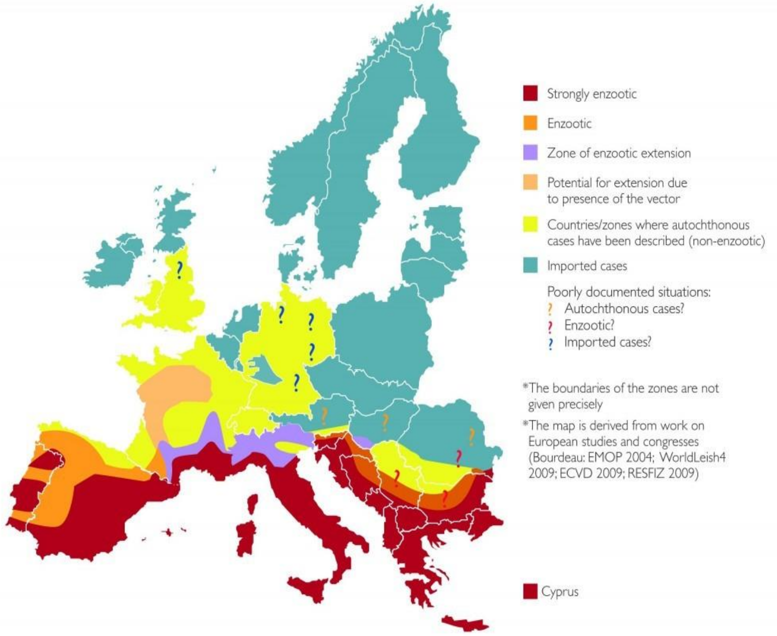
Assess health of a population

1. **determine** the extent of disease.

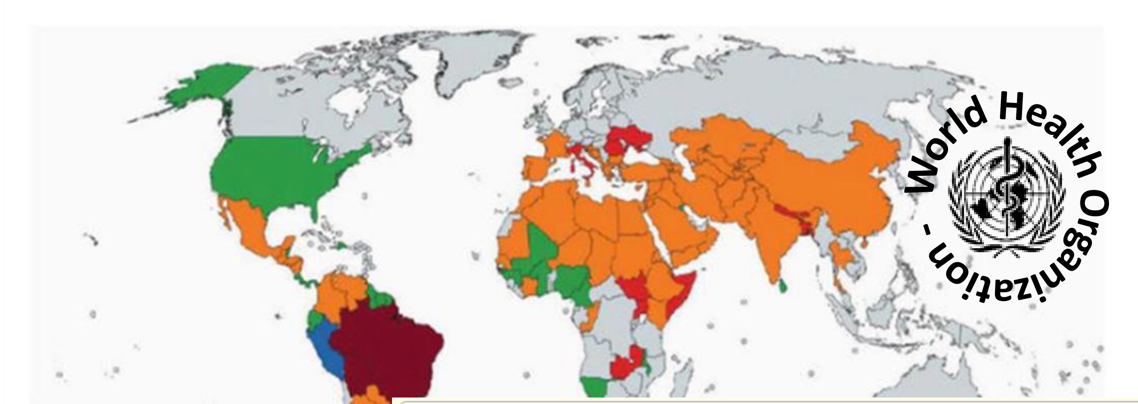
Canine leishmaniosis in Europe (Pr. P. BOURDEAU Original)

(Courtesy Prof P. Bourdeau) shows the current broad epidemiological situation in Europe.



The surveillance activity is focused in Europe on the main synanthropic reservoir of the disease: the dog and develops at a regional level on the basis of some considerations:

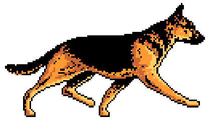
- Canine reservoir on the rise in non-endemic areas
- Rapidly spreading vector phlebotomine habitat
- Interregional Dog Handling
- Improved information flow Human and animal health



OPEN ACCESS PEER-REVIEWED CHAPTER
Epidemiology of Leishmaniasis
Stephen Kyari

Clinical forms	Leishmania parasite	Geographical distribution
CL	*L. major*, *L. tropica*, *L. infantum*, and *Labrus donovani*; *L. braziliensis*: *Lutzomyia neivai*, *Lu. Whitmani*, *L. Cortelezzii complex* (*L. Cortelezzii–L. Sallesi*), *L. Migonei*, and *L. Pessoai*, *L. (L.) peruviana*, *L. lainsoni*, *L. amazonensis*, *L. infantum chagasi*, *L. Mexicana*, *Leptodactylus colombiensis* and *L. equatoriensis*	Morocco, Algeria, Tunisia, Libya, Egypt; Chad; Sudan, South Sudan, Ethiopia, Kenya, Uganda and Somalia; Niger, Nigeria, Senegal and Mali; Cameroon, Burkina Faso, Mauritania, Gambia and Guinea, Ghana; Syria, Lebanon, Israel, Philistines, Iran, Saudi Arabia, Iraq, Pakistan, Afghanistan, Turkmenistan; Greece; United State of America; Bolivia, Brazil, Colombia, Peru; Sri Lanka, China, Nepal Bangladish; India, and
MCL	*L. viannia braziliensis*, *L. viannia amazonensis*, *L. viannia panamensis* and *L viannia guyanensis*	
DCL	*L. Mexicana*, *L. acthiopica*, *L. amazonensis*, *L. pifanoi*, *L. guyanensis*, and *L. panamensis*	
VL	*L. donovani*, *L. infantum*, *L. tropica*, *L. chagasi*	

Table 2.
The table below shows the clinical form of leishm



- Canine leishmaniasis is present in >70 countries
- Infected dogs in Italy, Spain, France and Portugal are around 2.5 million
- Many more in South America

Determine causes of any health problems

1. **study** the progression of the disease.

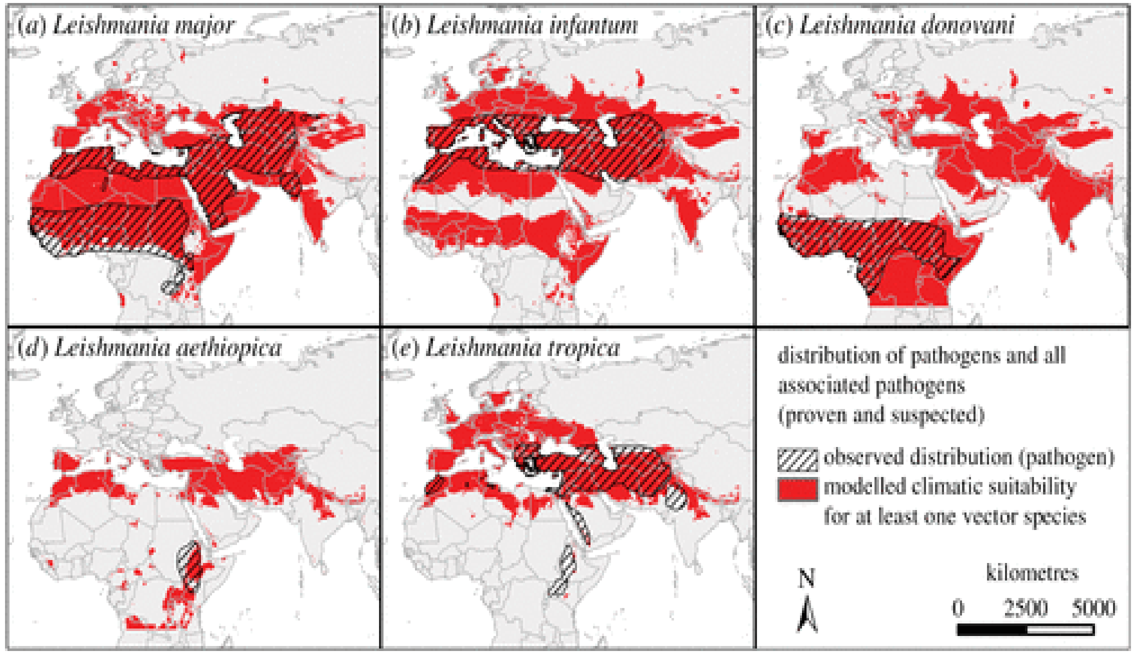
Where are we?

Its strategic location at the centre of the Mediterranean has made the island a crossroads of history, a pawn of conquest and empire, and a melting pot for ethnic groups, vegetal inflorescence and...arthropods!

Why do we care so much about climate changes?

The arthropod vectors of diseases are ETEROTHERMIC organisms (without temperature regulation system) and therefore they depend on the environmental temperature

Climatic suitability of vector species and distribution of associated pathogens. Hatched areas indicate the observed distribution of the five Leishmania species, red indicates areas with suitable climatic conditions based on the binary modelling results using equal training sensitivity and specificity threshold projected for at least one of the associated vector species (with confirmed or strongly suspected vector-competence for the respective Leishmania species).

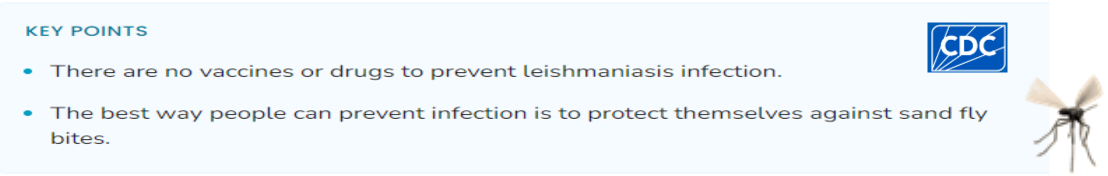


Leishmaniasis in Eurasia and Africa: geographical distribution o
Issue: 5, DOI: (10.1098/rsos.190334)

Determine causes of any health problems

1. **evaluate** preventive and therapeutic measures for a disease

Preventing Leishmaniasis



KEY POINTS

- There are no vaccines or drugs to prevent leishmaniasis infection.
- The best way people can prevent infection is to protect themselves against sand fly bites.

Joint Effort – Applied Surveillance Purpose:

- ✓ Track sand fly populations
- ✓ Evaluate Control effectiveness
- ✓ ID sand fly & disease "hot spots"
- ✓ Determine Leishmania infection rates
- ✓ Which trap designs are most effective

Prevention

Leishmaniasis is mainly prevented by suppressing and killing sandfly vectors which transmit the disease (vector control measures). Vector control measures are critical to reducing disease incidence in the absence of an effective vaccine.

The primary strategies of vector control are indoor residual spraying (IRS) and long-lasting insecticide-treated nets (LLINs) with pyrethroid insecticides. IRS involves spraying the walls and other surfaces of houses and buildings, LLINs offer protection to individuals.

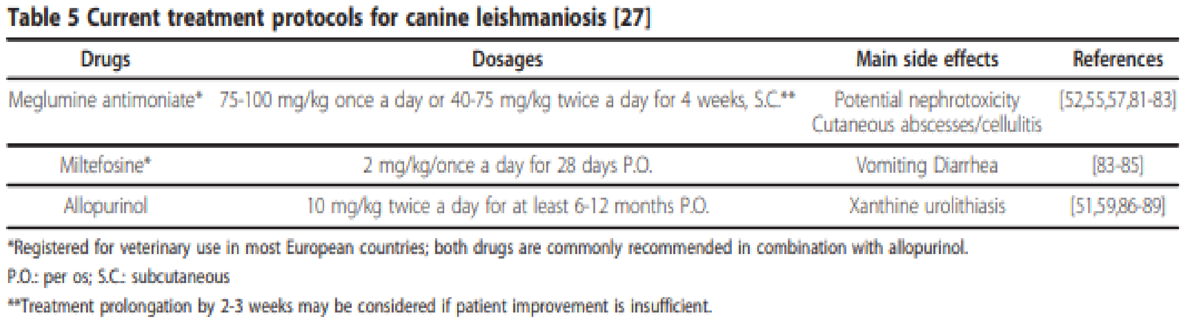


Table 5 Current treatment protocols for canine leishmaniosis [27]

Drugs	Dosages	Main side effects	References
Meglumine antimoniate*	75-100 mg/kg once a day or 40-75 mg/kg twice a day for 4 weeks, S.C.**	Potential nephrotoxicity Cutaneous abscesses/cellulitis	[52,55,57,81-83]
Miltefosine*	2 mg/kg/once a day for 28 days P.O.	Vomiting Diarrhea	[83-85]
Allopurinol	10 mg/kg twice a day for at least 6-12 months P.O.	Xanthine urolithiasis	[51,59,86-89]

*Registered for veterinary use in most European countries; both drugs are commonly recommended in combination with allopurinol.

P.O.: per os; S.C.: subcutaneous

**Treatment prolongation by 2-3 weeks may be considered if patient improvement is insufficient.

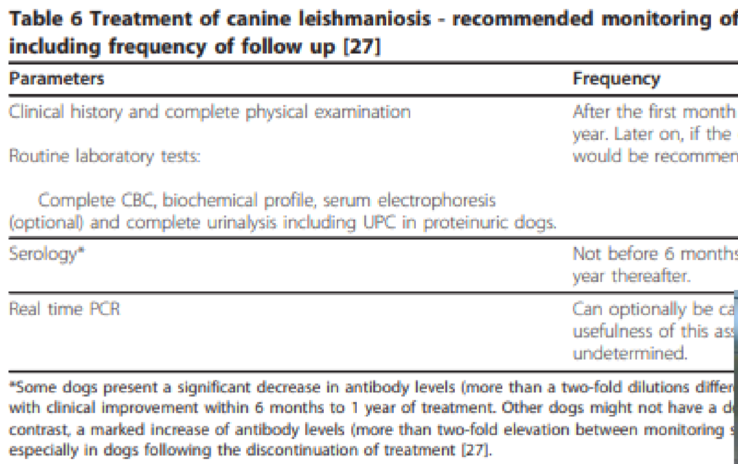
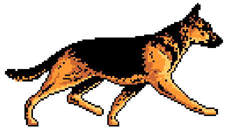


Table 6 Treatment of canine leishmaniosis - recommended monitoring of clinicopathological parameters and serology including frequency of follow up [27]

Parameters	Frequency
Clinical history and complete physical examination Routine laboratory tests: Complete CBC, biochemical profile, serum electrophoresis (optional) and complete urinalysis including UPC in proteinuric dogs.	After the first month of treatment and then every 3-4 months during the first year. Later on, if the dog is fully recovered clinically with treatment, a recheck would be recommended every 6 months or once a year.
Serology*	Not before 6 months after initial treatment and every 6 months or once a year thereafter.
Real time PCR	Can optionally be ca usefulness of this as undetermined.

*Some dogs present a significant decrease in antibody levels (more than a two-fold dilutions differ
with clinical improvement within 6 months to 1 year of treatment. Other dogs might not have a d
contrast, a marked increase of antibody levels (more than two-fold elevation between monitoring s
especially in dogs following the discontinuation of treatment [27].



Solano-G
http://w

LeishVet
of canin

World Organisation for Animal Health
Founded in 1924

WOAH Regional Workshop on Vector Borne diseases in Asia and the Pacific

Implement & evaluate solutions

1. **develop** public health policy.

Actually

Sandfly biting activity is strongly seasonal, restricted to summer months in most areas

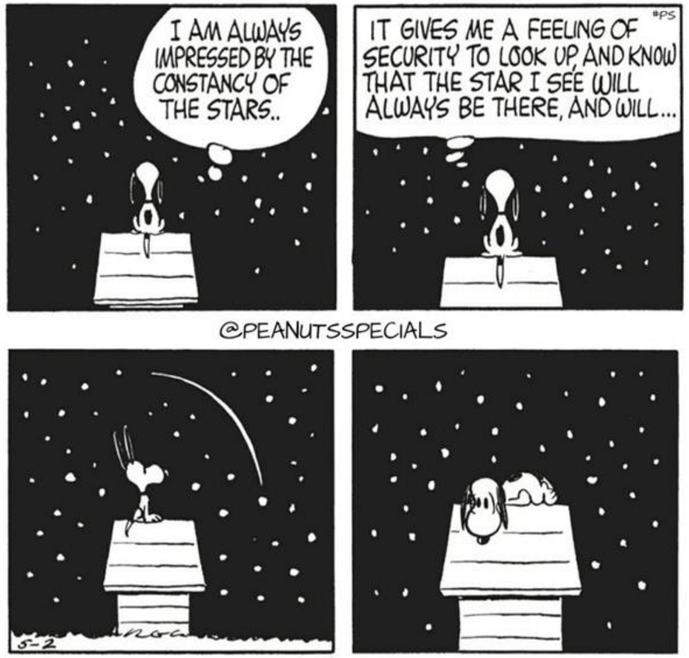
(e.g. Southern Europe, below 800m above sea level)

Future & climate change

Prolonged activity periods and shorter diapause periods (overwintering)

Extend northwards and into higher altitudes

At present, no good prediction models available



What needs

- *Public health surveillance at the International level* (mandatory notification system in all countries?)
- Educate people on interventions against sandflies
  - Insect repellents Insecticides
  - Use of insecticide impregnated nets and bed nets
  - Dog: topical applications and impregnated collars
- Further research on
  - Alternative modes of transmission
  - Effective vaccine for human leishmaniasis
    - immunisation strategy for human populations
  - Effective vaccine for canine leishmaniasis
    - to control the infections in reservoir population (dogs, cats, hares,
  - Better predictive modelli

Leishmaniases remain widespread and under-reported. Measures for leishmaniases prevention and control, access to valid diagnostic methods and guidelines, and access to effective treatments vary considerably between countries. This variation and the lack of resources in some countries or regions, could have important disease implications including increased incidence; unnoticed spread of Leishmania spp. into new areas; increased treatment failure and development of resistance to treatments.

TECHNICAL REPORT Surveillance, prevention and control of leishmaniases, EFSA, ECDC

Leishmaniasis: An example of how essential the concept of One Health is

- **Medical** doctors to recognize and treat human clinical forms (CL / VL)
- **Veterinarians** to recognize and treat animal clinical forms
- **Biologists** to optimize research laboratories
- **Entomologists** to monitor vectors
- **Wild experts** to identify non-anthropized reservoirs
- **Ecologists** to make health authorities responsible for the principles of public hygiene
- **Epidemiologists** to outline surveillance strategies
- **Media** to inform about risks and prevention

Thank you …

Summary from pre-meeting questionnaire

Arjun Pandit, Hokkaido University

Kevin Chyi, D.V.M, APHIA Chinese Taipei

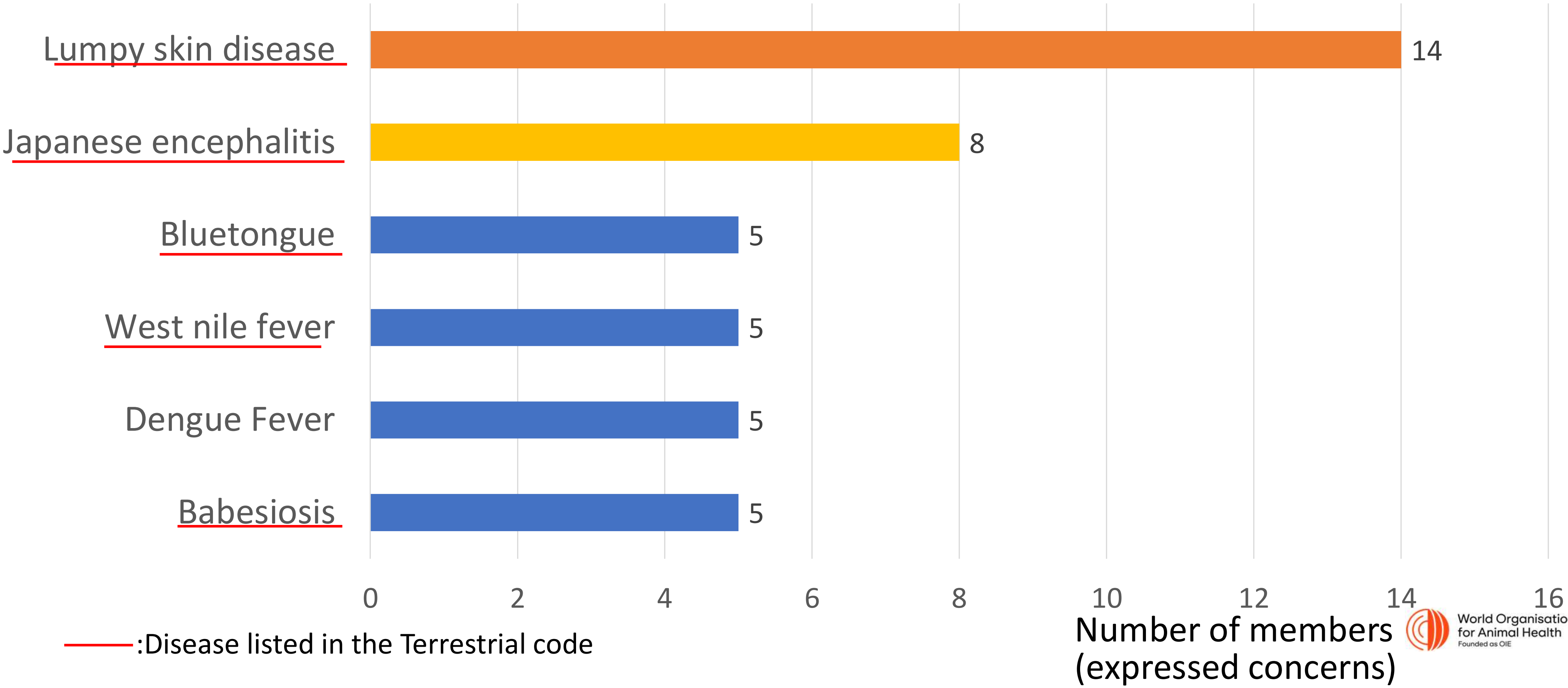
WOAH Interns

19 September 2024
Tokyo, Japan

World Organisation
for Animal Health
Founded as OIE

VBD(s) concerned by Regional Members-1/2

Diseases of concerns



——:Disease listed in the Terrestrial code

World Organisation for Animal Health
Founded as OIE

VBD(s) concerned by Regional Members-2/2

LSD, JE, BTV, WNF, Dengue fever, Babesiosis are of the most concerns,

1. Widespread in the region
2. Doing their best to prevent, eradicate or contain in the territory
3. Zoonotic diseases

- Anaplasmosis
- Theileriosis
- African horse sickness
- African swine fever
- Trypanosomiasis
- Leishmaniosis
- Rift valley fever

