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SVPF
SOCIÉTÉ VÉTÉRINAIRE PRATIQUE DE FRANCE

XIIe Rencontres de Santé publique vétérinaire
École du Val de Grâce, le 04 décembre 2024
« Actualités des maladies vectorielles : connaissances, lutte, gestion »

Maladies vectorielles

quels mécanismes d'émergence ?

Thomas Balenghien
balenghien@cirad.fr

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Définition
maladie à transmission vectorielle

Maladie associée à un agent infectieux qui est transmis d’un organisme à un autre organisme par un arthropode piqueur de manière active

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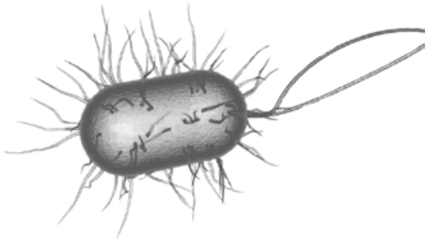

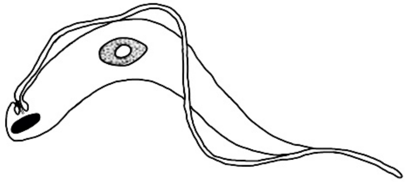

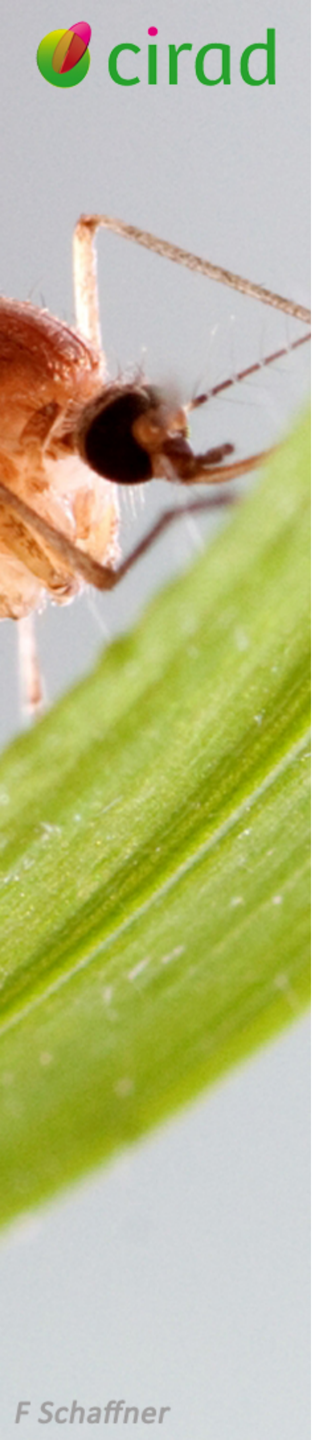

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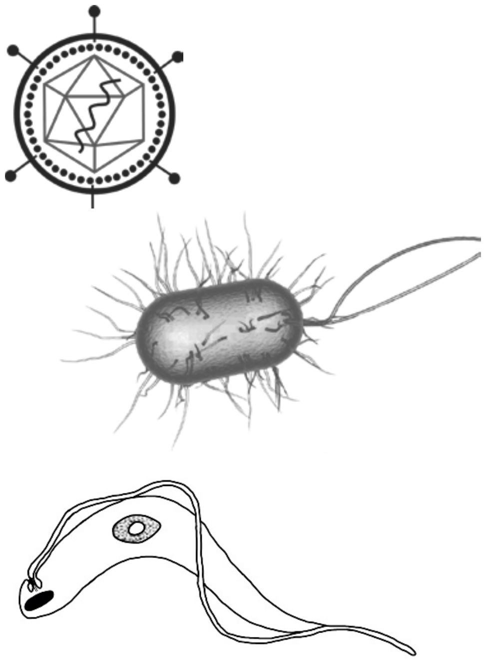

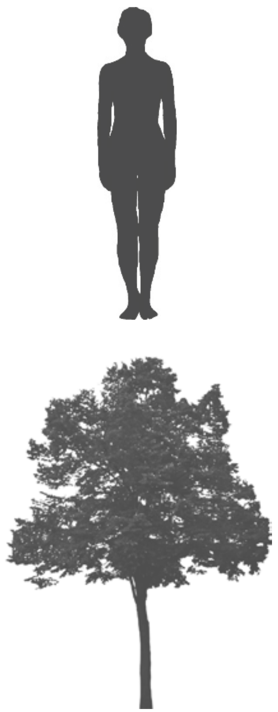

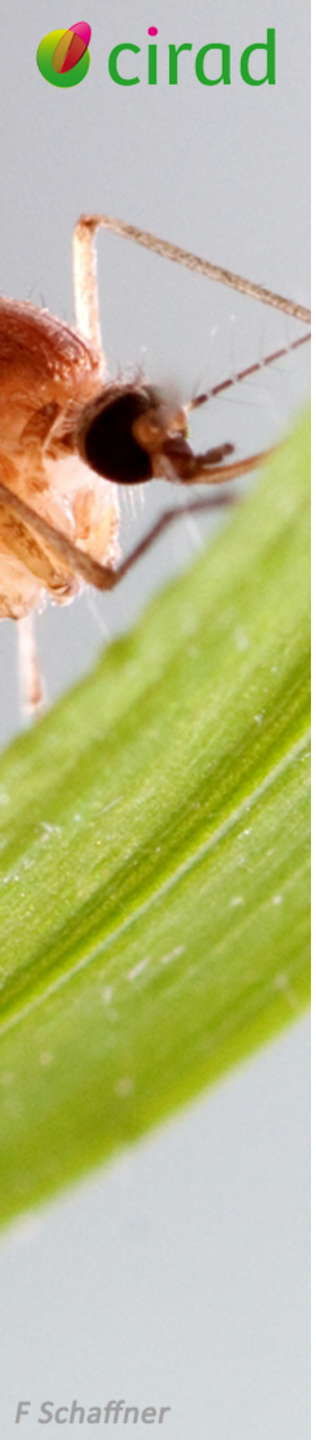

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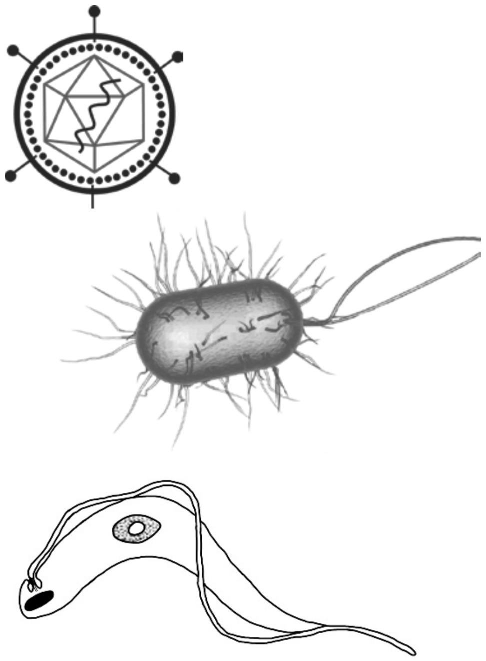

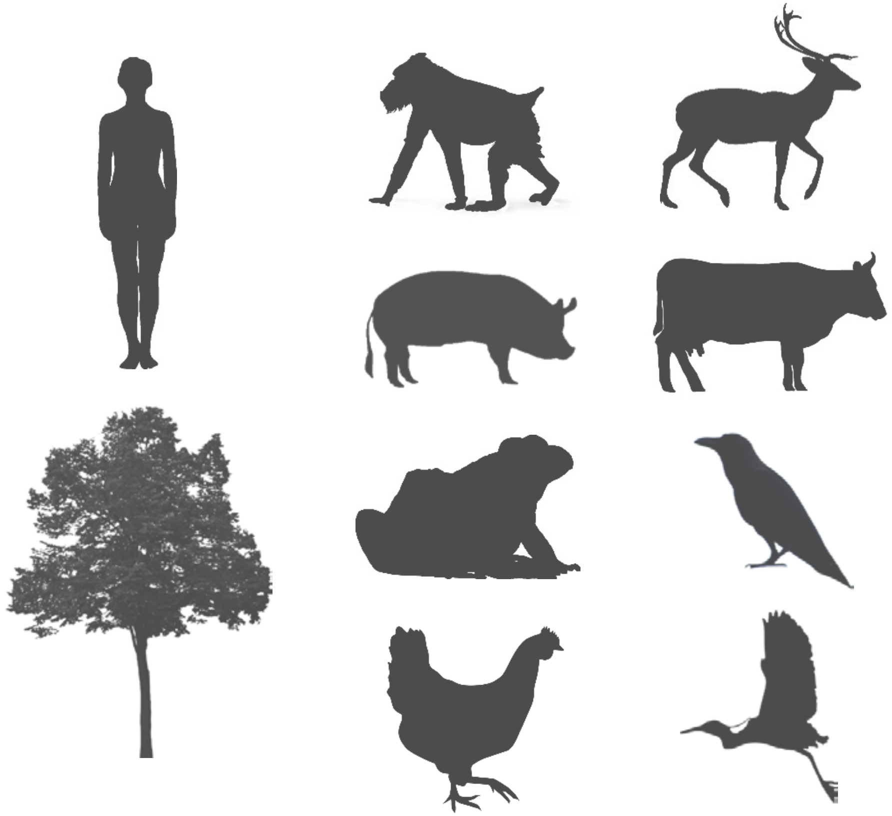

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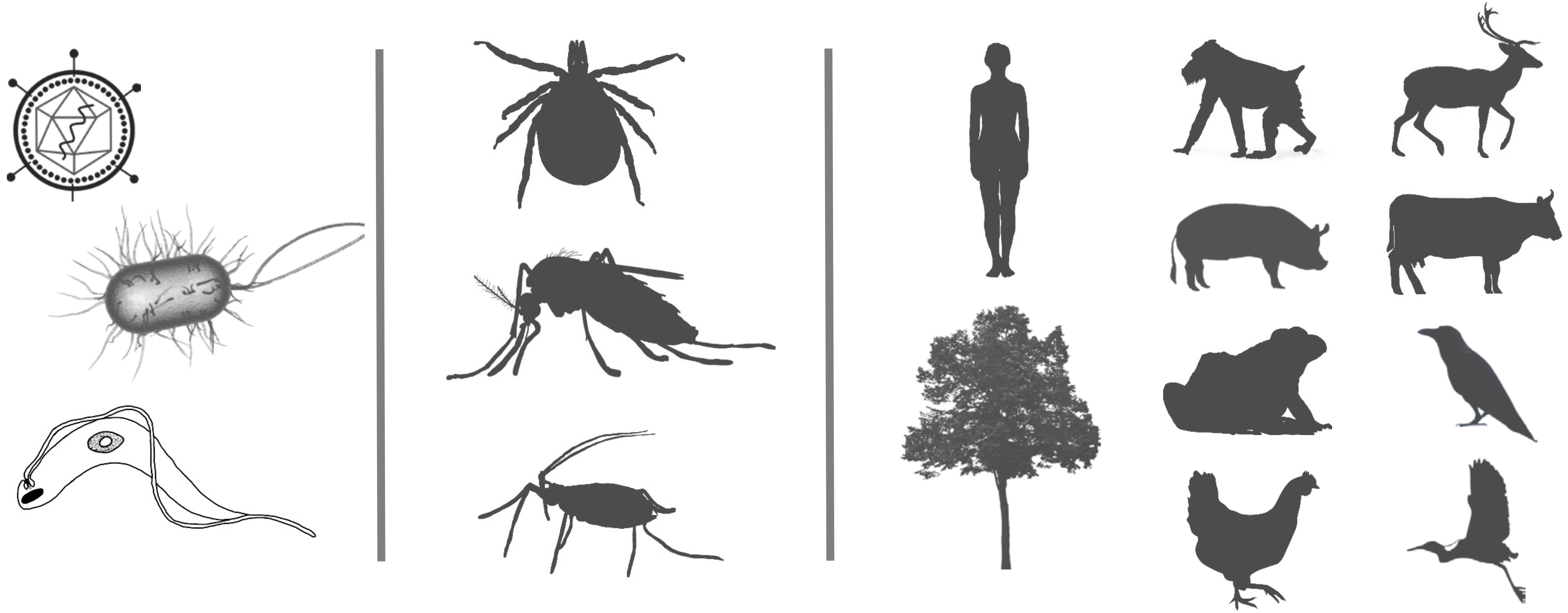
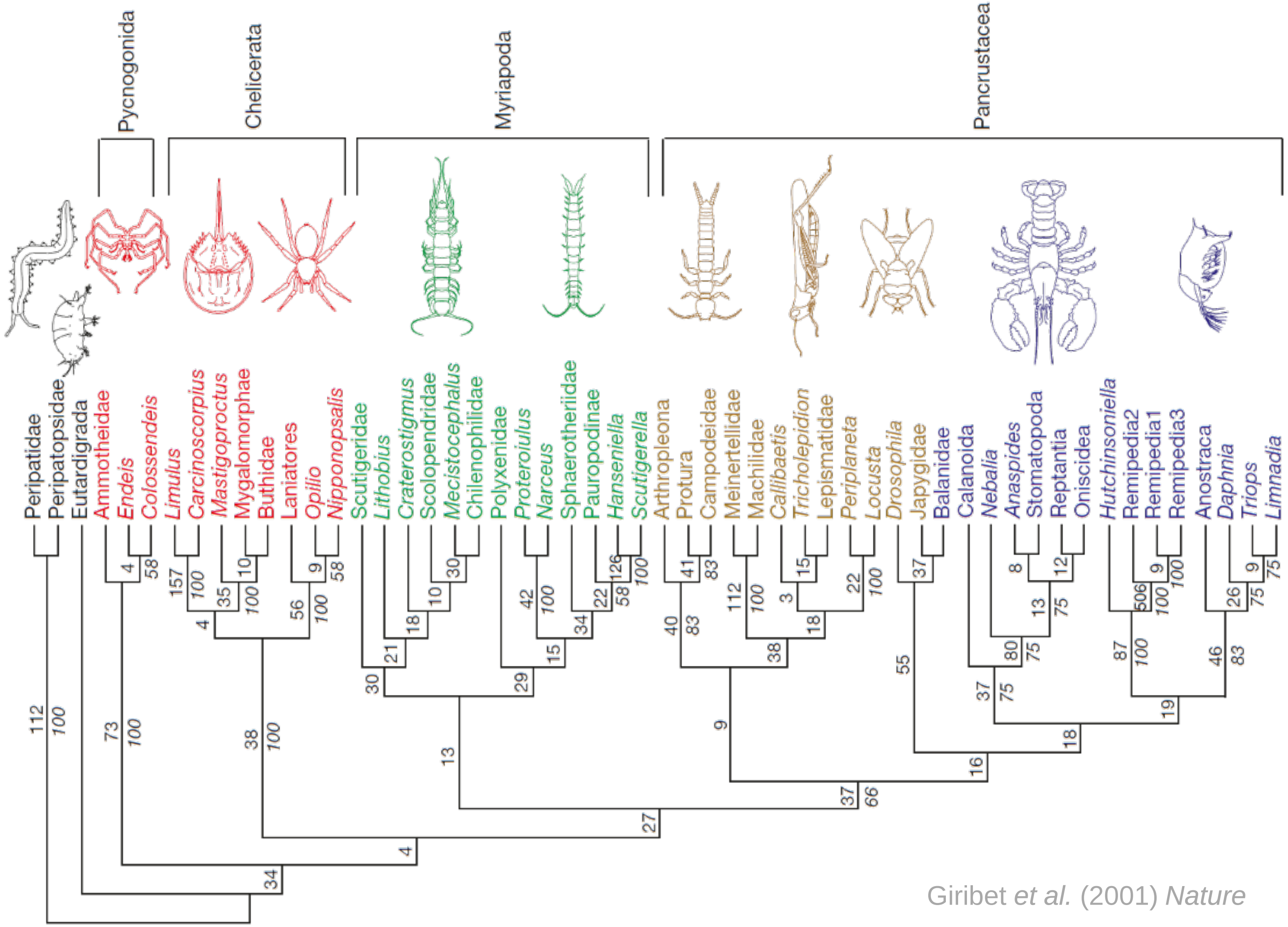


Hématophagie et évolution
grande diversité des vecteurs



Giribet *et al.* (2001) *Nature*

<u>Arthropode</u> (500 Ma)

- du grec :
  arthron « articulation »
  podos « pied »
- corps segmenté :
  métamères hétéronomes, munis chacun d'une paire d'appendices articulés
- cuticule (exosquelette)
  mue de croissance
  mue de métamorphose
- groupe le plus divers,
  le plus abondant

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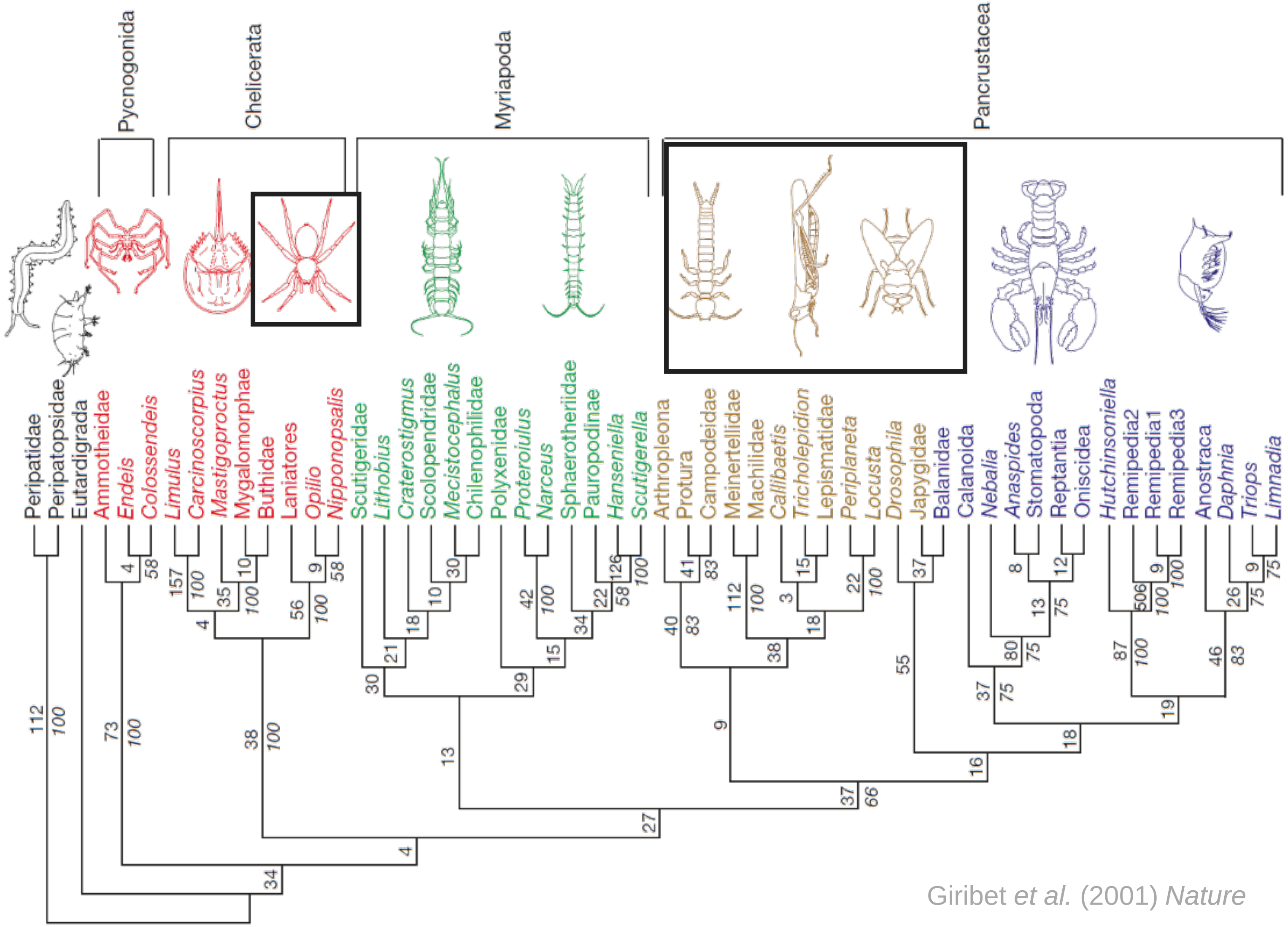

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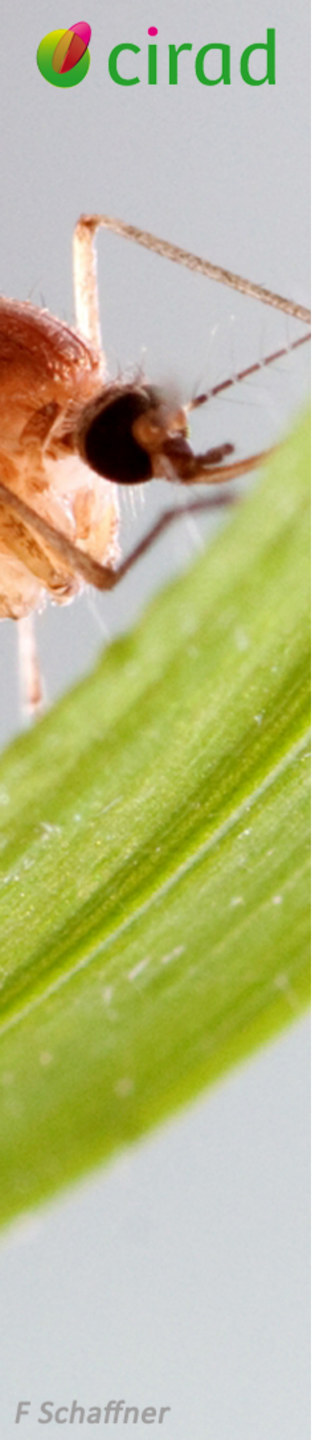

Hématophagie et évolution
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Hexapoda (sous-embranchement),
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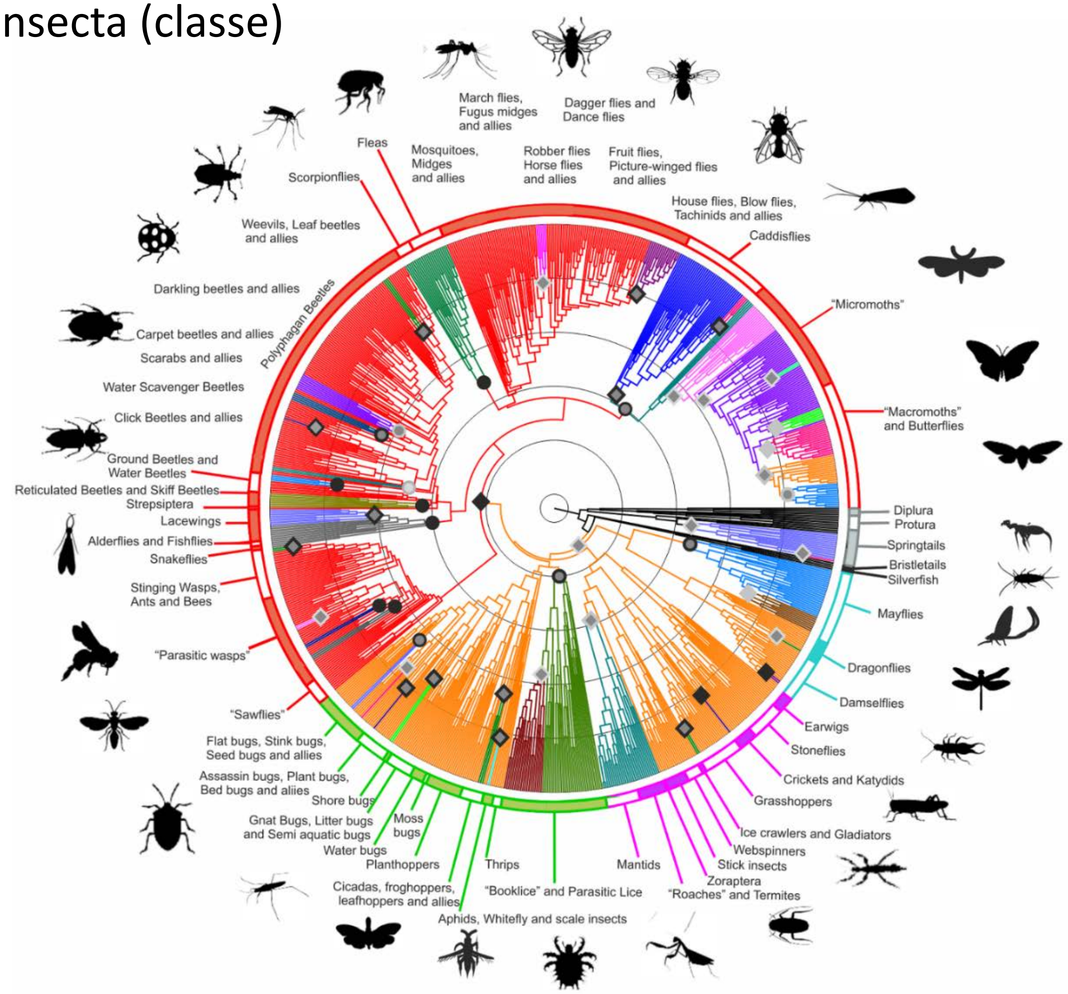

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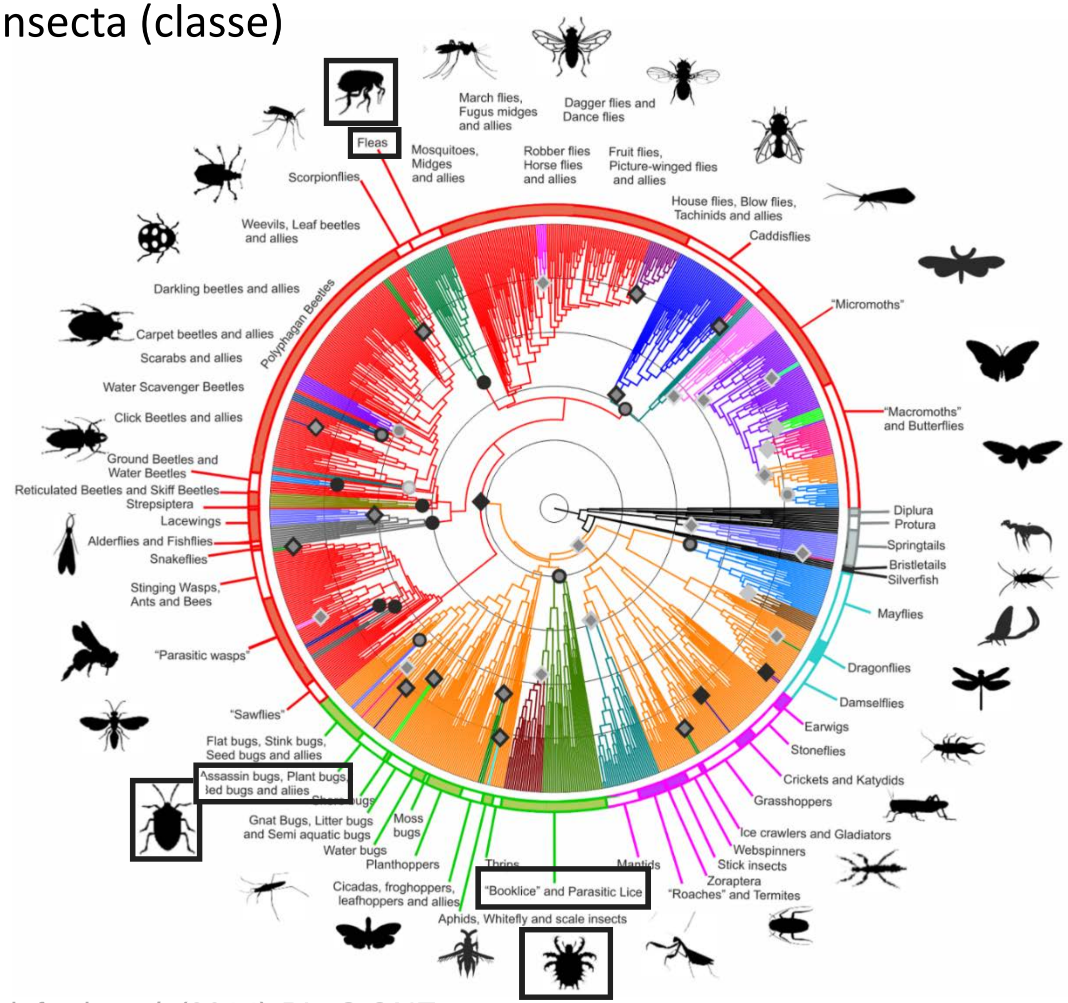

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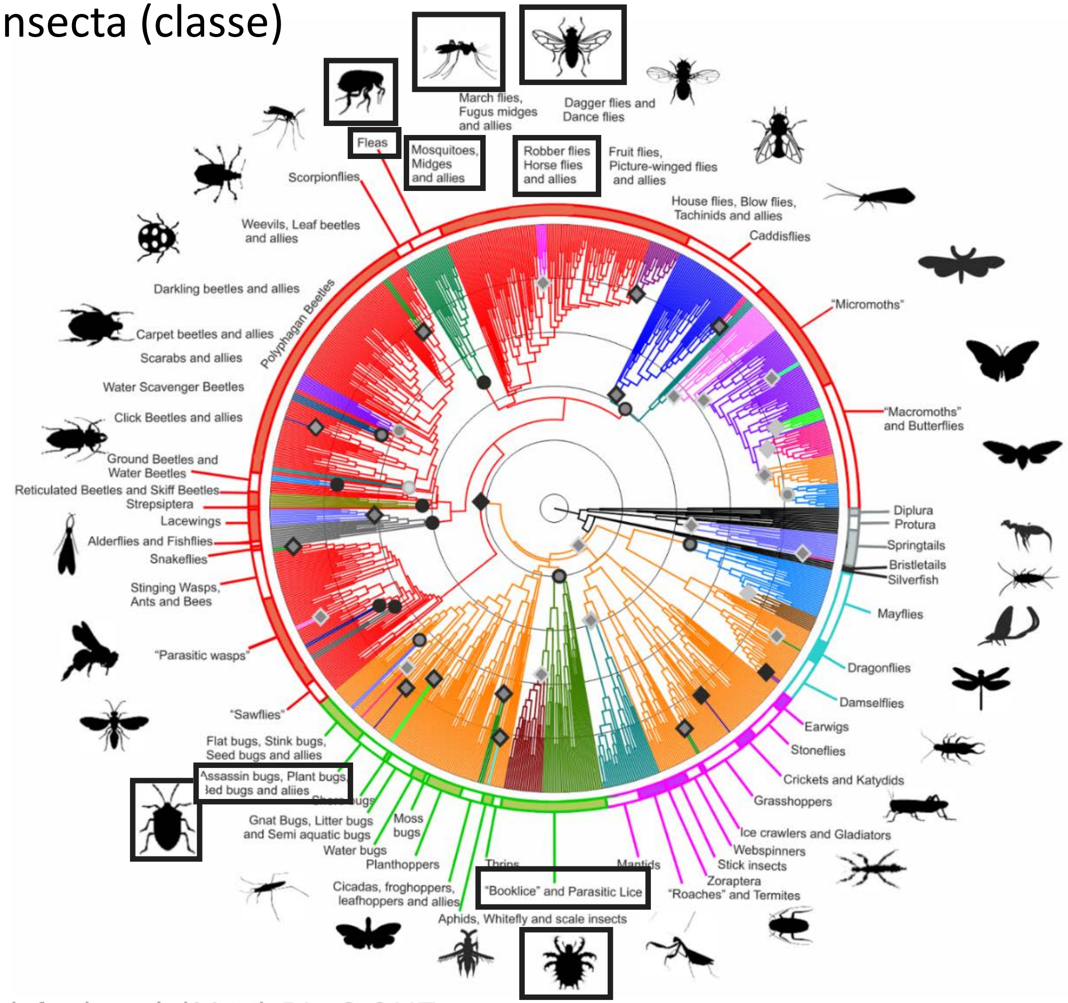

