

POINT SUR L'EXTENSION GEOGRAPHIQUE DES ARBOVIROSES

Dr Thomas Perpoint

Maladies Infectieuses et Tropicales

Hôpital de la Croix-Rousse Lyon

- ARBOVIROSE → • **TRIADE** HOTE VECTEUR VIRUS
- GEOGRAPHIE PARTAGEE → • **EPIDEMIOLOGIE** GEOGRAPHIQUE
- EXPANSION → • **DYNAMISME** D'EMERGENCE

- ARBOVIROSE → • **TRIADE** HOTE VECTEUR VIRUS
- GEOGRAPHIE PARTAGEE → • **EPIDEMIOLOGIE** GEOGRAPHIQUE
- EXPANSION → • **DYNAMISME** D'EMERGENCE +++

MALADIES LIEES A DES VIRUS

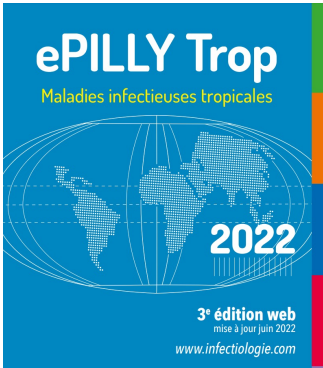


Tableau 1. Principales arboviroses tropicales

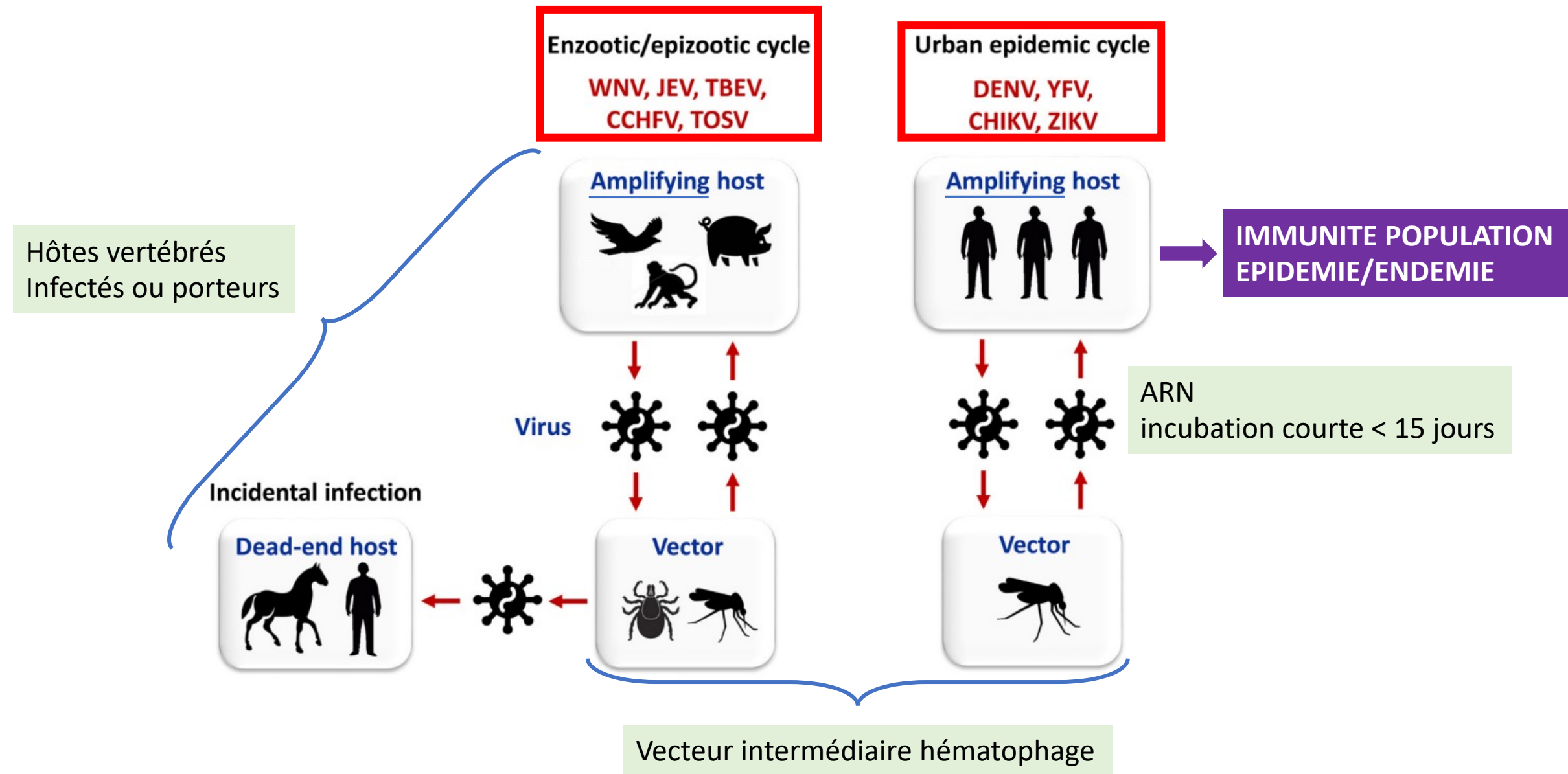
Famille	Genre	Arboviroses
Flaviviridae	Flavivirus	Dengue (M) ★
		Fièvre jaune (M)
		Encéphalite japonaise (M)
		West Nile (M, T) ★
		Encéphalite Saint Louis (M)
		Fièvre de la forêt de Kyasanur (T)
		Zika (M) ★
		Sepik (M) Encéphalite à tique (T) ★
		Koutango (T)
Bunyaviridae	Nairovirus	Crimée-Congo (T) ★
	Phlébovirus	Fièvre de la vallée du Rift (P)
		Fièvre à phlébotomes (P) Toscana (P)
	Bunyavirus	Bunyamwera (M)
Togaviridae	Alphavirus	Chikungunya (M) ★
		O'Nyong Nyong (M)
		Sindbis (M)
		Mayaro (M)
		Ross River (M)
		Encéphalites équine Est, Ouest, du Venezuela (M)
Reoviridae	Orbivirus	Orungo (M)
Transmission par des moustiques (M), des phlébotomes (P), des tiques (T)		