- Epizootic hemorrhagic disease
- Q fever
- Akabane disease
- Crimean-Congo haemorrhagic fever
- Malaria*
- *Mycoplasma haemocanis*
- Dirofilaria
- Schistosomiasis

- Severe Fever with Thrombocytopenia Syndrome(SFTS)
- Hepatozoon
- Chuzan virus
- Chikungunya
- Bovine ephemeral fever
- *Ehrlichia canis*
- *Rickettsia felis*

——:Diseases listed in the Terrestrial code

Responses to VBD(s)-1/2

- Surveillance
  - Vector surveillance (mosquito, biting midge, stable fly, fly, tick...)
  - Active surveillance (LSD, JE, BTV, WNF, AHS, Akabane disease, RVF …)
- Preventive measures
  - Vector control (Repellant, insecticide, vector trap…)
  - Biosecurity on farm
  - Vaccination (LSD, JE, Q-fever, Akabane disease…)
  - Contingency plan
- Response during a disease outbreak
  - Movement control (LSD, JE, AHS, ASF…)
  - Treatment (Q-fever, Surra, tick…)
  - Stamping out (LSD, AHS, ASF…)

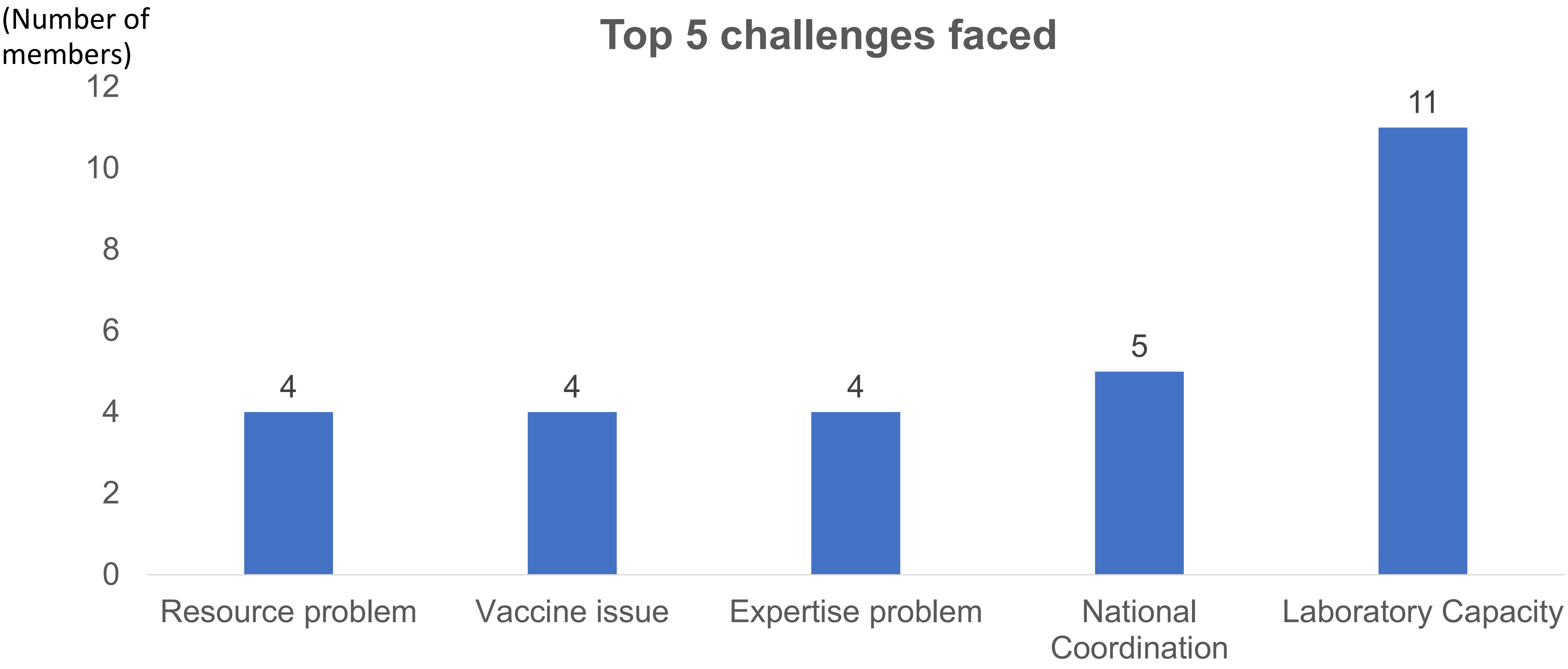
Responses to VBD(s)-2/2

- Public awareness
  - Training and education
  - Communication (Using One Health approach. Conducting awareness campaigns to the general public)
- Diagnostic ability
  - Development of the detection method (diagnostic kit for detection Surra)
  - Diagnostic training

Impact of actions

- Successfully prevent or eradicate VBD (14)
  - Reduce the risk of exposure (11)
  - To regain VBD-free status (3)
- Diagnostic and Surveillance efficiency increased (8)
  - Enhanced diagnostic and surveillance ability (6)
  - Importance of early warning system (2)
- Vaccination is effective in controlling VBD (5)
  - Vaccination is an effective measure to combating VBD (4)
  - Make stockpiles of vaccines possible (1)
- Other impact
  - Strengthen awareness and education, data-sharing
  - Improved policy and strategies, established list of priority, identify the risk, enhanced biosecurity

Summary of challenges faced by members

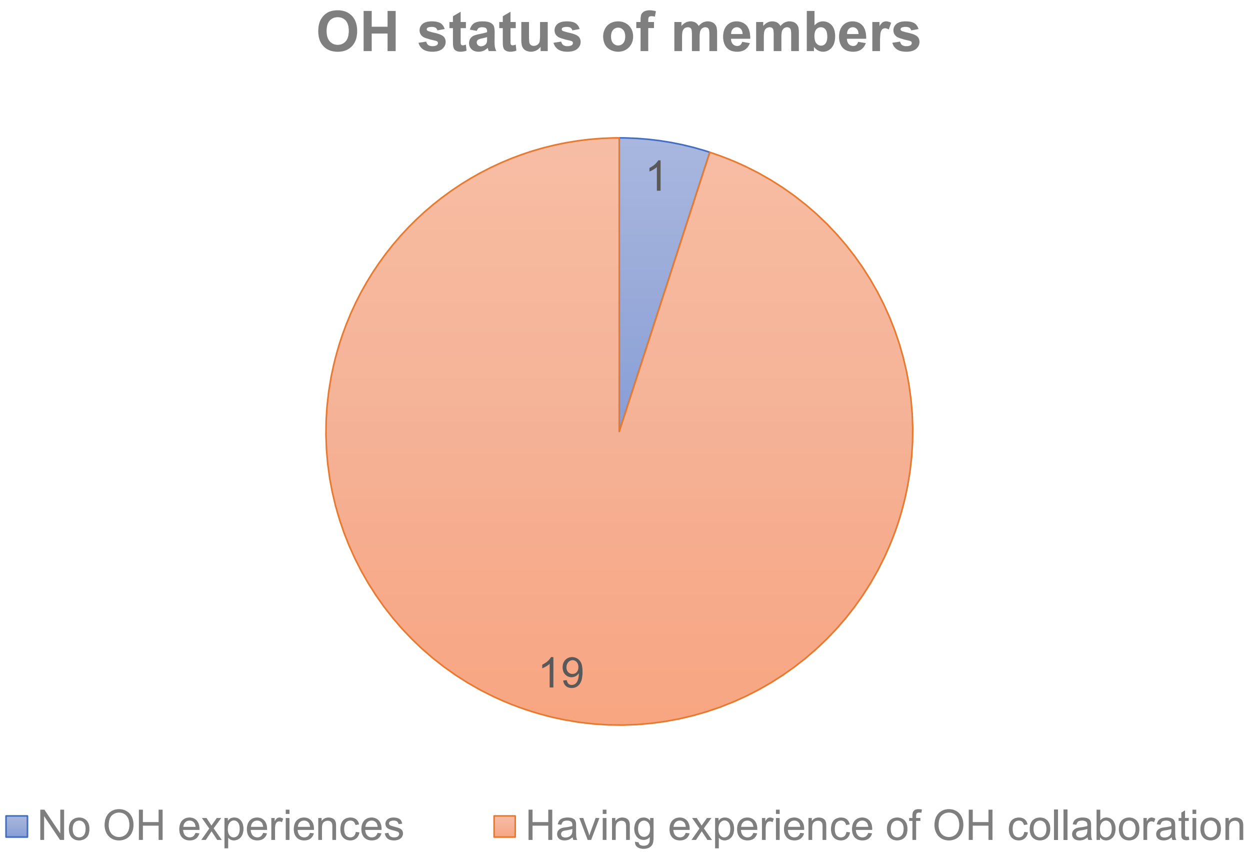


Other problems: Awareness problems, under-reporting, and surveillance problems

Possible solutions to overcome the challenges

- **Capacity development**
  - Diagnostic to field staff
  - Continued education
  - Vector and vaccine development training
- **Coordination with partners**
  - Strengthen cross-border collaboration between partners
  - Cost-sharing (PPP with development partners),
  - Coordination from sub-national to International level
- **Surveillance facilitation**
  - **Data sharing and some innovations (**PCR on feral pig tonsils, chew ropes for monitoring tools for pigs: Australia),
  - Country-level sustainable **active surveillance**

Collaboration with other sectors under One Health approach



Collaboration with other sectors under One Health approach

- **Multisectoral collaboration**
  - Shared surveillance information/Protocol/Publication/collaborative risk assessments (New Zealand)
  - Multisectoral collaboration from the sub-national to the international level
  - Co-writing of contingency plans (New Caledonia)

- **Joint surveillance**
  - Joint surveillance of feral animals and other animals (Australia)
  - Arbovirus surveillance (Japan)
  - JE and wildlife disease surveillance (Malaysia)
  - integrated surveillance (New Caledonia)

Possible actions to strengthen One Health approach

- **Multisectoral collaboration**
  - Data and Information Sharing
  - Joint surveillance framework
  - Multisectoral expert networking
  - Joint research projects
  - Collaborative preparedness resilience
  - Zoonoses simulation exercises
  - Joint capacity building

- **Regular stakeholder meeting**
  - Frequent meetings between stakeholders
  - Creating platforms for knowledge-sharing
  - Information sharing frameworks
  - Regular resource funding.

Expectations for the VBDs workshop

- **Experiences of members**
  - VBDs epidemiology in the climate change context
  - Success stories and experience of members (Epizootic hemorrhagic diseases in Europe, Akabane disease and Blue Tongue in China and India)
  - SFTS management
  - Early warning systems
  - Contingency plans of different members

- **Information from experts on specific diseases**
  - Management strategy
  - Latest global epidemiology of LSD, WNF, and AHS
  - Cost-effective early warning system of VBDs.

Thank you

WOAH Regional Workshop on Vector borne diseases in Asia and the Pacific
Tokyo, Japan, 19 – 20 September 2024 09:10 – 09:30

Zoonotic and human related diseases and their control

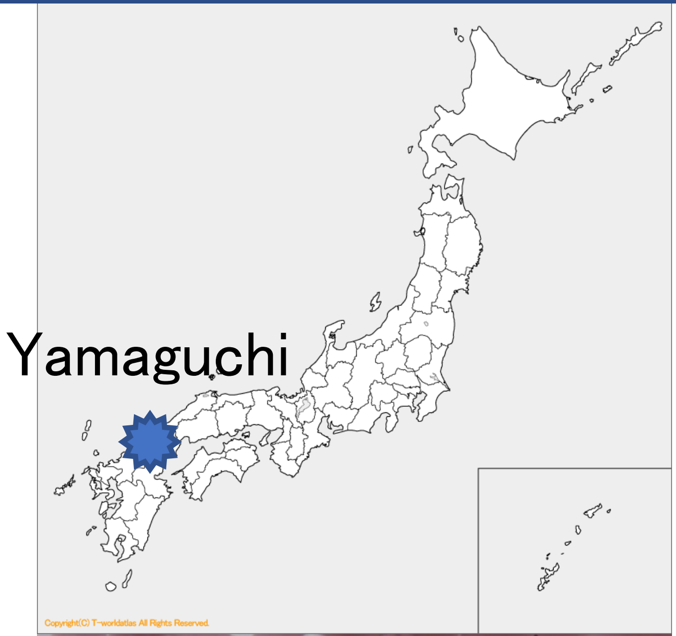
Ken Maeda, Ph.D., D.V.M.
Director
Department of Veterinary Science
National Institute of Infectious Diseases (NIID)

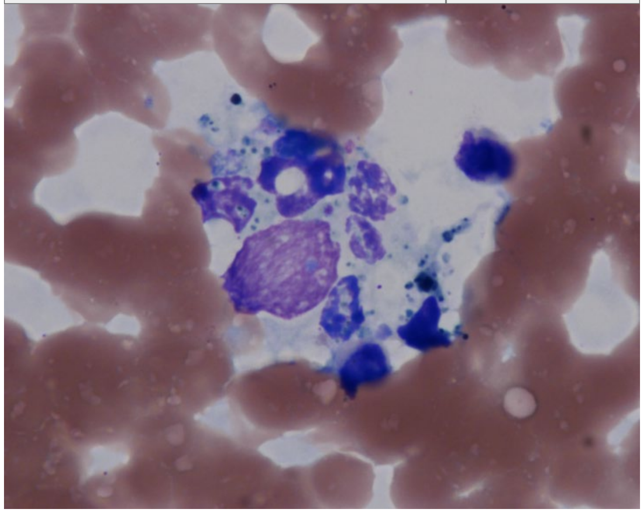
Major emerging viral zoonosis in Japan

Date	Emerging viral diseases	Vector	Animals
Dec, 2012	First report of severe fever with thrombocytopenia syndrome (SFTS) in Japan	Tick	Many mammalians
Aug, 2014	Endemic of dengue fever in Tokyo after 69 years	Mosquito	Non-human primates (sylvatic type)
Jul, 2016	Tick-borne encephalitis after 23 years	Tick	Rodents, Wild animals
May, 2019	First discovery of Yezo virus in the world	Tick	Wild animals?
Nov, 2019	First report of B virus infection in Japan (2 cases)		Macaque
Jan, 2020	Pandemic of COVID-19 in Japan		Bat?
May, 2020	Rabies in Japan after 14 years		Dog, Bats
Jul, 2022	Mpox in Japan		Rodents etc.
Summer, 2022	Oz virus infection in Chiba	Tick	Wild animals

The first case of SFTS in Japan

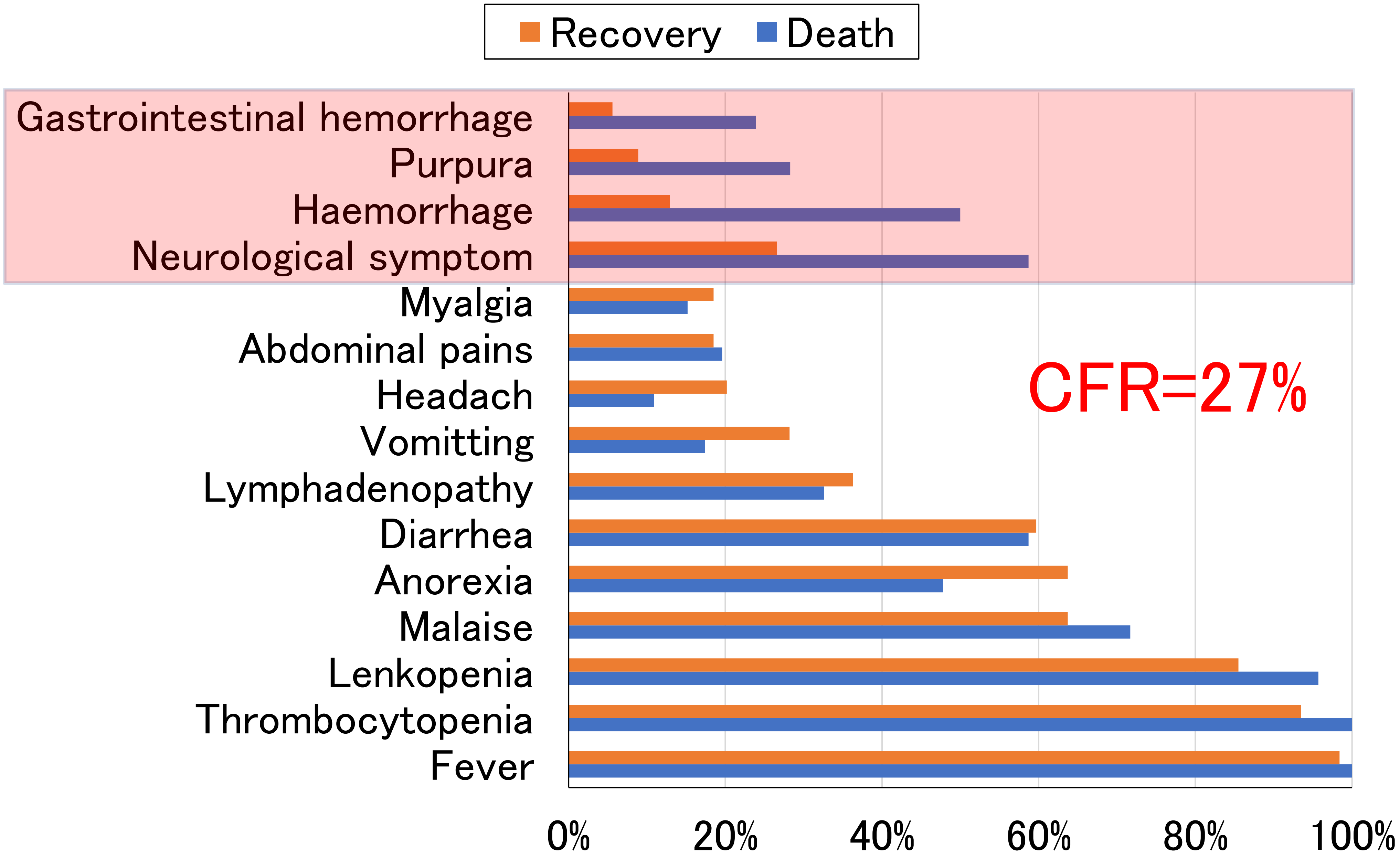
- Patient：Female aged 50’s without oversea travel
- Onset time and location： Autumn 2012, Yamaguchi prefecture
- Symptoms: Fever, general fatigue, vomiting, melena (bloody diarrhea)
- Laboratory findings: Leukopenia (400 /mm^3) and Thrombocytopenia (8.9X10^4 /mm^3) in TBC;
  Elevated AST, ALT, LDH, CK;
  Extremely elevated ferritin in serum chemistry;
  Hematuria and proteinuria in urinalysis;
  Hemophagocytosis with hypocellularity findings in bone marrow aspiration



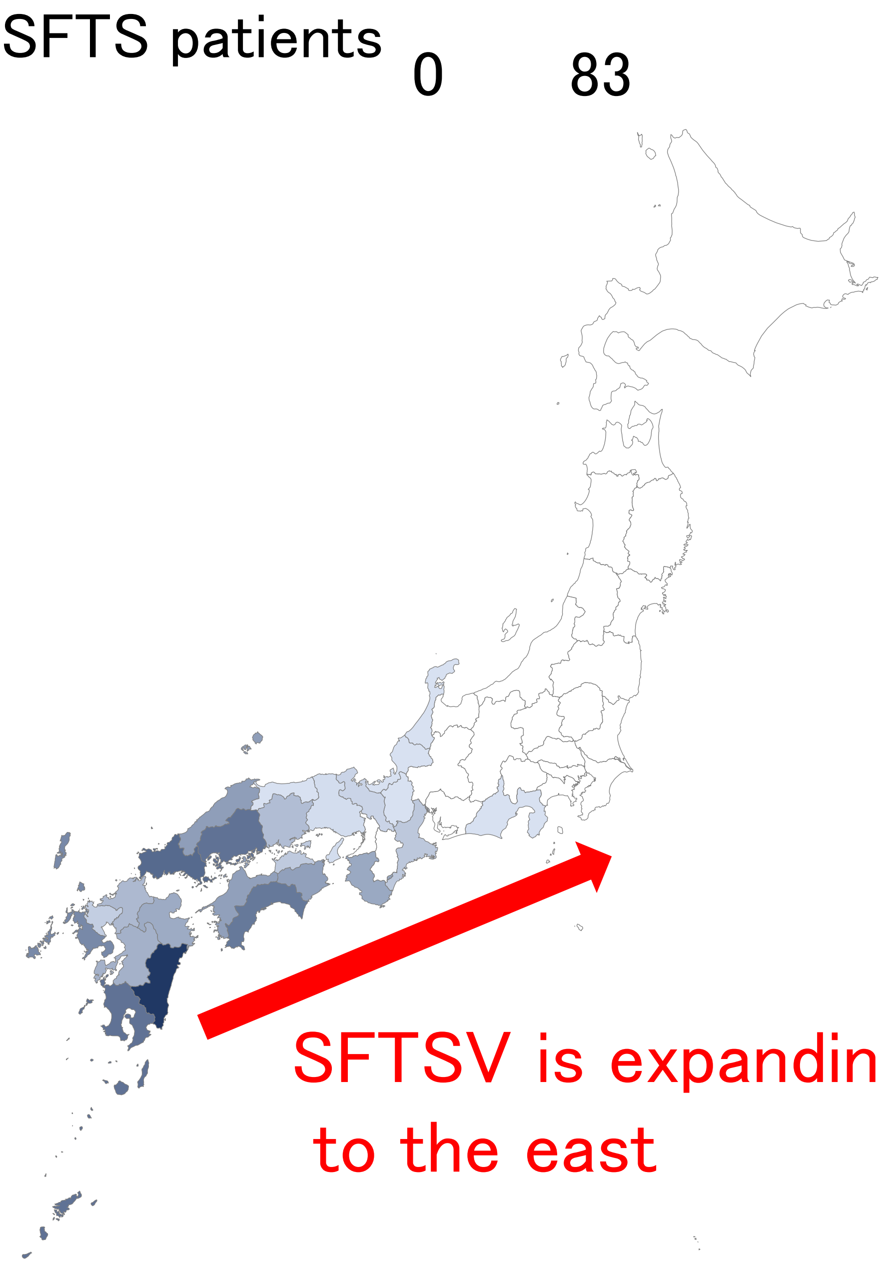


Takahashi T, Maeda K, Suzuki T, Ishido A, Shigeoka T, Tominaga T, Kamei T, Honda M, Ninomiya D, Sakai T, Senba T, Kaneyuki S, Sakaguchi S, Satoh A, Hosokawa T, Kawabe Y, Kurihara S, Izumikawa K, Kohno S, Azuma T, Suemori K, Yasukawa M, Mizutani T, Omatsu T, Katayama Y, Miyahara M, Ijuin M, Doi K, Okuda M, Umeki K, Saito T, Fukushima K, Nakajima K, Yoshikawa T, Tani H, Fukushi S, Fukuma A, Ogata M, Shimojima M, Nakajima N, Nagata N, Katano H, Fukumoto H, Sato Y, Hasegawa H, Yamagishi T, Oishi K, Kurane I, Morikawa S, Saijo M. The first identification and retrospective study of Severe Fever with Thrombocytopenia Syndrome in Japan. J Infect Dis. 2014 Mar;209(6):816-27. doi: 10.1093/infdis/jit603. Epub 2013 Nov 14. PMID: 24231186; PMCID: PMC7107388.