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Diptera (ordre)

Ceratopogonidae

Culicidae

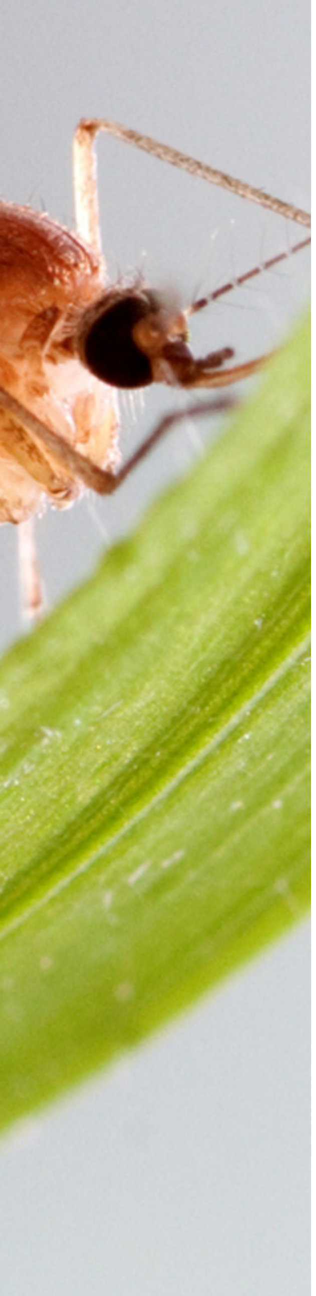
Tabanidae

Muscidae

Psychodidae

Simuliidae

Glossinidae



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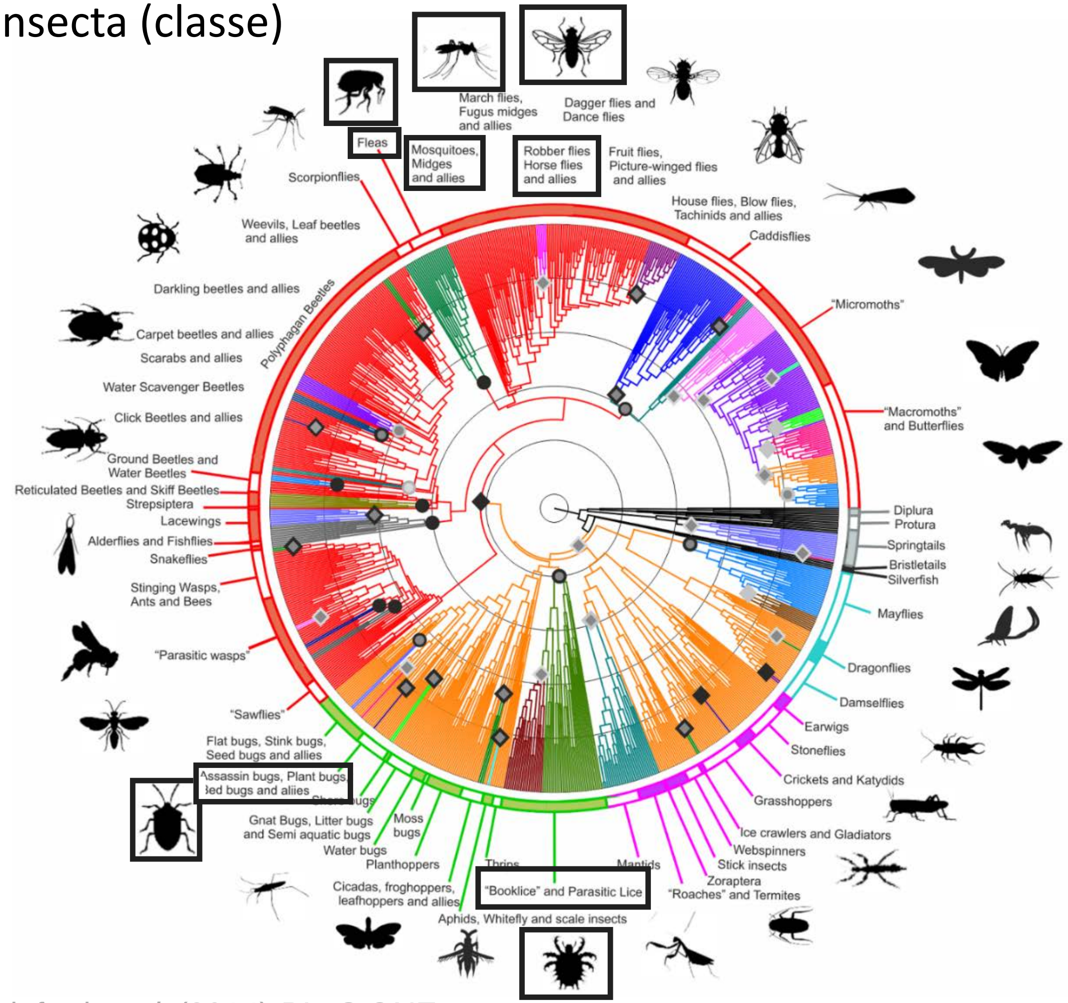

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Diptera (ordre)

Fièvre catarrhale ovine,
Maladie épizootique hémorragique,
Schmallenberg, Oropouche

Ceratopogonidae

Culicidae

Fièvre West Nile,
Fièvre de la
vallée du Rift

Tabanidae

Dermatose nodulaire contagieuse,
Besnoitiose bovine

Muscidae

Leishmaniose,
Phlebovirus

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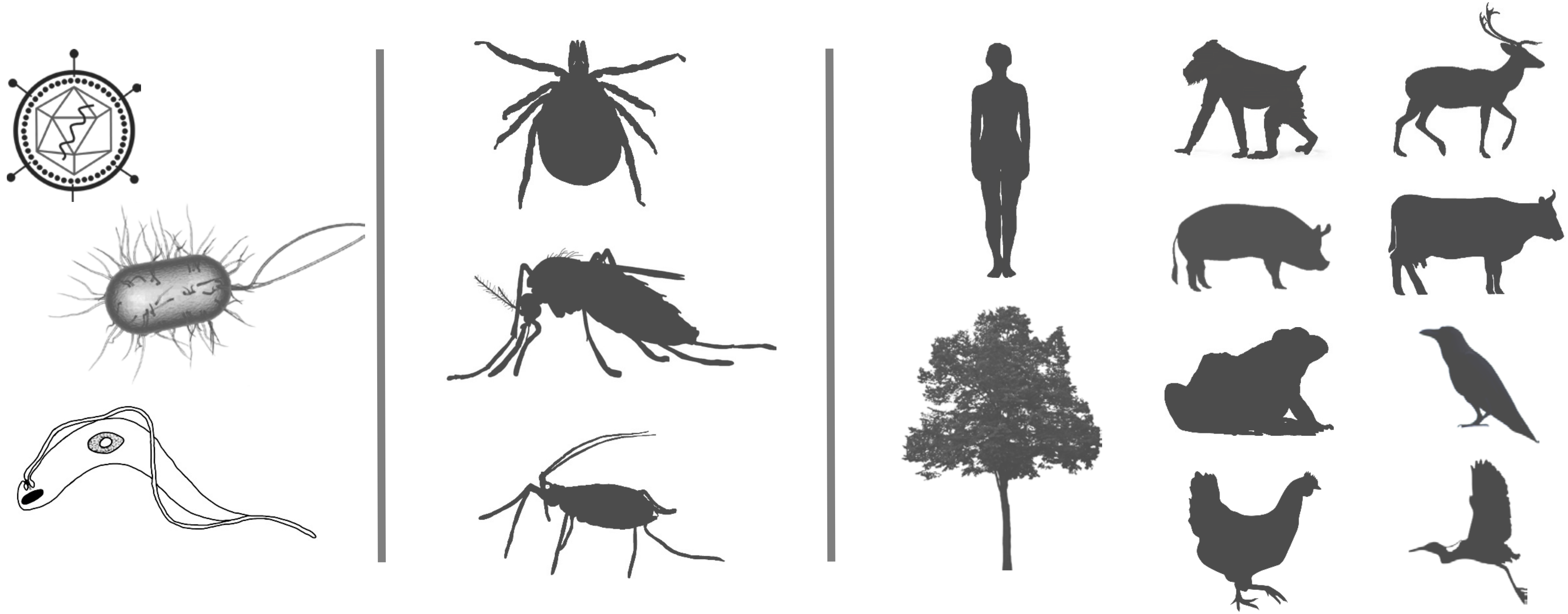

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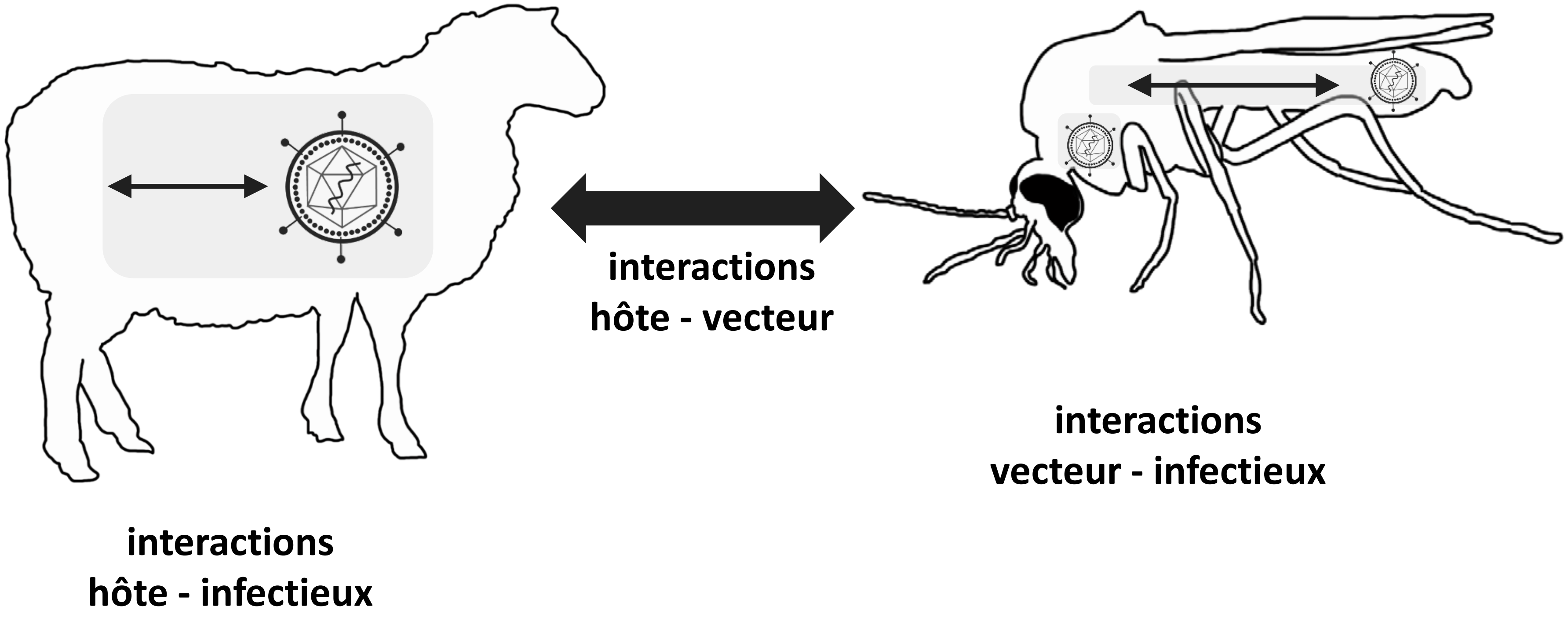
Les systèmes vectoriels
interactions entre trois acteurs



Les systèmes vectoriels

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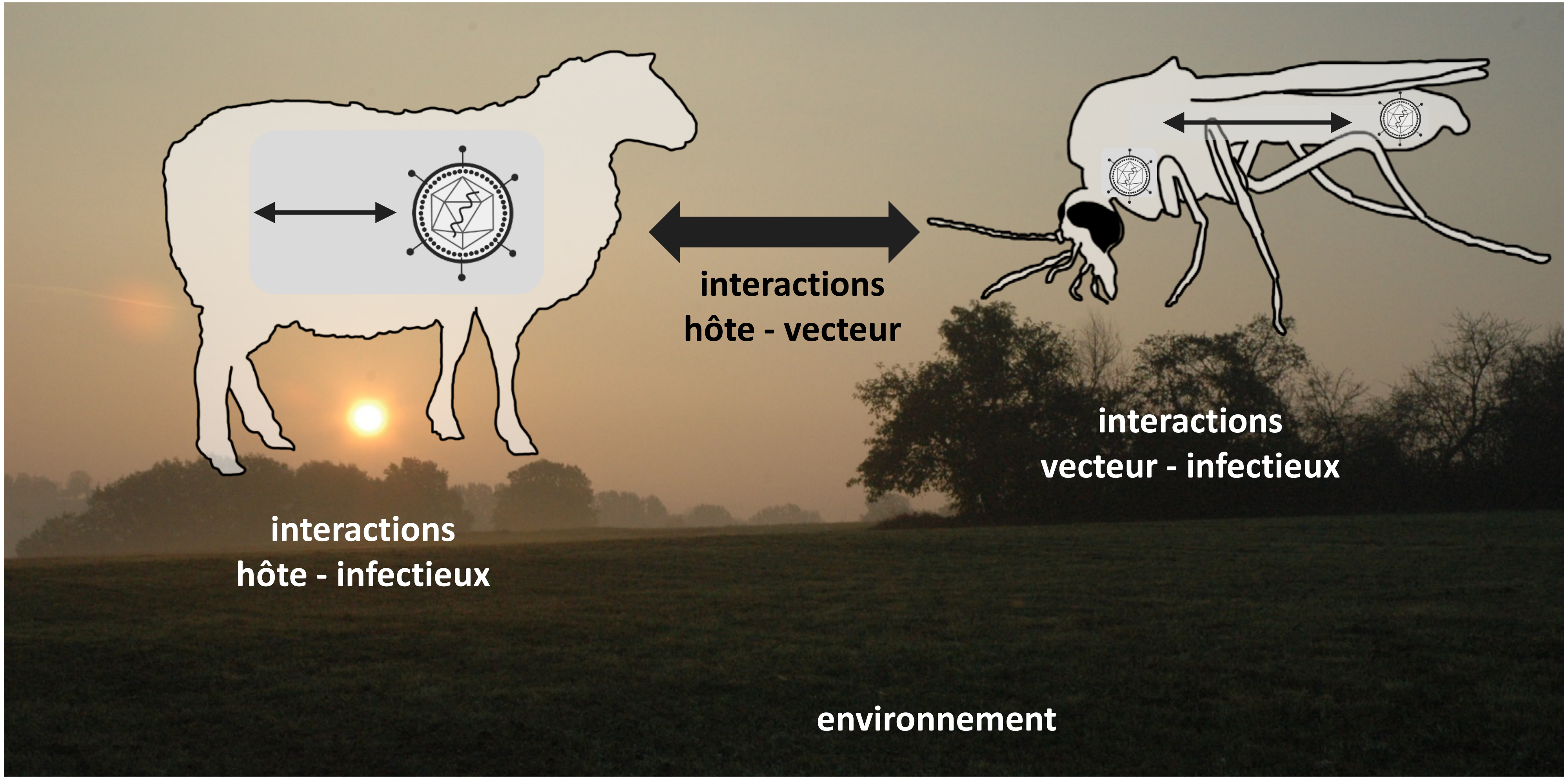
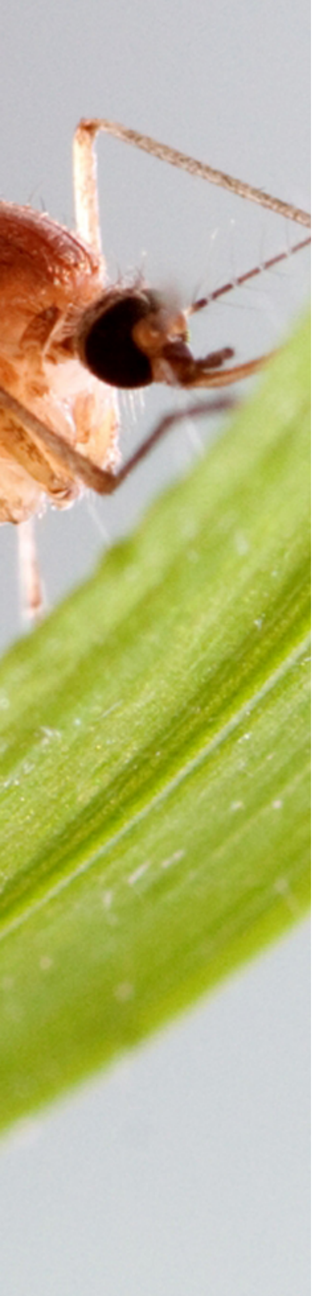


Emergence, recrudescence

un seul exemple illustrant la période



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Le Monde
MARDI 10 SEPTEMBRE 2024

Epizooties : la triple plaie du bétail français

Elevages ovins, bovins et caprins sont touchés par trois virus, véhiculés par des moucherons culicoïdes

Depuis un an, ce ne sont pas un, ni deux, mais bien trois fléaux qui se sont abattus sur les élevages ovins et bovins français. Ce fut d'abord, en août 2023, la détection d'une nouvelle souche du sérotype 8 de la fièvre catarrhale ovine (FCO) dans l'Aveyron puis, en septembre 2023, l'arrivée sur le territoire de la maladie hémorragique épizootique (MHE) depuis l'Espagne vers les Pyrénées-Atlantiques, et enfin, le 5 août, la détection d'un premier cas d'un nouveau sérotype, le 3, de la FCO en provenance de Belgique vers le Nord. Trois épizooties potentiellement mortelles pour les bêtes. Trois virus véhiculés par les mêmes moucherons, les culicoïdes.

« La situation française actuelle est inédite en Europe, donc ça nous inquiète », s'alarme Emmanuel Garin, vétérinaire épidémiologiste pour le réseau des Groupements de défense sanitaire (GDS France). *« Pour un élevage, être touché par une maladie, ça a des impacts sur la santé et le bien-être des bêtes, sur la production, sur le coût des traitements vétérinaires. Mais si en plus, quelques mois après, c'est au tour d'une deuxième puis d'une troisième maladie, on ne sait pas ce que ça va avoir comme conséquence ; c'est une grande inconnue »*, explique l'expert, qui conseille les éleveurs pour améliorer la santé et le bien-être de leurs animaux.

La carte retraçant l'avancée des différents fronts – régulièrement mise à jour par le GDS France – fait déjà état de plusieurs cas de cocirculation virale. Un grand quart sud-ouest est touché à la fois par le sérotype 8 de la FCO et la MHE, tandis que la Nièvre, la Saône-et-Loire et le Doubs accueillent les deux sérotypes de la FCO.

Injection d'antibiotique à une bête atteinte de la fièvre catarrhale ovine, à Aspremont (Hautes-Alpes), le 7 septembre. THIBAUT DURAND/MAXPPP

qualité des produits (viande, lait) issus des animaux malades.

Depuis la réémergence de la maladie en 2015, les symptômes semblaient s'être atténués, peut-être en raison d'une immunité collective acquise au gré des vagues successives. La FCO est depuis considérée comme endémique ; le vaccin contre le sérotype 8 n'est plus remboursé par l'Etat. L'arrivée d'une nouvelle souche il y a un an a pourtant durement touché les élevages. *« Personne ne s'attendait à l'émergence d'une nouvelle sou-*

Si elle peut avoir des conséquences graves pour les animaux, la fièvre catarrhale ovine n'affecte pas les humains

culicoïde. Il faudrait plutôt raisonner au pluriel, tant les espèces sont nombreuses (80 à 100 en France, plus de 1400 dans le monde), et tant il est difficile de le distinguer pris isolément – les anglophones parlent de *« no-see-ums »* (expression dérivée de *« no-see-them »* : « on ne les voit pas »).

Moucherons portés par le vent

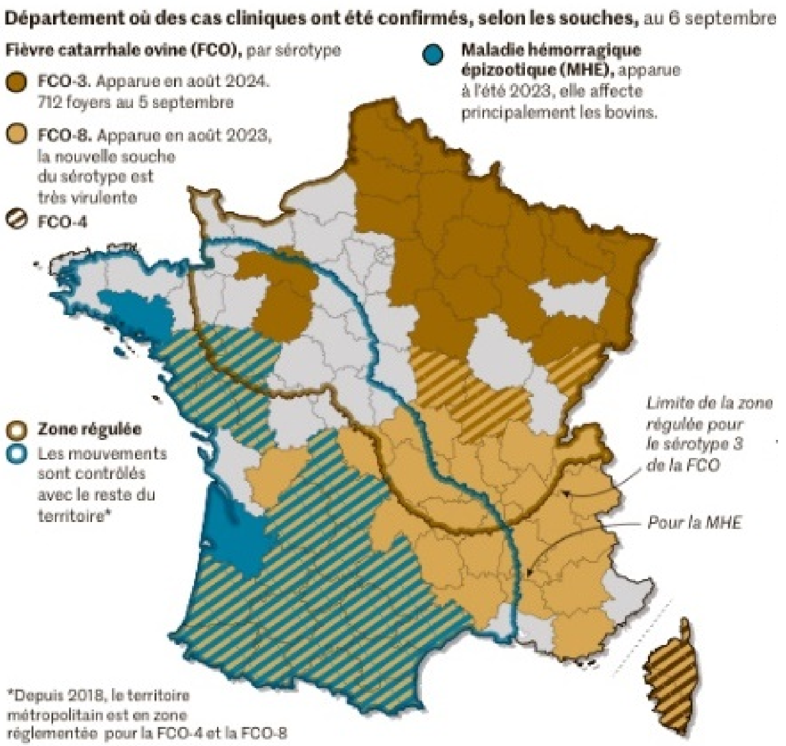
A l'image du moustique-tigre transportant les virus de la dengue et du chikungunya dans sa salive, les culicoïdes sont les vecteurs de

pération internationale en recherche agronomique pour le développement, qui précise que la souche française est identique à celle retrouvée en Tunisie. *« Les culicoïdes ne sont pas des espèces invasives, mais elles se dispersent facilement »*, explique la chercheuse. Quant à l'introduction des différents sérotypes de la FCO, les experts privilégient plutôt le transport d'animaux déjà contaminés, dont le sang, aspiré par une femelle culicoïde pour faire maturer ses œufs, est ensuite transporté

La maladie épizootique hémorragique, surtout présente chez les bovins, provoque fièvre, anorexie, détresse respiratoire

pératures augmentent, plus le temps nécessaire au virus pour passer des intestins aux glandes salivaires de l'insecte, et donc rendre possible une nouvelle contamination, est réduit. *« C'est un paramètre très important parce que si un moucheron met plutôt cinq ou vingt jours pour répliquer son virus, ça joue beaucoup sur sa capacité de transmission »*, souligne l'entomologiste.

Mais alors, pour se prémunir de ces propagateurs de virus, ne suffirait-il pas de s'en débarrasser ? Plus facile à dire qu'à faire. A la différence des moustiques, les culicoïdes ne pondent pas leurs œufs en milieu aquatique, ce qui rend impossible l'usage de larvicides ciblés. Ils privilégient des endroits humides et riches en matières organiques comme les trous dans l'écorce des arbres, les fruits en décomposition ou plus particulièrement le fumier. La vaporisation d'insecticide dans les hangars n'a pas prouvé son efficacité. Quant à l'application de crème à base de deltaméthrine (un insecticide) directement sur les animaux, il faudrait la renouveler tous les dix jours pour une protection à long terme. Avec des risques de diffusion dans l'environnement de ce pesticide connu pour engendrer de la résistance



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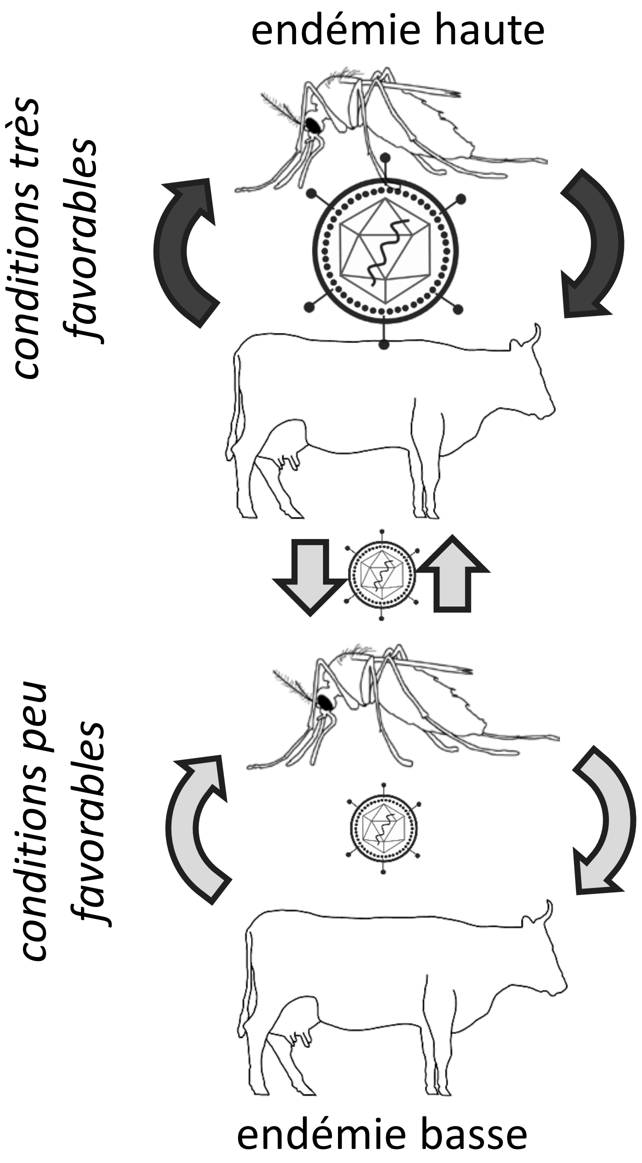

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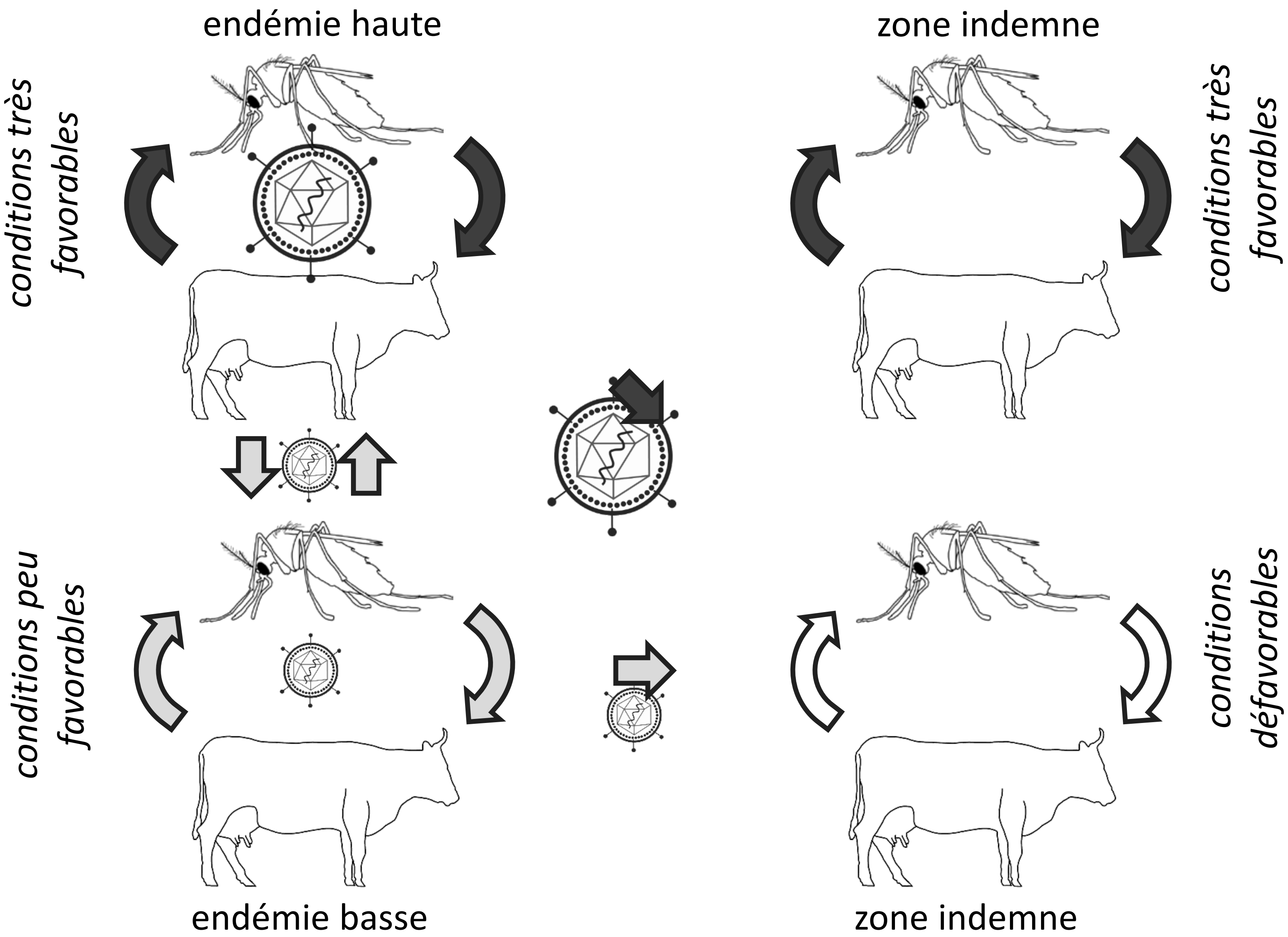