Forme pauci ou asymptomatique
Forme clinique
Forme grave

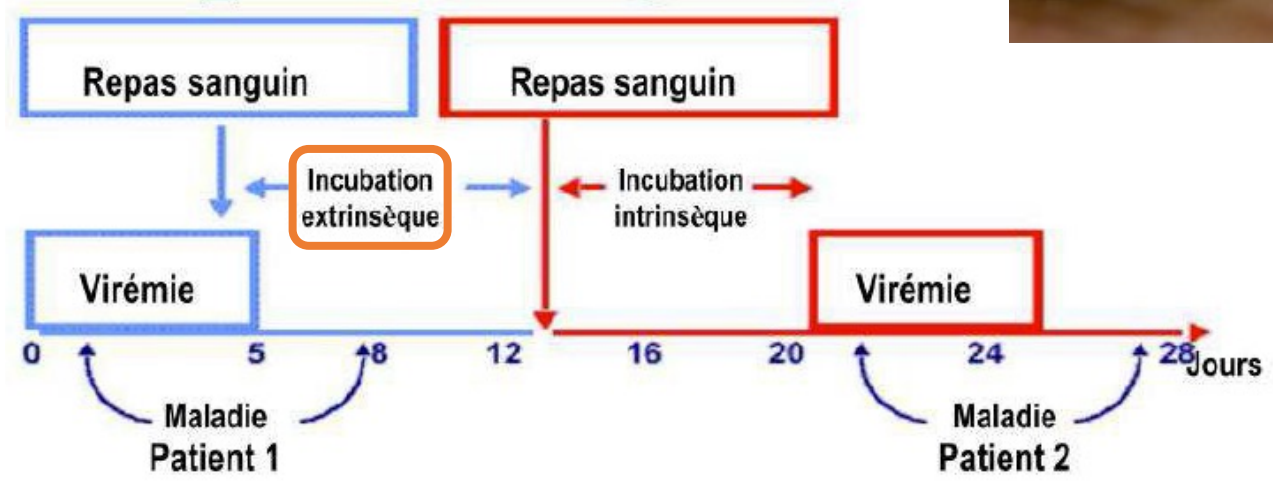
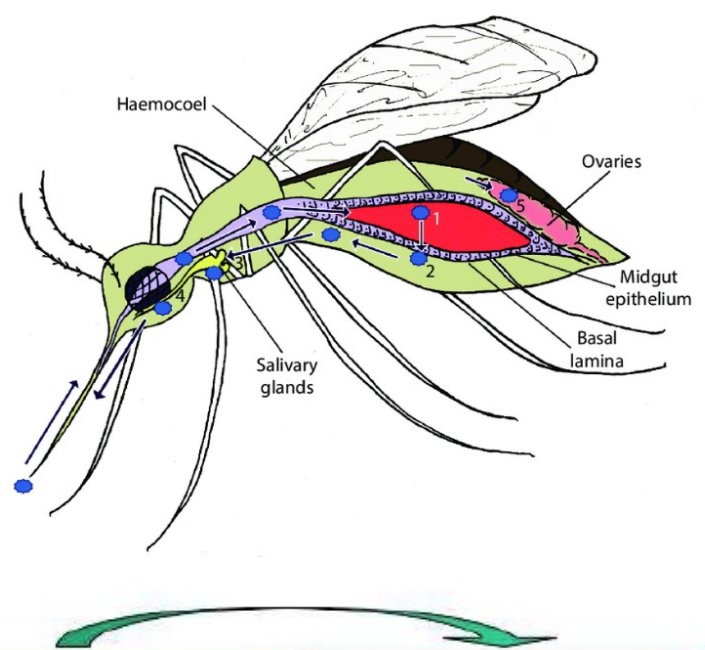
Tableau 2. Principaux syndromes dus aux arboviroses