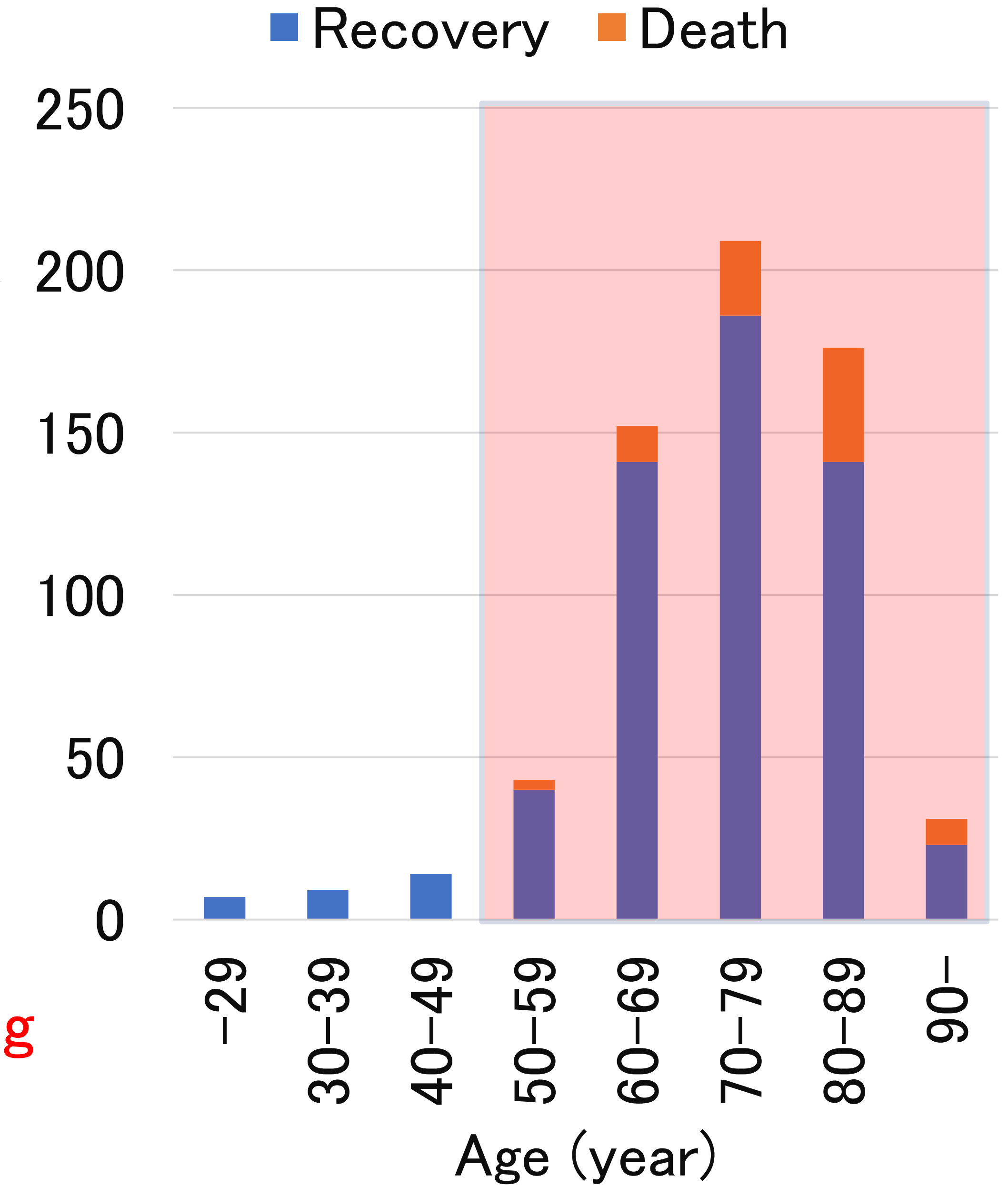
Clinical symptoms in human patients



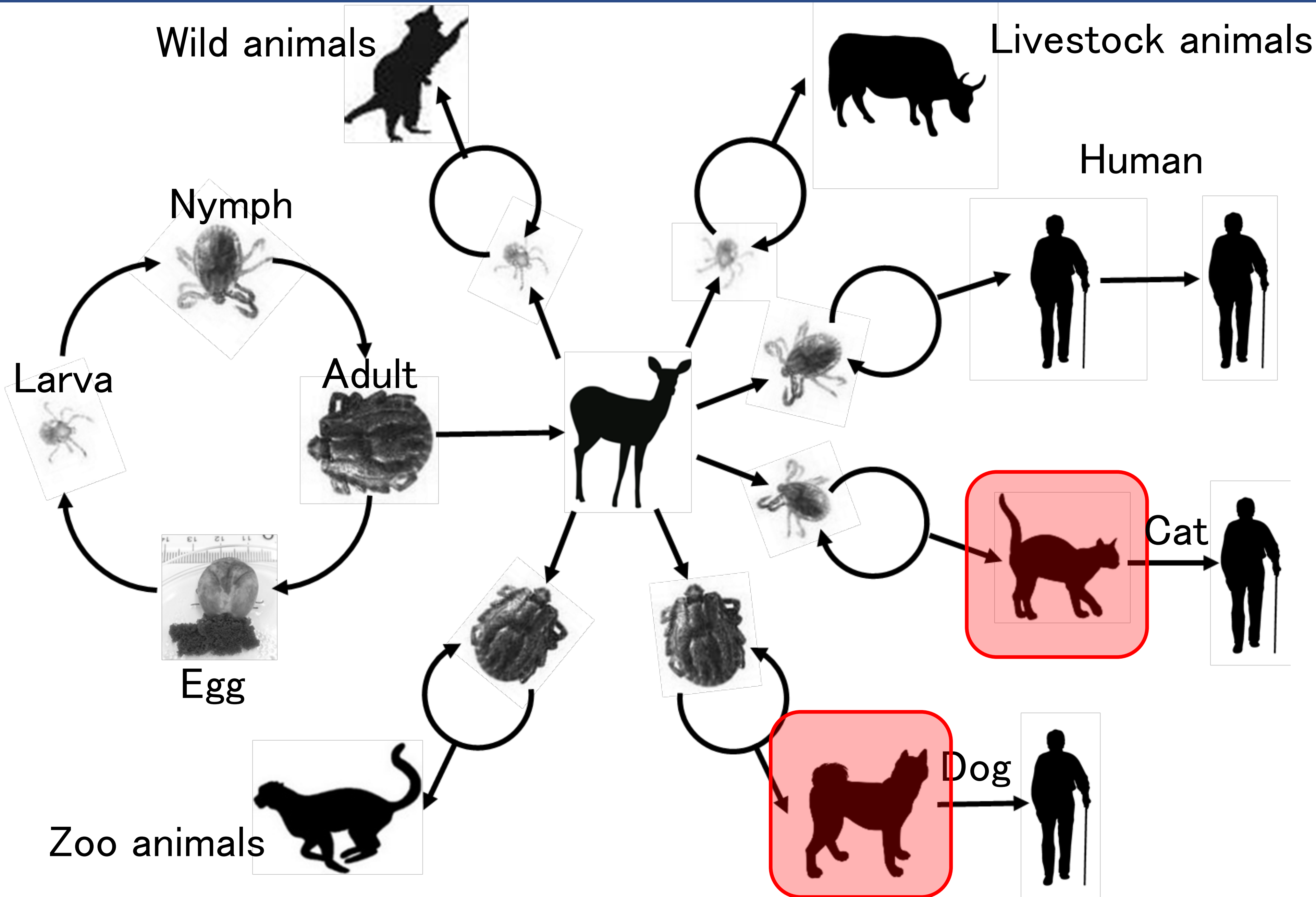
Distribution and age of SFTS patients in Japan



SFTSV is expanding to the east



Transmission cycle of SFTSV



Clinical symptoms in SFTS cats

	No. of Positive /No. of Total	Ratio
Low activity・Anorexia	97/97	100%
Vomiting	44/95	46%
Diarrhea	5/95	5%
Jaundice	43/43	100%
Death	41/69	59%

First SFTS dog and symptoms in SFTS dogs

- June, 2017
- Mix
- Spayed female
- 4 years old
- Every year 6 combination vaccine and rabies vaccine
- Heartworm and tick preventives

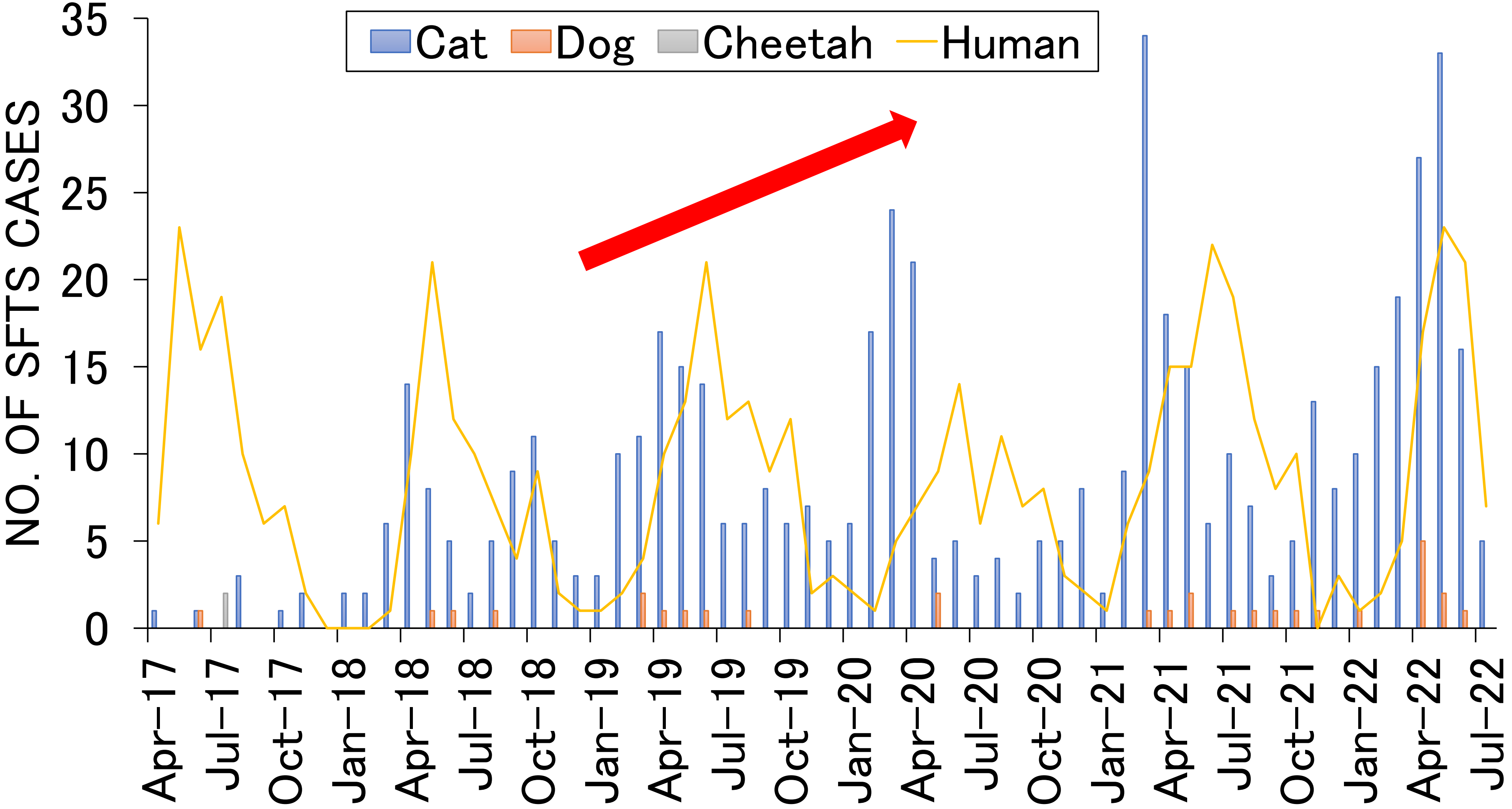
Clinical findings in seven SFTS dogs

Clinical findings	Number of dogs with abnormal values (%)
Anorexia and less activity	7 (100%)
Vomit	2 (29%)
Loose stool	2 (29%)
Dead	3 (43%)
Fever (>39℃)	7 (100%)
Leukocytopenia (<6,000/μl)	7 (100%)
Thrombocytopenia (<200,000/μl)	7 (100%)
Tick parasite	5 (71%)

Owner of this SFTS dog was also infected with SFTSV without tick-bite

Oshima H et al., Jpn J Infect Dis. 2022 Jul 22;75(4):423-426.
Ishijima K et al., Viruses. 2022 Sep 4;14(9):1963

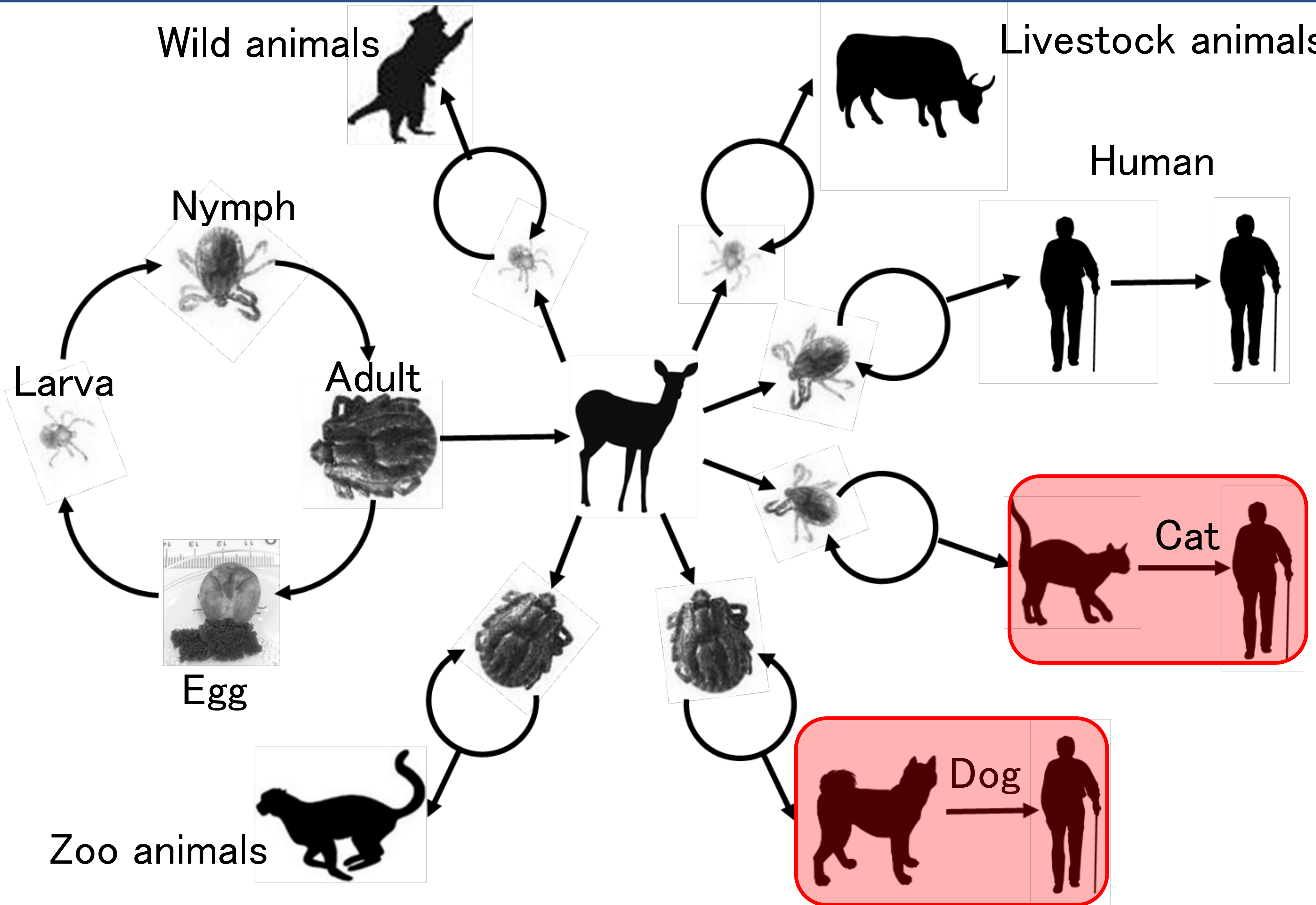
Number of SFTS cases in animals and humans



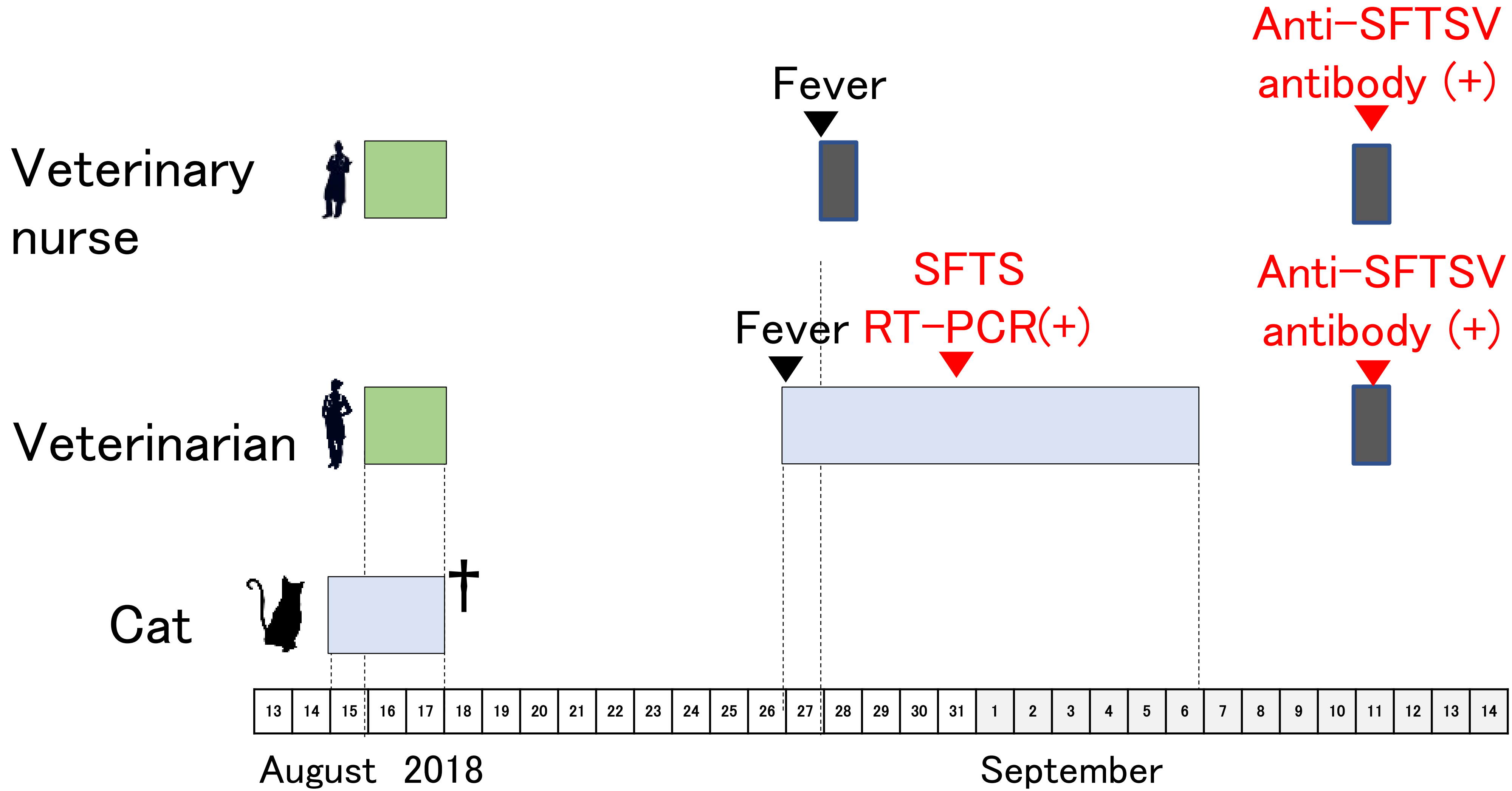
The tendency is similar to that of human cases.