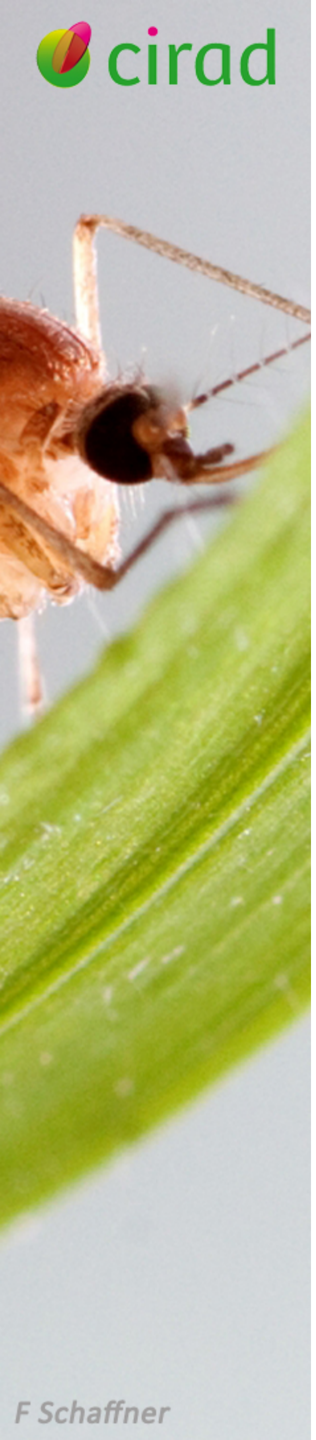

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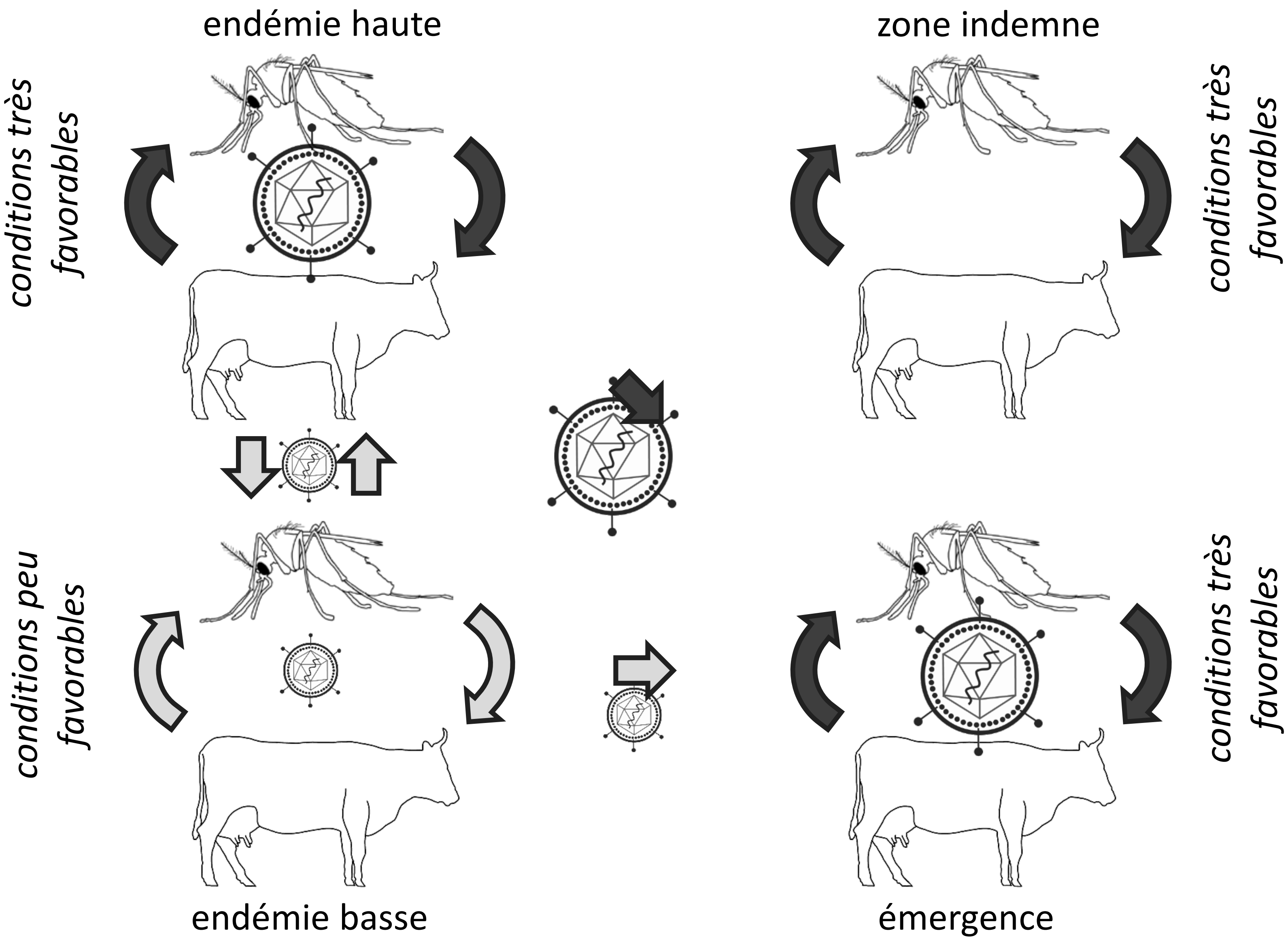

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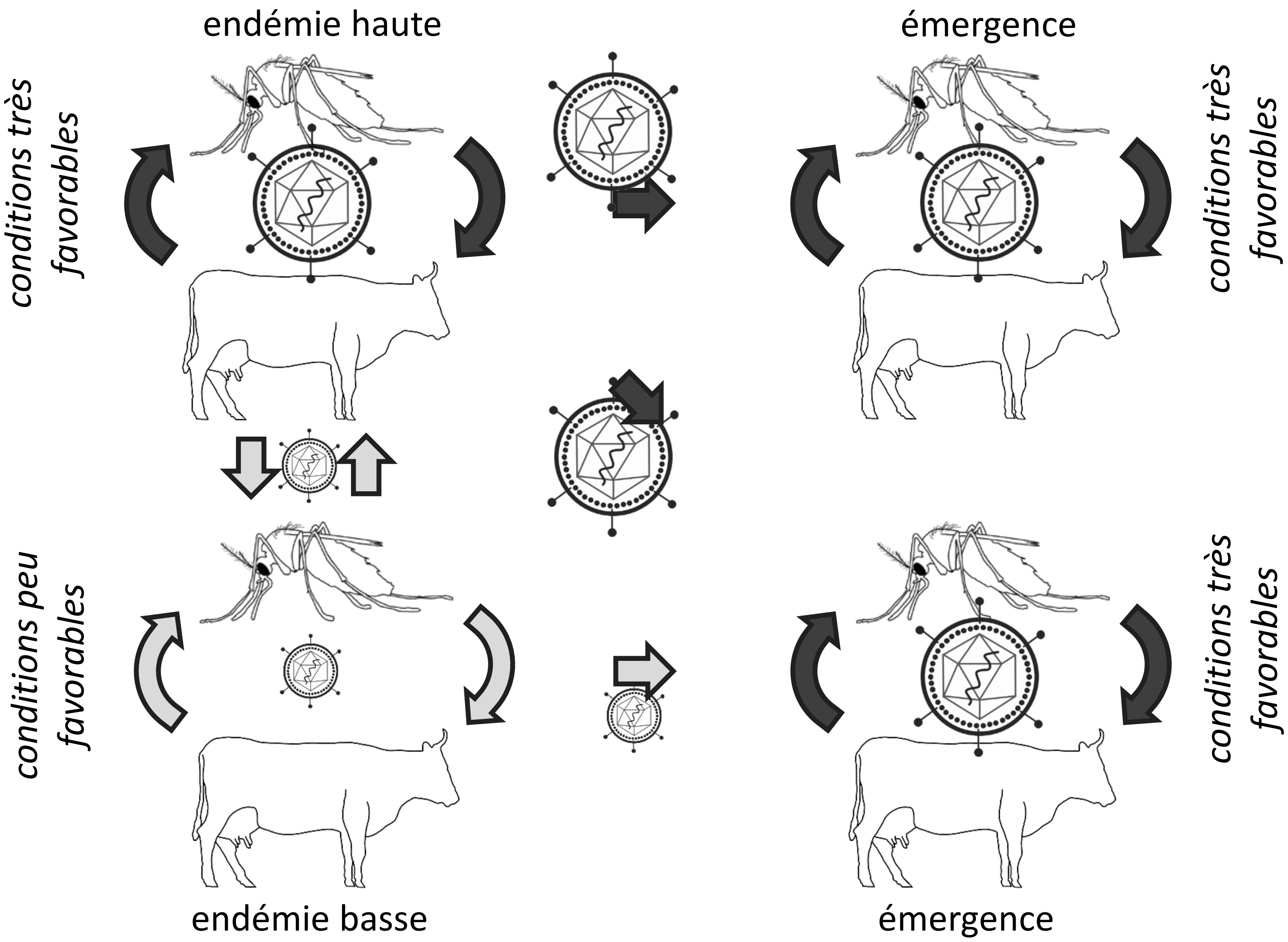

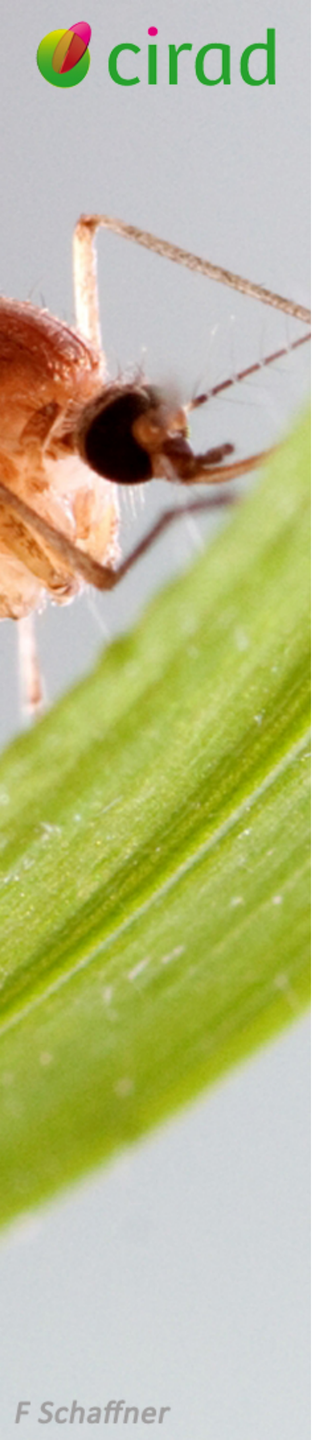

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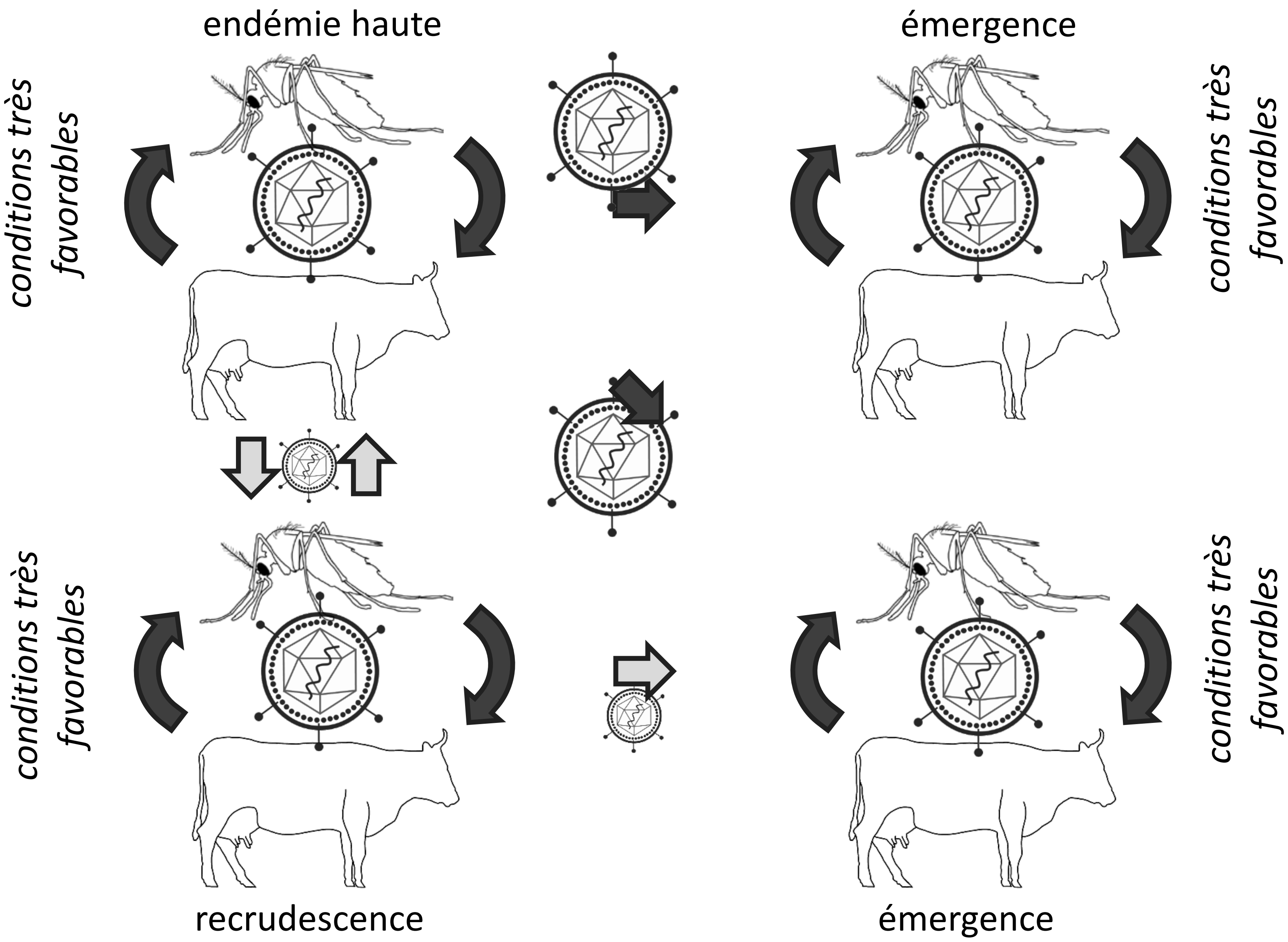

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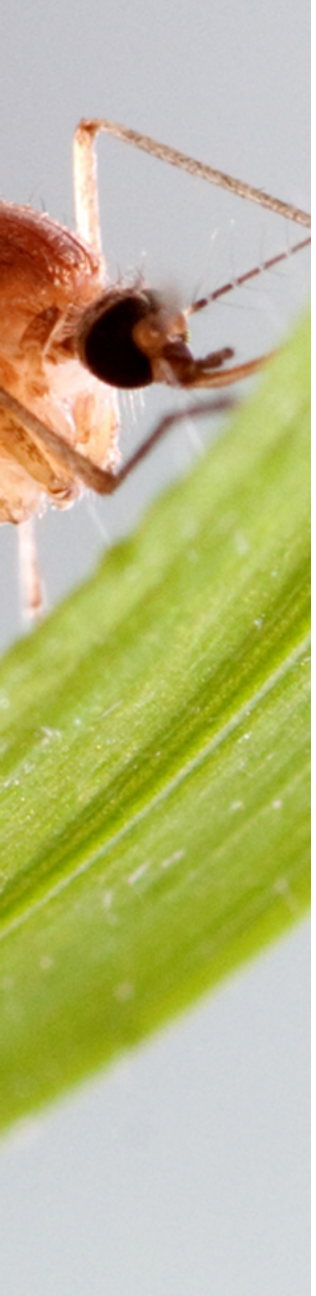
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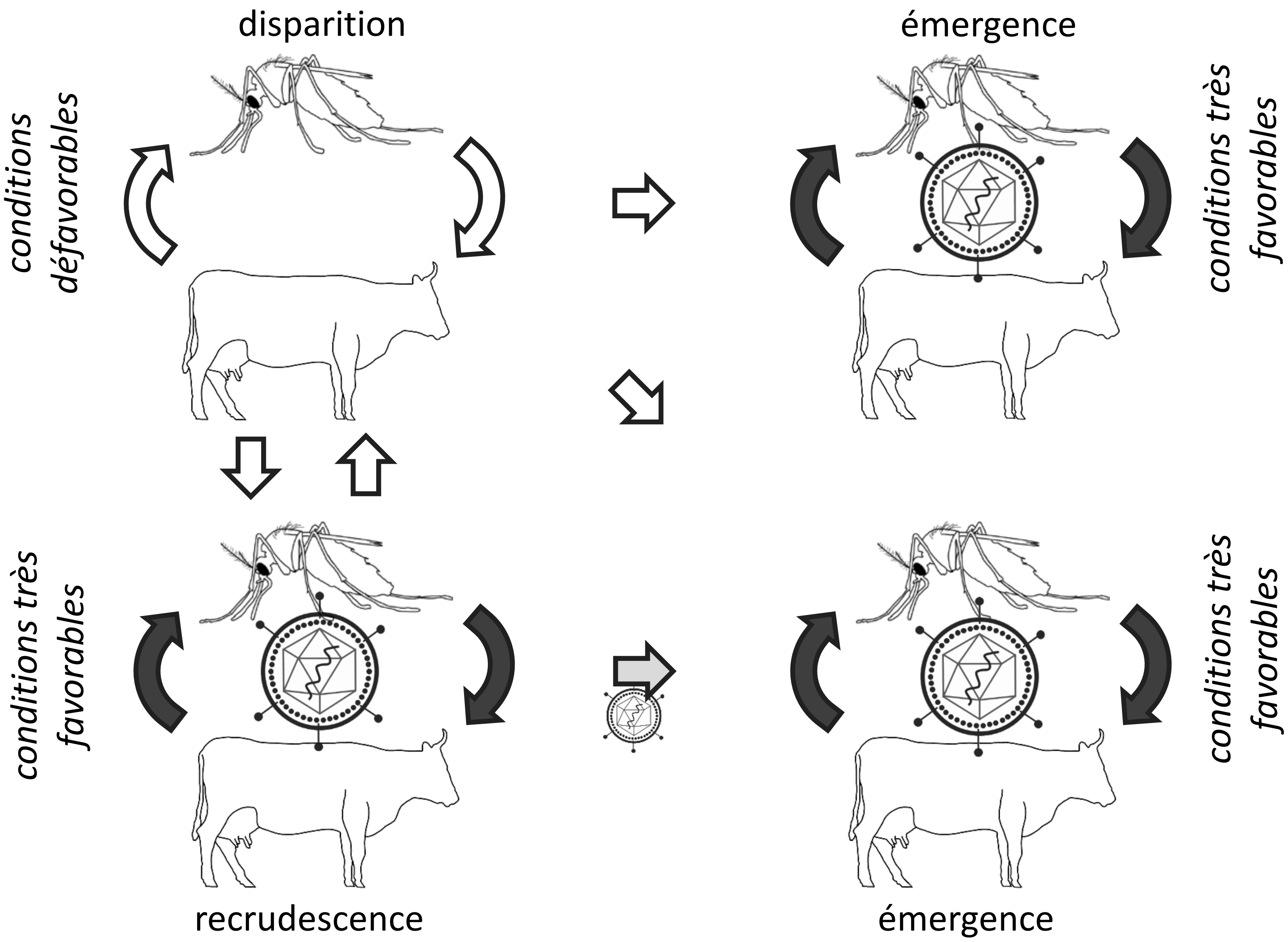

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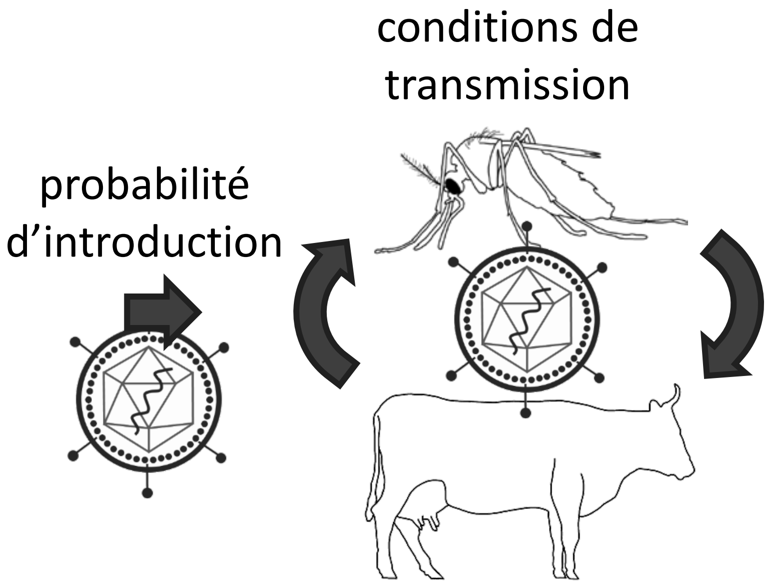

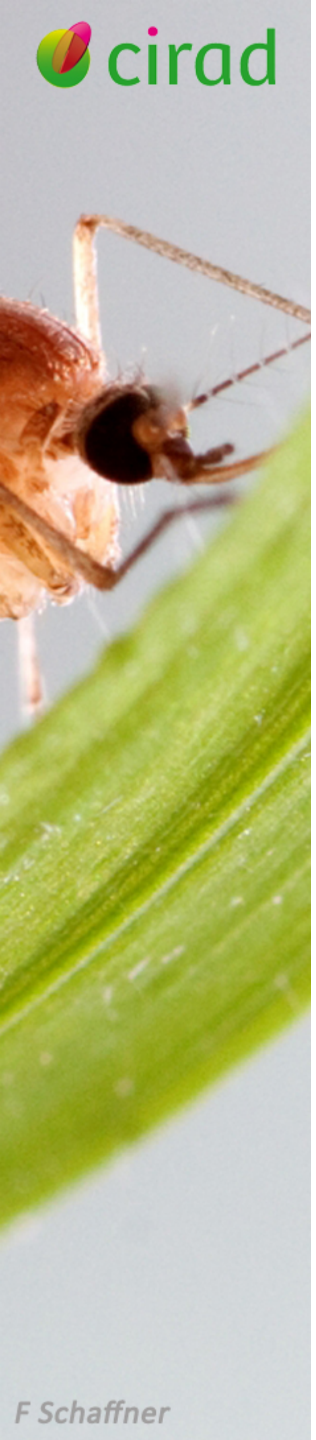

Emergence, recrudescence

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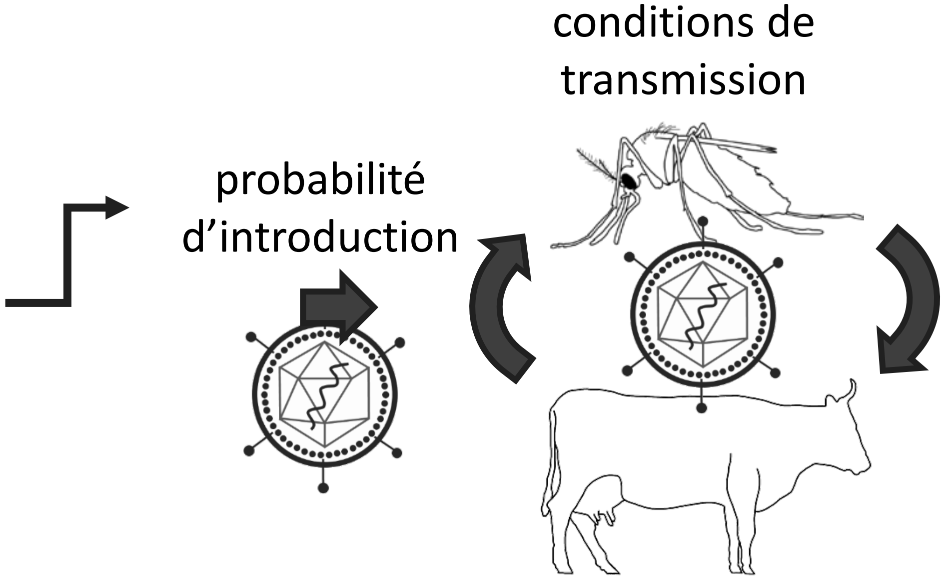
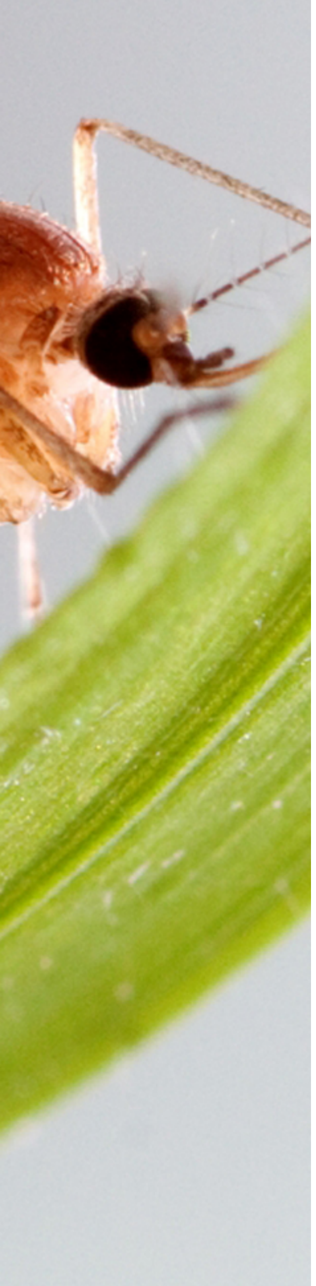
Mobilité des hôtes
et des vecteurs





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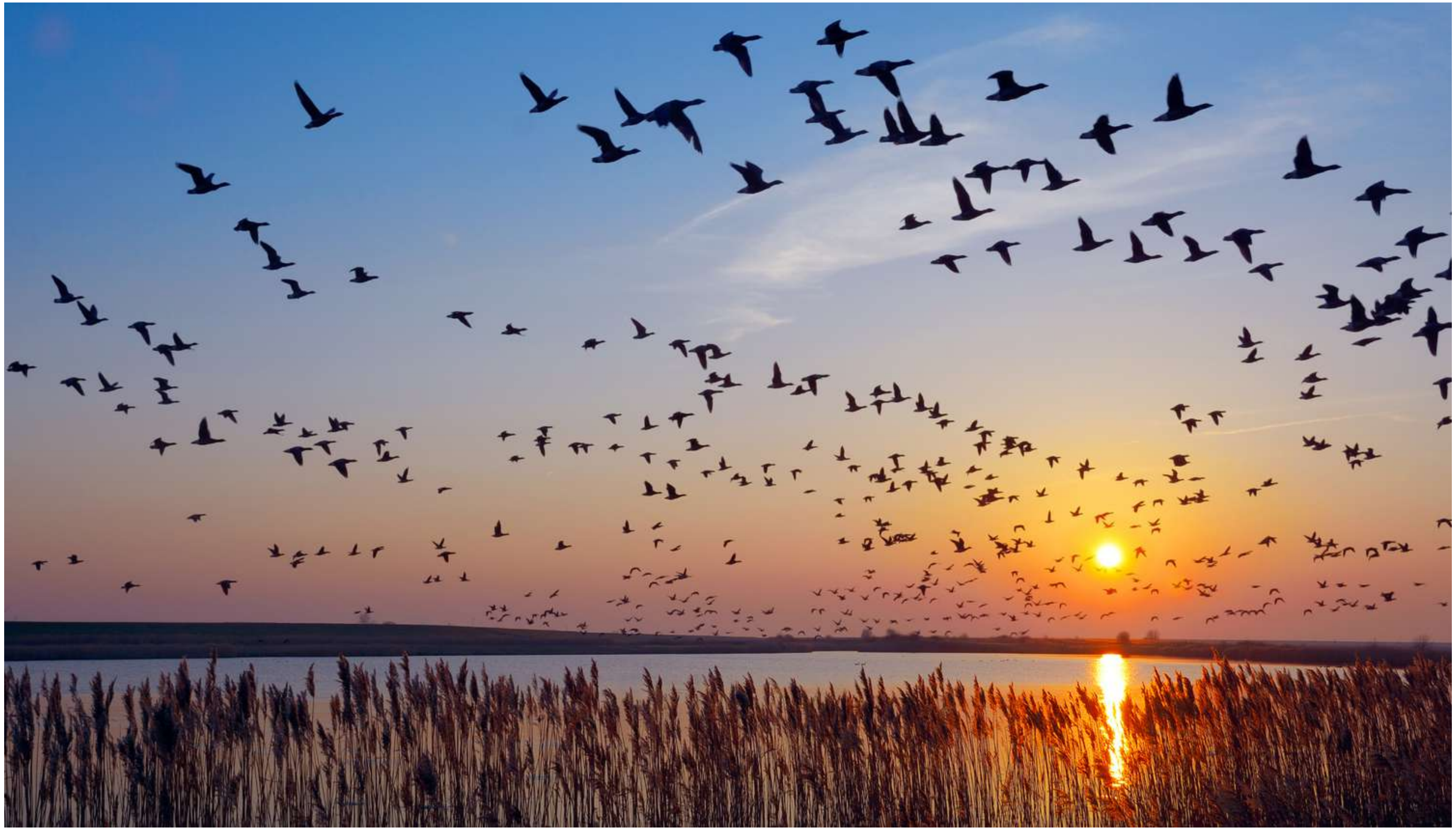
Migrations animales

agents infectieux chez les hôtes



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Transports passifs
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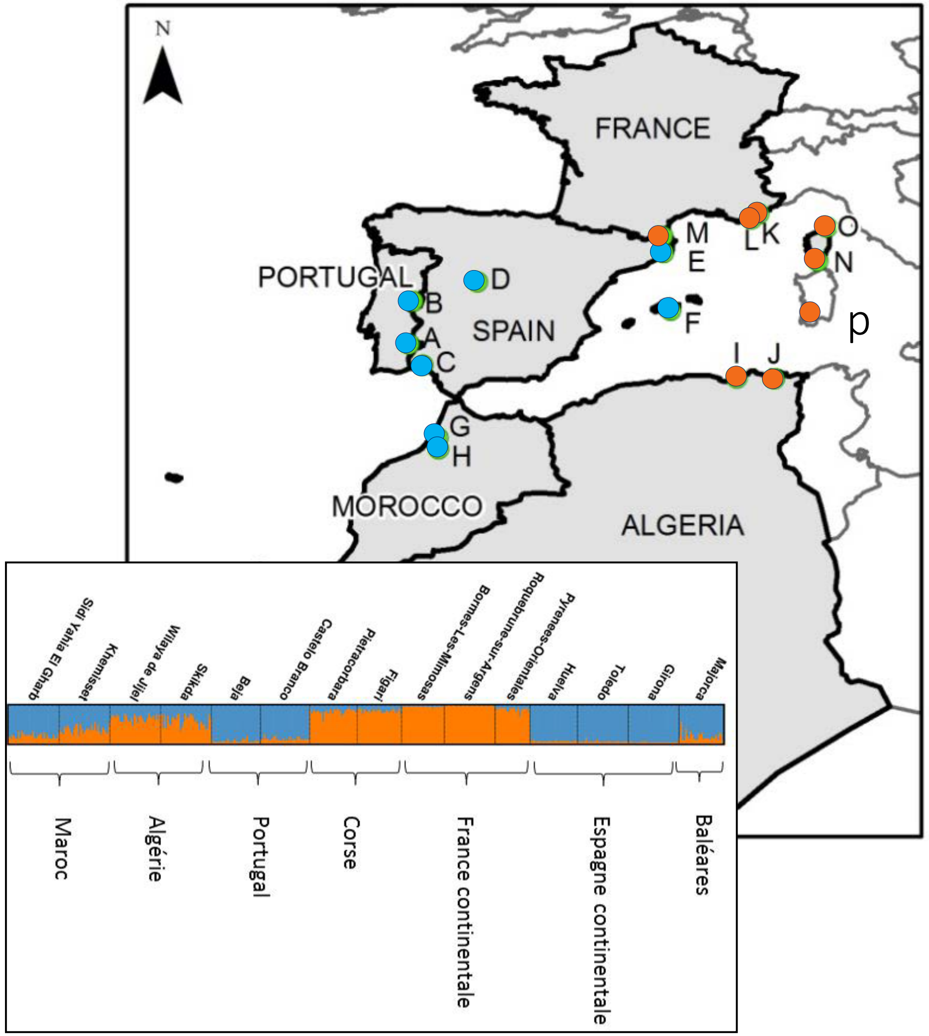