Syndrome algique	Syndrome hémorragique	Syndrome méningo-encéphalitique
Dengue	Crimée Congo	Encéphalite japonaise
Chikungunya	Dengue	Encéphalite Saint Louis
Zika	Kyasanur	Encéphalites équine
Mayaro	Fièvre de la Vallée du Rift	West Nile
O'Nyong Nyong	fièvre jaune	Fièvre de la Vallée du Rift
Ross River		Rarement : dengue et Chikungunya
Hépatite-néphrite	fièvre jaune	

TRIADE HOTE VECTEUR VIRUS



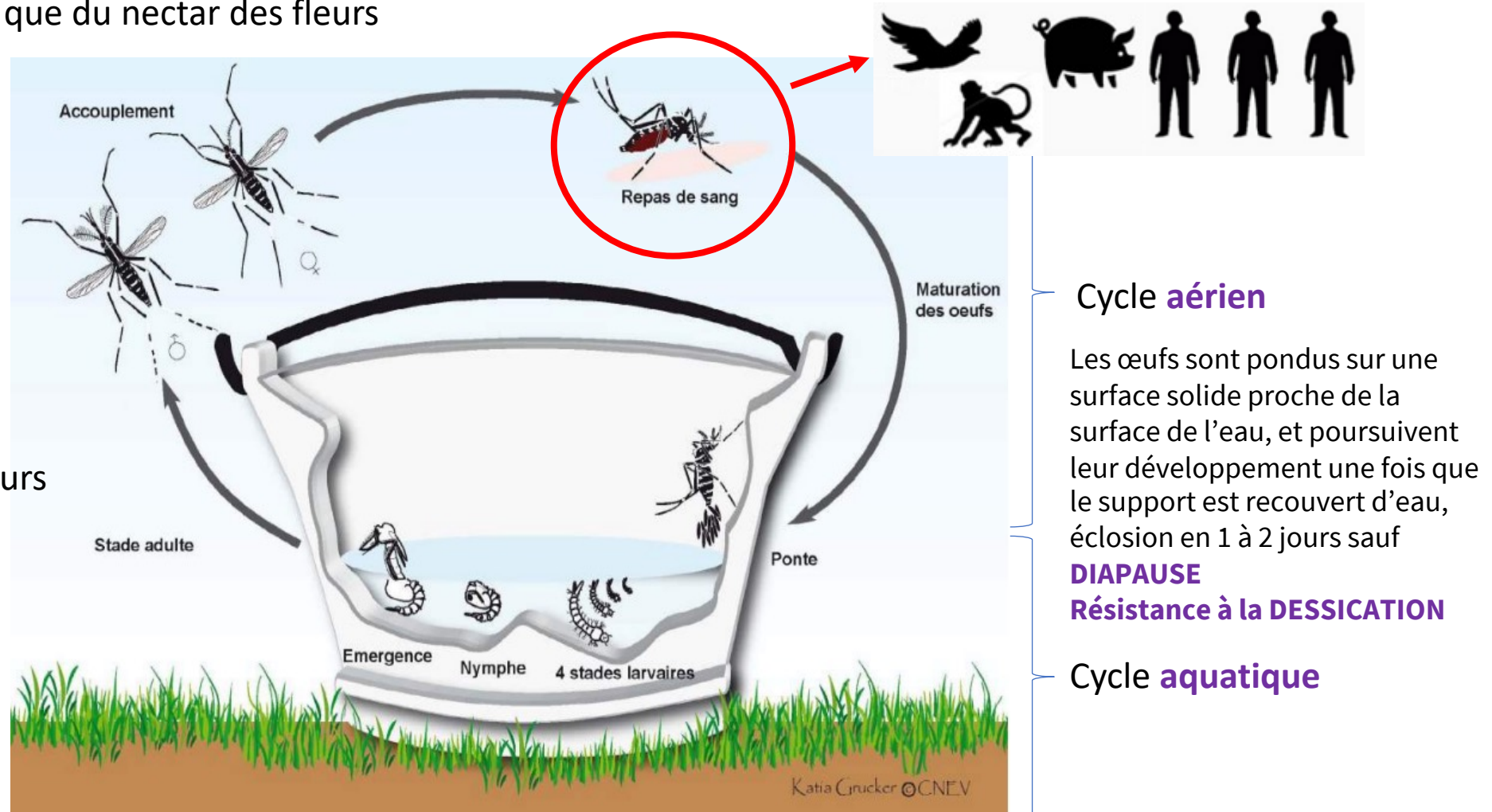
VECTEURS



VECTEURS DETERRITORIALISATION DE LA FORET A LA VILLE

VECTEURS AEDES / SON CYCLE

Seules les **femelles** après avoir été fécondées piquent pour récupérer les **protéines** nécessaires à la maturation des ses œufs
Les mâles ne se nourrissent que du nectar des fleurs



VECTEURS DETERRITORIALISATION

DYNAMIQUE DU VECTEUR AEDES / DIFFERENCES AEGYPTI ALBOPICTUS



Aedes Aegypti

Vit en milieu **urbain**
avec ou sans végétation

Dans les maisons

Furtif

Préfère l'**humain**

Principal vecteur de la
dengue

Sites de ponte
artificiels, autour ou
dans les **maisons**

Compétence vectorielle
+++



Aedes Albopictus

Vit au contact de la
végétation

Jardin

agressif

Autant humain que
mammifère domestique
ou sauvage

Vecteur secondaire de
la dengue

Sites de ponte naturels
ou artificiels plus
éloignés des habitations

Compétence vectorielle
+

Adaptation aux zones
tempérées, plasticité

- **DIAPAUSE** = capacité de passer
l'hiver pour le moustique tigre

ŒUFS = capable de résister au **froid** qui
arrête leur maturation pendant des
mois. Eclosion au printemps quand la
température et de l'eau reviendra

LARVES: idem développement arrêté si
température < 15° en restant dans
l'eau et reprise secondaire

ADULTE dernière génération,
accumulation de graisse et
« hibernation »

VECTEURS DETERRITORIALISATION et ANTHROPISATION

VECTEUR AEDES / GITES ANTHROPIQUES

cnév

Centre National d'Expertise
sur les Vecteurs



MINISTÈRE
DES AFFAIRES SOCIALES
ET DE LA SANTÉ

Exemples de gîtes larvaires liés au bâti



Photos : Différents lieux propices au développement d'*Aedes aegypti* et *Aedes albopictus*.