Cat cases are more than human cases

Transmission from cats and dogs to human



SFTSV transmission from a cat to humans



Anti-SFTSV antibody (+)

Fever

Veterinary nurse

SFTS RT-PCR(+)

Fever

Anti-SFTSV antibody (+)

Veterinarian

Cat

†

13 14 15 16 17 18 19 20 21 22 23 24 25 26 27 28 29 30 31 1 2 3 4 5 6 7 8 9 10 11 12 13 14

August 2018

September

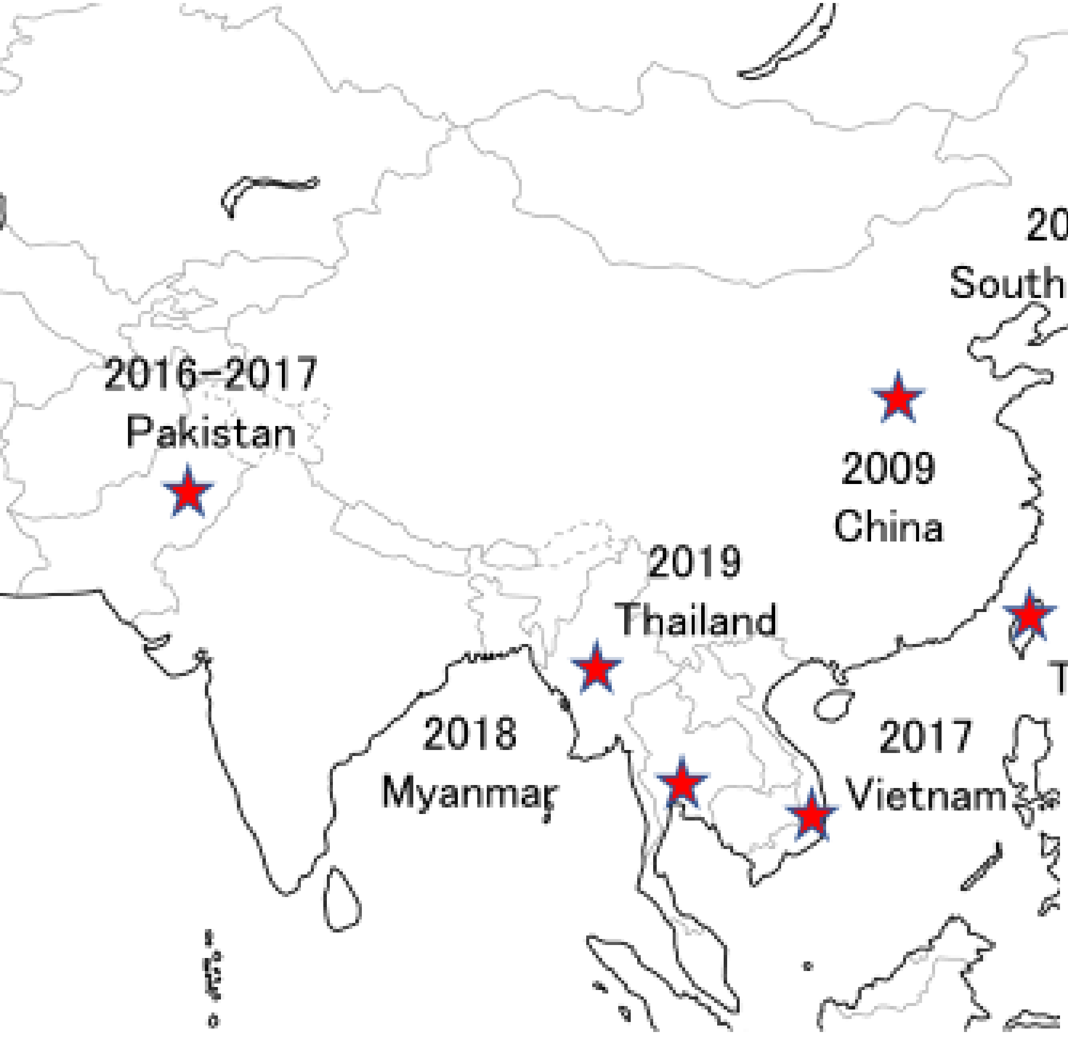
🟩: Contact with cat ⬜: Hospitalization ⬛: Outpatient care

Yamanaka A et al., Emerg Infect Dis. 2020 Dec;26(12):2994-2998

Direct transmission from animals to human

Jun, 2017	Dog⇒Owner
Aug, 2018	Cat⇒Veterinarian and nurse
Oct, 2018	Cats⇒Veterinarian
Oct, 2018	Cat⇒Owner（Dead）
May, 2019	Cat bite⇒Owner
Aug, 2019	Cat⇒Owner
Nov, 2019	Cat⇒Veterinarian
Mar, 2020	Cat⇒Owner
Jun, 2020	Cat⇒Veterinarian
Feb, 2021	Cat⇒Veterinarian
Feb, 2021	Cat⇒Veterinarian
Jun, 2021	Cat⇒Veterinarian

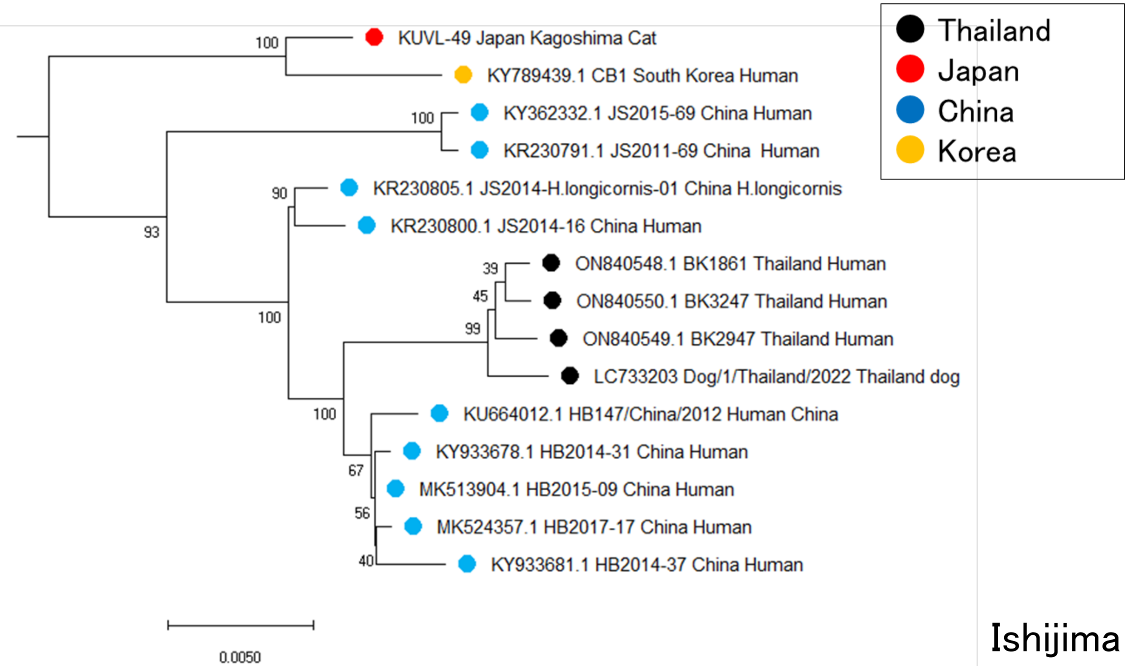
Distribution of SFTSV in Asian countries



Yu XJ et al., N Engl J Med. 2011 Apr 21;364(16):1523-32
Kim YR et al. Emerg Infect Dis. 2018 Nov;24(11):2103-2105
Takahashi T et al. J Infect Dis. 2014 Mar;209(6):816-27
Tran XC et al. Emerg Infect Dis. 2019 May;25(5):1029-1031.
Peng SH et al. Emerg Infect Dis. 2020 Jul;26(7):1612-1614.
Win AM et al. Emerg Infect Dis. 2020 Aug;26(8):1878-1881
Ongkittikul S et al. *Bangkok Med J* 16, 2 (Sep. 2020), 204.
Zohaib A et al. Emerg Infect Dis. 2020 Jul;26(7):1513-1516.
Kirino Y et al. J Infect Chemother. 2022 Jun;28(6):753-756.

Prevalence of SFTSV infection in Thai dogs

Province	District	ELISA(OD＞0.129)		FRNT$_{50}$(≧1:10)		Minimum Positive Ratio
		No. of Examined Dogs	No. of Positive Dogs	No. of Examined Dogs	No. of Positive Dogs	
Prachinburi		17	1	1	0	0.0%
Bangkok		143	12	12	6	4.2%
Chachoengsao		18	2	2	2	11.1%
Samutprakan		81	19	16	10	12.3%
Rayong		14	2	2	1	7.1%
Chonburi	Mueang Chonburi	27	6	6	3	11.1%
	Banglamung	56	5	5	3	5.4%
	Sattahip	95	56	52	50	52.6%
	Pattaya city	7	3	2	1	14.3%
Total		458	106	98	76	16.6%



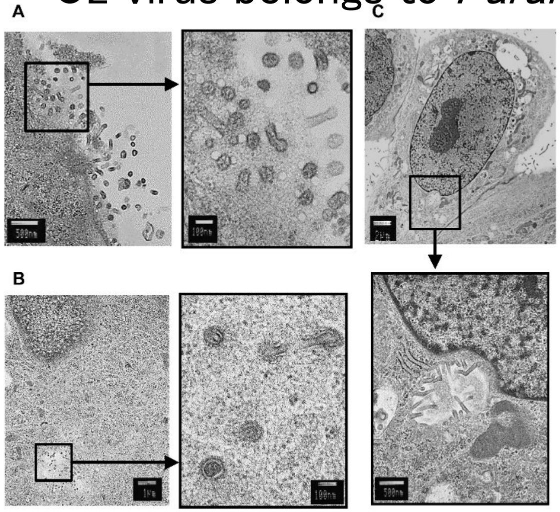
Ishijima *et al*., 2023, Viruses

Summary of SFTS infection

- SFTS is a tick-borne disease
- SFTSV causes severe disease in human
- CFR in human is 27% in Japan
- SFTSV can infect to many animals
- SFTSV causes lethal disease in cats and the CFR is 60%
- SFTSV can transmit from diseased animals to humans
- Pet owners and veterinarians are at high risk of SFTSV infection
- Veterinarians should protect themselves by PPE (glove, mask, gown, goggles, face shield)

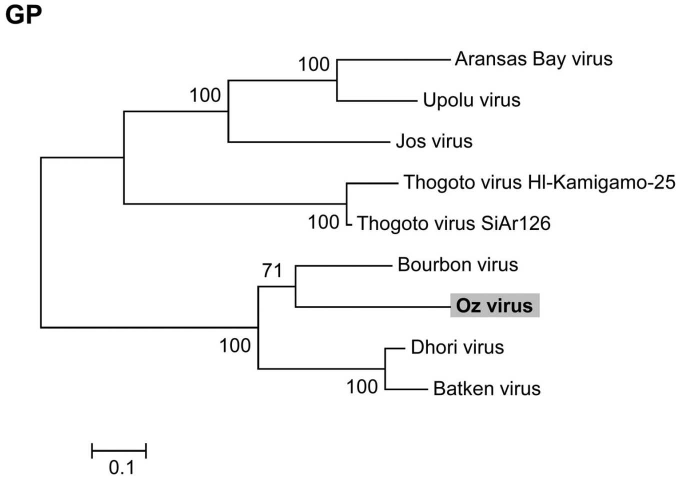
Characterization of Oz virus

Oz virus belongs to *Paramyxoviridae*

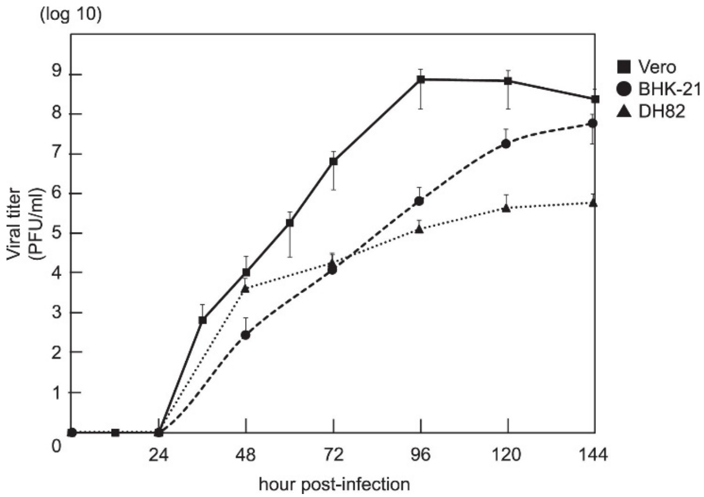


Pleomorphic viral particles, including both filamentous and round particles, budded directly from the plasma membrane of infected cells

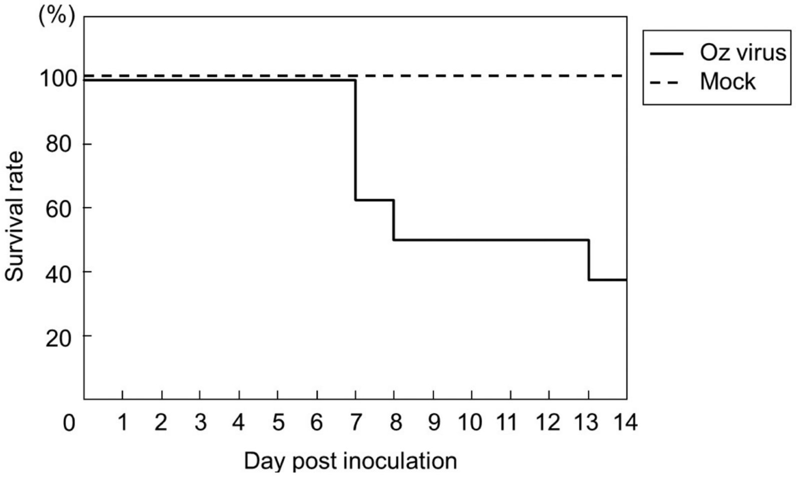
Oz virus is similar to Bourbon virus in U.S.A



Oz virus can grow well in mammalian cell lines



Oz virus can kill suckling mice



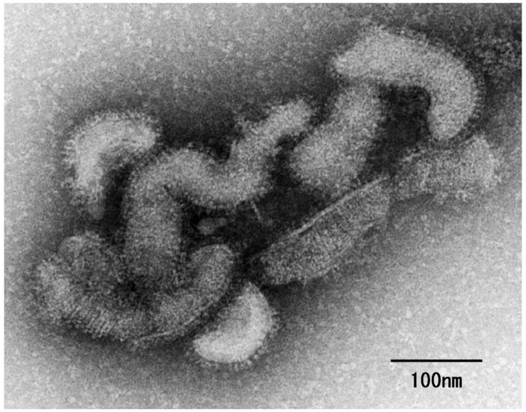
Ejiri H, Lim CK, Isawa H, Fujita R, Murota K, Sato T, Kobayashi D, Kan M, Hattori M, Kimura T, Yamaguchi Y, Takayama-Ito M, Horiya M, Posadas-Herrera G, Minami S, Kuwata R, Shimoda H, Maeda K, Katayama Y, Mizutani T, Saijo M, Kaku K, Shinomiya H, Sawabe K. Characterization of a novel thogotovirus isolated from Amblyomma testudinarium ticks in Ehime, Japan: A significant phylogenetic relationship to Bourbon virus. Virus Res. 2018 Apr 2;249:57–65.

Oz virus infects many mammalian species

Species	Year	VN titer							Ratio
		<1:10	1:10	1:20	1:40	1:80	1:160	1:320	
Human	2015	22	0	0	1	1	0	0	8.3%
Monkey	2012–2019	91	0	4	5	4	9	7	24.2%
Wild boar	2013–2015	49	2	12	10	15	20	16	60.5%
Sika deer	2014–2015	20	5	8	11	12	13	7	73.7%

Tran NTB, Shimoda H, Ishijima K, Yonemitsu K, Minami S; Supriyono; Kuroda Y, Tatemoto K, Mendoza MV, Kuwata R, Takano A, Muto M, Sawabe K, Isawa H, Hayasaka D, Maeda K. Zoonotic Infection with Oz Virus, a Novel Thogotovirus. Emerg Infect Dis. 2022 Feb;28(2):436–439. doi: 10.3201/eid2802.211270. PMID: 35075999; PMCID: PMC8798690.

The first patient with Oz virus infection



図．患者検体から分離された OZV 粒子の電子顕微鏡写真

Date: early summer of 2022

Patient: female in her 70s, resident of Ibaraki Prefecture, underlying hypertension and dyslipidemia, no history of overseas travel

Symptoms: fatigue, loss of appetite, vomiting, joint pain, and a fever of 39 ℃, ultimately resulting in viral myocarditis and death

Blood tests: thrombocytopenia (66,000/μL), liver disorder, renal disorder, high serum markers of inflammation (CRP 22.82 mg/dL), high CK (2049 U/L, CK-MB 14 IU/L), high LDH (671 U/L), high ferritin (10729 ng/mL), simple CT normal.

On hospitalization: Engorged ticks in the right inguinal region. No rickettsia or SFTS, blood culture negative.

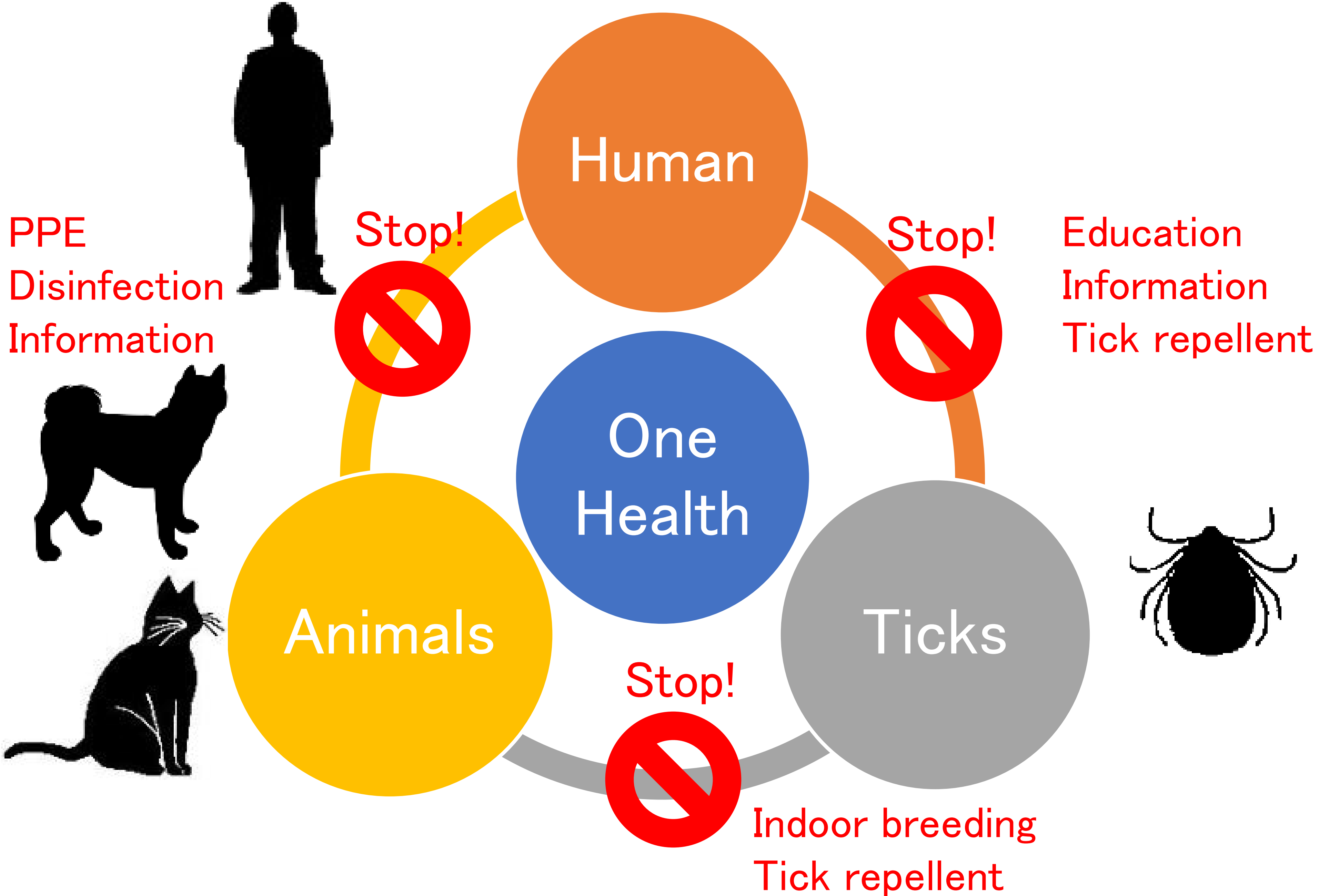
During hospitalization: Pacemaker implanted due to atrioventricular block. Various tests suspected myocarditis. The pacemaker was removed after approximately 10 days, when the patient's pulse stabilized. On the 20th day of hospitalization, consciousness disorder and multiple cerebral infarctions were observed, and anticoagulation therapy was started. The patient had persistent fever, but thoracoabdominal pelvic contrast CT could not point out any obvious foci or organ enlargement that could be the source of the fever.