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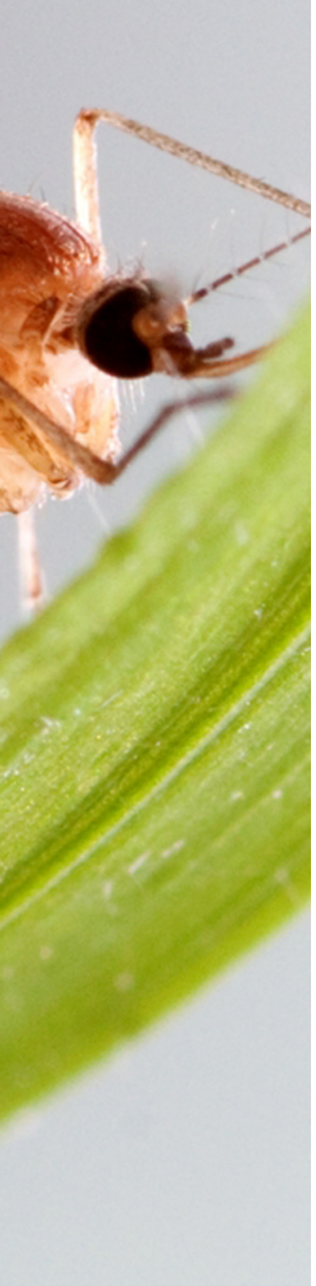

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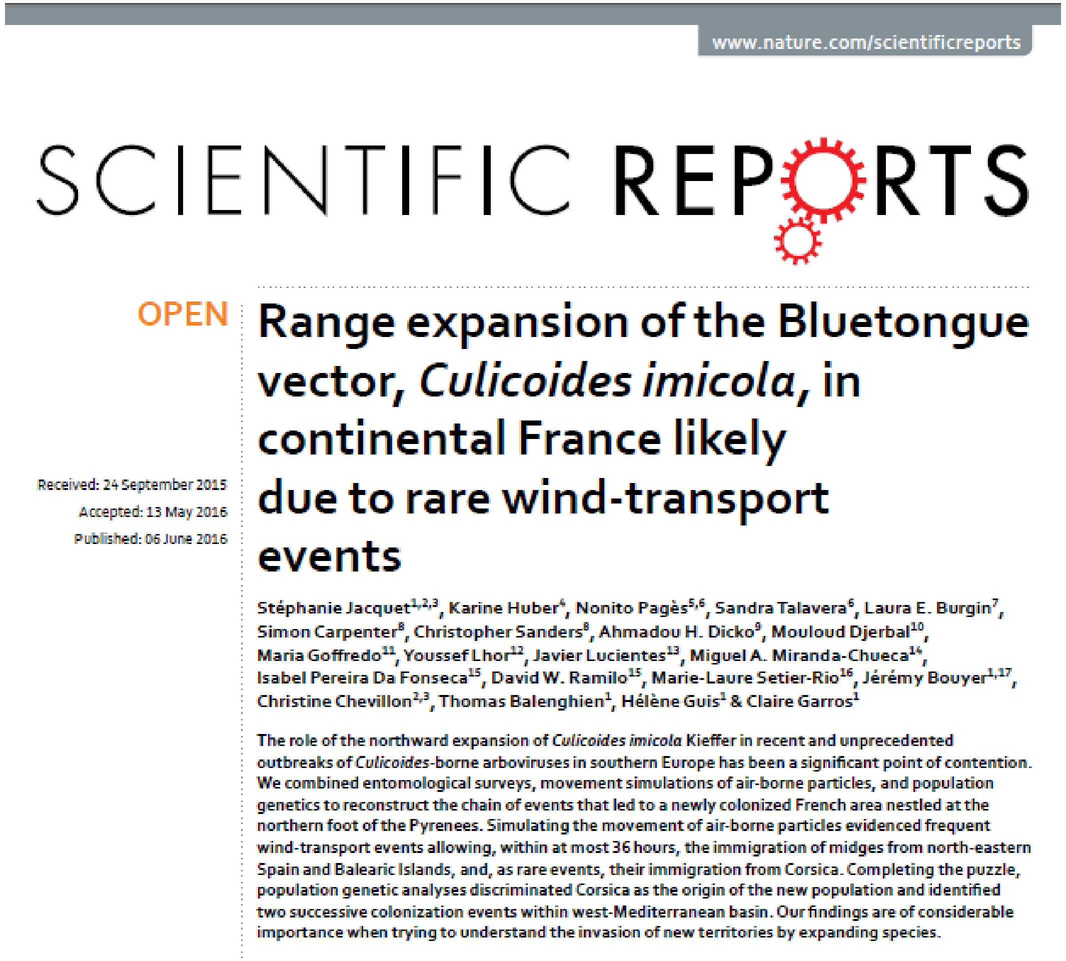

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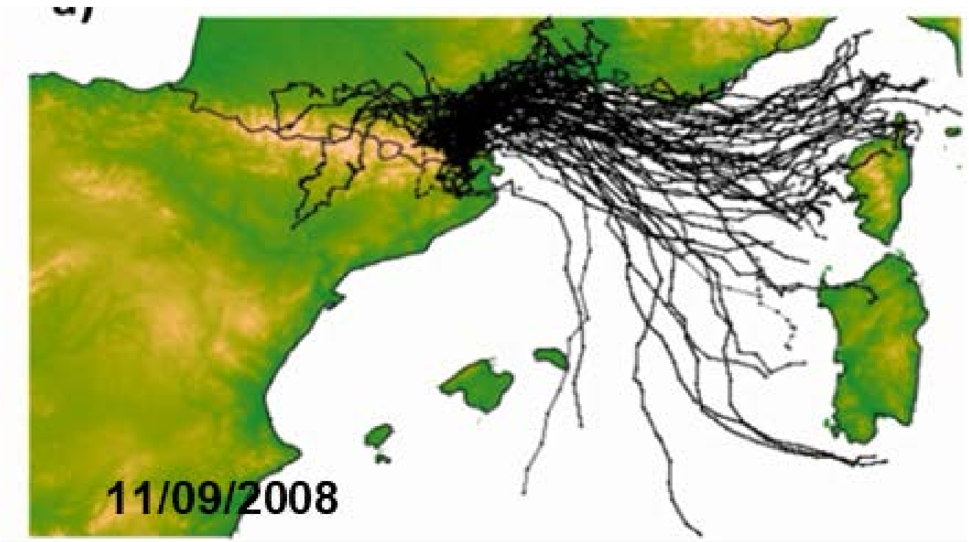
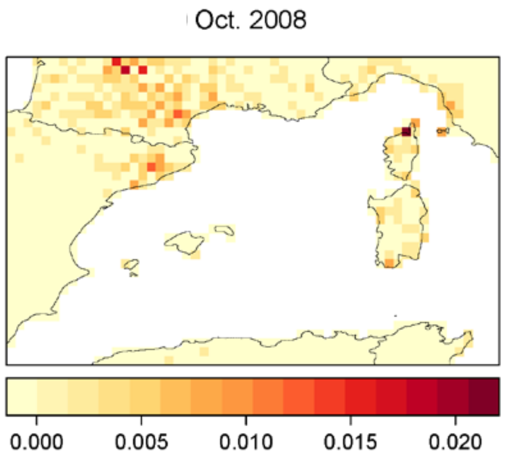
The role of the northward expansion of *Culicoides imicola* Kieffer in recent and unprecedented outbreaks of *Culicoides*-borne arboviruses in southern Europe has been a significant point of contention. We combined entomological surveys, movement simulations of air-borne particles, and population genetics to reconstruct the chain of events that led to a newly colonized French area nestled at the northern foot of the Pyrenees. Simulating the movement of air-borne particles evidenced frequent wind-transport events allowing, within at most 36 hours, the immigration of midges from north-eastern Spain and Balearic Islands, and, as rare events, their immigration from Corsica. Completing the puzzle, population genetic analyses discriminated Corsica as the origin of the new population and identified two successive colonization events within west-Mediterranean basin. Our findings are of considerable importance when trying to understand the invasion of new territories by expanding species.





Transports passifs

agents infectieux chez les vecteurs

Laura Burgin[1] · Marie Ekström[2] · Suraje Dessai[3]

Received: 25 July 2016 / Revised: 16 December 2016 / Accepted: 17 December 2016 / Published online: 14 January 2017
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Abstract Bluetongue, an economically important animal disease, can be spread over long distances by carriage of insect vectors (*Culicoides* biting midges) on the wind. The weather conditions which influence the midge's flight are controlled by synoptic scale atmospheric circulations. A method is proposed that links wind-borne dispersion of the insects to synoptic circulation through the use of a dispersion model in combination with principal component analysis (PCA) and cluster analysis. We illustrate how to identify the main synoptic situations present during times of midge incursions into the UK from the European continent. A PCA was conducted on high-pass-filtered mean sea-level pressure data for a domain centred over north-west Europe from 2005 to 2007. A clustering algorithm applied to the PCA scores indicated the data should be divided into five classes for which averages were calculated, providing a classification of the main synoptic types present. Midge incursion events were found to mainly occur in two synoptic categories; 64.8% were associated with a pattern displaying a pressure gradient over the North Atlantic leading to moderate south-westerly flow over the UK and 17.9% of the events occurred when high pressure dominated the region leading to south-easterly or easterly winds. The winds indicated by the pressure maps generally compared well against observations from a surface station and analysis charts. This technique could be used to assess frequency and timings of incursions of virus into new areas on seasonal and decadal timescales, currently not possible with other dispersion or biological modelling methods.

Keywords Bluetongue · *Culicoides* · Wind · Synoptic pattern · Map classification · Dispersion modelling

Introduction

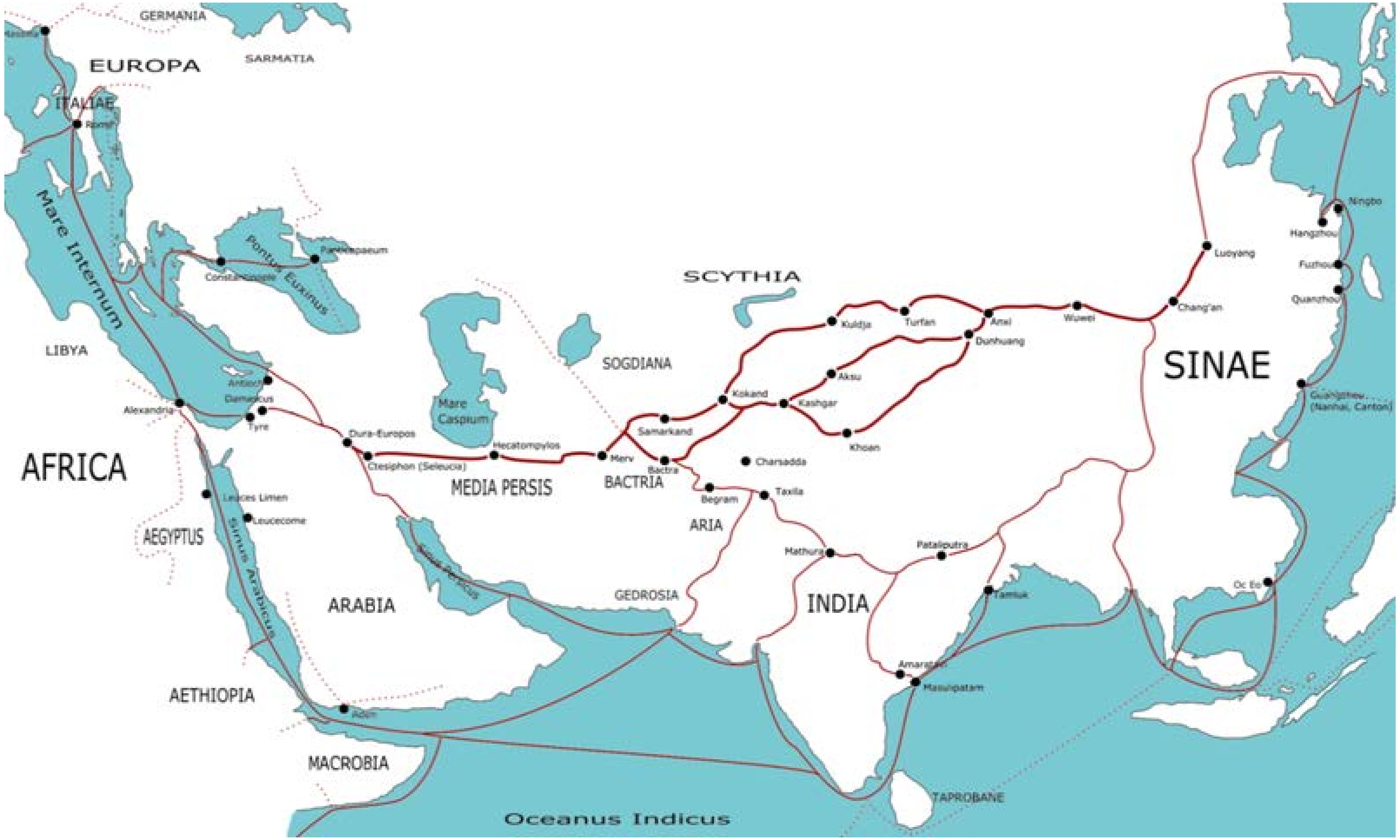
The biting midge *Culicoides* is the principal vector for several viruses causing economically important animal diseases including bluetongue (BT), African horse sickness and epizootic haemorrhagic disease. Northern Europe first experienced outbreaks of the disease in 2006 and has suffered from periodic outbreaks since. During a peak epidemic in 2007, losses due to death, sickness and reduced productivity of infected farm animals and movement restrictions applied to infected regions were estimated to be in the order of many hundreds of millions of pounds (Hoogendam 2007; Wilson and Mellor 2008).

The spread of vector-borne diseases is influenced directly and indirectly through a large range of environmental factors that influence the pathogen, the vector and the host. Development rates, activity levels, survival, timing of emer-

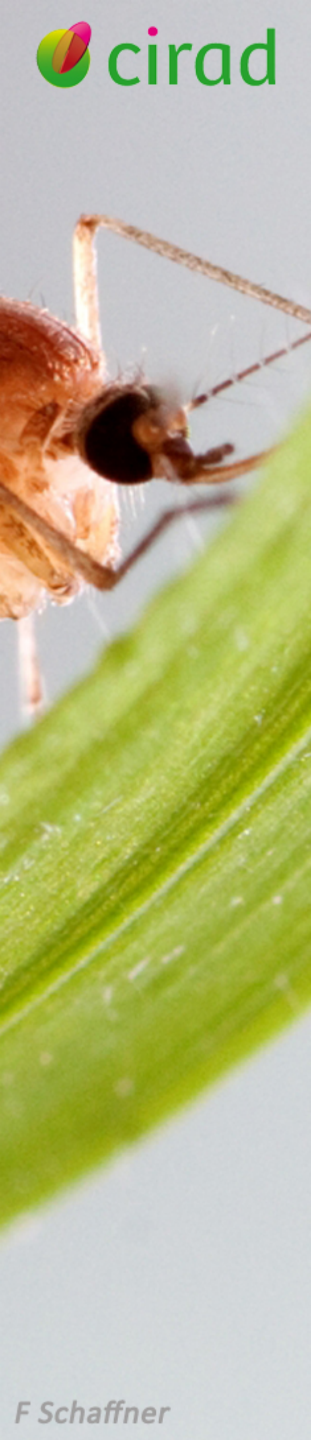
Electronic supplementary material The online version of this article (doi:10.1007/s00484-016-1301-1) contains supplementary material, which is available to authorized users.

Fig. 1 Example of output from the NAME model used to ermine 'midge days'

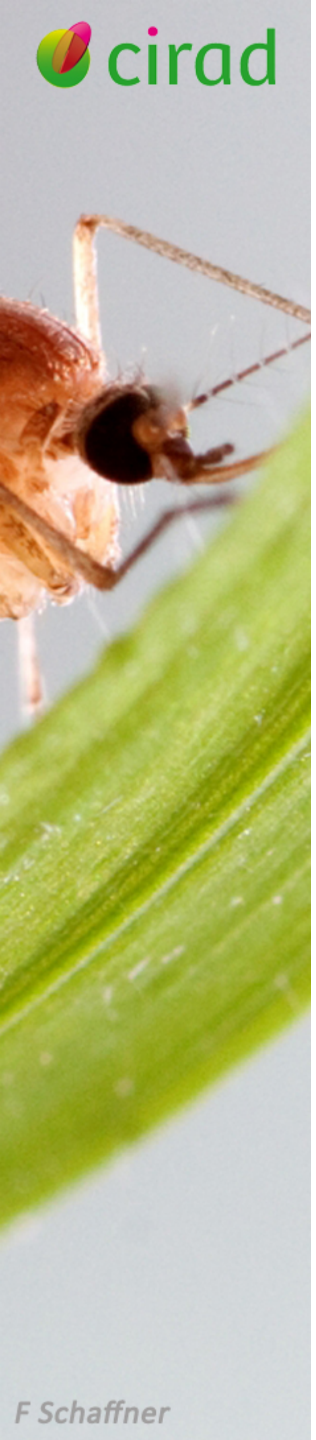
Migration et commerce
Asie-Europe, pestes moyenâgeuses



Migration et commerce
Asie-Europe, pestes moyenâgeuses



Colonisations européennes
« commerce triangulaire »

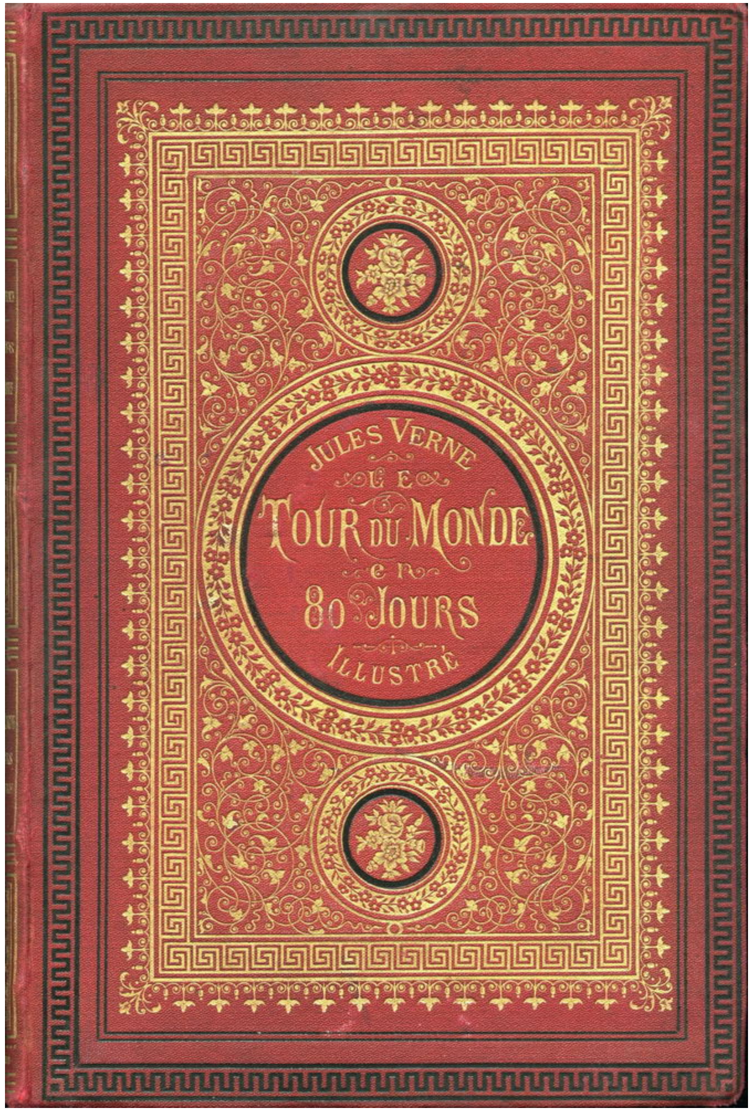


Révolution industrielle
marine à vapeur et aviation

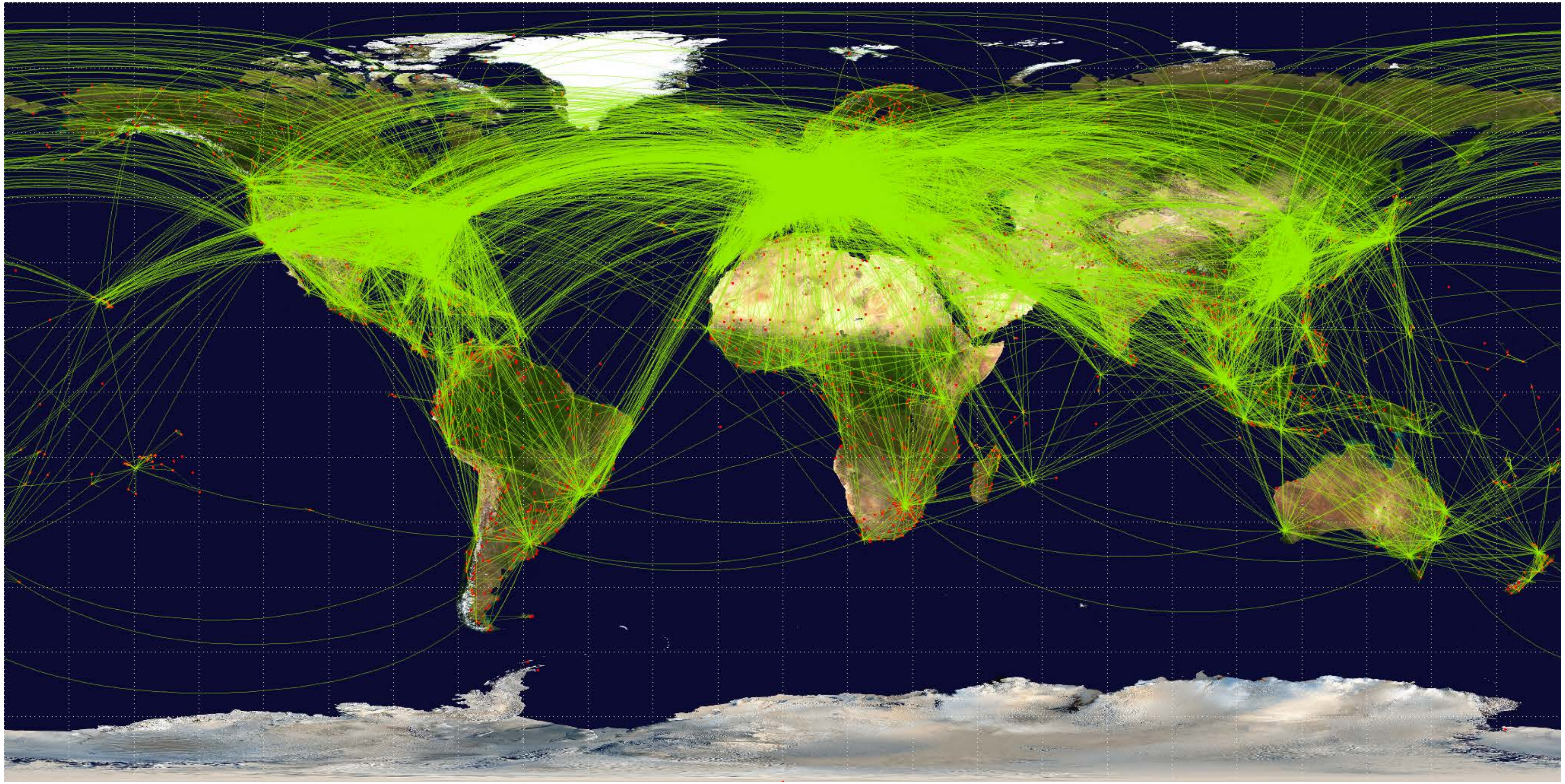
Temps de parcours à partir de Paris (en jours)

	1765	1780*
Lyon	5	5
Marseille	12	8
Toulouse	15	7

*** mise en place du réseau des diligences**



Révolution industrielle
marine à vapeur et aviation



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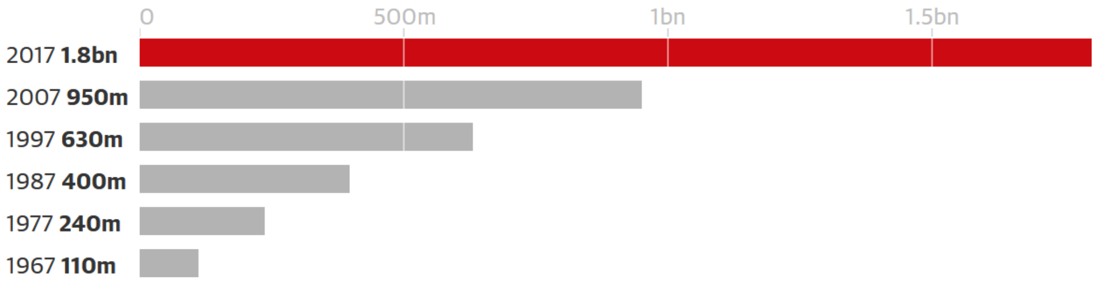
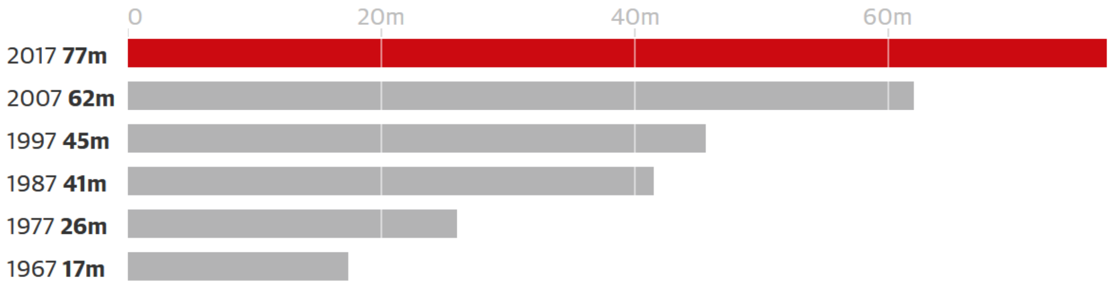
La mondialisation
échanges dans le village planétaire

Almost 2bn live chickens were transported around the world in 2017

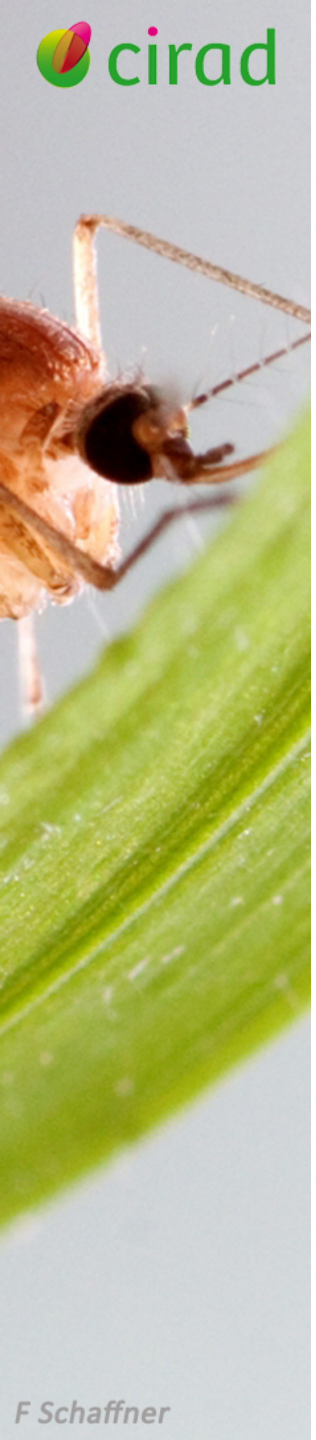


Guardian graphic | Source: The UN's Food and Agricultural Organization

More than 75m live pigs, cattle, sheep and goats were trucked and shipped around the world in 2017



Guardian graphic | Source: The UN's Food and Agricultural Organization



La mondialisation
échanges dans le village planétaire

Veterinary Microbiology, 33 (1992) 129–142
Elsevier Science Publishers B.V., Amsterdam

African horse sickness in Spain

M. Rodriguez[a], H. Hooghuis[b] and Ma. Castaño[a]
[a]*Departamento de Patología Animal - II, Facultad de Veterinaria, Universidad Complutense, Madrid, Spain*
[b]*Laboratorio de Sanidad y Producción Animal Algete, Ministerio de Agricultura, Pesca y Alimentación, Madrid, Spain*

(Accepted 26 June 1992)

ABSTRACT

Rodriguez, M., Hooghuis, H. and Castaño, Ma., 1992. African horse sickness in Spain. *Vet. Microbiol.*, 33: 129–142.

