



SC2 Dissemination Event
Sustainable Food Security

Vmerge : Emerging viral vector-borne diseases



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Vmerge project outline

What are the challenges? Why do they matter?

- Predict, detect and anticipate the risk of vector-borne diseases: **Emerging threat**
- Enhance collaborations between European and African research institutes: **Capacity building**
- Enhance collaborations between research and animal health decision makers: **Mutual interest**



Vmerge project outline

What is the approach?

- Development of new diagnostic tools
- Field work to describe, understand, model and predict the transmission of vector-borne diseases
- Material exchange between partners and trainings
- Common workshop between Vmerge partners and Mediterranean animal health network (REMESA)





Vmerge project outline

What is the main objective?

Address the **risk of introduction, emergence and spread** of known - or still unknown - **vector-borne viruses (VBV)** associated with mosquitoes (*Aedes* and *Culex* genera), and *Culicoides* biting midges:

- Improve our understanding of these emerging VBV and their potential for spread throughout northern Africa and Europe;
- Improve epidemiological surveillance strategies and tools for better disease detection.



Vmerge project outline

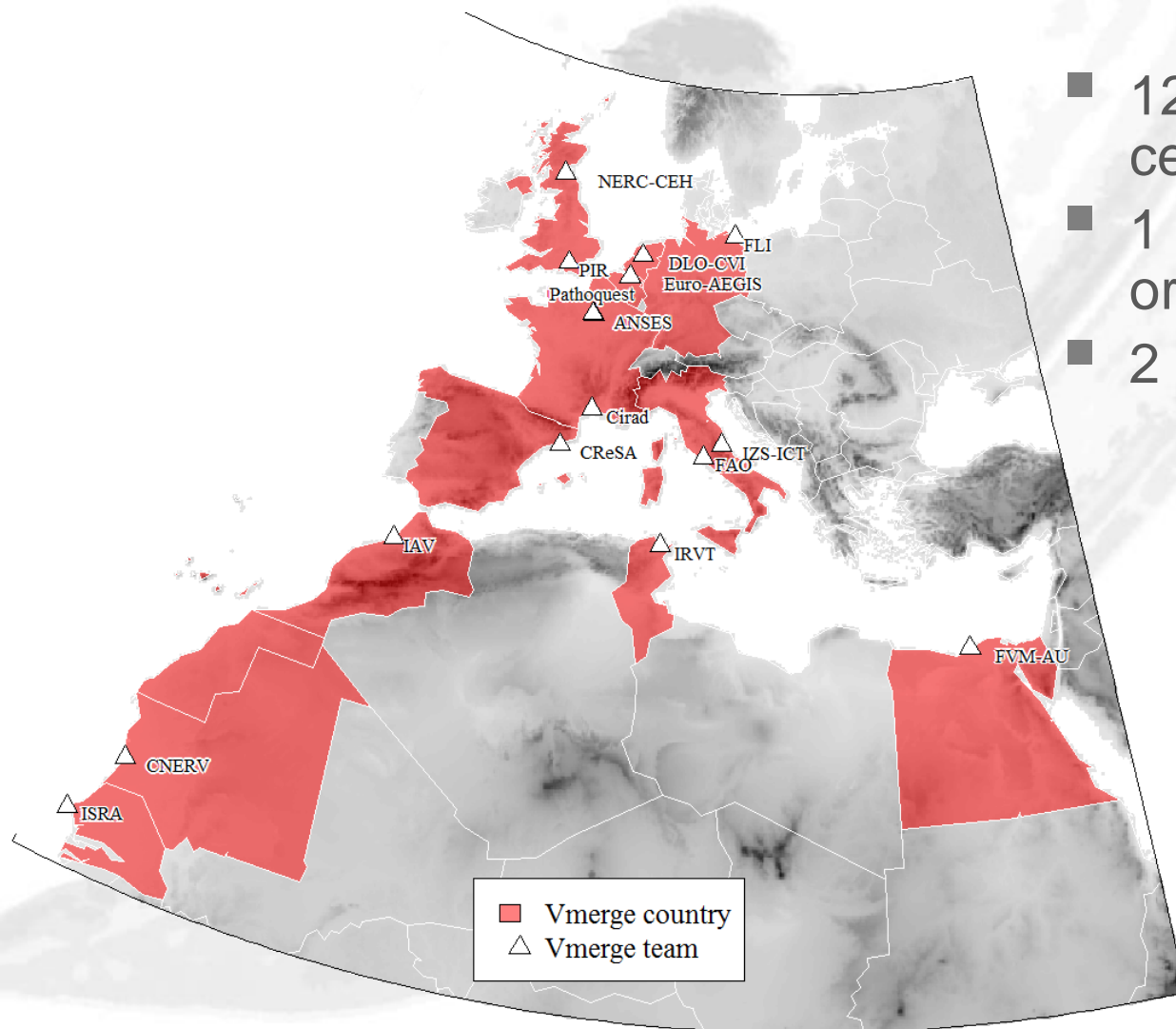
What are the main objectives?