IASR Vol.44 (7): p109-111:2023

Catalogue of tick–borne viruses in Japan

Viruses	Classification	Isolation	Tick	Animal	Human	Disease
SFTS virus	*Bunyavirales*	○	○	○	○	SFTS
Yezo virus	*Bunyavirales*	○	○	○	○	Like SFTS
Iwanai Valley virus	*Bunyavirales*	○	○			
Ama virus	*Bunyavirales*	○	○			
Tofla virus	*Bunyavirales*	○	○			
Toyo virus	*Bunyavirales*		○			
Kabuto Mountain virus	*Bunyavirales*	○	○	○	○	?
Okutama tick virus	*Bunyavirales*		○			
Mukawa virus	*Bunyavirales*	○	○	○		
Soft tick bunyavirus	*Bunyavirales*	○	○			
Kuriyama virus	*Bunyavirales*	○	○			
Tick–borne encephalitis virus	*Flaviviridae*	○	○	○	○	Encephalitis
Yamaguchi virus	*Flaviviridae*		○	○		
Negishi virus	*Flaviviridae*	○			○	Encephalitis
Saruyama virus	*Flaviviridae*		○	○		
Ohshima virus	*Orthomyxoviridae*		○			
Thogoto virus	*Orthomyxoviridae*	○	○	○	?	
Oz virus	*Orthomyxoviridae*	○	○	○	○	Myocarditis
Tarumizu tick virus	*Reoviridae*	○	○	○		
Muko virus	*Reoviridae*	○	○	○		
Kemerovo virus	*Reoviridae*	○	○	?	?	
Sekira virus	*Nyamiviridae*		○			
H. Flava Ifla virus	*Iflaviridae*		○			

One Health approach for tick-borne diseases



Human

One Health

Animals

Ticks

PPE
Disinfection
Information

Stop!

Stop!

Education
Information
Tick repellent

Stop!

Indoor breeding
Tick repellent

Acknowledgements

National Institute of Infectious Diseases
- Department of Veterinary Science
- Department of Virology I
- Department of Pathology
- Department of Medical Entomology
- Research Center for Influenza and Respiratory Viruses
- Research Center for Biosafety, Laboratory Animal and Pathogen Bank

Yamaguchi University
Kagoshima University
Nagasaki University
Okayama Science University
Miyazaki University
Tokyo University of Agriculture and Technology
The University of Tokyo
Hokkaido University
Hiroshima Veterinary Medical Association

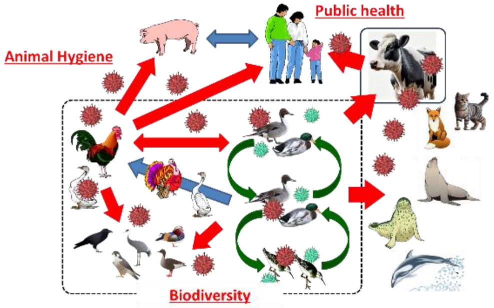
Veterinary Professionals throughout Japan

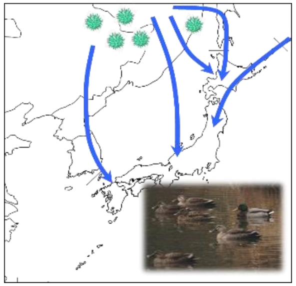
ひと、くらし、みらいのために
厚生労働省
Ministry of Health, Labour and Welfare

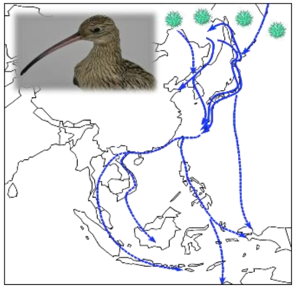
AMED

環境省
Ministry of the Environment

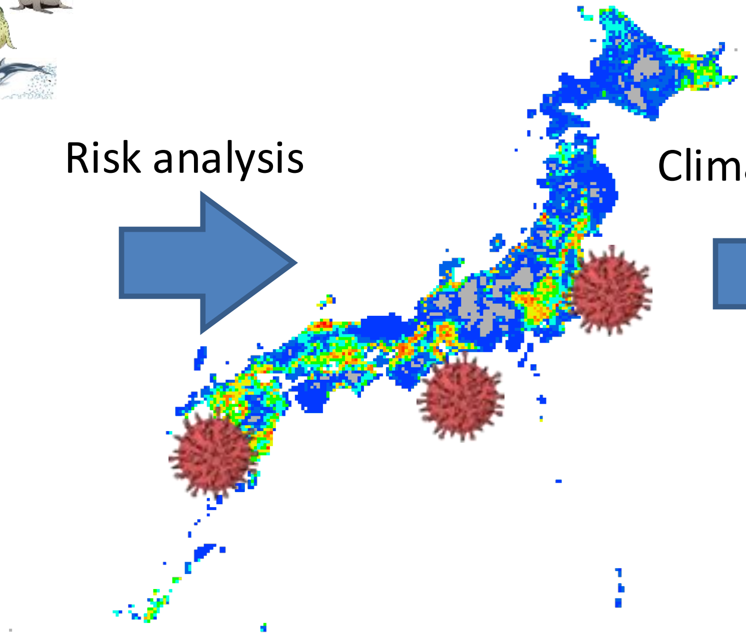
Climate change, wildlife and zoonoses: HPAIV as a model case



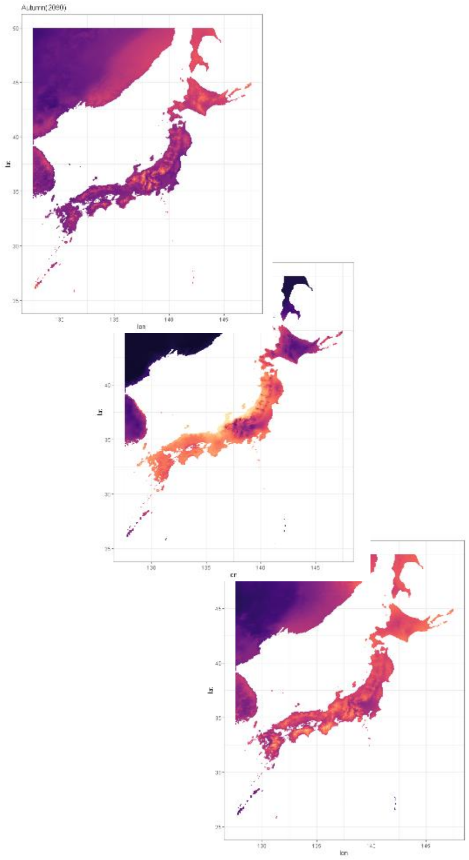




Risk analysis



Climate change



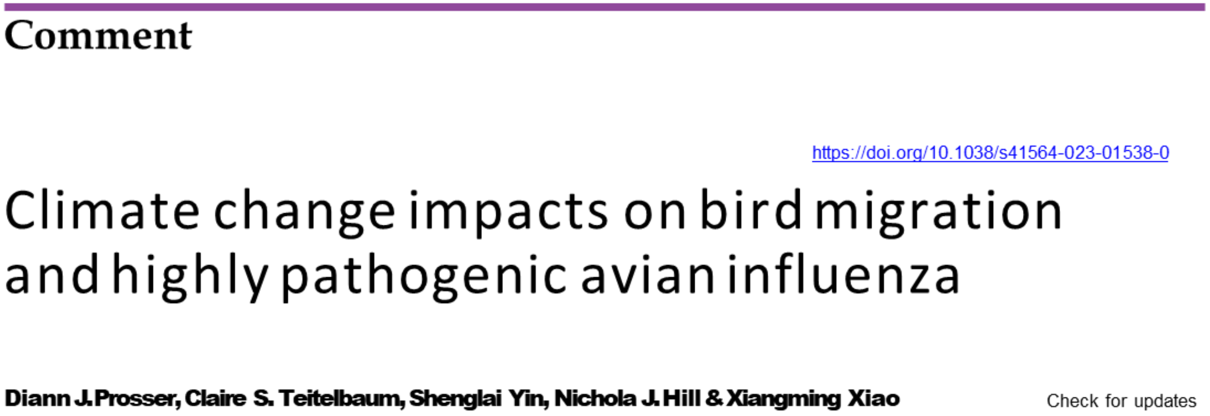
Koichi GOKA and Manabu Onuma
National Institute for Environmental Studies

RESEARCH

Wild Ducks as Long-Distance Vectors of Highly Pathogenic Avian Influenza Virus (H5N1)

Juthatip Keawcharoen,* Debby van Riel,* Geert van Amerongen,* Theo Bestebroer,* Walter E. Beyer,*
Rob van Lavieren,* Albert D.M.E. Osterhaus,* Ron A.M. Fouchier,* and Thijs Kuiken*

Emerging Infectious Diseases • www.cdc.gov/eid • Vol. 14, No. 4, April 2008



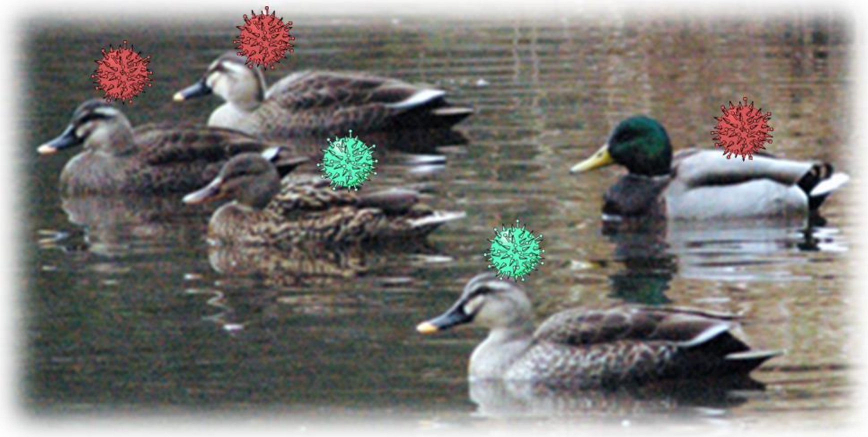
Comment

https://doi.org/10.1038/s41564-023-01538-0

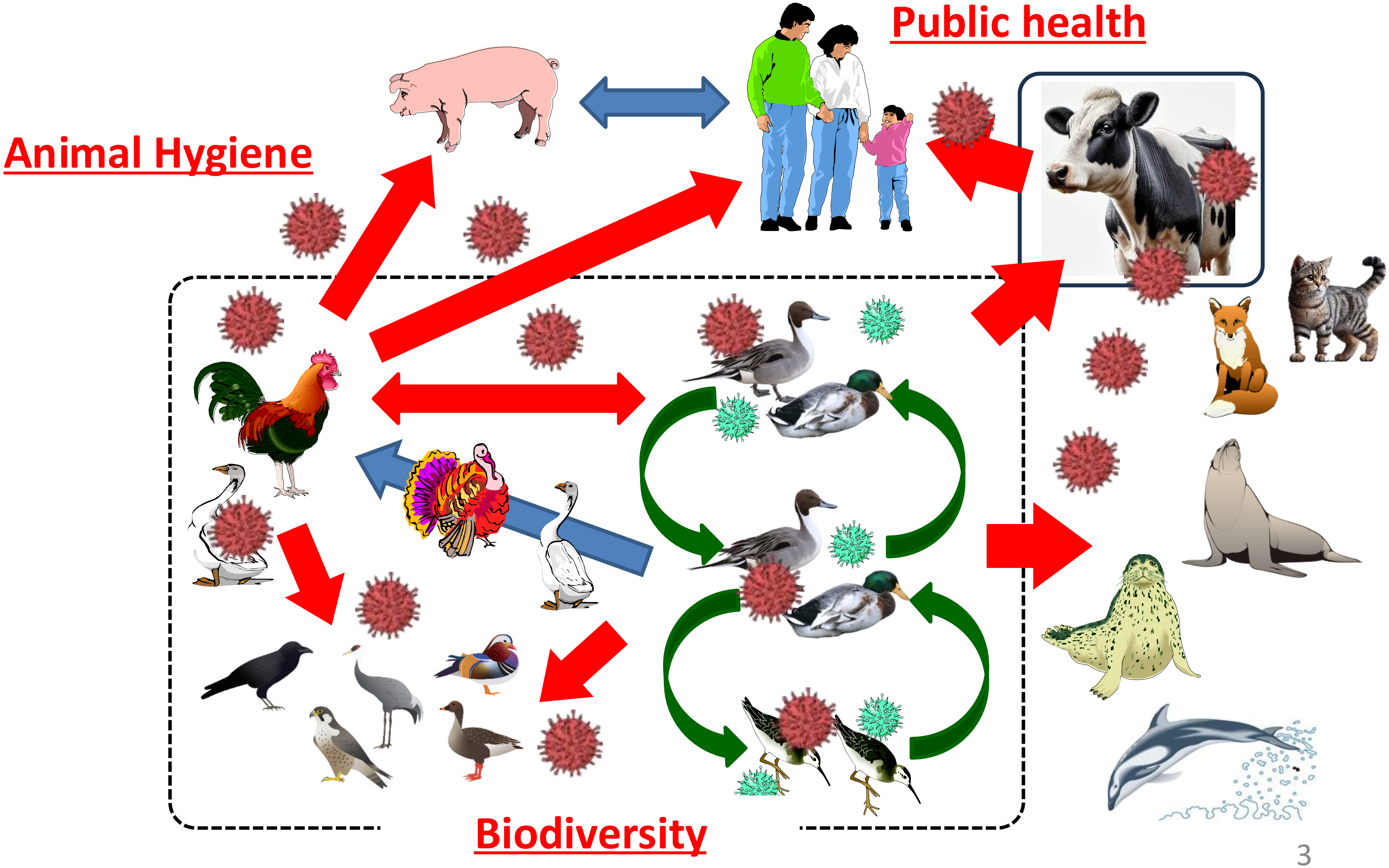
Climate change impacts on bird migration and highly pathogenic avian influenza

Diann J. Prosser, Claire S. Teitelbaum, Shenglai Yin, Nichola J. Hill & Xiangming Xiao

Check for updates



Animals infected with highly pathogenic avian influenza viruses



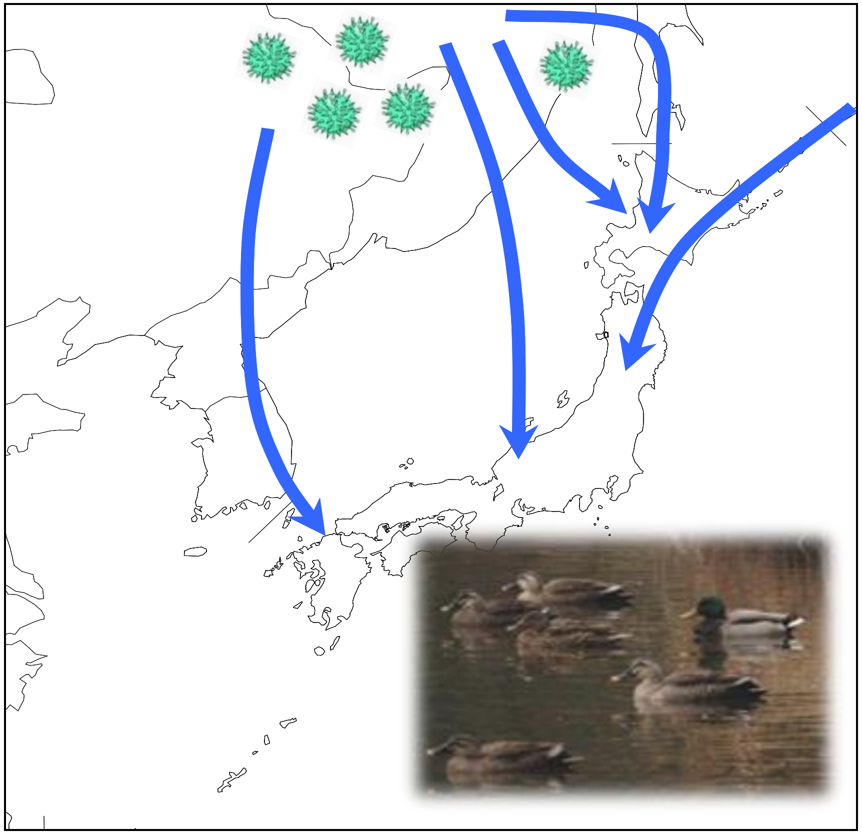
Public health

Animal Hygiene

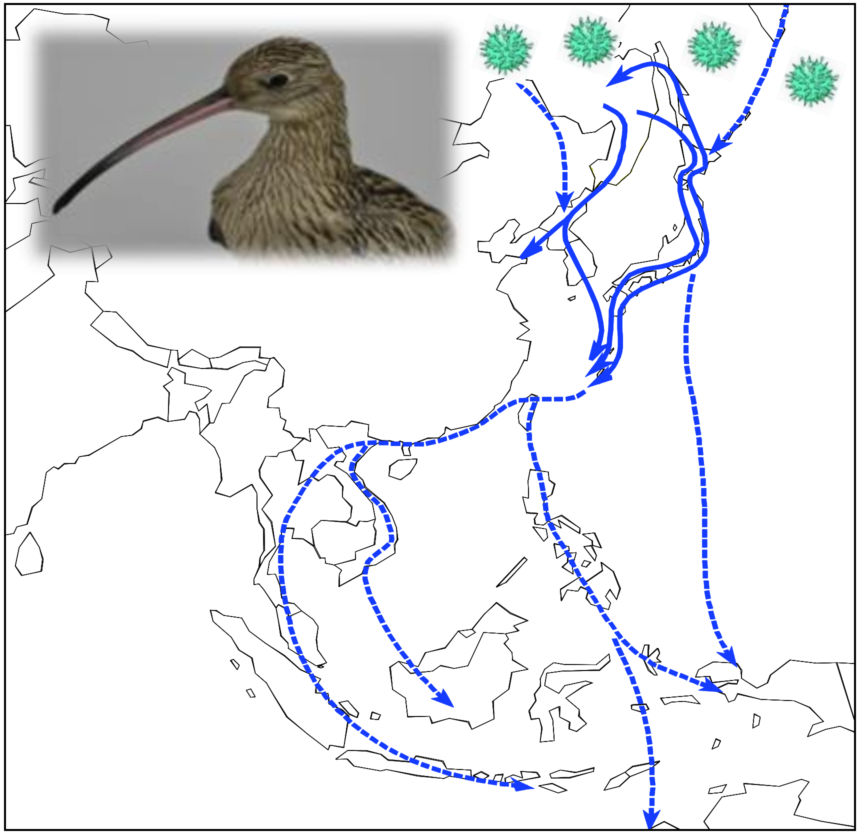
Biodiversity

Nationwide AIV surveillance in Japan

Wild ducks
（wintering in Japan）
(October – March)



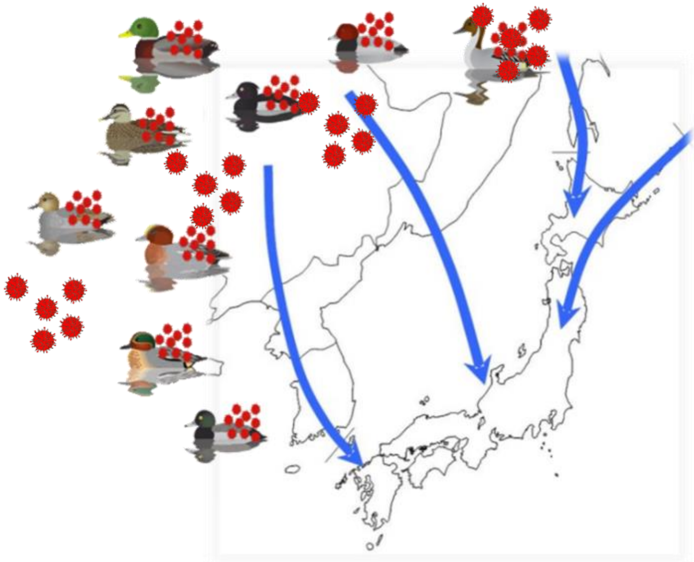
Shorebird
(The East-Asian Australasian Flyway)
(July – September)