The aetiology, pathogenesis and epizootiology of African horse sickness (AHS) are reviewed with special reference to recent outbreaks in the Iberian peninsula. AHS is a highly fatal insect-borne viral disease of Equidae. It is caused by an Orbivirus (family Reoviridae) and nine serotypes are recognised. Outbreaks occurred in central Spain in 1987 and in southern regions of the Iberian peninsula in 1988, 1989 and 1990. All were associated with serotype 4 of the virus, whereas other occurrences of AHS outside Africa have all been caused by serotype 9. The clinical picture in the outbreaks was mainly of the acute (pulmonary) form except in 1988 when the subacute (cardiac) form of disease predominated. Several hundred horses died or were destroyed as a result of the outbreaks. Further spread was contained by a combination of slaughter of sick animals, movement controls, and vaccination which was extended over an increasingly wide area in successive years. The 1987 outbreak is believed to be associated with infected zebras imported from Africa. Possible explanations for the recurrence of disease in Spain in successive years are considered to include (a) the climatic conditions in Southern Spain, which could permit continuous vector activity, (b) the relative clinical resistance of mules and donkeys, which may permit subclinical circulation of the virus, (c) incomplete population immunity among horses due to possible gaps in the vaccination strategy.

Bangkok Post

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THAILAND › GENERAL

Horse death toll in Korat rises to 146

Measures stepped up to prevent spread of African viral disease

PUBLISHED : 4 APR 2020 AT 19:37 WRITER: PRASIT TANGPRASERT

0 15

A horse is taken back to a farm in Pak Chong district in Nakhon Ratchasima. So far, a total of 146 horses at farms in this district have been killed by African horse sickness. (Photo by Prasit Tangprasert)

MOST RECENT »

THAILAND

B15m resort owned by retired major general being demolished

KANCHANABURI: The family of the dead nominee of a retired major general have agreed to dismantle all structures at the 15-million baht Phatsapada Resort, which encroaches on Khao Laem National Park.

17:09

WORLD

Anwar says to meet king to prove majority

KUALA LUMPUR: Malaysian opposition leader Anwar Ibrahim on Thursday said he will meet with the country's king next week to present his case for taking over the premiership from Muhyiddin Yassin.

17:03

THAILAND

Drunk cabbie attacked car with knife

A drunk taxi driver who attacked another vehicle with a long knife after a minor accident has been charged with damaging property, reckless driving causing damage and illegally carrying a weapon.

15:36

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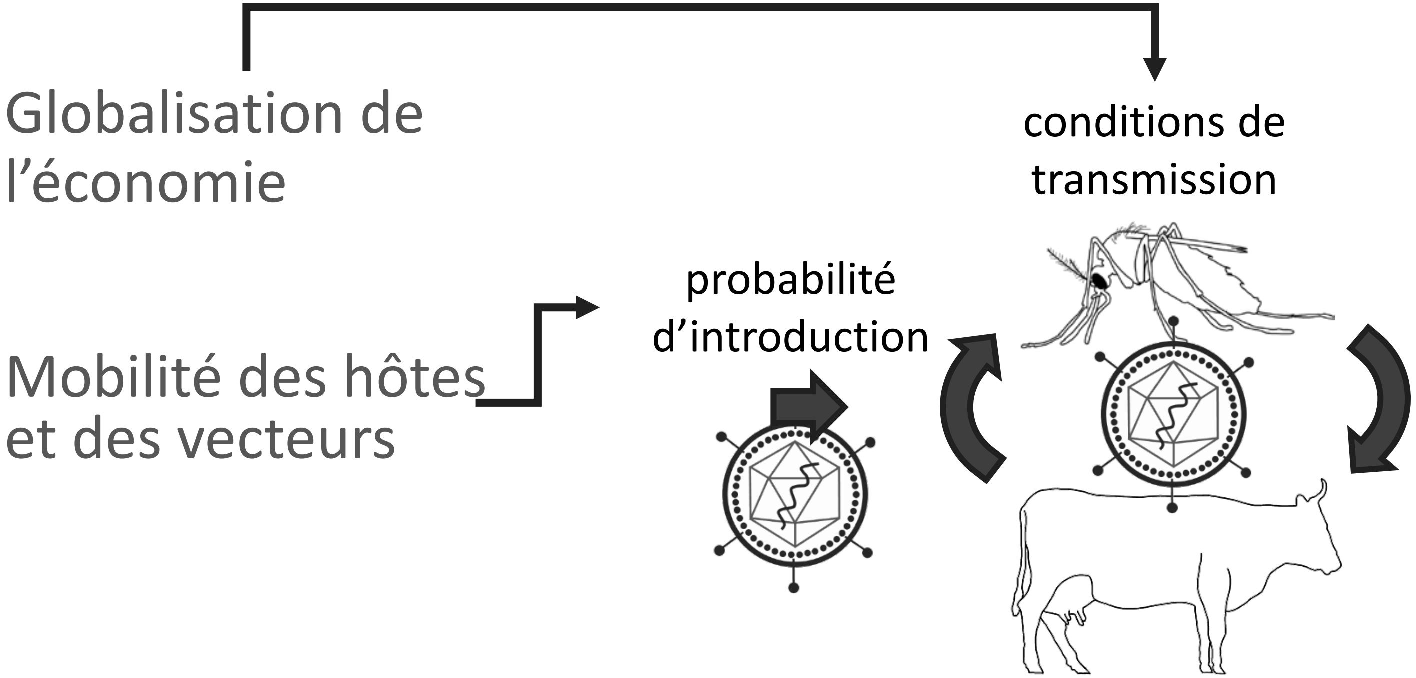
Emergence, recrudescence

quels mécanismes ?



La mondialisation
échanges dans le village planétaire

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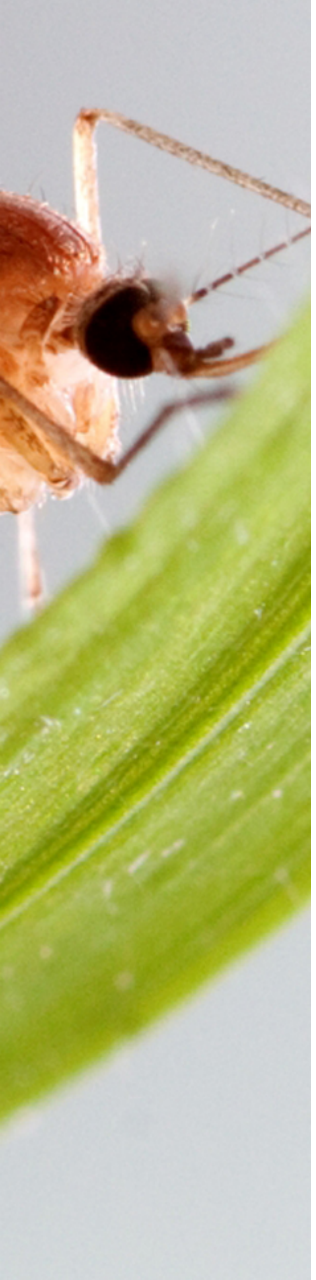

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Crédits : J Gathany

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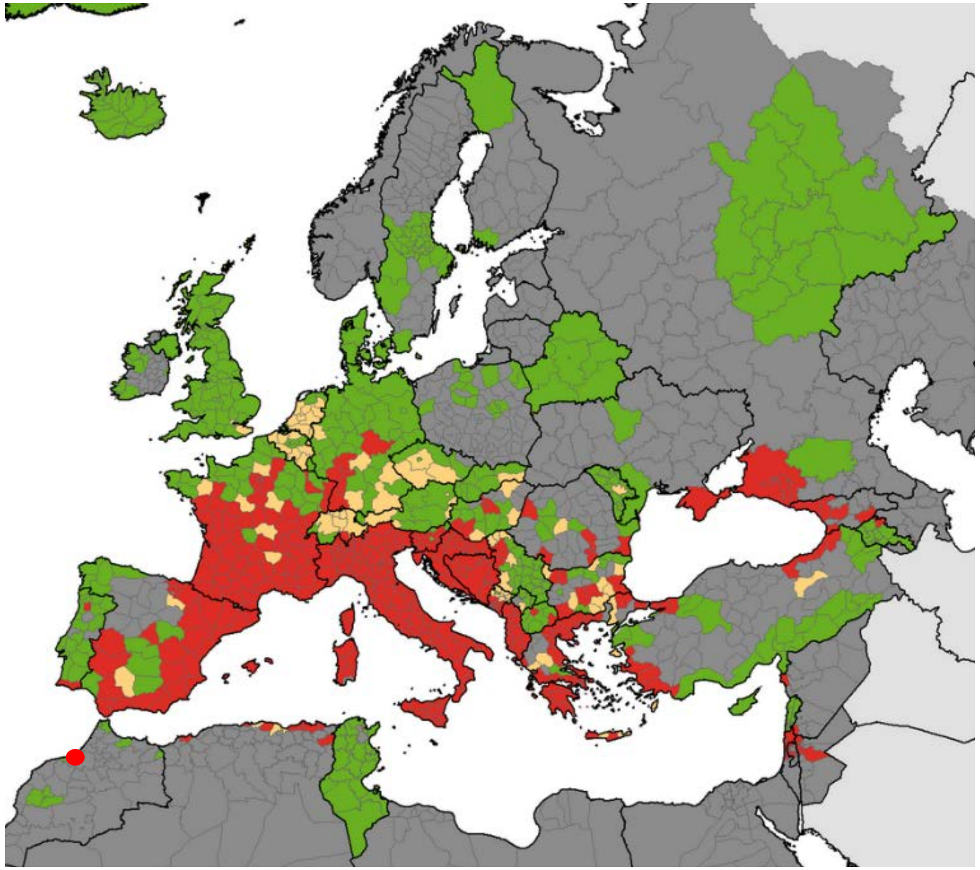

Crédits : *European Center for Disease Control*

La mondialisation

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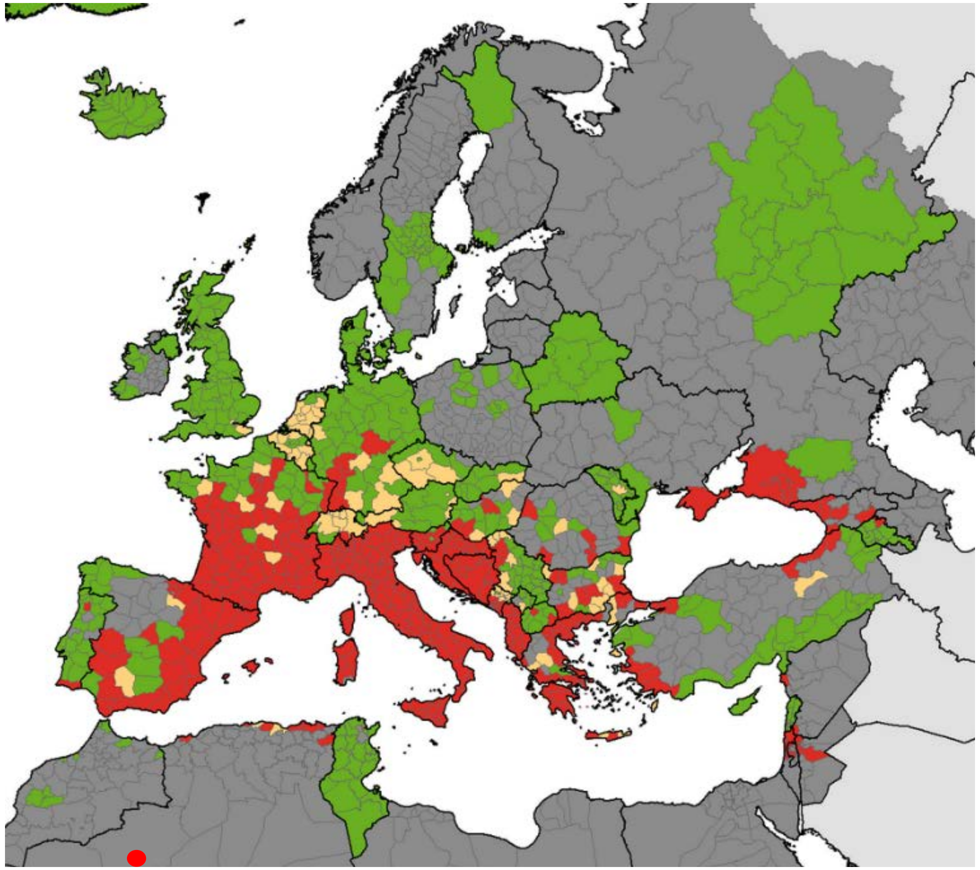


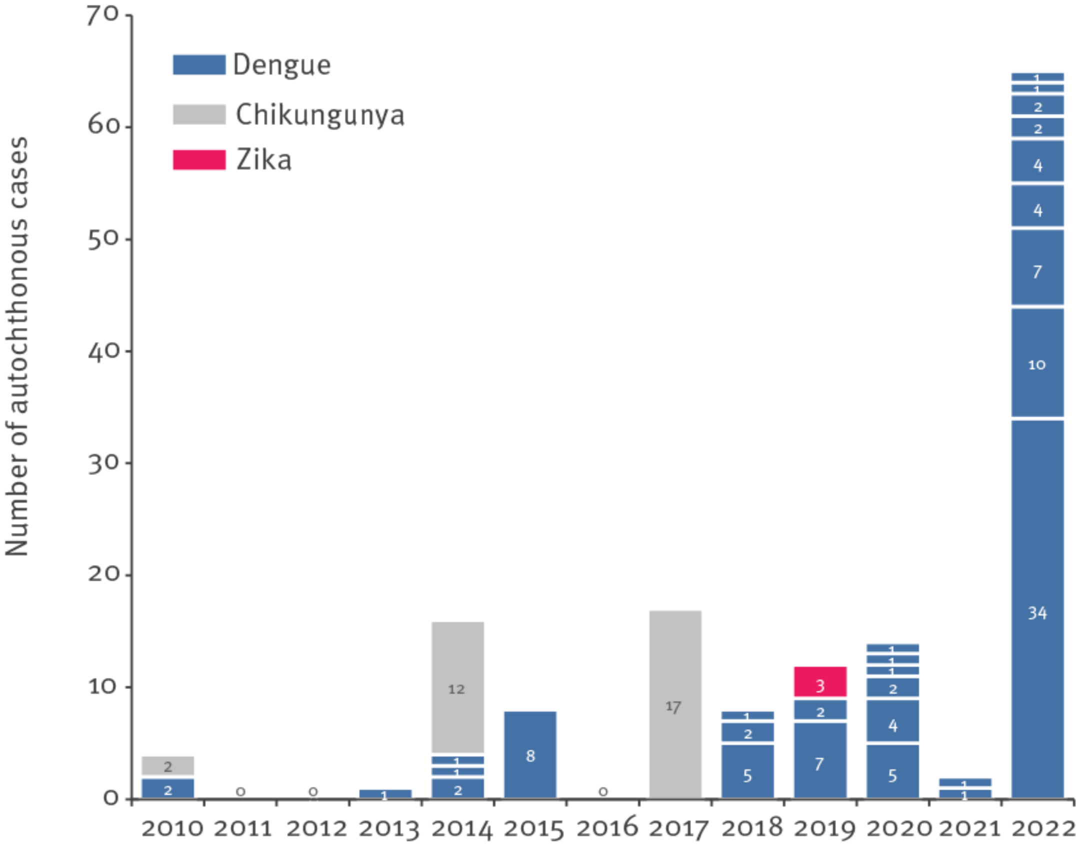
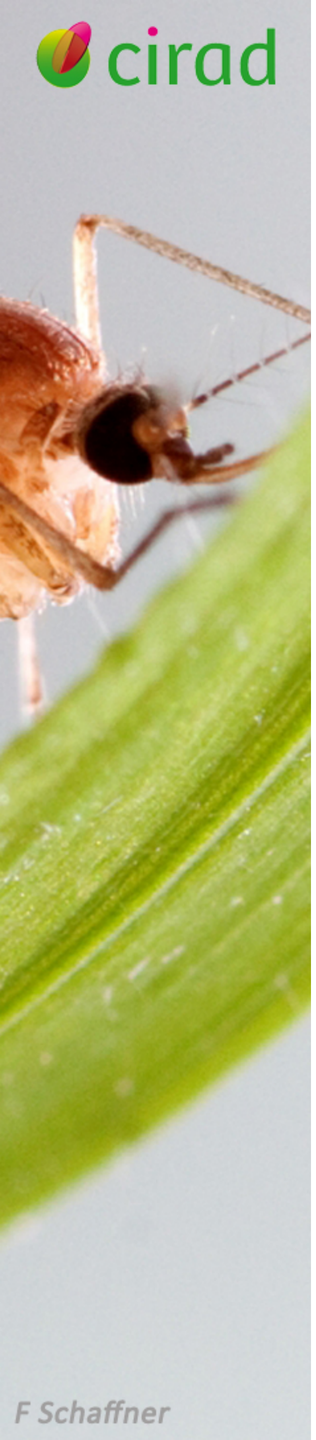


Figure 1. Distribution of arbovirus autochthonous events in mainland France, 2010–2022

Crédits : *European Center for Disease Control*

Cochet *et al.* (2022) *Euro Surveill*



Emergence, recrudescence

quels mécanismes ?

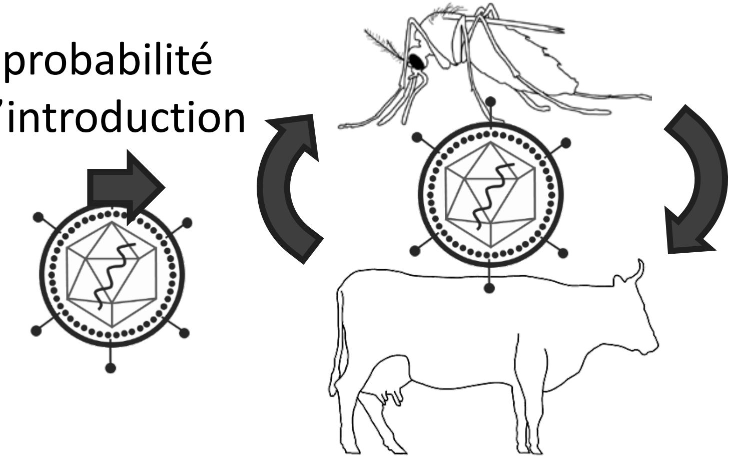
Changements sociaux
et modifications
environnementales

Globalisation de
l'économie

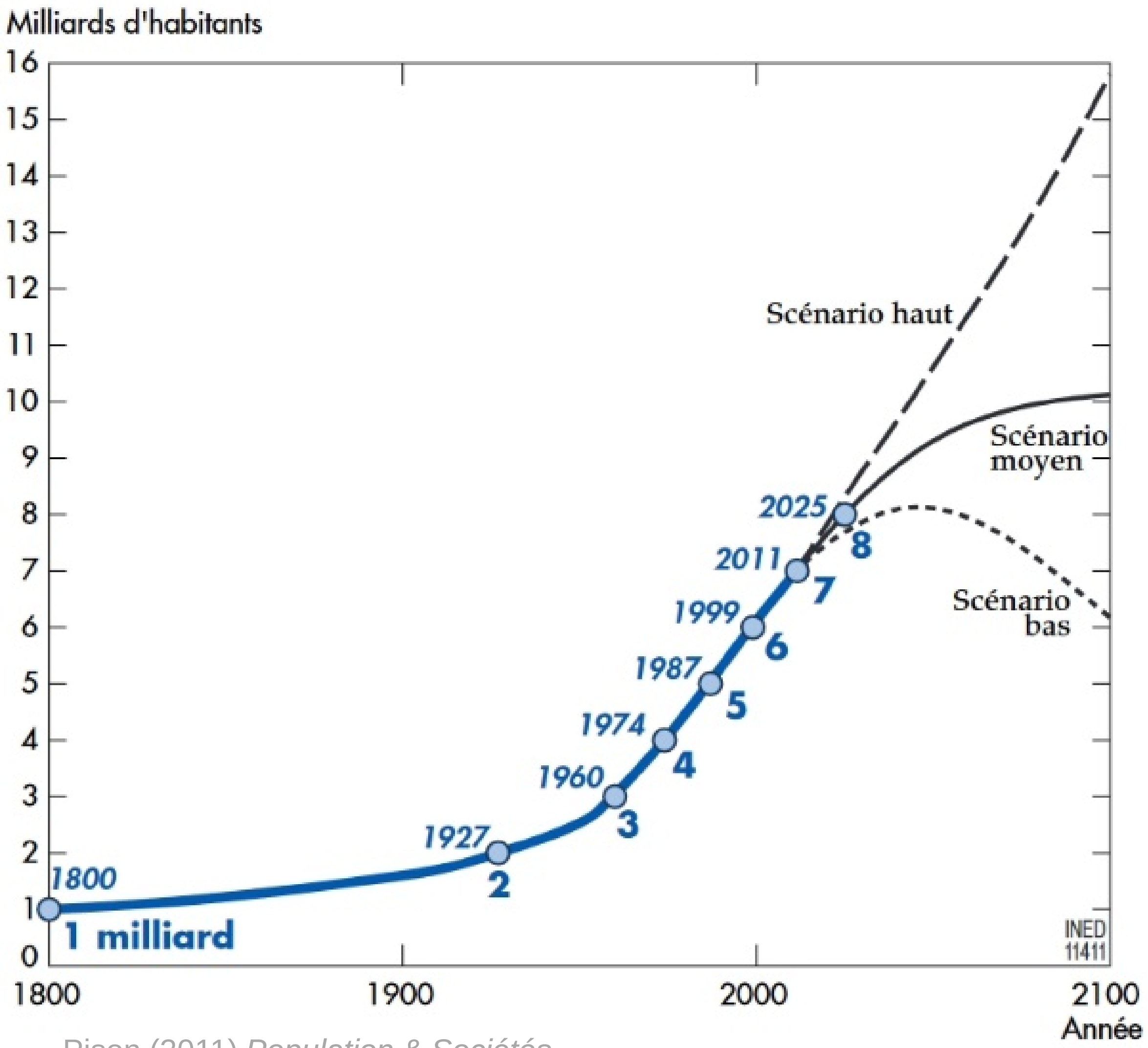
conditions de
transmission

Mobilité des hôtes
et des vecteurs

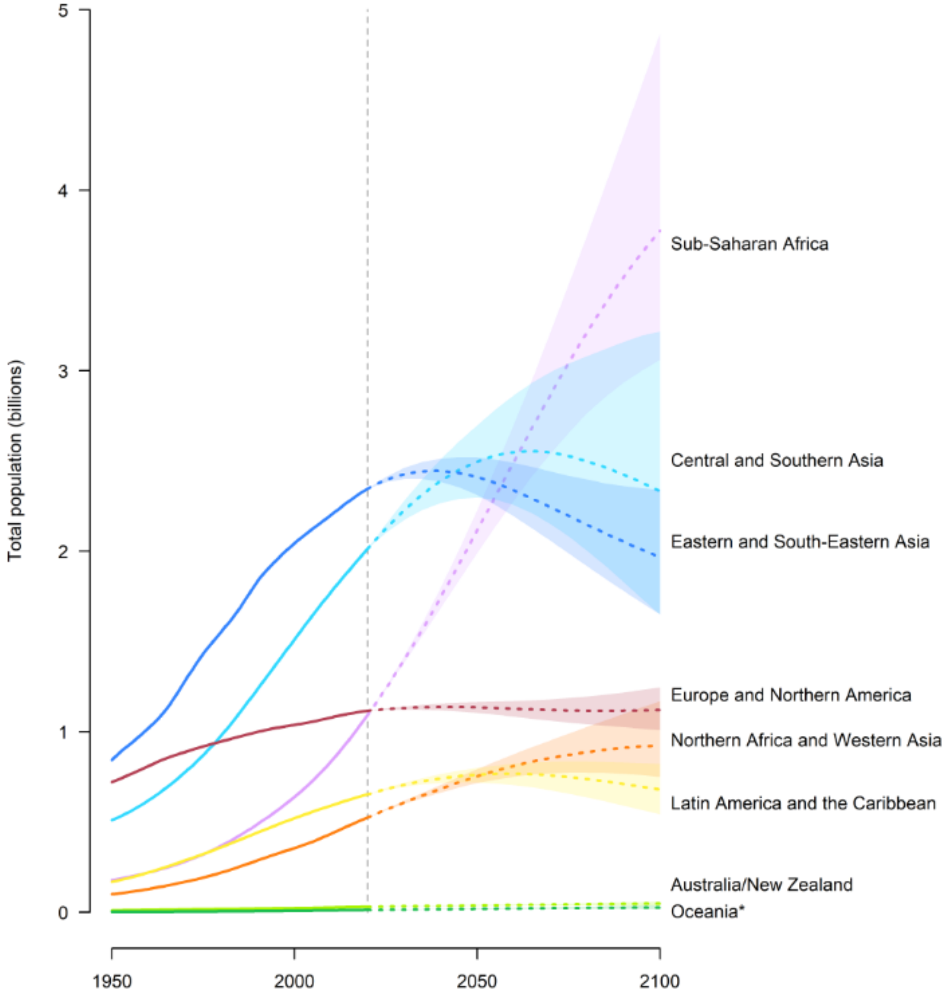
probabilité
d'introduction



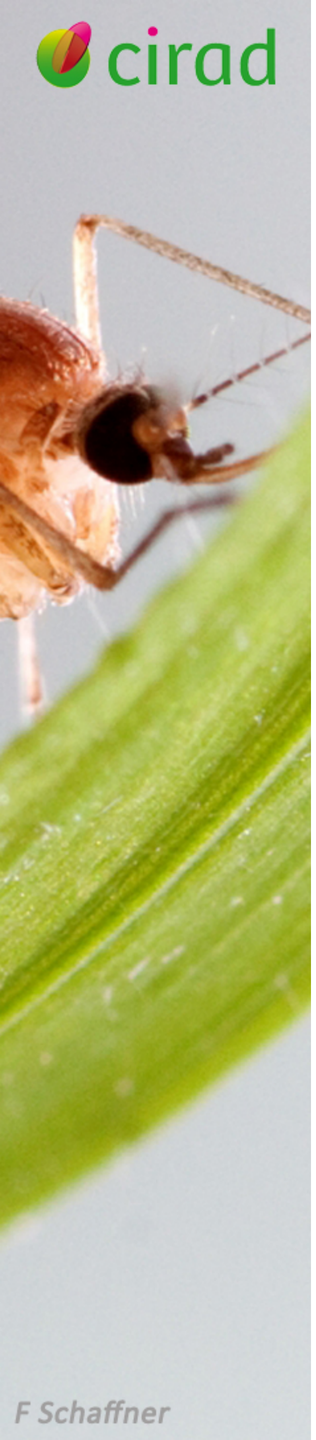
Croissance démographique

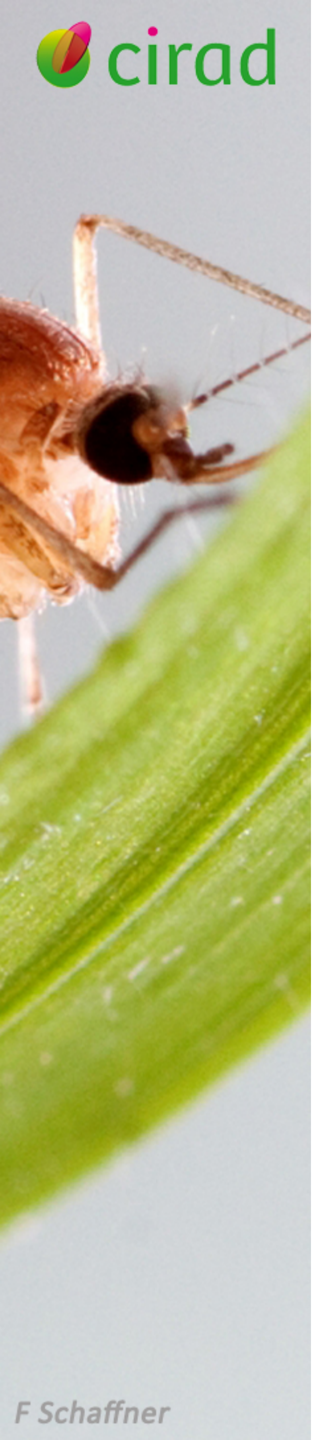


Pison (2011) *Population & Sociétés*



United Nations (2019) *World Population Prospects*





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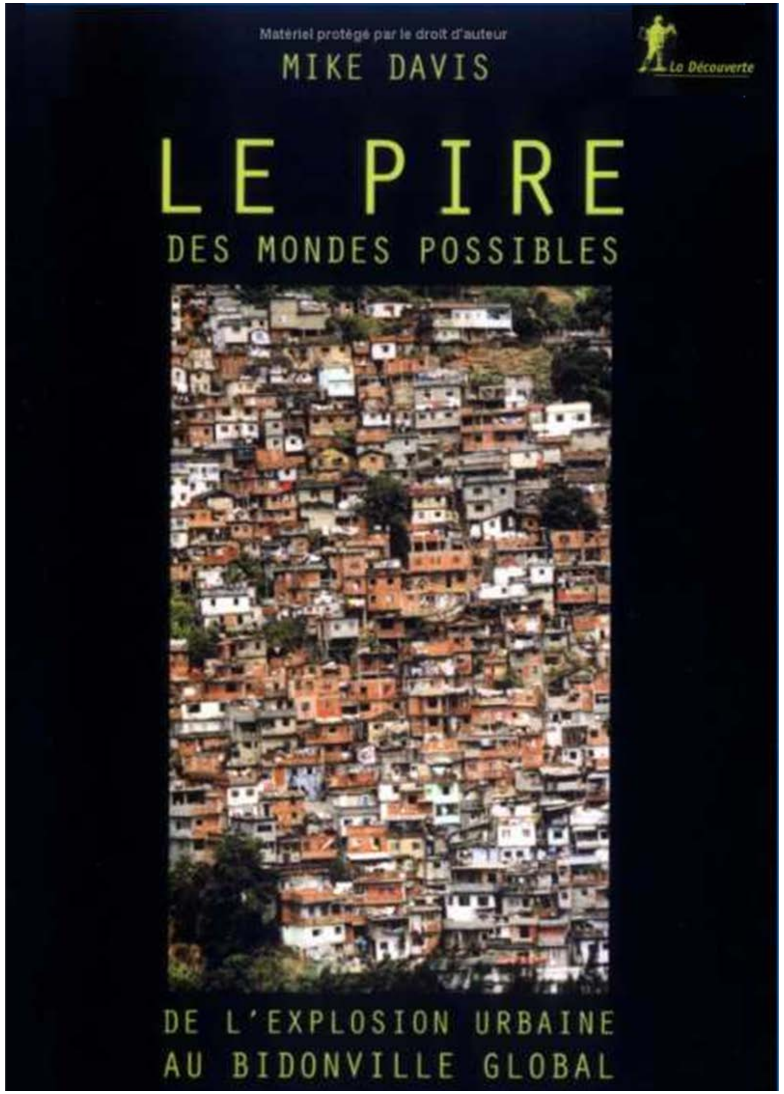
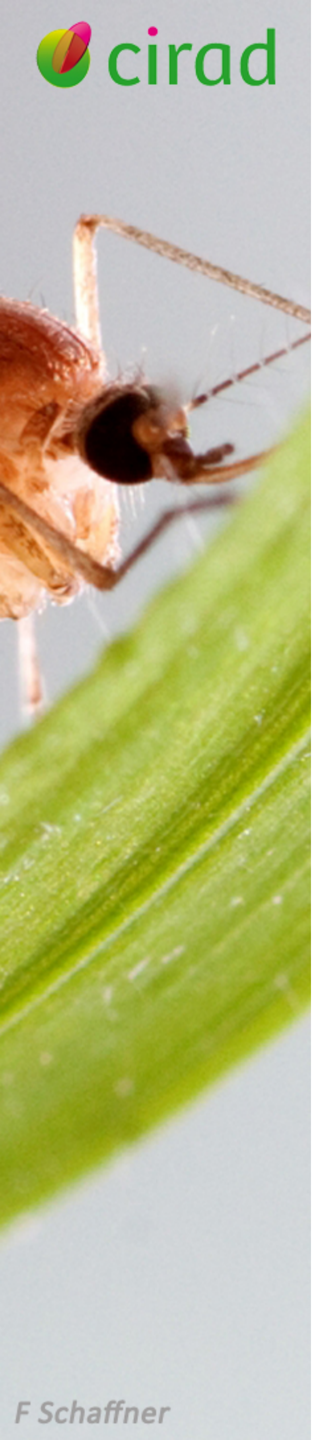
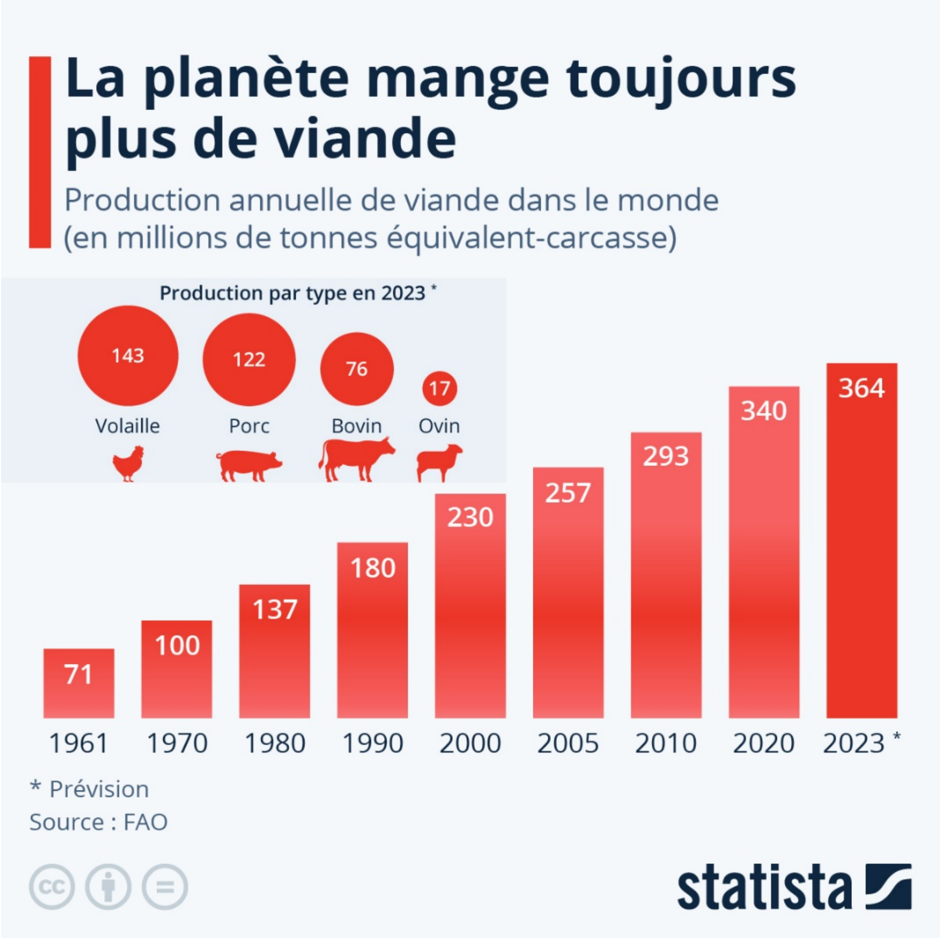
Croissance démographique
urbanisation et « bidonvillisation » du monde