- To provide innovations in diagnostic procedures for more reliable, more cost effective, and quicker identification of emerging VBV
- To improve our understanding of vector competence of insect populations in ecosystems at risk of emerging VBV;
- To model vector-population dynamics and virus transmission for better assessment of emergence and spread capacities of selected VBV
- To assess the existing surveillance networks for emerging VBV and propose new surveillance strategies



Vmerge consortium overview

16 partners, 12 countries



- 12 Research centres
- 1 International organization
- 2 SME



Project results





Vmerge results

- We produced new **DATA** to characterise interactions:
 - between virus and vectors
 - between vector populations/environment/hosts
- Dissemination via publications

Vmerge
Emerging viral vector-borne diseases

RESEARCH Project 2013-2016

Search

- ▶ Restricted access
- ▶ Data website
- ▶ Site map

The project | Overall strategy | What's new? | Related activities | **Publications**

Publications > Vmerge publications > The 2010 Northern Mauritania Outbreak in the *Camelus dromedarius* Species

Vmerge publications

- A High-Performance Multiplex Immunoassay for Serodiagnosis of Flavivirus-Associated Neurological Diseases in Horses (Vmerge 005)**
- Duplex Real-Time RT-PCR Assays for the Detection and Typing of Epizootic Haemorrhagic Disease Virus (Vmerge 004)**
- Complete Coding Genome Sequence of Putative Novel Bluetongue Virus Serotype 27 (Vmerge 003)**
- The 2010 Northern Mauritania Outbreak in the *Camelus dromedarius* Species**
- A First Attempt at Modelling Red Deer (*Cervus elaphus*) Distributions Over Europe (Vmerge002)**

Comprehensive Phylogenetic Reconstructions of Rift Valley Fever Virus (Vmerge000)

Another Vmerge paper!

Rift valley fever (RVF) is a mosquito-borne disease of domestic and wild ruminants caused by RVF virus (RVFV), a phlebovirus (Bunyaviridae). RVF is widespread in Sub-Saharan Africa. In September of 2010, an RVF outbreak occurred in northern Mauritania involving mass abortions in small ruminants and camels (*Camelus dromedarius*) and at least 63 human clinical cases, including 13 deaths. In camels, serological prevalence was 27.5–38.5% (95% confidence interval, $n=279$). For the first time, clinical signs other than abortions were reported in this species, including hemorrhagic septicemia and severe respiratory distress in animals. We assessed the presence of RVFV in camel sera sampled during this outbreak and generated whole-genome sequences of RVFV to determine the possible origin of this RVFV strain. Phylogenetic analyses suggested a shared ancestor between the Mauritania 2010 strain and strains from Zimbabwe (2269, 763, and 2373), Kenya (155_57 and 561B8), South Africa (Kakamas, SA75 and SAS1VanWyck), Uganda (Entebbe), and other strains linked to the 1987 outbreak of RVF in Mauritania (OS1, OS3, OS8, and OS9).

[Access to the publication](#)

[Ahmed Bezeid El Mamy](#)

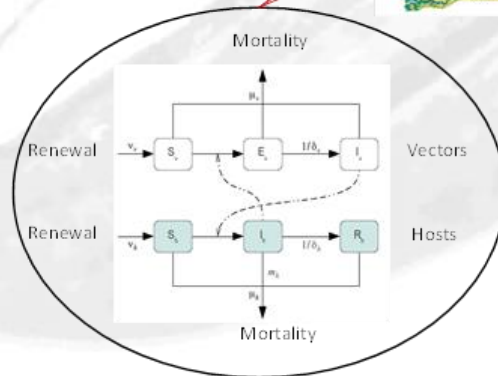
Centre National d'Elevage et de Recherches Vétérinaires

Mauritania



Vmerge results

- We produced new **TOOLS**:
 - Molecular and serological tools
 - Software to sample and predict distribution of vectors: VECMAP
 - Models to predict risk of transmission in endemic and potentially epidemic areas
- Dissemination via publications, and technology transfer to partners



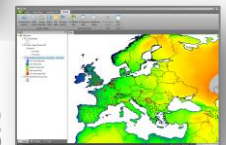
Administrato



Field teams

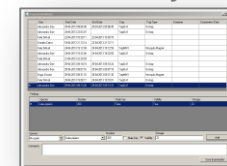


platform



GIS

Laboratory





Vmerge results

- We produced **SUPPORT to decision/policy makers**:
 - Information and analysis of the risk of emergence
 - Analysis of the current surveillance system
 - Guidelines for surveillance
- Dissemination via regular newsletters, and common workshops Vmerge/Animal health networks



Impact and Lessons learnt

UK Netherlands
Belgium
France Germany
Spain Italy
Morocco Tunisia
Mauritania Egypt
Senegal





Impact

- **Better understanding** on how **vector-borne diseases** emerge, are introduced and spread
- **Increase capacities of national laboratory** to detect the diseases
- **Disseminate tools** to better predict the risk of transmission
- **Increase the level of preparedness** of countries against the vector-borne diseases

Impact

- **Enhance interactions** between research institutes and animal health services:
 - Join Vmerge/REMESA workshops during the project
 - Join meeting Vmerge/Animal health networks in Mediterranean basin and West and Central Africa for the Vmerge final meeting
 - Regional policy meeting between Vmerge and Chief veterinary officers





Lessons learnt

- Enhancing collaborations between north/southern research institutes and between research/surveillance-policy actors

- Is facilitated by:
 - Long history of collaborations between partners
 - Many research institutes involved have long history of interactions with animal health decision makers

- Is made difficult by:
 - Different expectations between partners (high-level publications *versus* capacity building)
 - Different time scales, different interaction cultures between research, risk management and policy



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Thank you