(a) toiture terrasse favorisant la stagnation de l'eau, (b) avaloirs pluviaux, (c) caniveau sur voirie, (d) et (e) coffrets techniques, (f) bonde d'évacuation siphon de sol (g) et (h) terrasse sur plots, (i) gîte créé lors de travaux d'aménagement - Crédits photo : CNEV



Photo 2. Différents lieux propices au développement d'*Aedes aegypti* et *Aedes albopictus*. (a) toiture terrasse favorisant la stagnation de l'eau, (b) avaloirs pluviaux, (c) soucoupes de pots de fleurs, (d) bidon de récupération d'eau de pluie, (e) divers récipients contenant de l'eau (e.g. arrosoir).

EPIDEMIOLOGIE GEOGRAPHIQUE

**EG = TERRITOIRE
AVEC VECTEUR
MAMMIFERE dont HUMAIN
INFECTE par VIRUS**



**EG = 2 TYPES DE TERRITOIRE
EN EXPANSION**

- **TROPICAUX**
- **NON TROPICAUX**



IMMUNITE DES POPULATIONS?

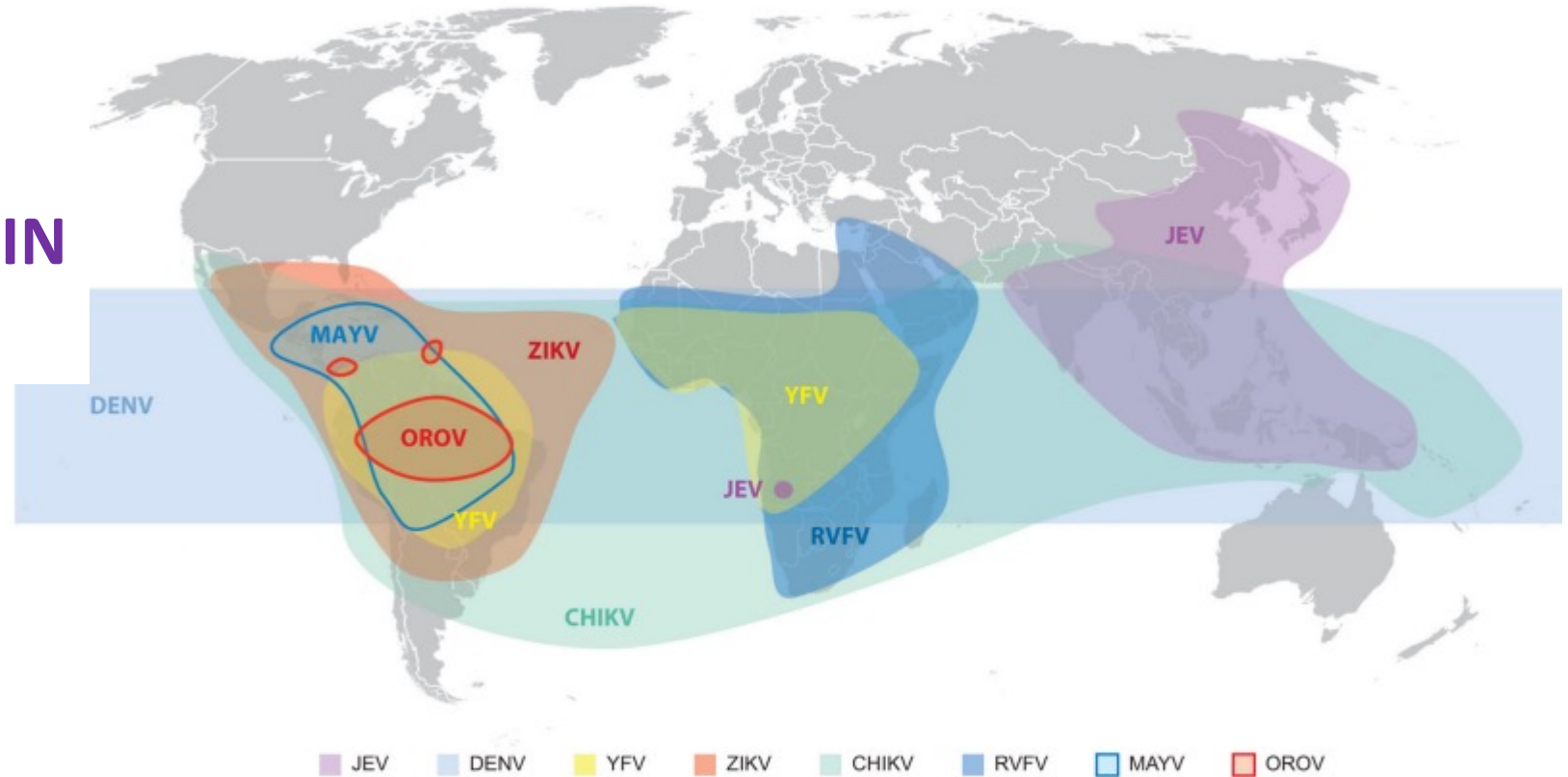


Figure 2.

Map showing the reported distributions of emerging arboviruses discussed in this review. Abbreviations: CHIKV, chikungunya virus; DENV, dengue virus; JEV, Japanese encephalitis virus; MAYV, Mayaro virus; OROV, Oropouche virus; RVFV, Rift Valley fever virus; YFV, yellow fever virus; ZIKV, Zika virus.

PHENOMENE DYNAMIQUE

DYNAMIQUE EPIDEMIOLOGIQUE / EXPANSION

- **Déterritorialisation** du vecteur (de la forêt à la ville)
- Déterminants **humains** à l'expansion
- Environnement et changement **climatique**

- 1 International trade and commerce
- 2 Human demographics and behaviour
- 3 Human susceptibility to infection
- 4 Poverty and social inequality
- 5 War and famine
- 6 Breakdown of public-health measures
- 7 Technology and industry
- 8 Changing ecosystems
- 9 Climate and weather