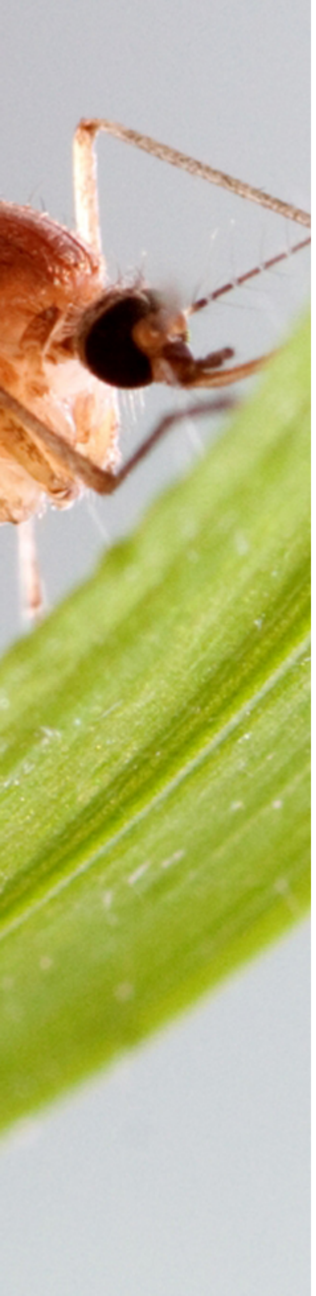


Croissance démographique
intensification de l'élevage





Modifications environnementales
complexité des systèmes



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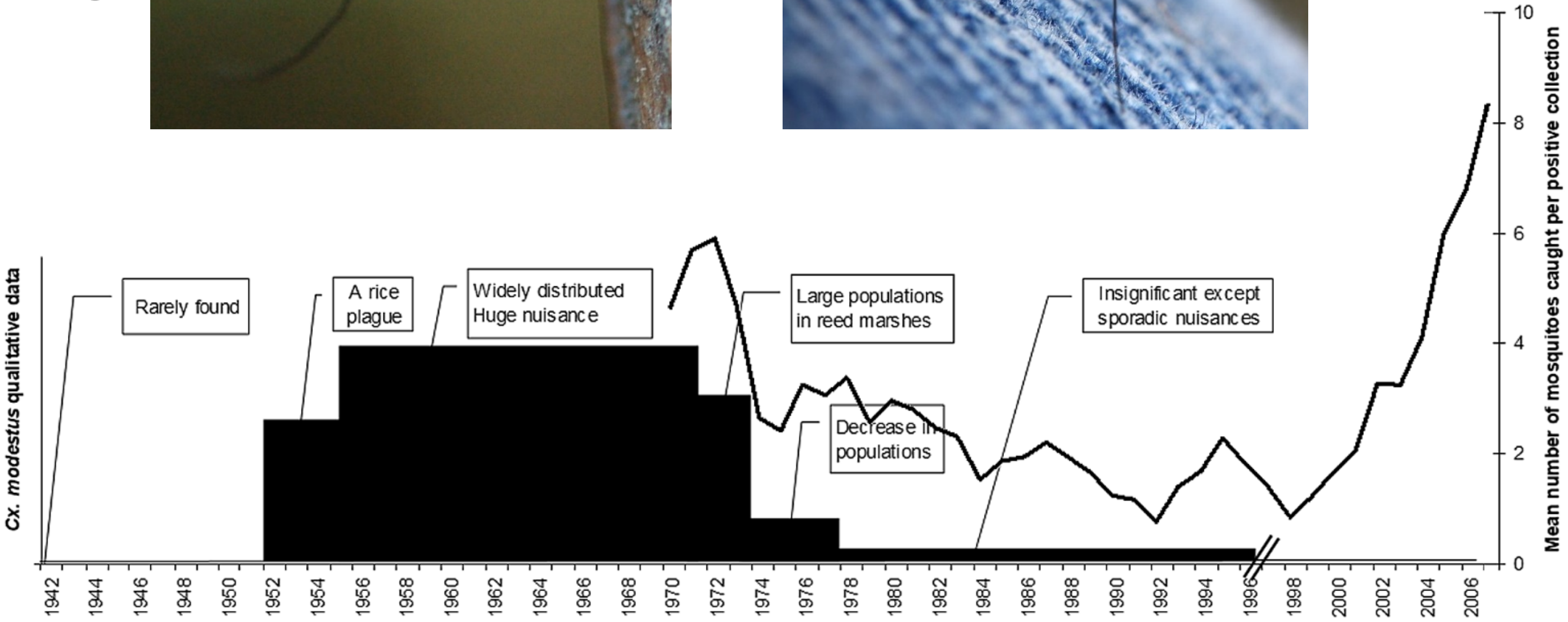
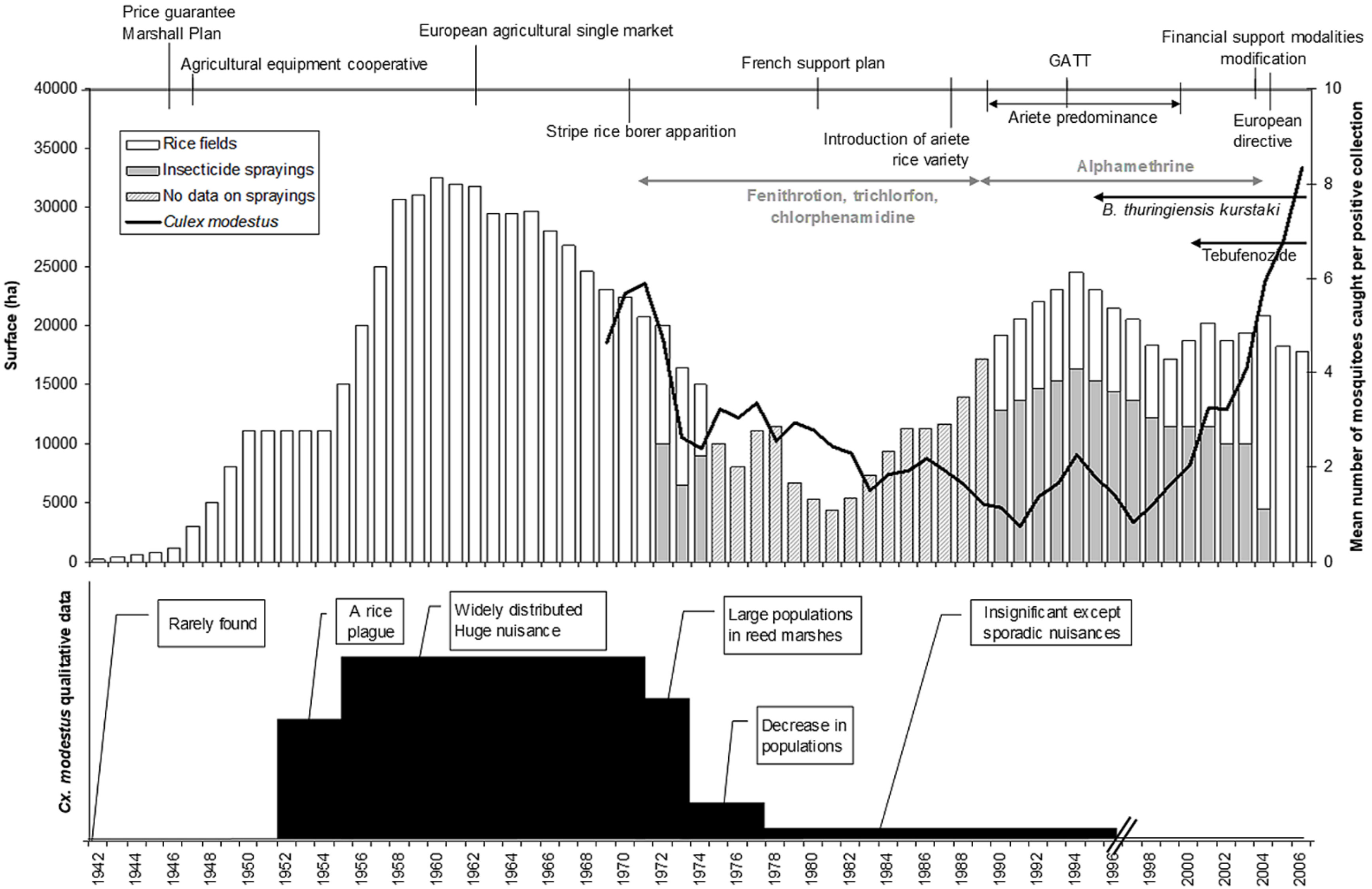
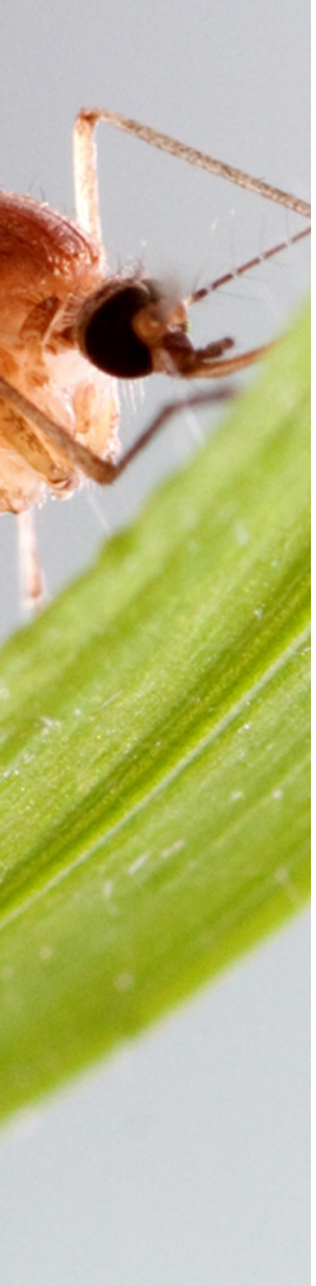


Ponçon *et al.* (2007) *Emerg Inf Dis*

Modifications environnementales
complexité des systèmes



Ponçon *et al.* (2007) *Emerg Inf Dis*



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Modifications environnementales
déforestation et …

292 *Mem Inst Oswaldo Cruz*, Rio de Janeiro, Vol. *112*(4): 292-298, April 2017

Vegetation loss and the 2016 Oropouche fever outbreak in Peru

Daniel Romero-Alvarez[1]/[+], Luis E Escobar[2]

[1]Hospital General Enrique Garcés, Unidad de Epidemiología, Quito, Ecuador
[2]University of Minnesota, Department of Fisheries, Wildlife and Conservation Biology, St. Paul, MN, USA

BACKGROUND *Oropouche virus* causes Oropouche fever, an arboviral disease transmitted mainly by midges of the genus *Culicoides* and *Culex* mosquitoes. Clinical presentation of Oropouche fever in humans includes fever, headache, rash, myalgia, and in rare cases spontaneous bleeding and aseptic meningitis. Landscape change has been proposed as a driver of Oropouche fever emergence.

OBJECTIVE To investigate the landscape epidemiology of the Oropouche fever outbreak that began in April 2016 in Cusco, Peru.

METHODS We used information of vegetation and multivariate spatial analyses including ecological niche modeling. Vegetation was characterised using16-day composite enhanced vegetation index (EVI) images at 500 m spatial resolution from the MODIS sensor carried by the Terra satellite.

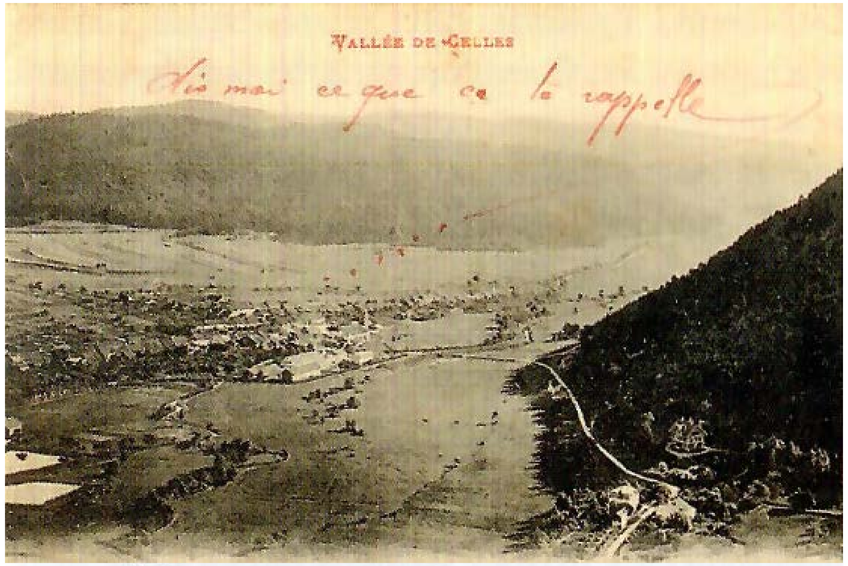
FINDINGS Cases were distributed across seven Peruvian districts in two provinces. La Concepcion was the province with most of the affected districts. EVI time series across 2000 to 2016 suggested a decline in the vegetation in sites with Oropouche fever cases before the epidemic. Our ecological niche modeling suggests that other areas in Junin, Apurimac, and Madre de Dios departments are at risk of Oropouche fever occurrence.

MAIN CONCLUSIONS Our results may provide a guide for future fieldwork to test hypotheses regarding Oropouche fever emergence and habitat loss in tropical Latin America.

Key words: Oropouche - ecological niche modeling - vegetation - outbreak - *Culicoides* - MODIS

Crédits : D Louppe

Modifications environnementales
déforestation et … reforestation



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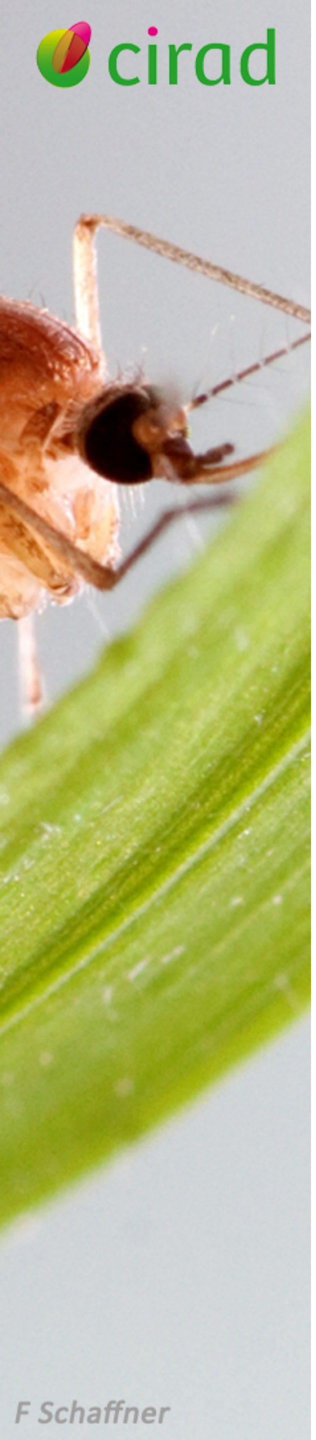


Emergence, recrudescence

quels mécanismes ?

Changements sociaux et modifications environnementales

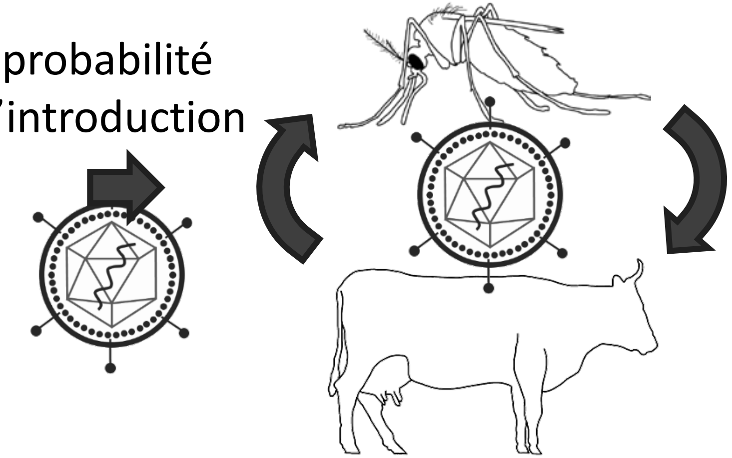
Augmentation globale des températures

Globalisation de l'économie

conditions de transmission

Mobilité des hôtes et des vecteurs

probabilité d'introduction



Température et expansion des vecteurs
la raison du sens commun

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La petite mangouste indienne pourrait arriver en France dans les prochaines décennies ©wikimedia commons

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Température et expansion des vecteurs *réelle ou apparente ?*

Journal of Medical Entomology, XX(X), 2018, 1–4
doi: 10.1093/jme/tjy036
Short communication

Vector-Borne Diseases, Surveillance, Prevention

OXFORD

Apparent Range Expansion of *Culicoides (Hoffmania) insignis* (Diptera: Ceratopogonidae) in the Southeastern United States

Stacey L. Vigil,[1] Mark G. Ruder, David Shaw, John Wlodkowski, Kayla Garrett, Matthew Walter, and Joseph L. Corn

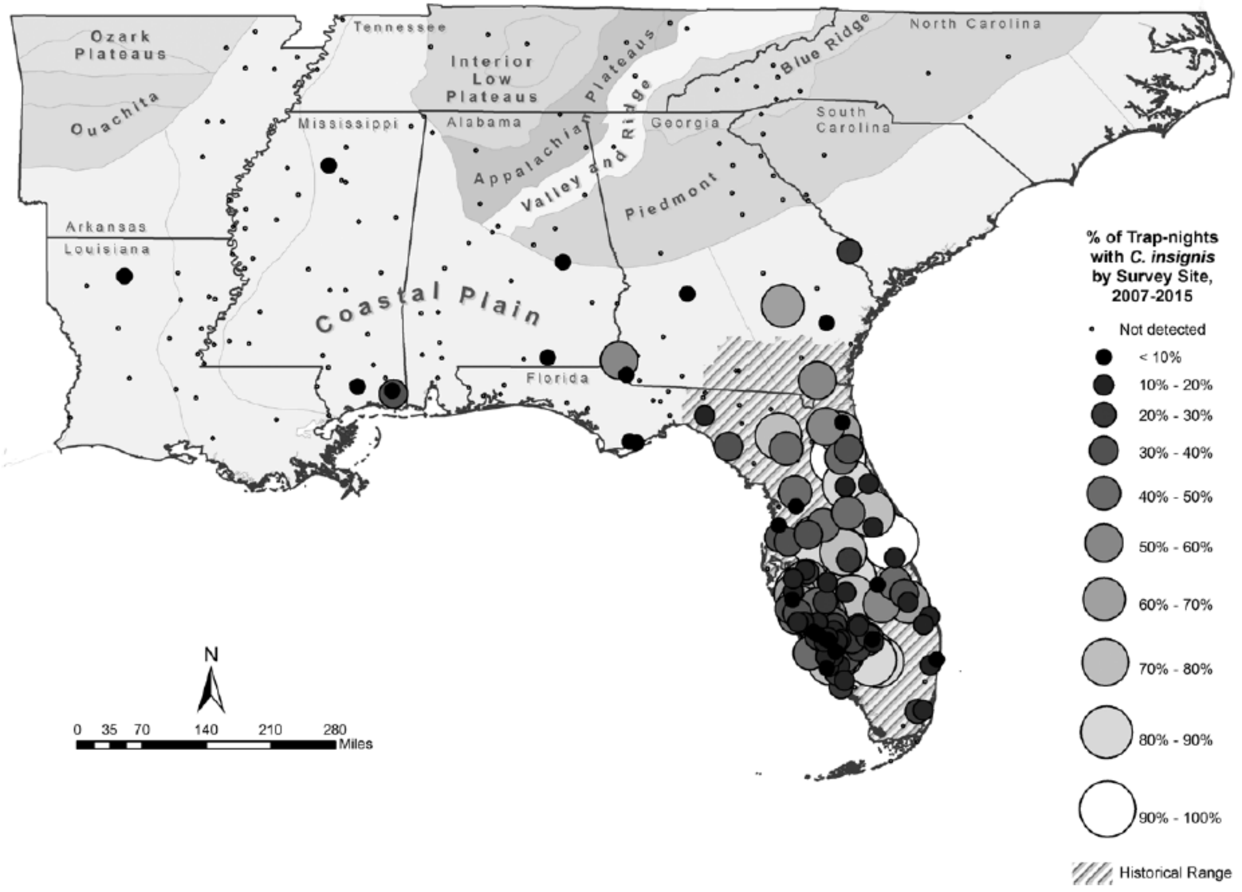
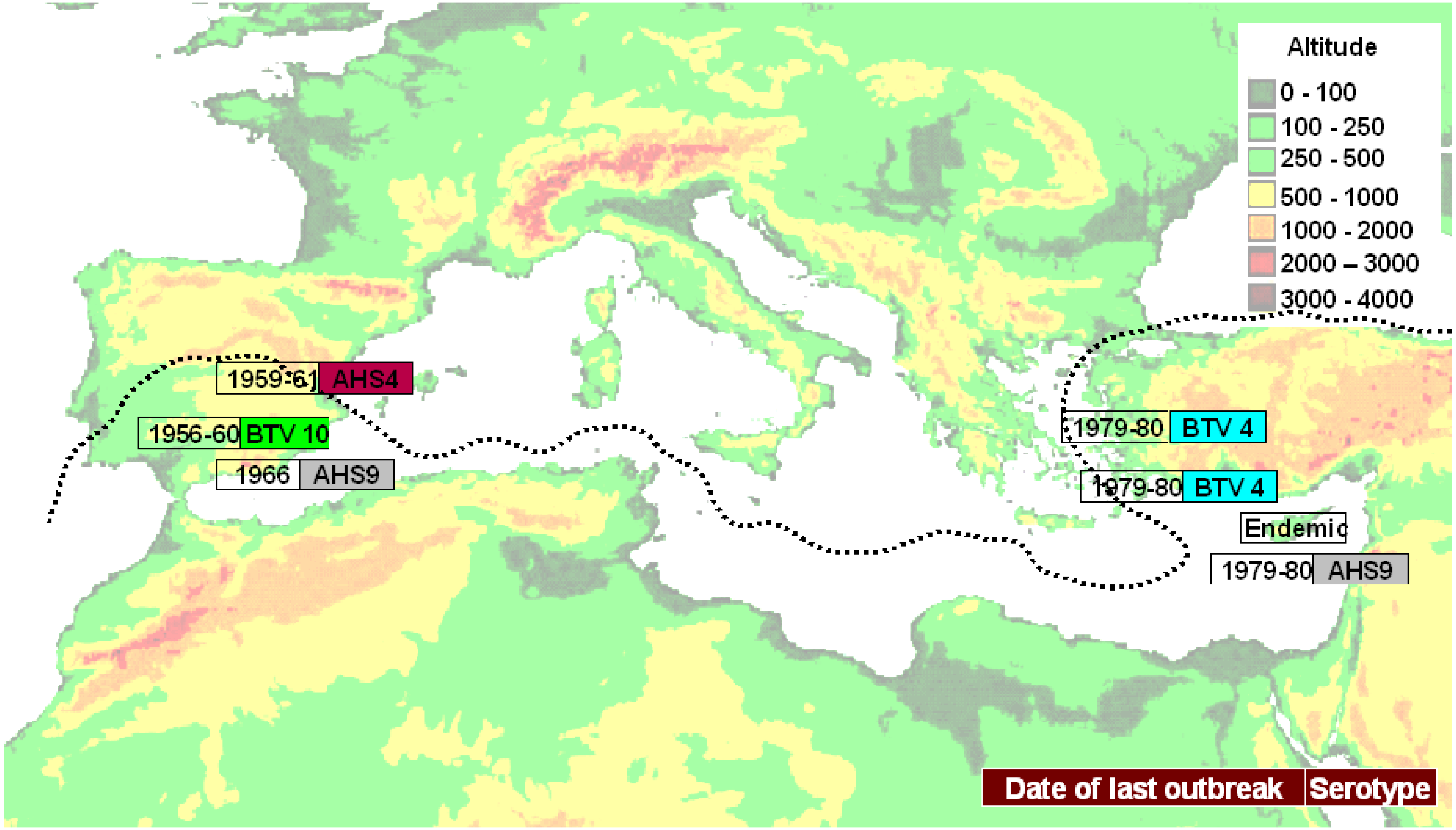


Fig. 1. SCWDS *Culicoides* survey sites in the southeastern United States where *Culicoides insignis* was detected, with the percentage of traps-nights in which it was collected at each site, 2007–2015. Historical range indicates the *C. insignis* range published by Kramer et al. (1985a).