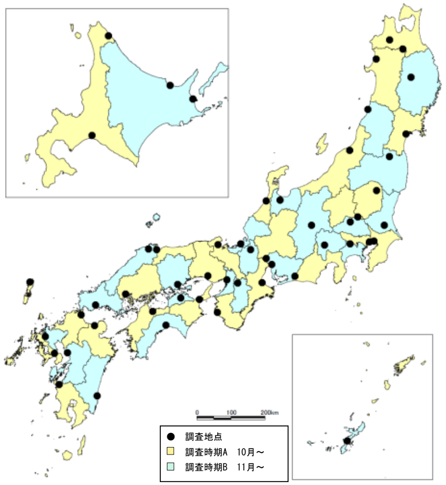
Funded by MOE

Funded by NIES

Nationwide AIV surveillance using fecal samples of Wild ducks (2008-2020)



52 locations
(Oct.-May)



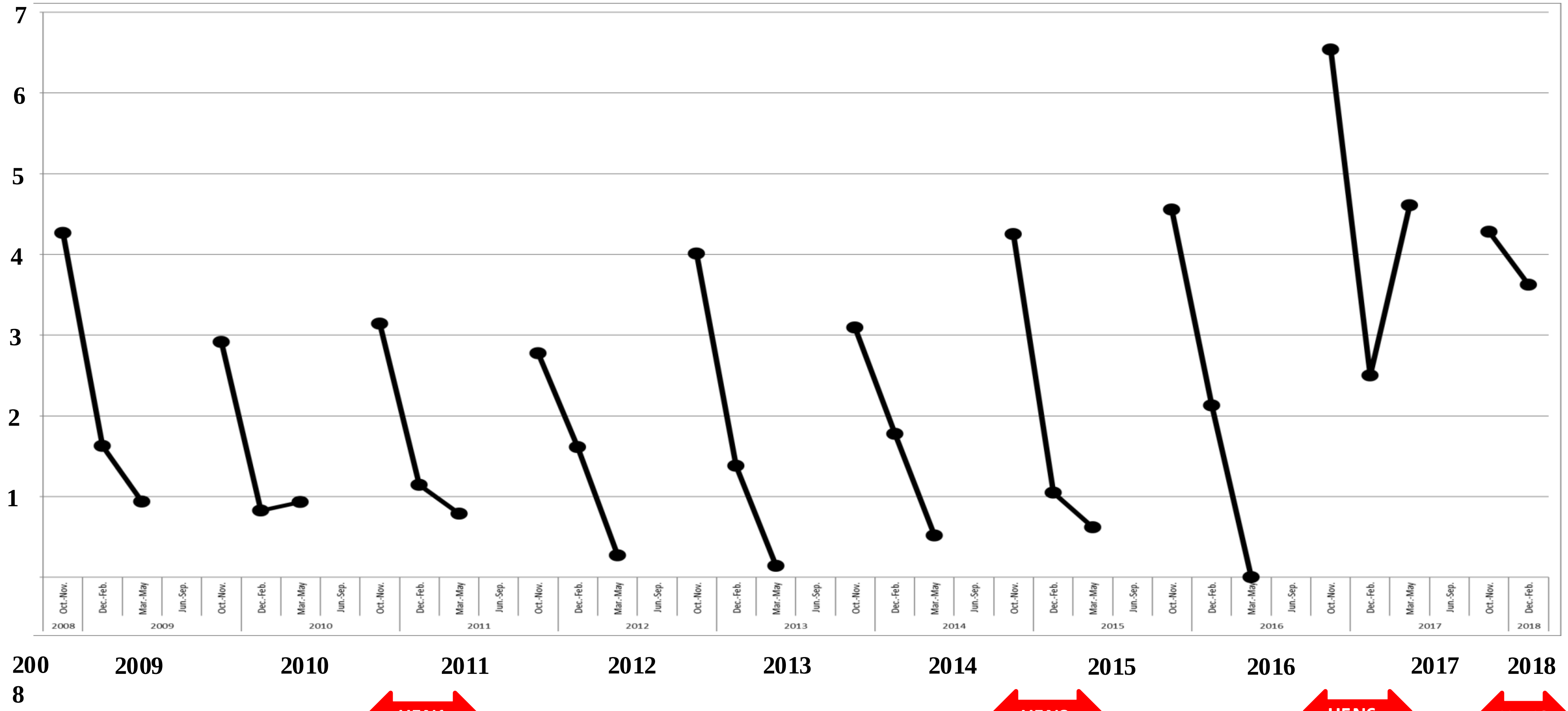
≈3,000 tubes
/season

5 feces/tube

Temporal change of AIV prevalence (2008-2018)

RT-LAMP positive rate in fecal samples (%)

Onuma M. Unpublished data



H5N1

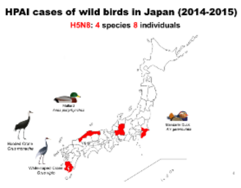
H5N8

H5N6

H5N6

HPAI cases of wild birds in Japan (2004-2011)

H5N1: 17 species & 1 unknown species, 75 individuals

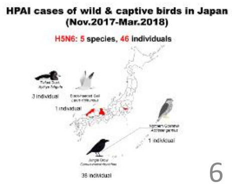


HPAI cases of wild birds in Japan (2014-2015)

H5N8: 4 species 8 individuals

HPAI cases of wild & captive birds in Japan (Oct.2016-Apr.2017)

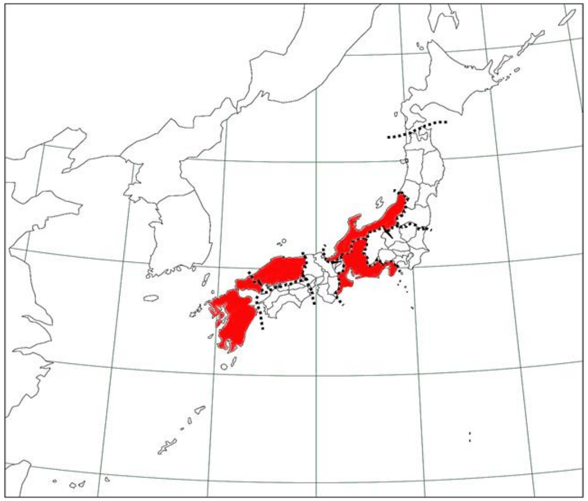
H5N6: 25 species & 1 unknown species, 210 individuals



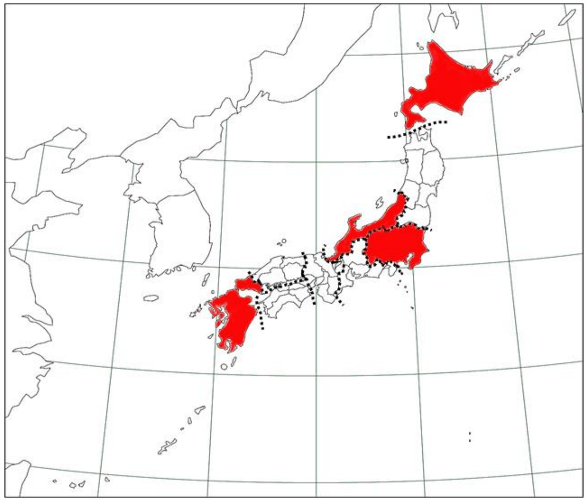
HPAI cases of wild & captive birds in Japan (Nov.2017-Mar.2018)

H5N6: 5 species, 46 individuals

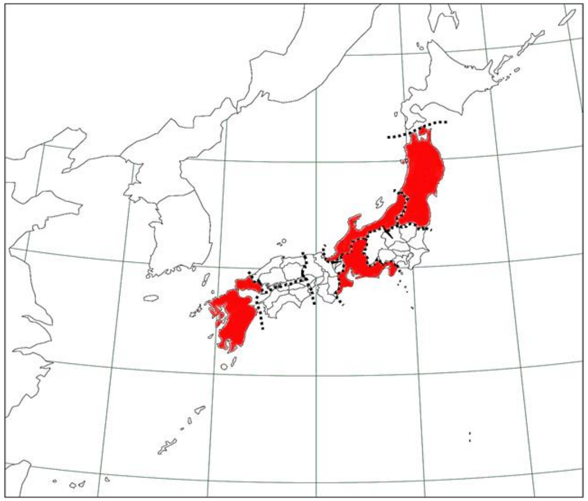
Time series changes in positivity rates (by region)



Autum migration
（Oct.～Nov.）



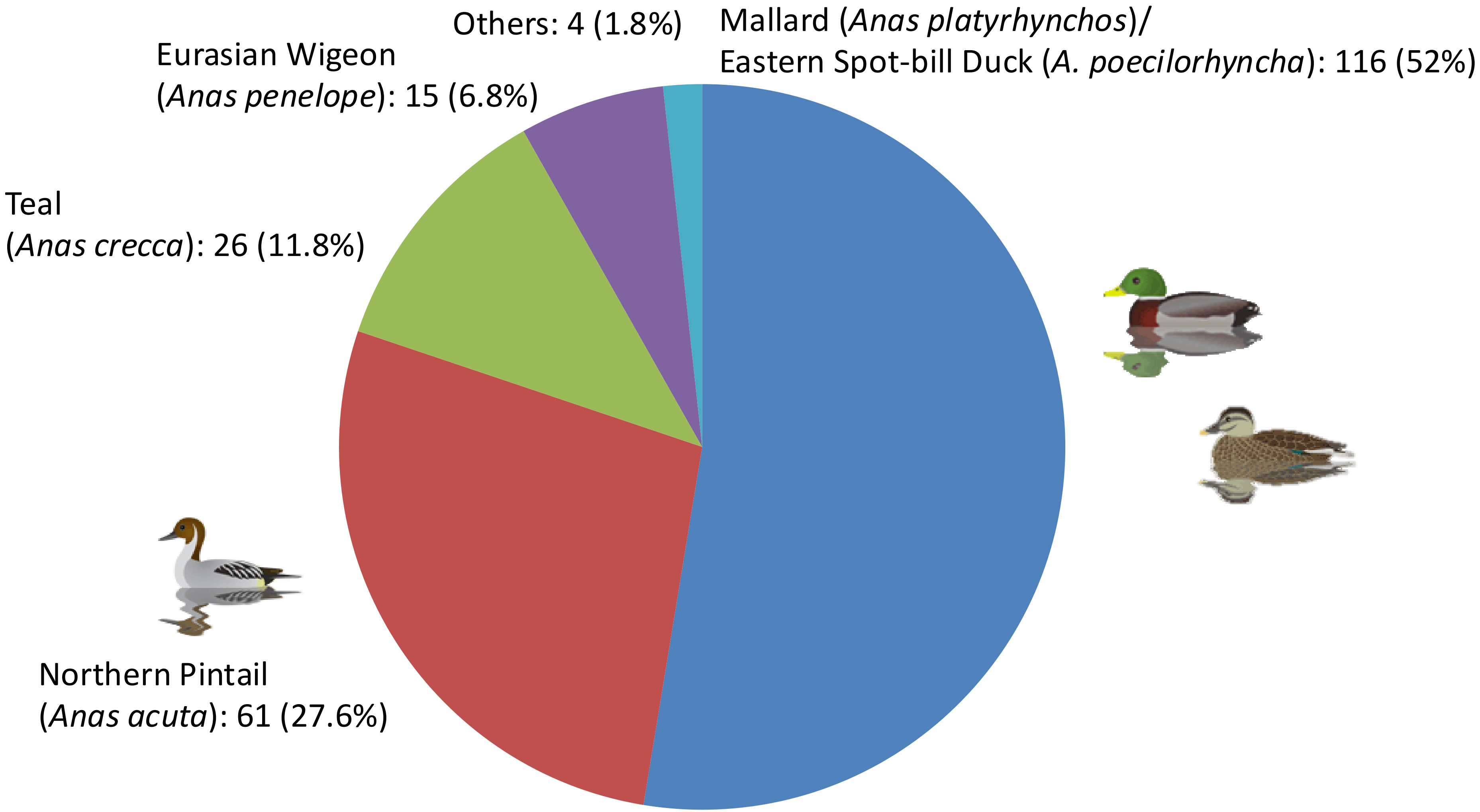
Wintering
（Dec.～Feb.）



Spring migration
（Mar.～May）

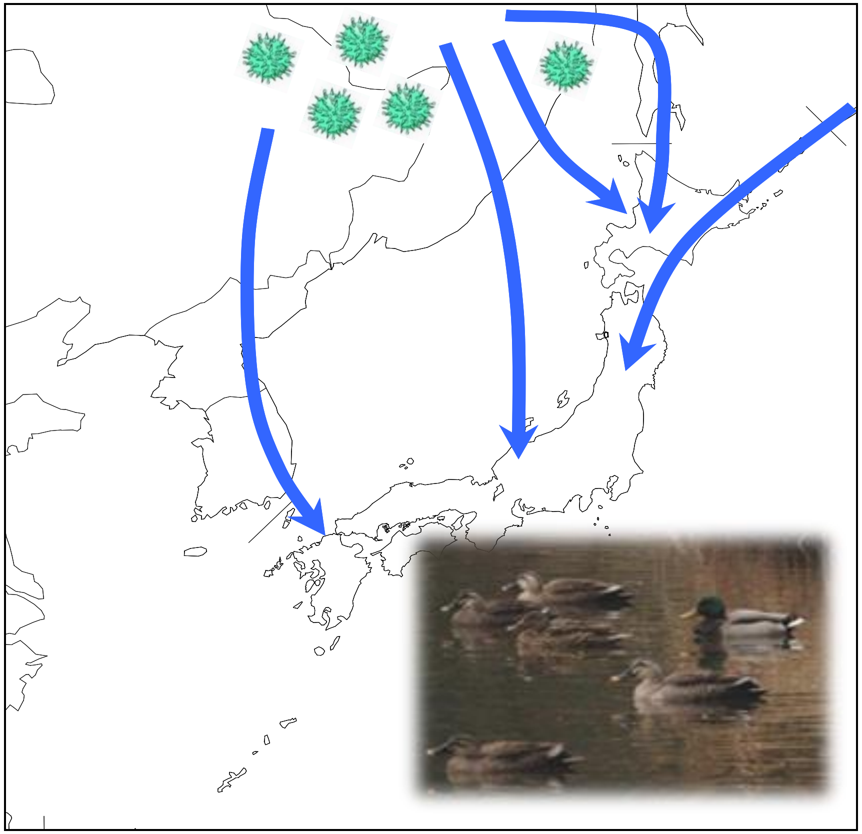
🟥 Regions with positivity rates above the national average

Result of species identification by DNA barcoding



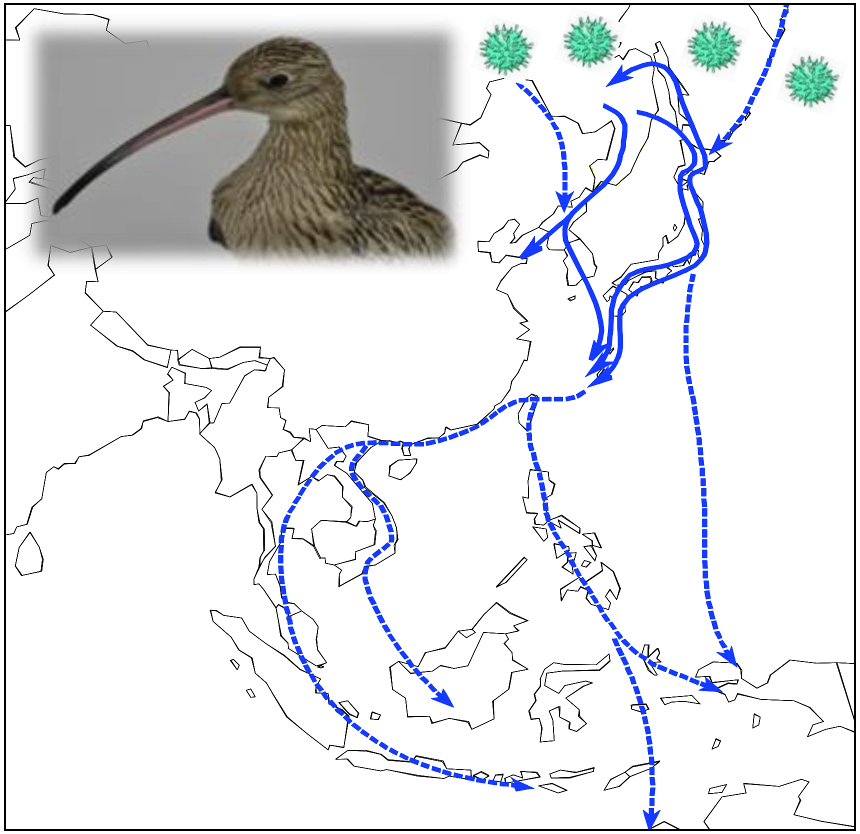
Nationwide AIV surveillance in Japan

Wild ducks
（wintering in Japan）
(October – March)



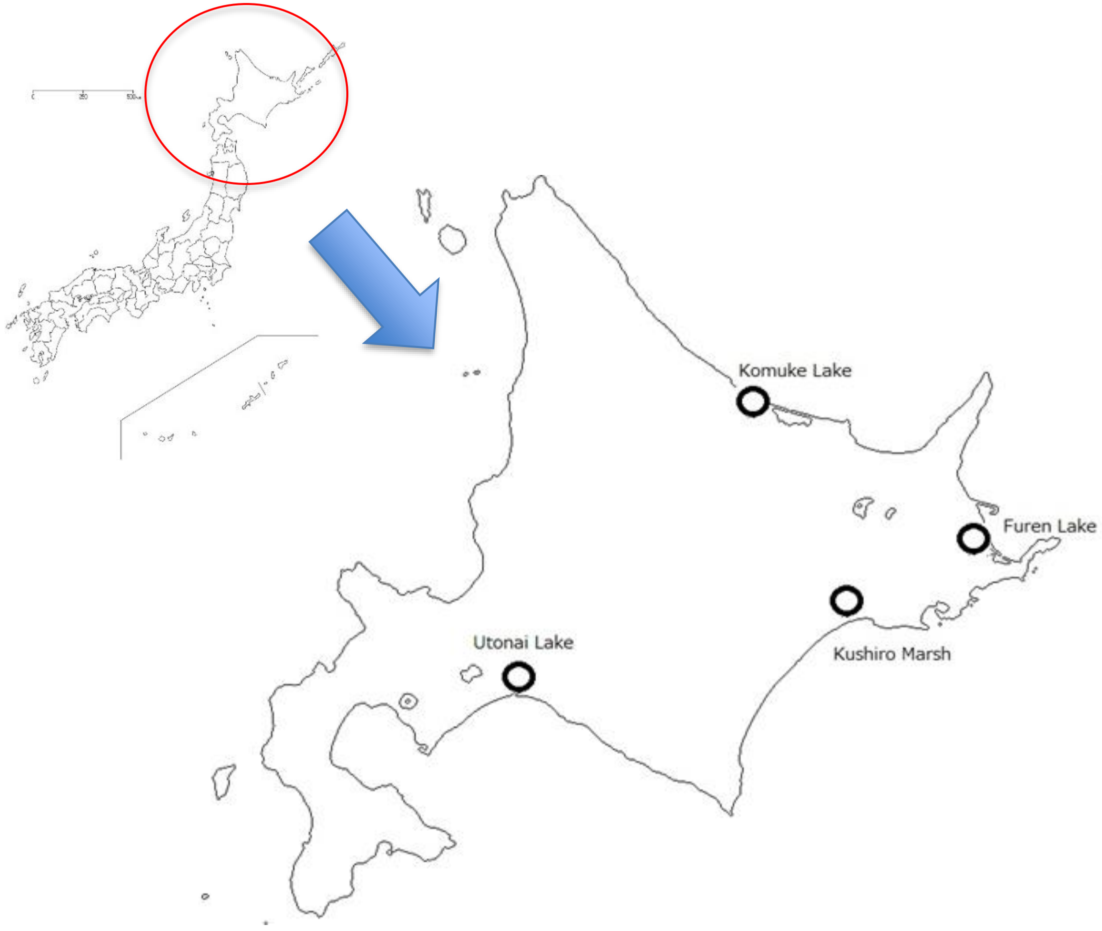
Funded by MOE

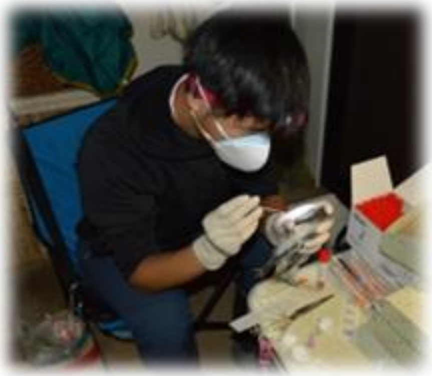
Shorebird
(The East-Asian Australasian Flyway)
(July – September)



Funded by NIES

Nationwide AIV surveillance in shorebirds





Result: AIV detection (by RT-LAMP)