- 10 Intent to harm
- 11 Lack of political will
- 12 Microbial adaptation and change
- 13 Economic development and land use

Emerging infections: a perpetual challenge

David M Morens, Gregory K Folkers, Anthony S Fauci

Table 1. Some major factors that underlie disease emergence and reemergence [2,5]. *Lancet Infect Dis 2008;*

The Microbial Agent	The Human Host	The Human Environment
Genetic adaptation and change	Human susceptibility to infection	Climate and weather
Polymicrobial diseases	Human demographics and behavior	Changing ecosystems
	International trade and travel	Economic development and land use
	Intent to harm (bioterrorism)	Technology and industry
	Occupational exposures	Poverty and social inequality
	Inappropriate use of antibiotics	Lack of public health services
		Animal populations
		War and famine
		Lack of political will

doi:10.1371/journal.ppat.1003467.t001

- De nouveaux territoires **tropicaux**
- Une immixtion **autochtone** dans des territoires non tropicaux **tempérés**

DYNAMIQUE EPIDEMIOLOGIQUE / FIEVRE JAUNE



Outbreaks of YFV transmission in the Caribbean and continental Americas, as well as in Europe, are also well documented back to the sixteenth century, **facilitated by the slave trade from Africa**. However, among these three viruses plus DENV, only YFV is known to have initiated an enzootic NHP–mosquito cycle, transmitted within the Amazon, Araguaia, and Orinoco river basins of South America by *Haemagogus* and *Sabethes* spp. arboreal mosquitoes

OPEN ACCESS Freely available online

PLOS PATHOGENS

Out of Africa: A Molecular Perspective on the Introduction of Yellow Fever Virus into the Americas