Température et expansion des vecteurs *réelle ou apparente ?*



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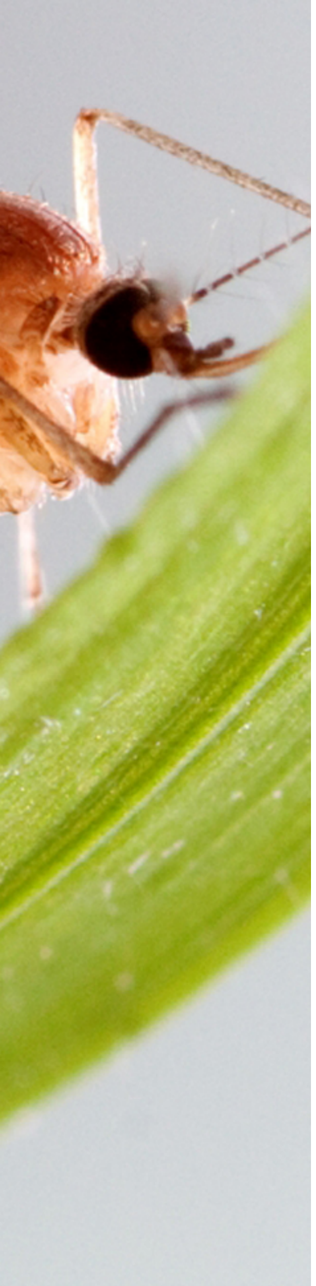

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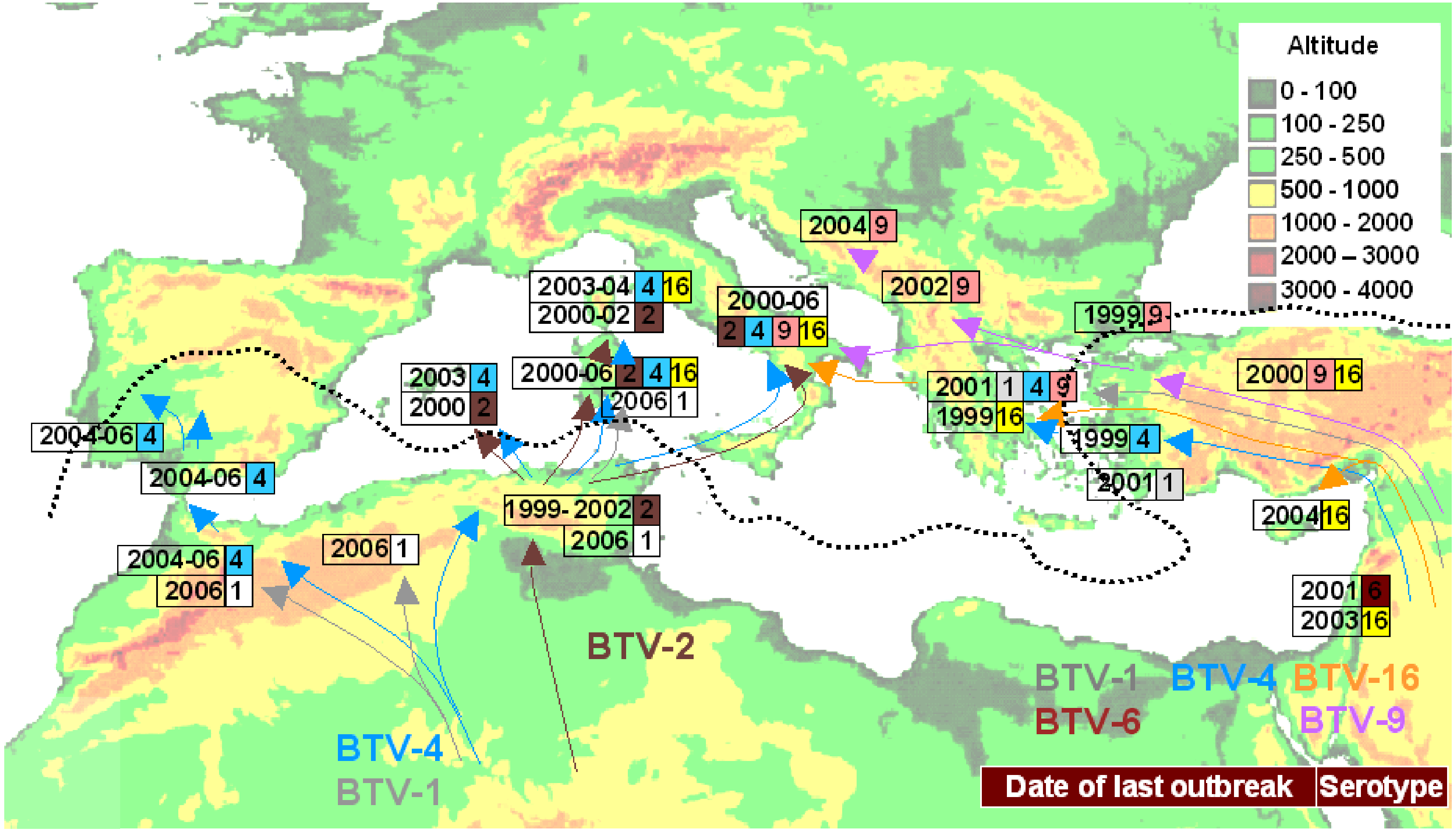
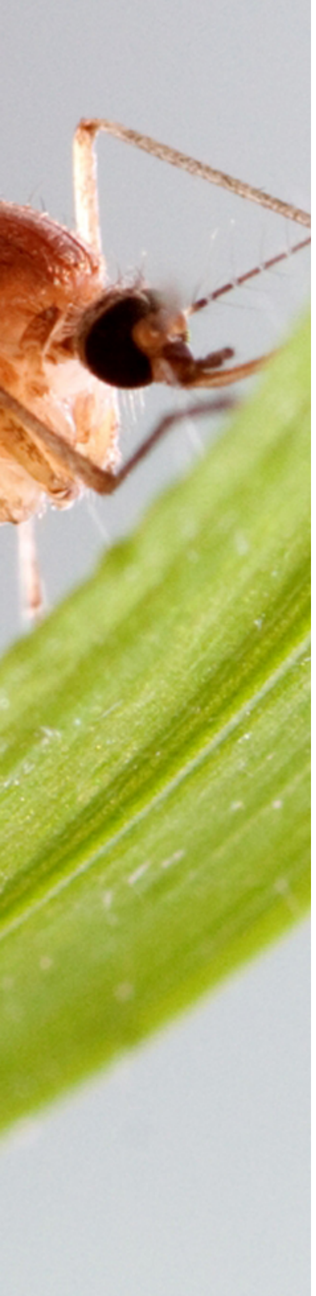
Température et expansion des vecteurs
réelle ou apparente ?





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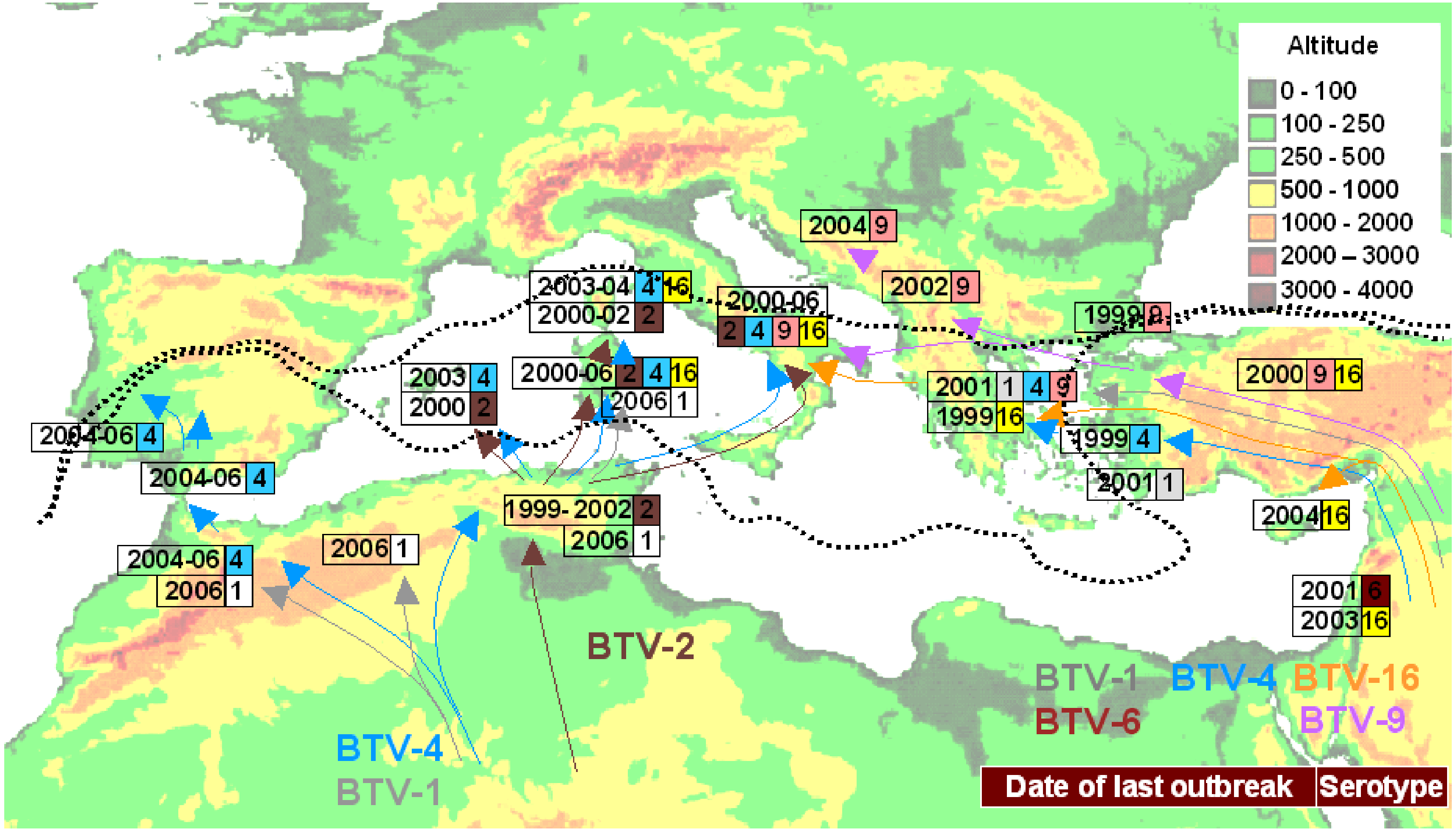
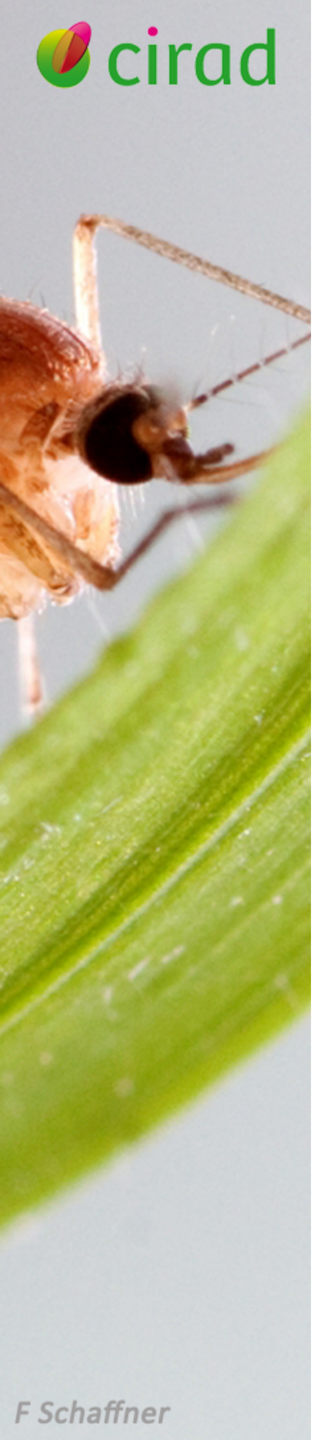
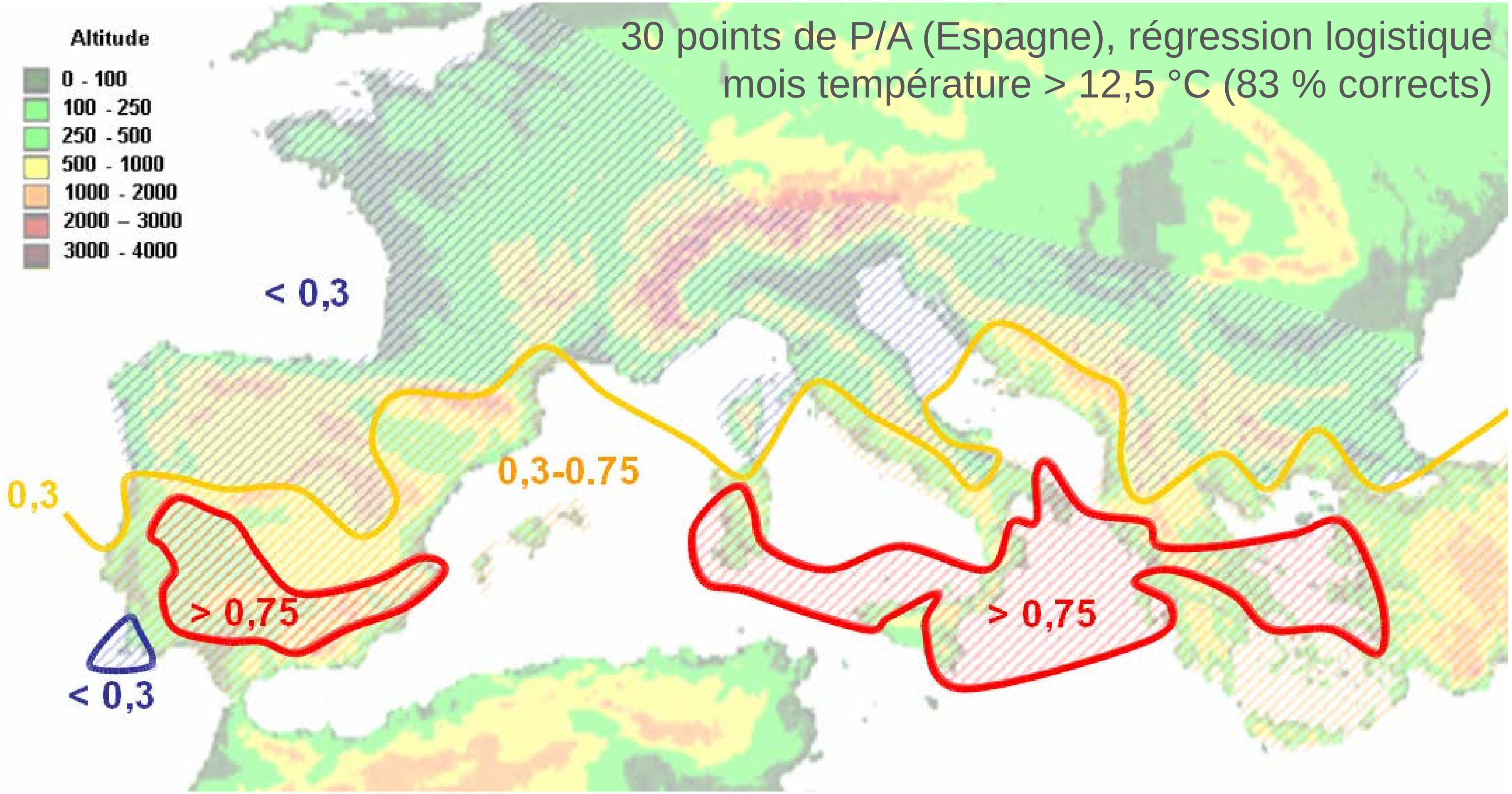
Température et expansion des vecteurs *réelle ou apparente ?*



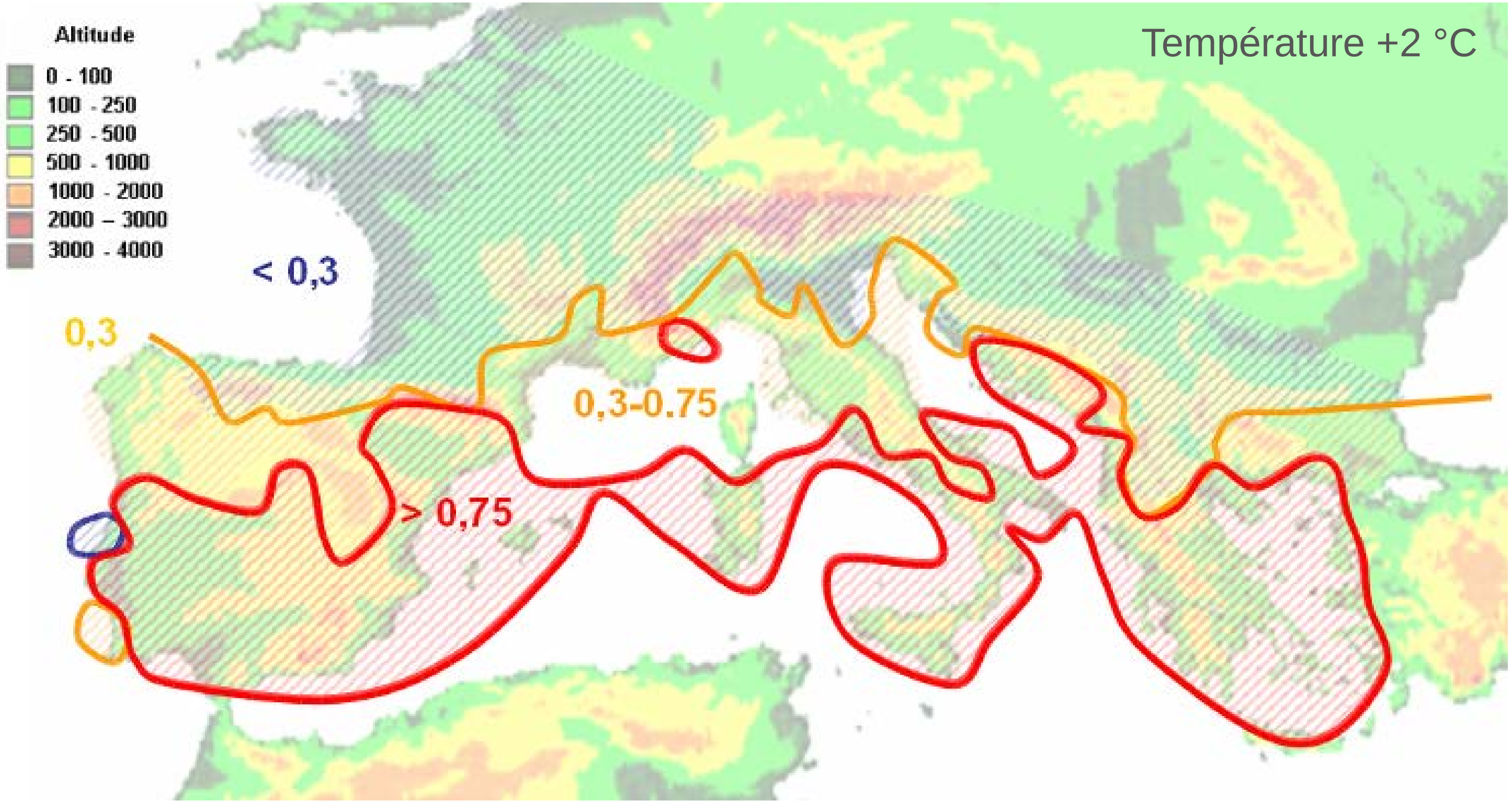


Température et expansion des vecteurs
prophétie auto-réalisatrice



Wittamann *et al.* (2001) *Rev. sci. tech. Off. int. Epiz*

Température et expansion des vecteurs
prophétie auto-réalisatrice



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Température et expansion des vecteurs
prophétie auto-réalisatrice

Journal of Applied Ecology

British Ecological Society

Journal of Applied Ecology 2009, **46**, 1332–1339 doi: 10.1111/j.1365-2664.2009.01723.x

Eight years of entomological surveillance in Italy show no evidence of *Culicoides imicola* geographical range expansion

A. Conte[1]*, M. Gilbert[2,3] and M. Goffredo[1]

[1]Istituto Zooprofilattico Sperimentale dell'Abruzzo e del Molise 'G. Caporale', Via Campo Boario, 64100 Teramo, Italy;
[2]Biological control and Spatial ecology, Université Libre de Bruxelles, av FD Roosevelt 50, B-1050 Brussels; and
[3]Fonds National de la Recherche Scientifique, rue d'Egmont 5, B-1000 Brussels, Belgium

Summary

1. Assessing changes in species range is based on identifying new occurrences in areas where absence has been inferred due to lack of previous records. This technique depends on creating a consistent observational dataset, based on comparable detection methods.

2. In Mediterranean countries, the midge *Culicoides imicola* is the principal vector of bluetongue virus (BTV) that causes an infectious disease of domestic and wild ruminants. Over the last 10 years, BTV has invaded Mediterranean countries (1998) and much of Northern Europe (2006); this unprecedented spread is reported to be a possible consequence of climate change. In southern Europe, based on recent observations found in northern latitudes, BTV spread has been attributed in part to changes in *C. imicola* distribution. However, current sampling of *Culicoides* spp. is far more intensive and targeted than that undertaken before the first BTV epidemics; this obviously results in new information from areas in which collections would have had little chance of positive identification in the past.

3. Since 2001, a national surveillance programme based on permanent traps was established in Italy to follow *C. imicola* population dynamics in space and time. Based on data from 2000 to 2001 cross-sectional studies, Italy was divided into three zones (I: endemicity; II: transition; III: absence) in which longitudinal data on *C. imicola* presence and abundance were analysed as a function of time between 2002 and 2007 through linear and quantile regressions.

4. The results from the surveillance programme demonstrate no detectable range expansion of the *C. imicola* population in Italy between 2002 and 2007.

5. *Synthesis and applications.* This study provides strong evidence that there has been no measurable range expansion between 2002 and 2007 in a species previously described as moving northwards as a result of climate change. For any reliable conclusions to be drawn on the range distribution of *C. imicola* or other similar vector species in Southern Europe, the *Culicoides* surveillance system across all European countries should be designed to provide comparable data based on a constant detection probability over time.

Key-words: Bluetongue, *C. imicola*, *Culicoides*, range expansion, spatial epidemiology, surveillance, vectors

MOLECULAR ECOLOGY

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Colonization of the Mediterranean basin by the vector biting midge species *Culicoides imicola*: an old story

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X. ALLENE,[1,2]† T. BALDET,[1,2]† C. CETRE-SOSSAH,[1,2,7]† A. CHASKOPOULOU,[8]†
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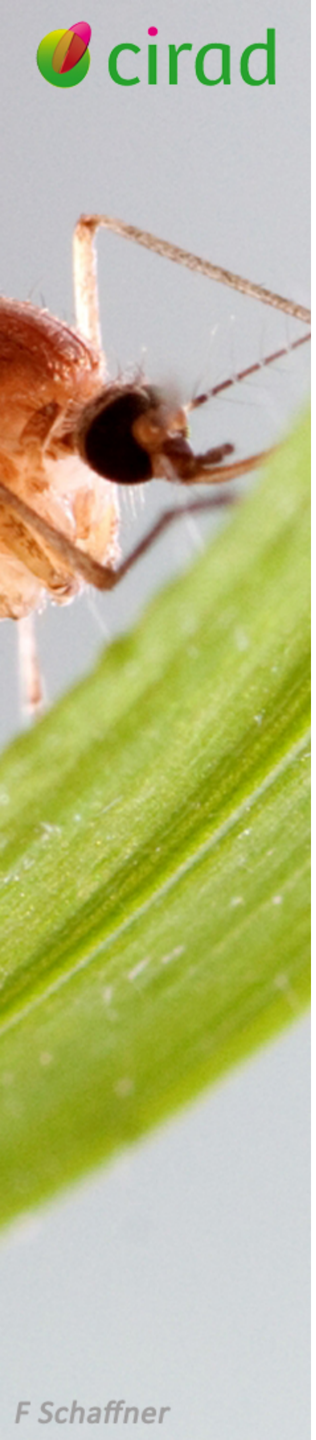
A. TABB
H. GUIS,

Abstract

Understanding the demographic history and genetic make-up of colonizing species is critical for inferring population sources and colonization routes. This is of main interest for designing accurate control measures in areas newly colonized by vector species of economically important pathogens. The biting midge *Culicoides imicola* is a major vector of orbiviruses to livestock. Historically, the distribution of this species was limited to the Afrotropical region. Entomological surveys first revealed the presence of *C. imicola* in the south of the Mediterranean basin by the 1970s. Following recurrent reports of massive bluetongue outbreaks since the 1990s, the presence of the species was confirmed in northern areas. In this study, we addressed the chronology and processes of *C. imicola* colonization in the Mediterranean basin. We characterized the genetic structure of its populations across Mediterranean and African regions using both mitochondrial and nuclear markers, and combined phylogeographical analyses with population genetics and approximate Bayesian computation. We found a west/east genetic differentiation between populations, occurring both within Africa and within the Mediterranean basin. We demonstrated that three of these groups had experienced demographic expansions in the Pleistocene, probably because of climate changes during this period. Finally, we showed that *C. imicola* could have colonized the Mediterranean basin in the Late Pleistocene or Early Holocene through a single event of introduction; however, we cannot exclude the hypothesis involving two routes of colonization. Thus, the recent bluetongue outbreaks are not linked to *C. imicola* colonization event, but rather to biological changes in the vector or the virus.

Keywords: approximate Bayesian computation, colonization, *Culicoides imicola*, microsatellites, mitochondrial genes



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Augmentation des températures
un exemple, la bluetongue

Guis *et al.* (2012) *Interface*

Modelling the effects of past and future climate on the risk of bluetongue emergence in Europe

Helene Guis[1,2,3], Cyril Caminade[4], Carlos Calvete[5], Andrew P. Morse[4], Annelise Tran[2,6] and Matthew Baylis[1,*]

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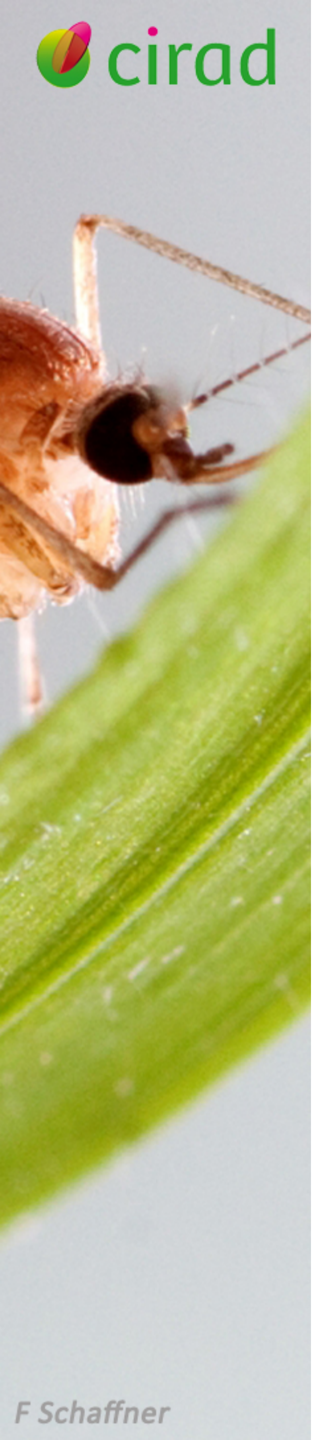

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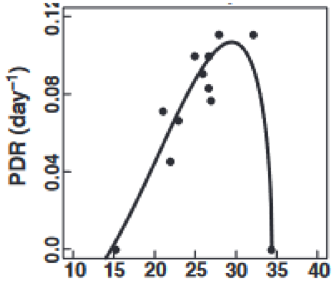
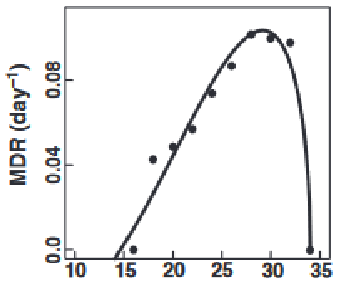
Durée d'incubation



Taux de développement



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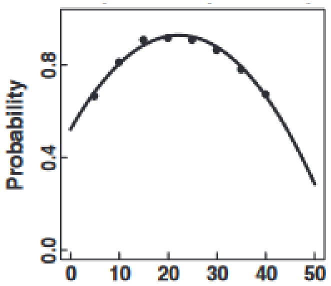

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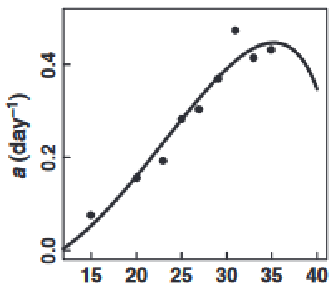

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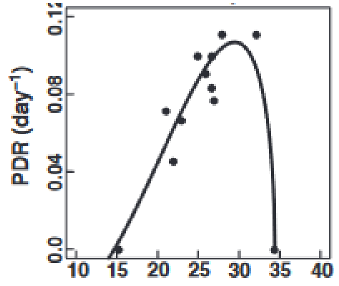

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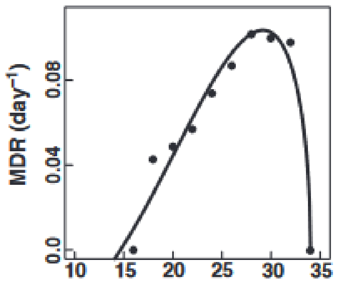

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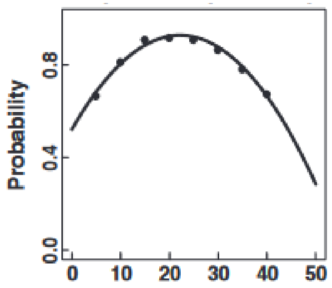

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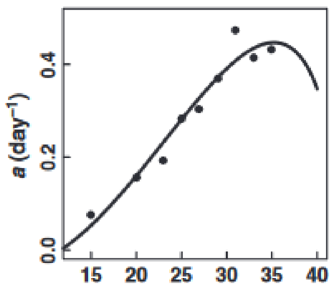

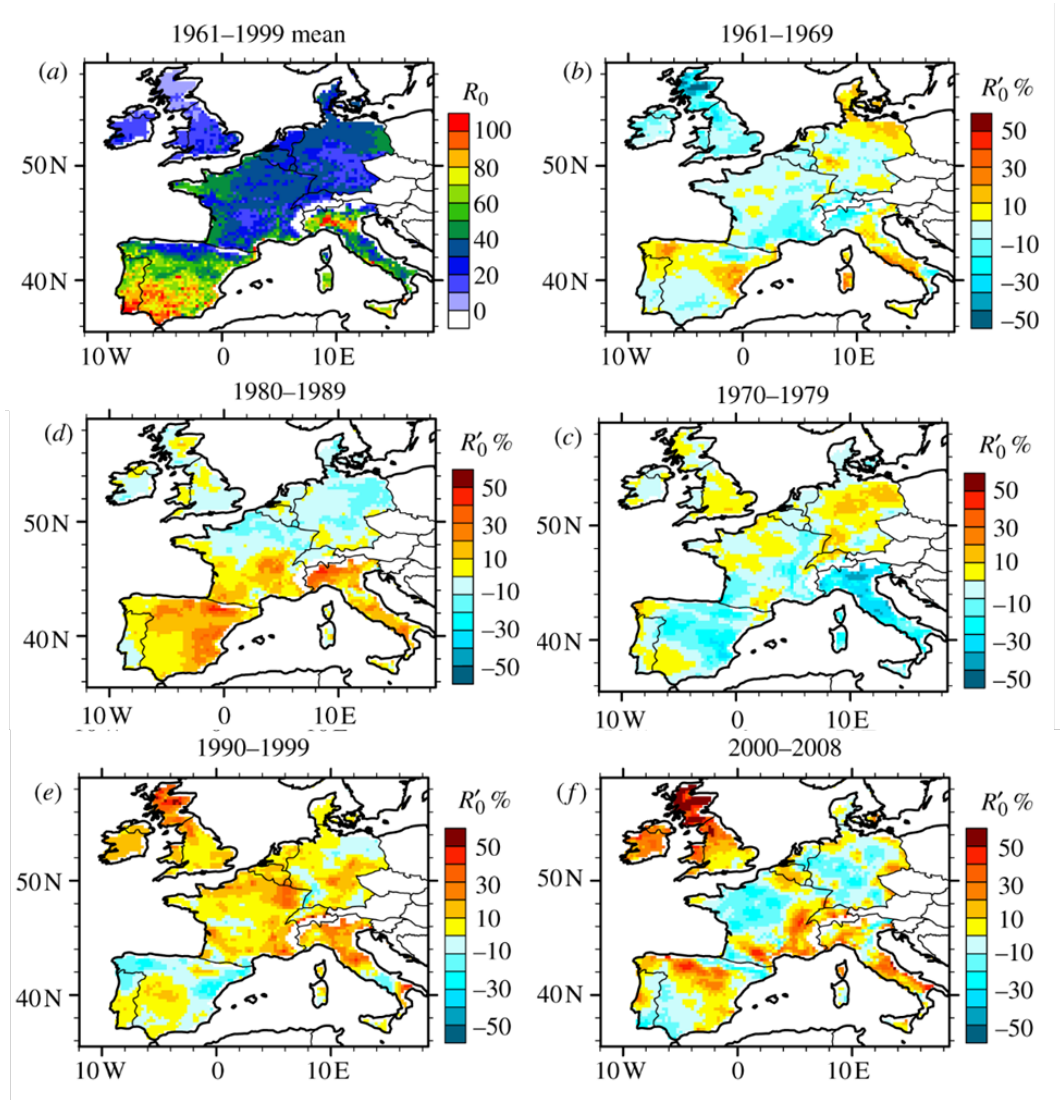

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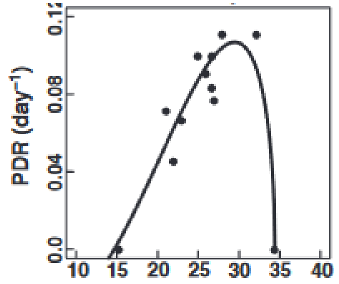