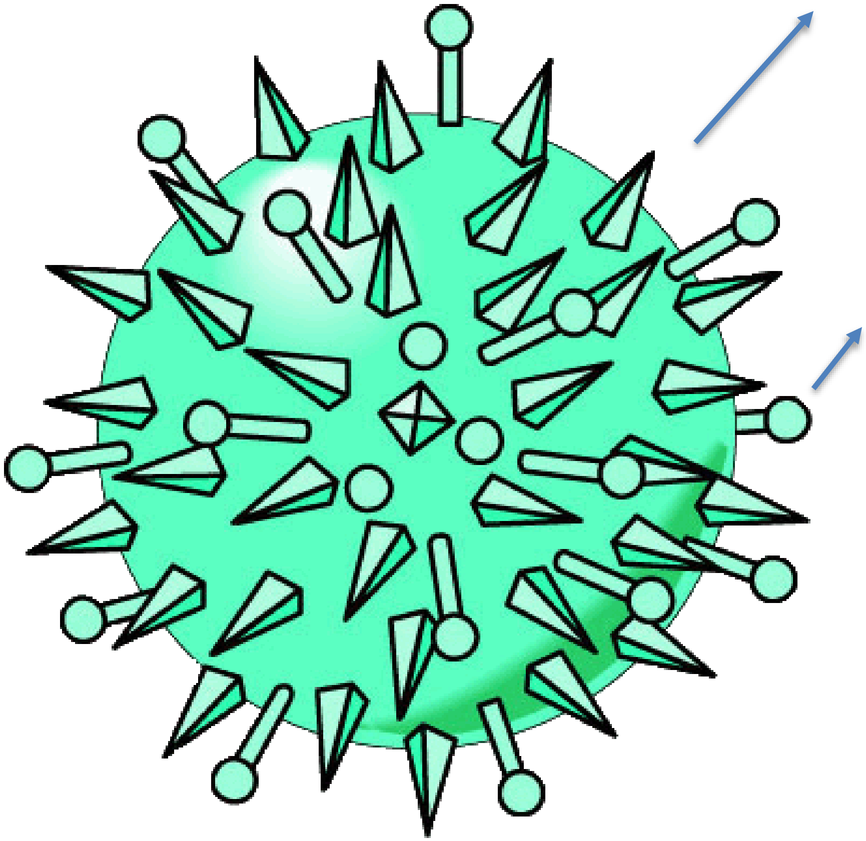
	2006	*2007	*2008	2009	*2010	Total
Number	340	289	210	329	579	1,747
Positive (%)	0	0	0	0	1 (0.2)	1 (0.1)

*** HPAIV positive cases in wild birds**

Lesser Sand Plover
(*Charadrius mongolus*)

Captured at Komuke lake
in September 3rd, 2010

Result: Subtyping (by sequencing)



HA: H10 (1,686 bp)
A/mallard/Korea/1242/2010(H10N6)
(99% identity)

NA: N7 (1,416 bp)
A/common teal/Hong Kong/
MPM1740/2011(H7N7) (99% identity)

Antibody prevalence of avian influenza virus in shorebirds (2017～)

Ruddy Turnstone

(*Arenaria interpres*)

34.8% (8/23)

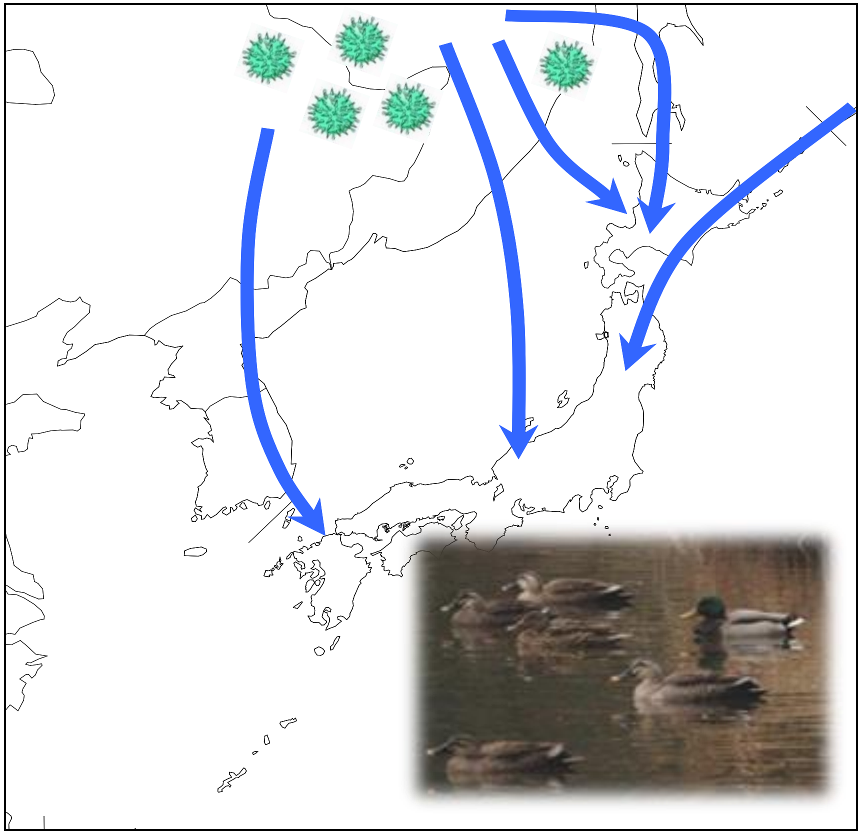
Whimbrel

(*Numenius phaeopus*)

36.4% (4/11)

Nationwide AIV surveillance in Japan

Wild ducks
（wintering in Japan）
(October – March)



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Shorebird
(The East-Asian Australasian Flyway)
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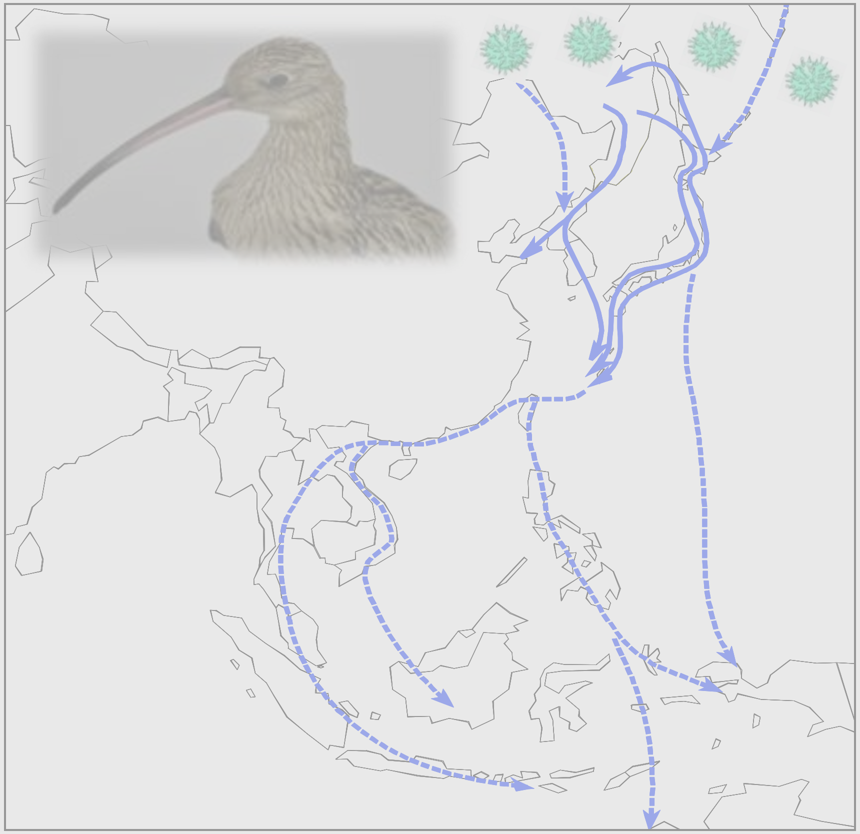
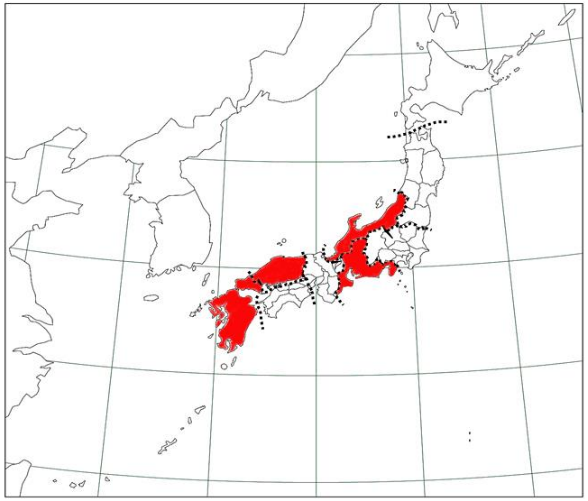
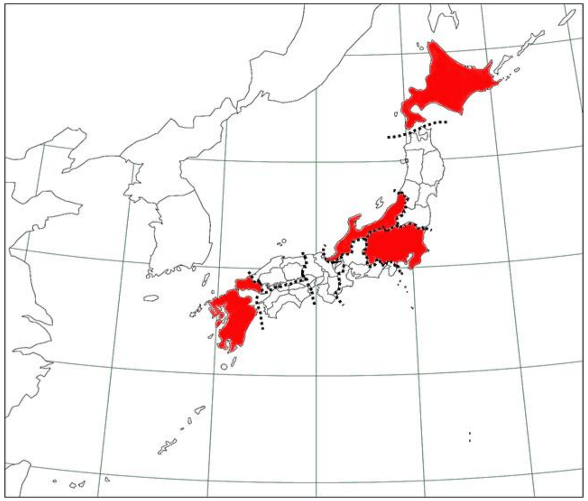


Funded by NIES

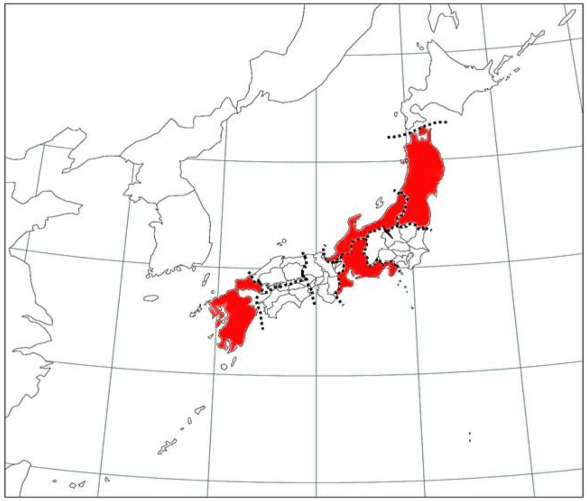
Identification of high-risk regions



Autum migration
（Oct.～Nov.）

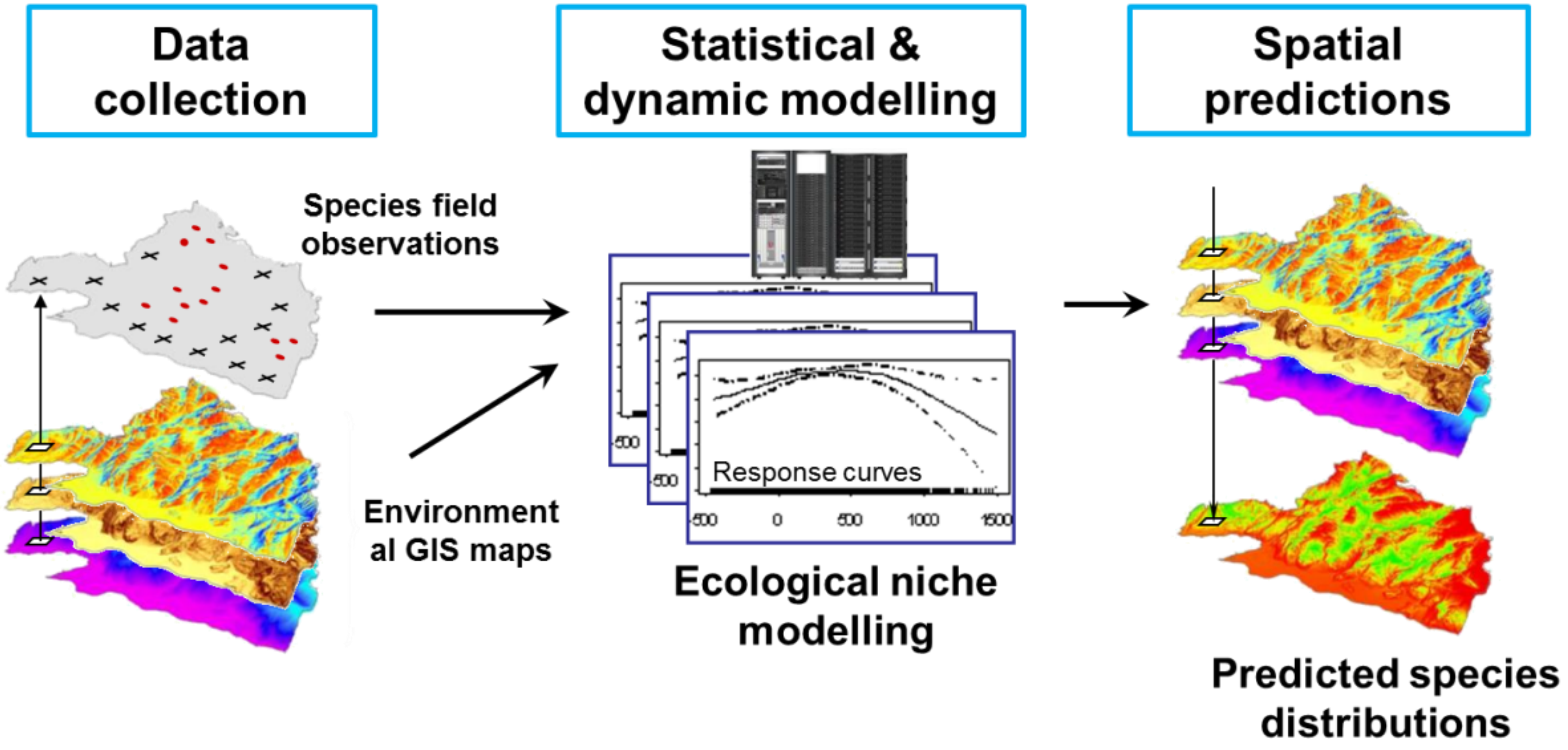


Wintering
（Dec.～Feb.）



Spring migration
（Mar.～May）

Environmental niche modelling



Data collection

Statistical & dynamic modelling

Spatial predictions

Species field observations

Environmental GIS maps

Ecological niche modelling

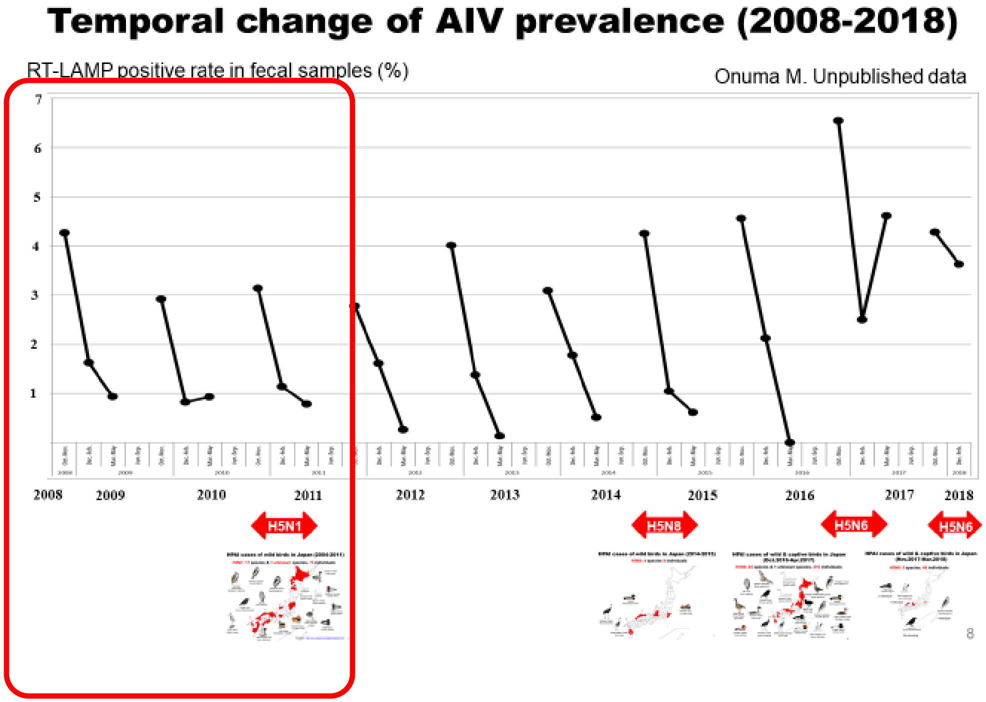
Predicted species distributions

https://www.unil.ch/webdav/site/idyst/shared/modeling.png

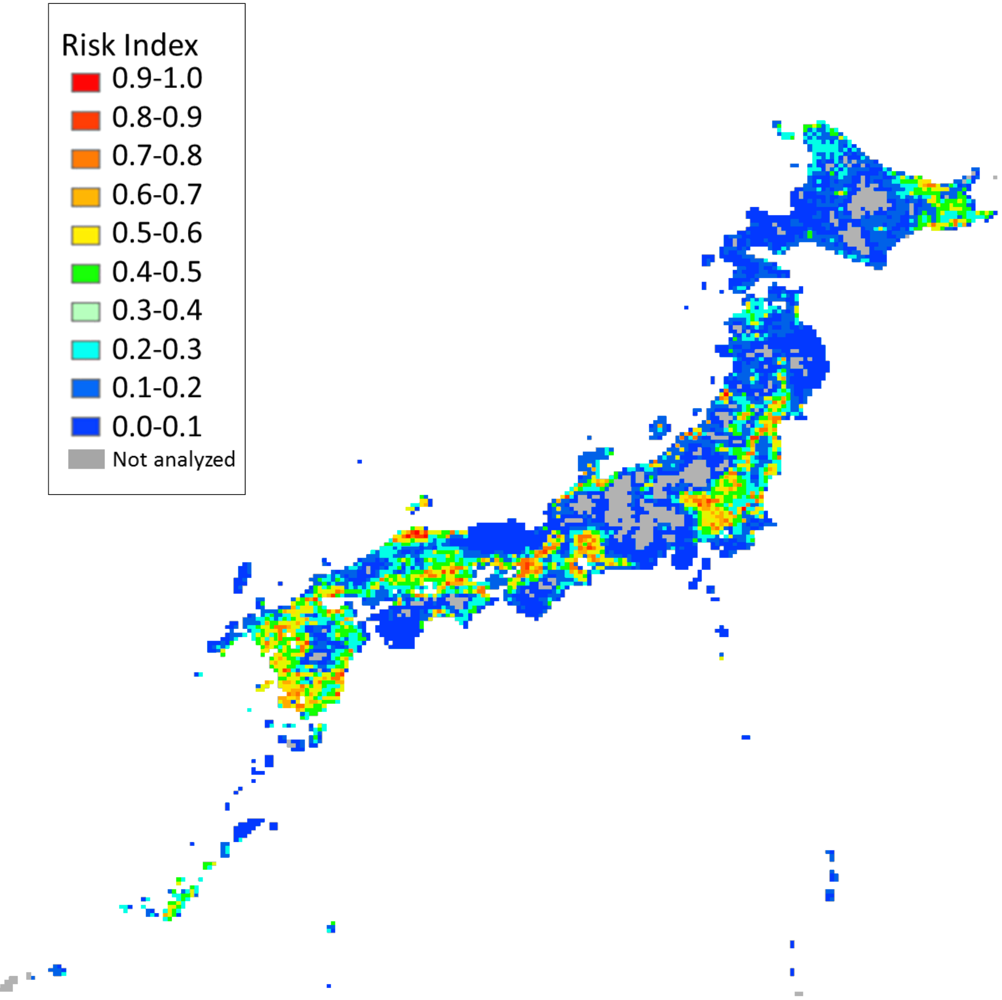
Method

Program: MaxEnt version 3.3.3e, Phillips et al., 2006
(The maximum entropy approach)

Data: Locations of LPAIV and HPAIV 2004-2011



Risk map for avian influenza in wild birds



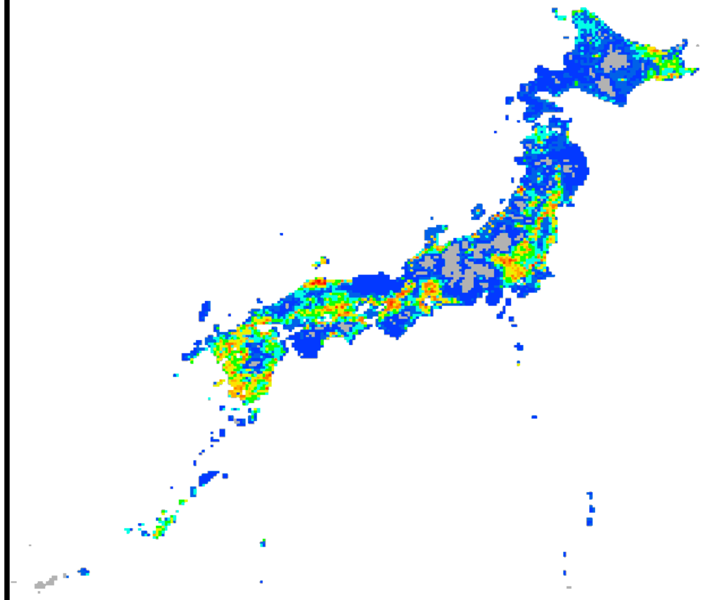
Contributions of independent variables to the model.

