

# Vector-borne animal diseases and the environment

## Understanding the biological factors in emergence

**B**etween 1990 and 2000, almost a quarter of the 300 diseases that emerged in man were vector-borne. Vector-borne diseases, which are transmitted by arthropods such as insects (mosquitoes, midges, bugs, etc) or mites (ticks, fleas, etc), are particularly sensitive to their environment, and any changes in that environment may contribute to their emergence. CIRAD's role is to explain the biological processes involved so as to come up with solutions for preventing, monitoring and controlling such diseases.



Restraining a zebu before taking a blood sample, Madagascar .  
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Small ruminant trade flows from countries in the Horn of Africa (Ethiopia, Kenya, Somalia, Eritrea) to Yemen and Saudi Arabia.

Source: *Abdo-Salem S et al., 2010*

**D**isease emergence has a range of causes. Over the past 60 years, more than 300 infectious diseases have emerged in man, of which two thirds are of zoonotic origin (transmitted between man and animals). Over the decade 1990-2000, around a quarter of the diseases that emerged were vector-borne. In fact, vector-borne diseases are particularly sensitive to changes in their environment, in terms of host population levels, climate, plant cover or movements of people and animals. Modelling serves to explain the mechanisms at play, assess the importance of the various factors, test control scenarios and anticipate the future.

### Rift Valley fever

#### Role of animal movements in the spread of the virus

Rift Valley fever (RVF) is a zoonotic arbovirus caused by a Phlebovirus (*Bunyaviridae*), transmitted by mosquitoes (genera *Aedes* and *Culex* in particular). Domestic ruminants are the usual hosts of the virus, but humans may also be infected. Certain major epidemics have affected tens of thousands of people. In addition to direct economic losses (abortion and neonatal mortality in ruminants), RVF is a strong constraint on animal and animal product exchanges. The geographical distribution of the disease, which was hitherto restricted to Africa, spread suddenly to the Arabian Peninsula in 2000 and the Indian Ocean in 2008.

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CIRAD, in collaboration with the Institut Pasteur in Madagascar and FOFIFA-DRZV, analysed the emergence factors and modelled the mechanisms by which RVF spreads, using social network analysis (SNA) methods. This work revealed that live ruminant trade contributed to the spread of the virus, on a local, regional and even continental scale. As the results of serological studies of small ruminants suggest, the RVF virus probably did not persist on the Arabian Peninsula after the 2000 epizootic. However, a risk analysis conducted in collaboration with Dhamar University and the veterinary services in Yemen showed that there was a real risk of its reintroduction via the trade in ruminants. The recent epizootic in northern Mauritania, in a particularly arid zone, demonstrated, if proof were needed, the virus' significant capacity to spread. Spatial and dynamic modelling by CIRAD has served to pinpoint zones at risk of transmission in the event of the disease being introduced into previously unaffected areas – Europe, Asia. It is thus possible to optimize surveillance methods, which are essential in protecting animal and human populations against the disease.

## Bluetongue

### Assessing the effect of climate change on the risk of transmission

Climate change may cause modifications in disease distribution (extension or reduction) and contribute to the emergence of certain diseases. The many factors involved are intrinsically linked. To estimate future risk, it is vital to quantify their effects precisely and understand the mechanisms at play.



Female *Culicoides nubeculosus* gorged with blood.  
© JB Ferre/EID Méditerranée

In collaboration with climate scientists and epidemiologists from the University of Liverpool, CIRAD has developed an approach that serves to assess the effect of past and future changes in climate on the risk of transmission of an infectious disease. The approach has been applied to bluetongue, a viral disease of ruminants transmitted by certain midges of the genus *Culicoides*. Bluetongue, which was seen as an exotic tropical disease until 1998, subsequently caused one of the most extensive epizootics ever seen in Europe (more than 110 000 foci in 14 countries).

The modelling approach showed that the climate over the past twenty years has favoured the emergence of the disease, albeit via different mechanisms in northern and southern Europe.

In southern Europe, the climate has favoured the spread of and increases in population levels of the Afro-Asian vector *Culicoides imicola*, whereas in the North, it has shortened the virus cycle within the vector and increased the daily biting rate of native *Culicoides*. The approach is also being used to simulate future changes in the risk of transmission in space and time and the uncertainty associated with such simulations.



Direct removal of *Culicoides* from a sheep to assess the biting rate.  
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Flock of sheep in Corsica.  
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## Partners

- **France:**  
ANSES, Agence nationale de sécurité sanitaire; Ministry of Agriculture, Food, Fisheries, Rural Affairs and Regional Planning

- **Madagascar:**  
FOFIFA-DRZV, Centre national de recherche appliquée au développement rural; Institut Pasteur

- **United Kingdom:**  
University of Liverpool

- **Yemen:**  
veterinary services; Dhamar University