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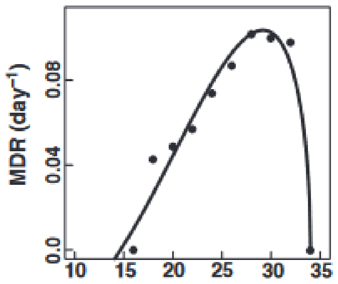

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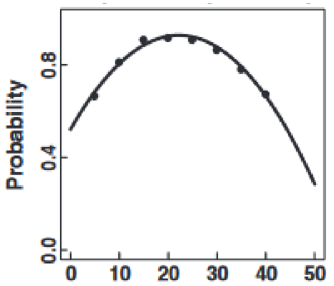

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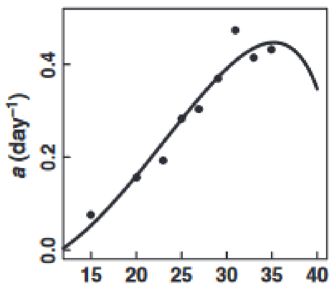
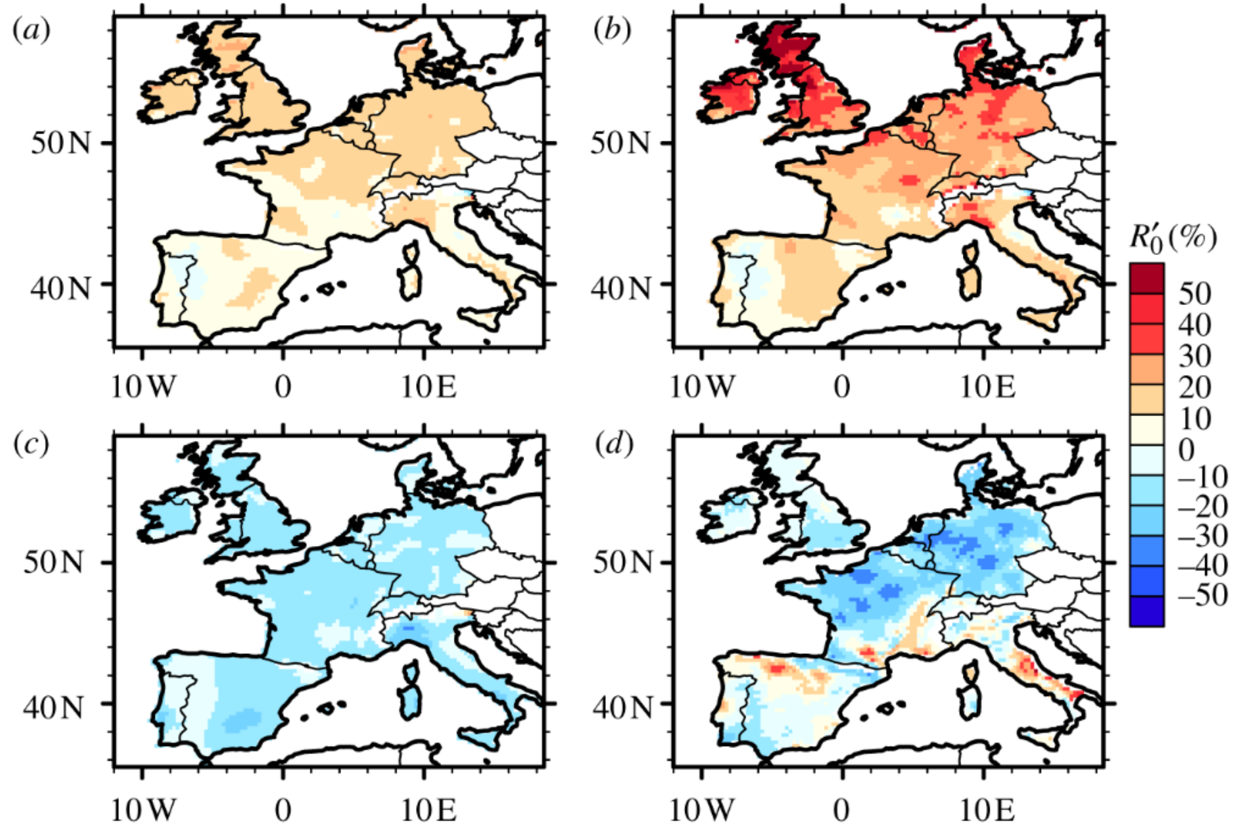


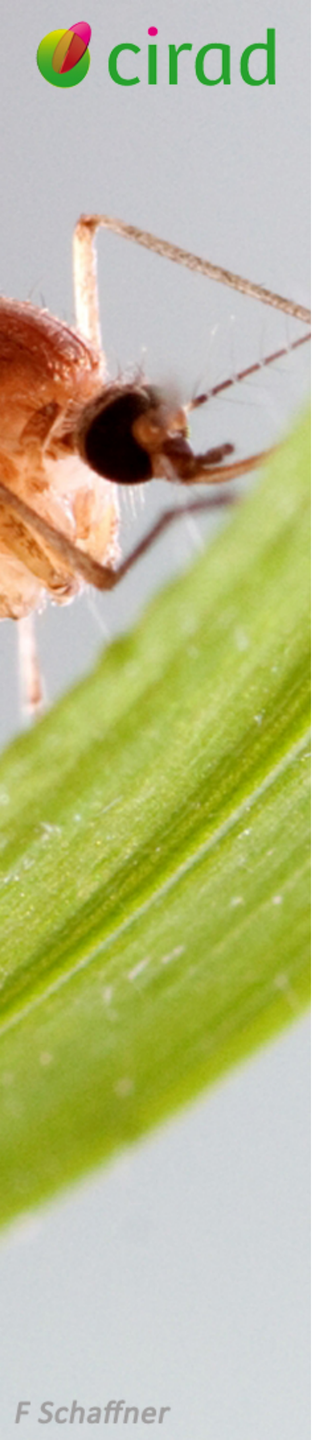
Taux piqûre

Incubation

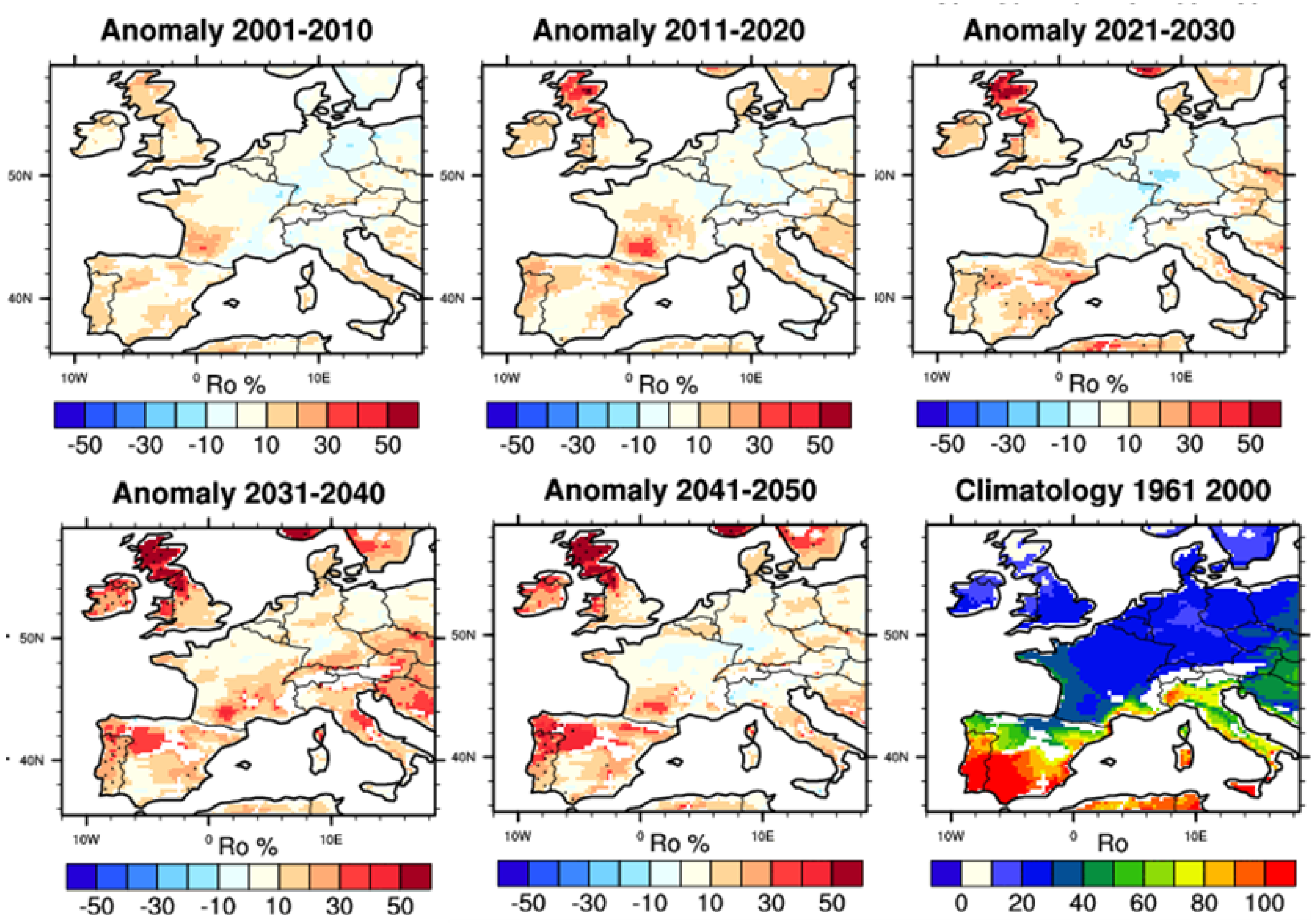


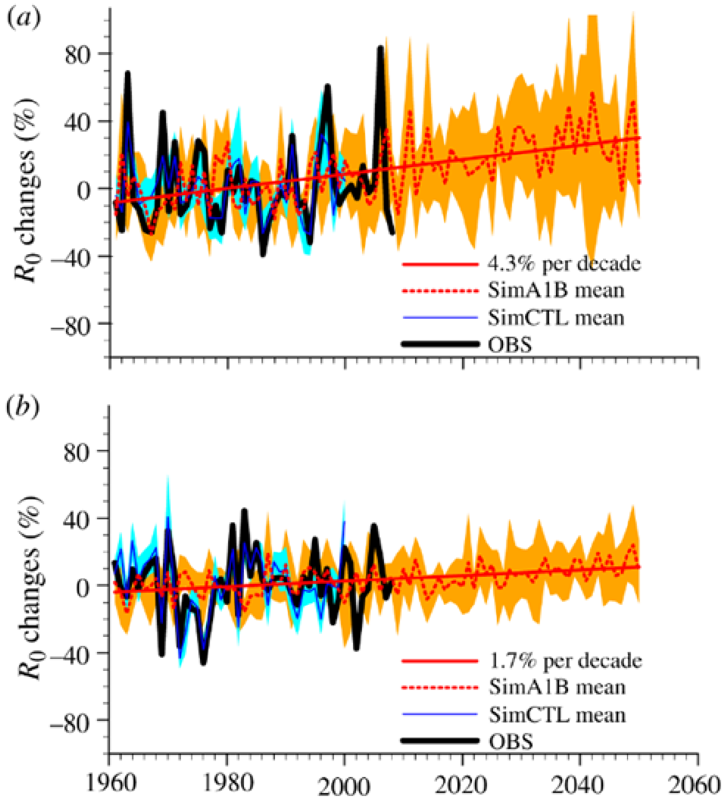
Mortalité

Abondance



Augmentation des températures
un exemple, la bluetongue





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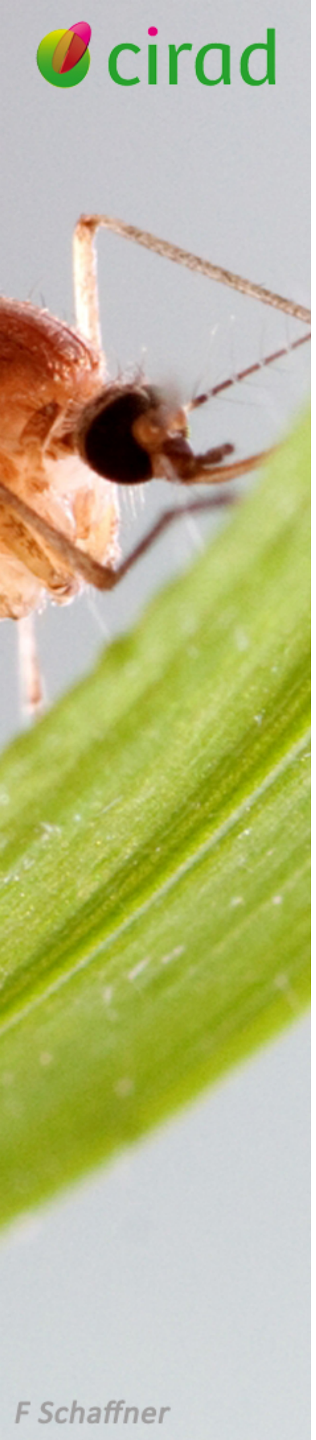


Emergence, recrudescence

quels mécanismes ?

Changements sociaux et modifications environnementales

Augmentation globale des températures

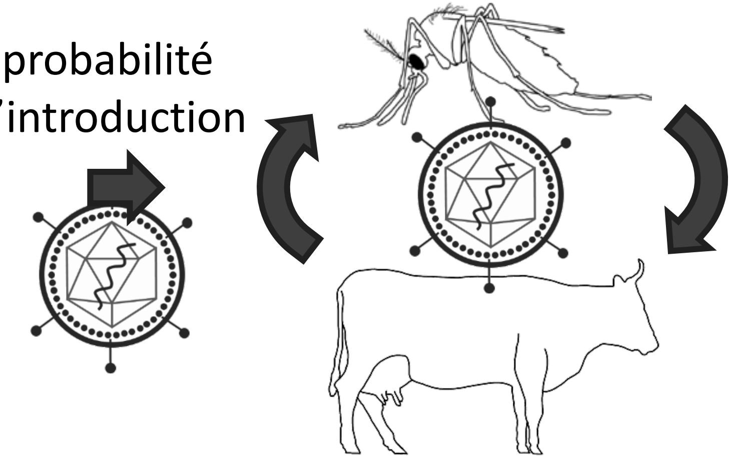
Mesures de lutte

Globalisation de l'économie

conditions de transmission

Mobilité des hôtes et des vecteurs

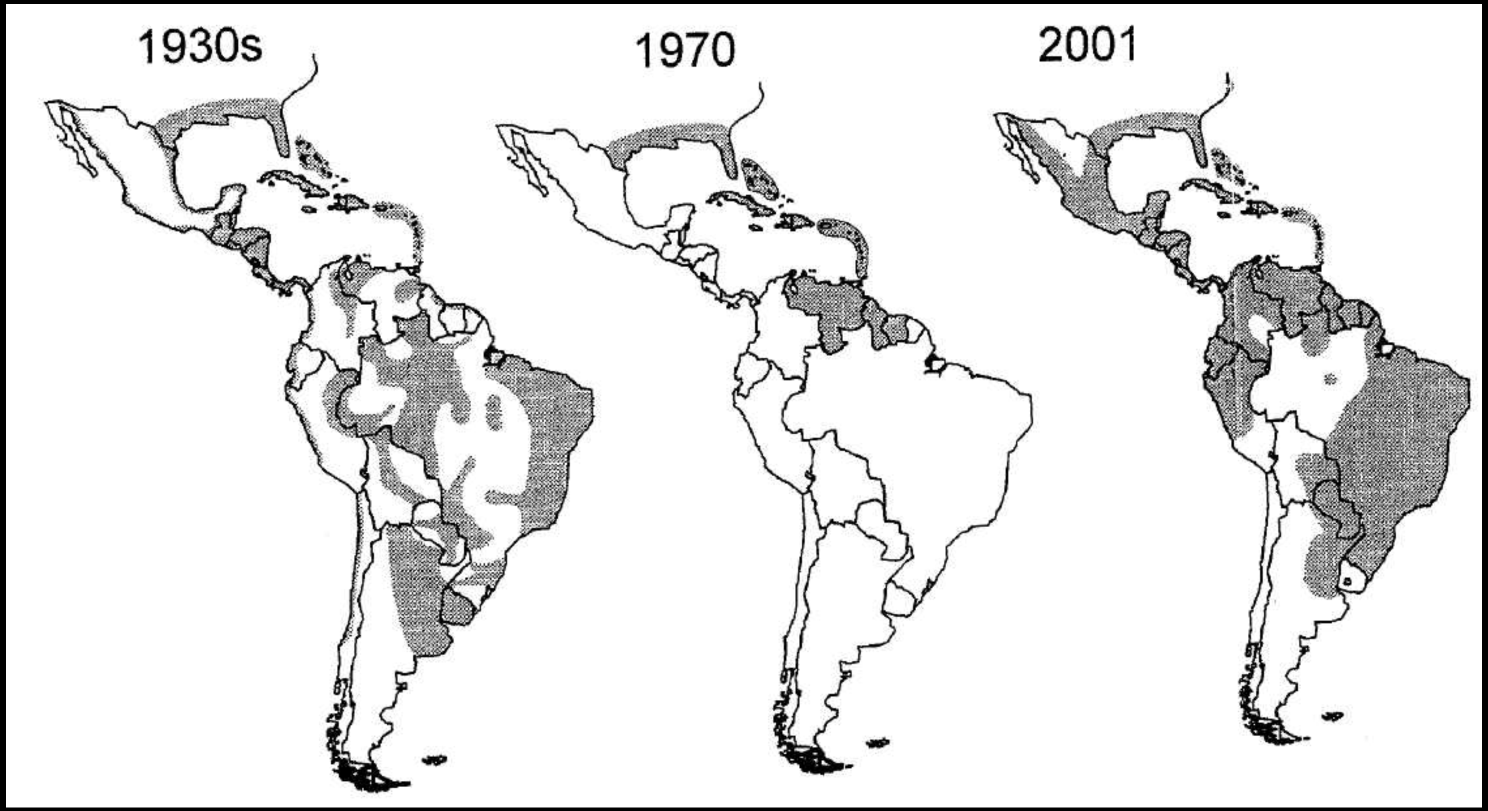
probabilité d'introduction



Programmes de lutte
fluctuation des activités

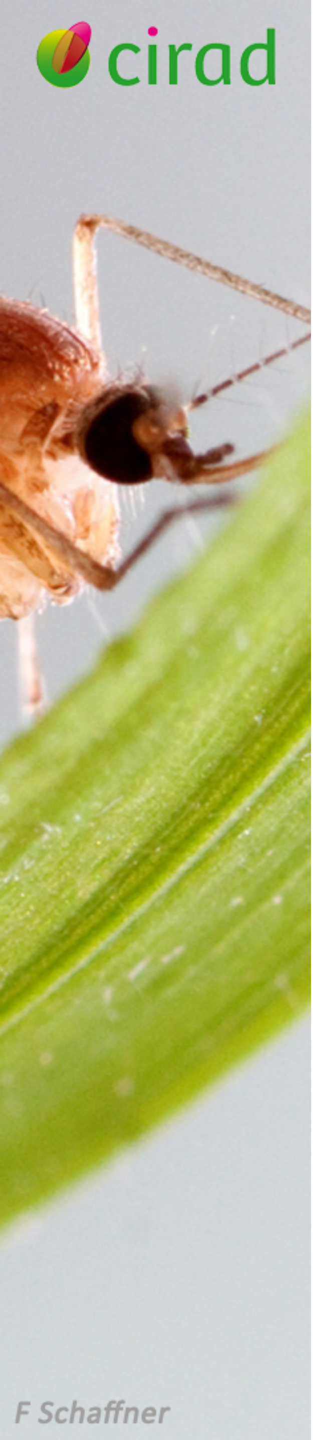
F Schaffner

Crédit : J Gathany



Gubler (2002) *Arch Med Res*

Quelques mots de conclusion



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Mobilité des hôtes et des vecteurs

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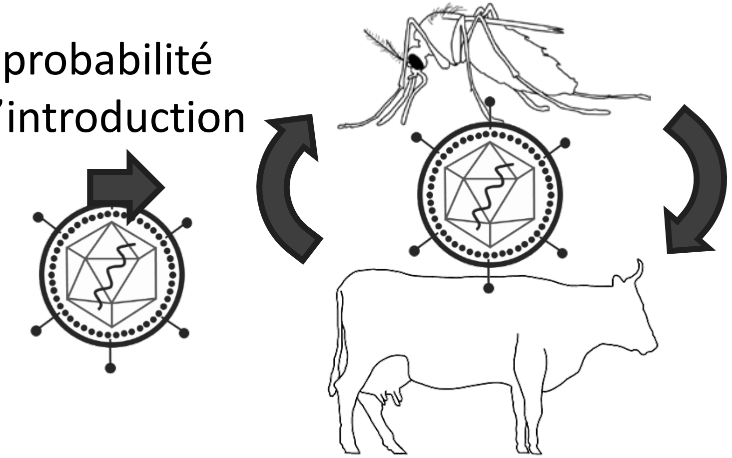
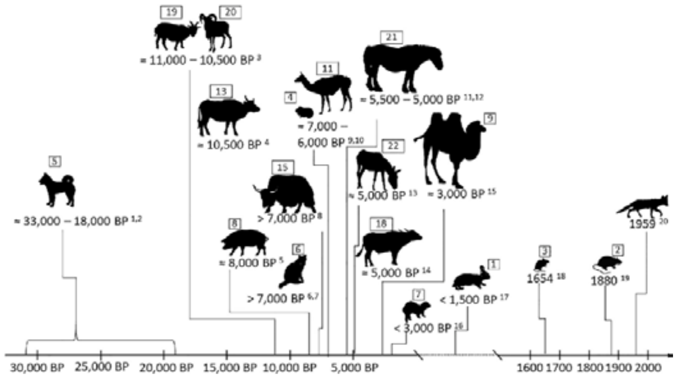
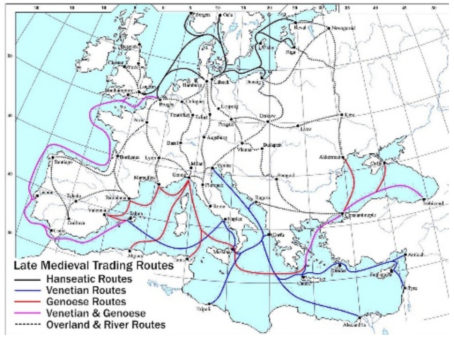


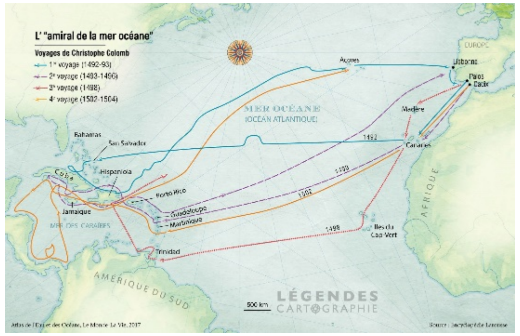
Transitions épidémiologiques



10 000 ans : sédentarisation (agriculture, élevage)

2 000 à 3 000 ans : contacts militaires et commerciaux (bassin méditerranéen, Asie Centrale et du Sud-Est)

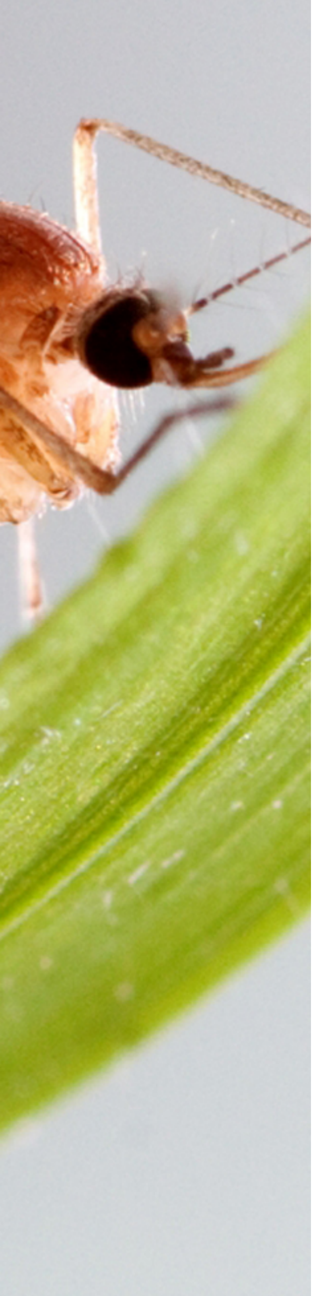




XVIe siècle : colonisations européennes, contacts trans-océaniques

capitalocène : échelle globale, changements démographiques, sociaux et environnementaux, augmentation globale de la température

McMichael (2004) *Phil. Trans. R. Soc. Lond.B*



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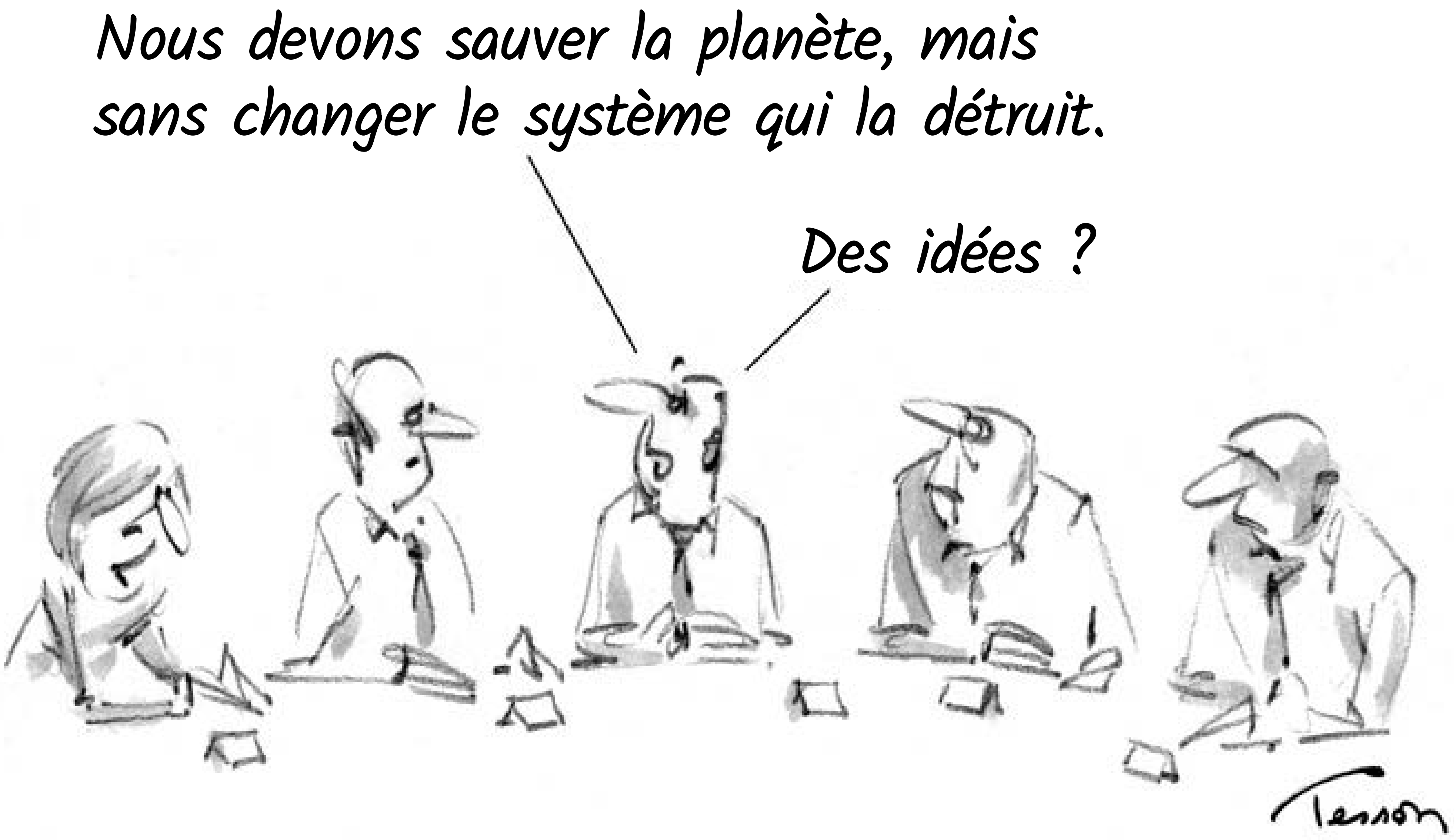
COP21



SOCIÉTÉ VÉTÉRINAIRE PRATIQUE DE FRANCE

XIIe Rencontres de Santé publique vétérinaire
École du Val de Grâce, le 04 décembre 2024
« Actualités des maladies vectorielles : connaissances, lutte, gestion »

Maladies vectorielles
quels mécanismes d'émergence ?

Thomas Balenghien
balenghien@cirad.fr

cirad