Independent variables	Contribution
Dabbling duck population	**49.4 ± 5.5**
Urban area	12.5 ± 3.5
Altitude	8.2 ± 2.3
Diving duck population	3.5 ± 3.5
Lake area	2.2 ± 1.5
Farmland area	0.9 ± 1.2
Poultry density	0.5 ± 0.5
Mean precipitation in winter	0.3 ± 1.0
Min temperature in winter	0.1 ± 0.1
Distance to lakes	0.0 ± 0.0
Sum of spatial filters	22.5 ± 5.6

(Moriguchi et. al., 2013)

Risk map of avian influenza in raptors

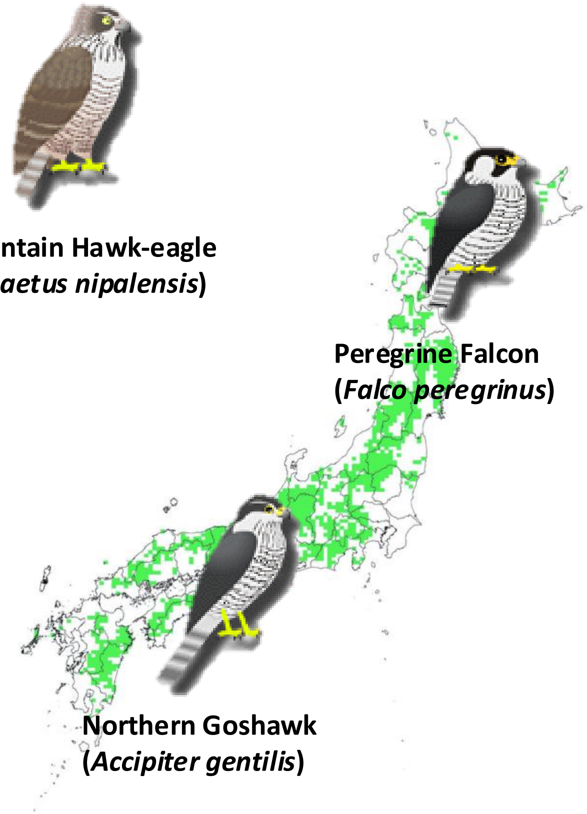
Risk map of AI



Moriguchi et al. (2013)

+

Distribution map

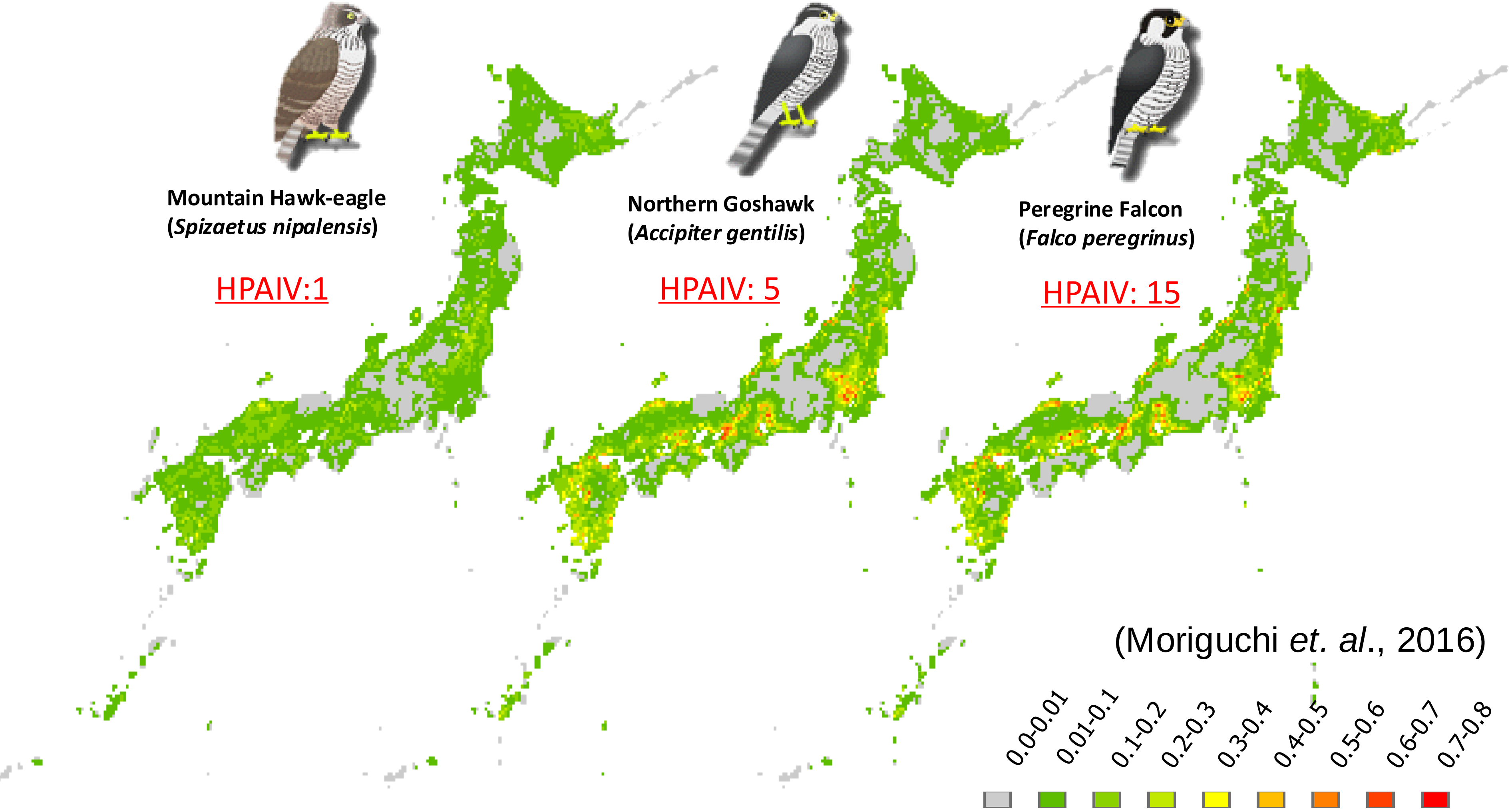


Mountain Hawk-eagle
(*Spizaetus nipalensis*)

Peregrine Falcon
(*Falco peregrinus*)

Northern Goshawk
(*Accipiter gentilis*)

Risk map of avian influenza in raptors



Mountain Hawk-eagle
(*Spizaetus nipalensis*)

HPAIV:1

Northern Goshawk
(*Accipiter gentilis*)

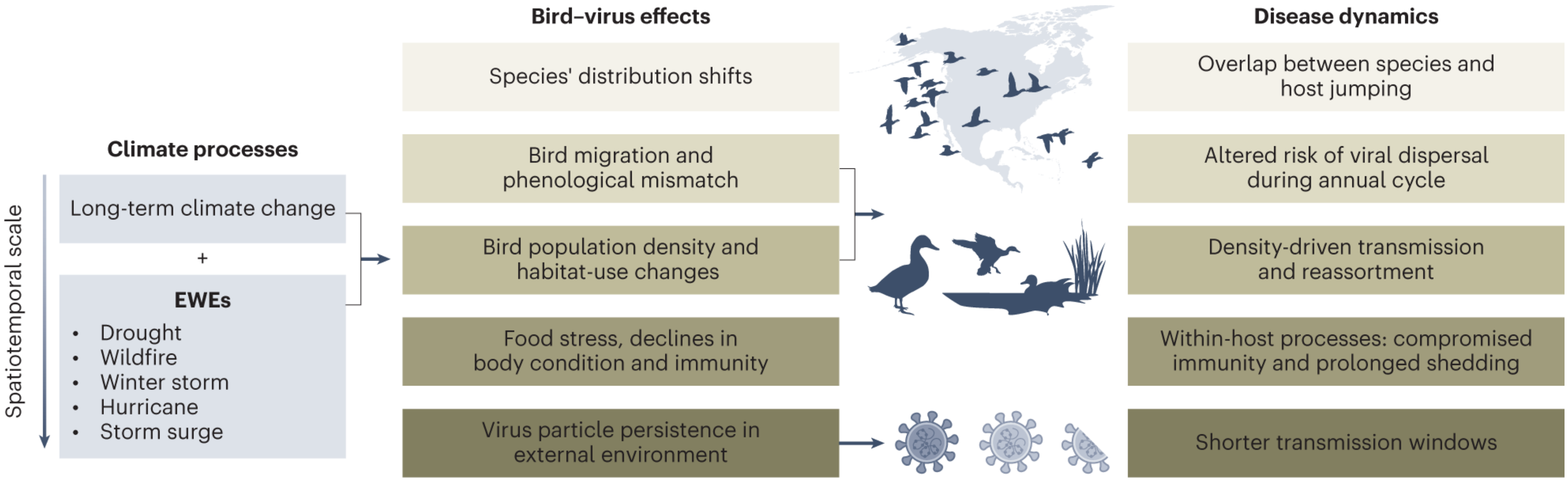
HPAIV: 5

Peregrine Falcon
(*Falco peregrinus*)

HPAIV: 15

(Moriguchi *et. al*., 2016)

Climate change impacts on bird migration and highly pathogenic avian influenza (Prosser et al. 2023)



Climate processes

Spatiotemporal scale

Long-term climate change

+

EWEs

- Drought
- Wildfire
- Winter storm
- Hurricane
- Storm surge

Bird–virus effects

Species' distribution shifts

Bird migration and phenological mismatch

Bird population density and habitat-use changes

Food stress, declines in body condition and immunity

Virus particle persistence in external environment

Disease dynamics

Overlap between species and host jumping

Altered risk of viral dispersal during annual cycle

Density-driven transmission and reassortment

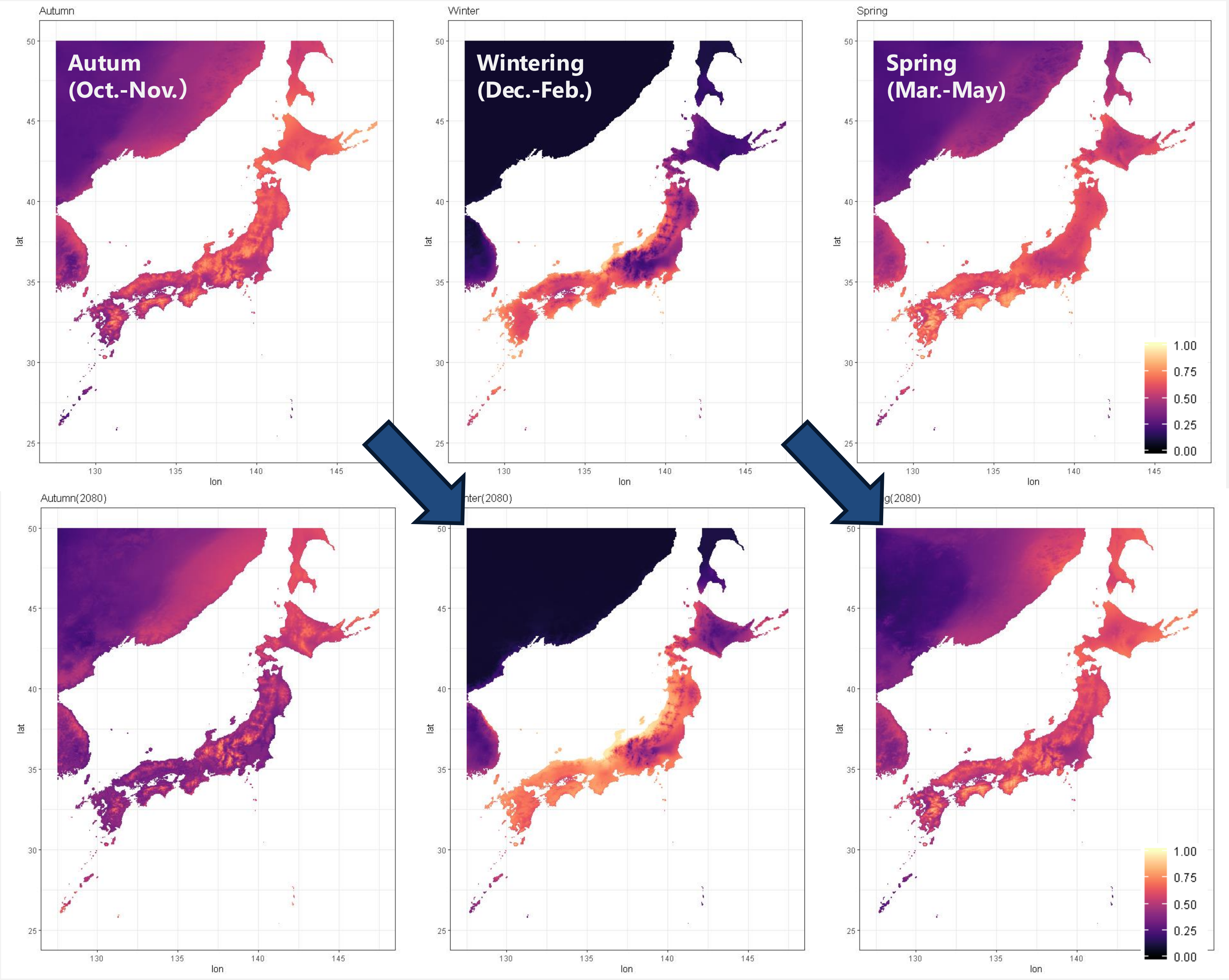
Within-host processes: compromised immunity and prolonged shedding

Shorter transmission windows

doi: 10.1038/s41564-023-01538-0.

“ long-distance migratory species tend **to track their niche** and select largely **similar environments through seasons**” Zurell et al. (2018, J. Biogeog.)

"Is it possible to estimate 'when' and 'where' migratory birds are using an ecological niche model with seasonal climate data?"



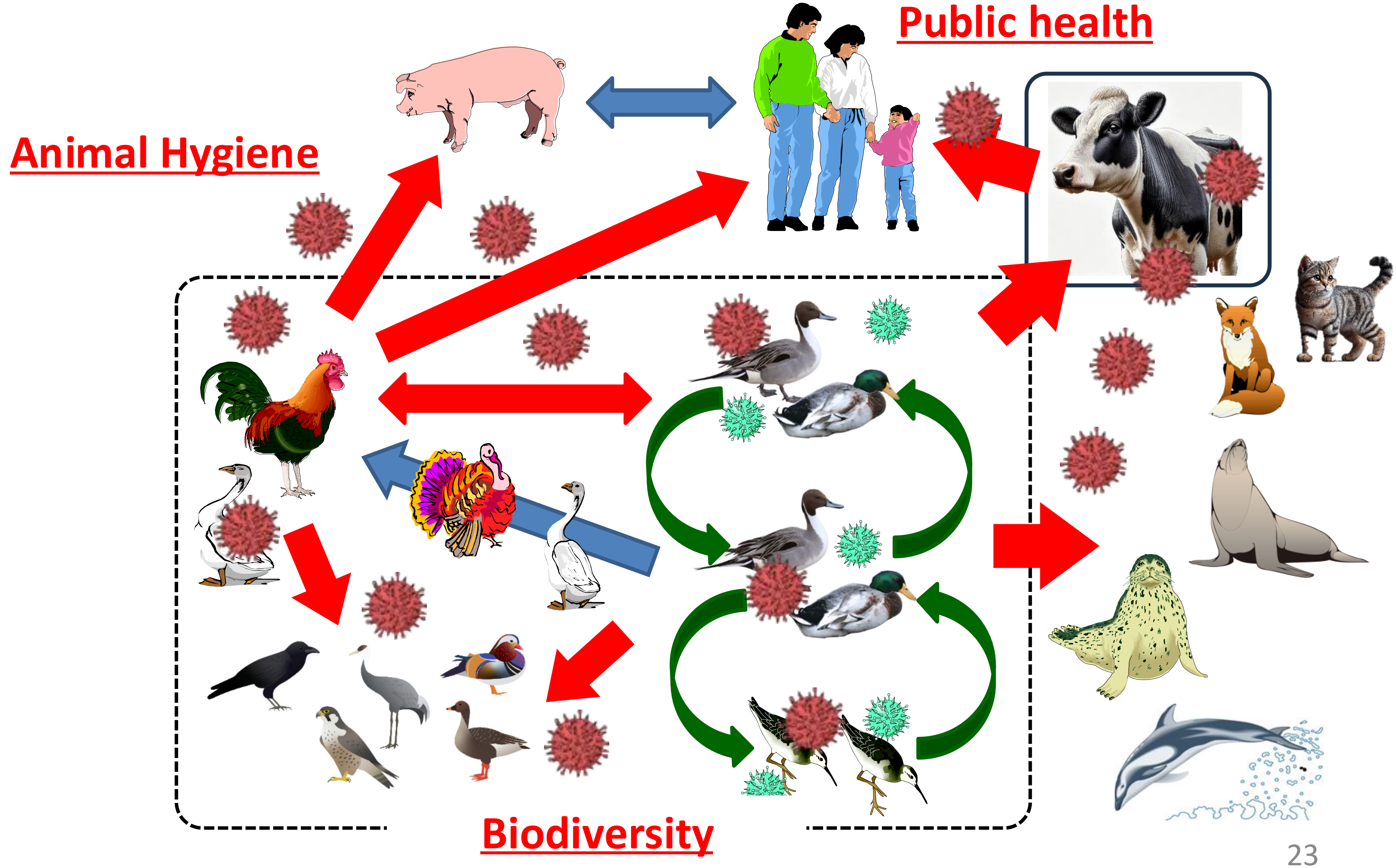
Present

2080

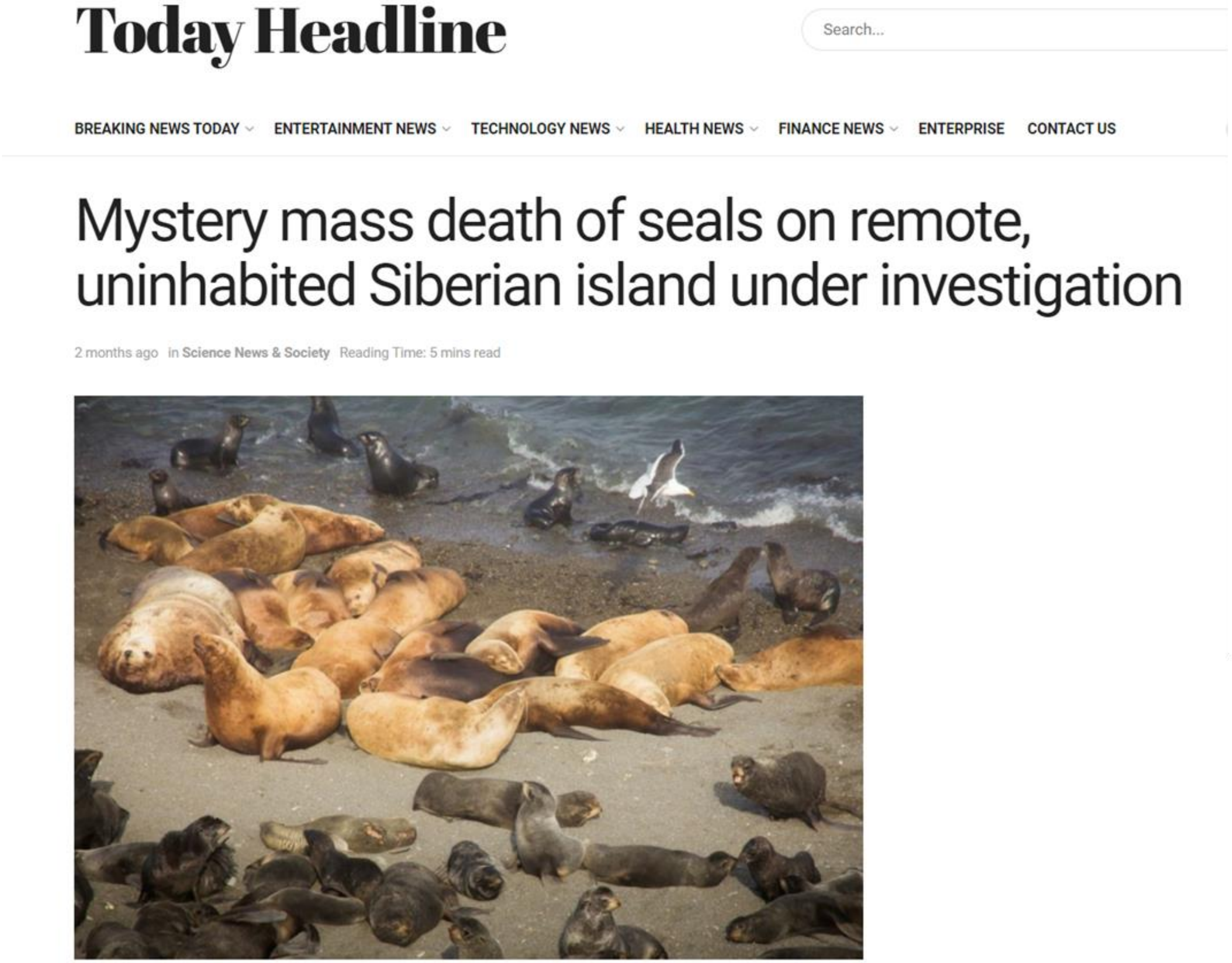
(RCP8.5)

Ikegami et al. unpublish data

Animals infected with highly pathogenic avian influenza viruses



Mass mortality event of marine mammals in Russia (Summer 2023)



Mystery mass death of seals on remote, uninhabited Siberian island under investigation

2 months ago in Science News & Society Reading Time: 5 mins read

https://todayheadline.co/mystery-mass-death-of-seals-on-remote-uninhabited-siberian-island-under-investigation/