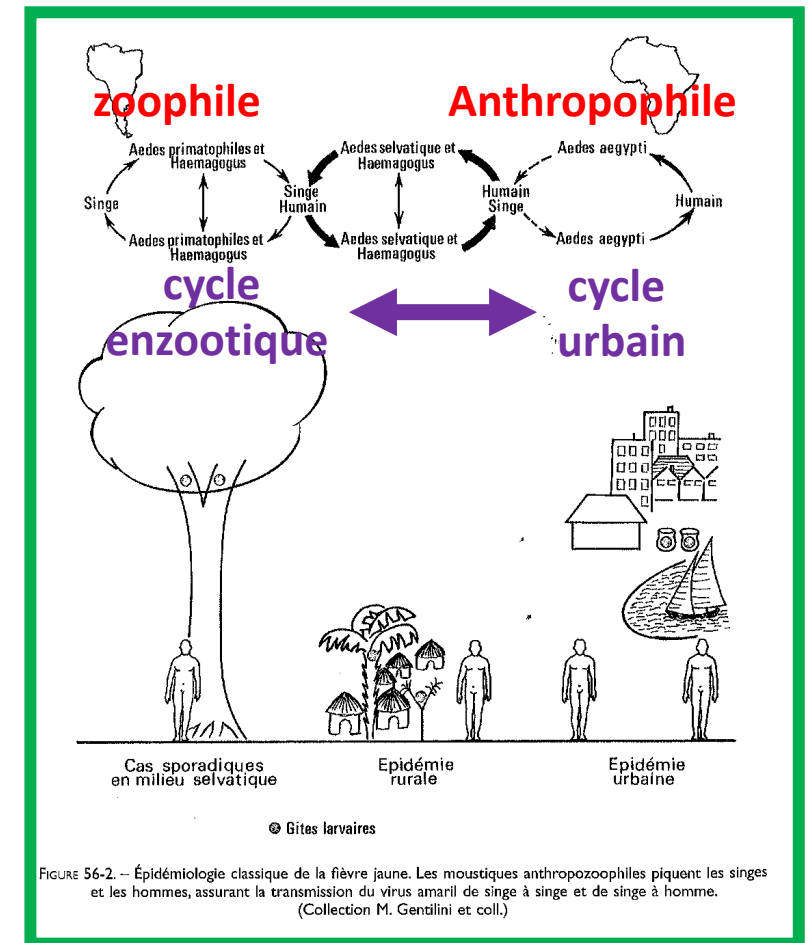
Juliet E. Bryant^{1,2,3,4*}, Edward C. Holmes^{5,6,7}, Alan D. T. Barrett^{1,2,3*}

May 2007 | Volume 3 | Issue 5 | e75

1 Department of Pathology, University of Texas Medical Branch, Galveston, Texas, United States of America, **2** Center for Biodefense and Emerging Infectious Diseases, University of Texas Medical Branch, Galveston, Texas, United States of America, **3** Institute for Human Infections and Immunity, University of Texas Medical Branch, Galveston, Texas, United States of America, **4** Institut Pasteur, National Center for Laboratory and Epidemiology, Vientiane, Lao People's Democratic Republic, **5** Department of Biology, The Pennsylvania State University, University Park, Pennsylvania, United States of America, **6** Center for Infectious Disease Dynamics, The Pennsylvania State University, University Park, Pennsylvania, United States of America, **7** Fogarty International Center, National Institutes of Health, Bethesda, Maryland, United States of America

Yellow fever virus (YFV) remains the cause of severe morbidity and mortality in South America and Africa. To determine the evolutionary history of this important reemerging pathogen, we performed a phylogenetic analysis of the largest YFV data set compiled to date, representing the *prM/E* gene region from 133 viral isolates sampled from 22 countries over a period of 76 years. We estimate that the currently circulating strains of YFV arose in Africa within the last 1,500 years and emerged in the Americas following the slave trade approximately 300–400 years ago. These viruses then spread westwards across the continent and persist there to this day in the jungles of South America. We therefore illustrate how gene sequence data can be used to test hypotheses of viral dispersal and demographics, and document the role of human migration in the spread of infectious disease.

Citation: Bryant JE, Holmes EC, Barrett ADT (2007) Out of Africa: A molecular perspective on the introduction of yellow fever virus into the Americas. PLoS Pathog 3(5): e75. doi:10.1371/journal.ppat.0030075



DYNAMIQUE EPIDEMIOLOGIQUE / DENGUE ZIKA CHIKUNGUNYA FIEVRE JAUNE

DYNAMIQUE DU VECTEUR AEDES / SA LOCALISATION

Aedes Aegypti

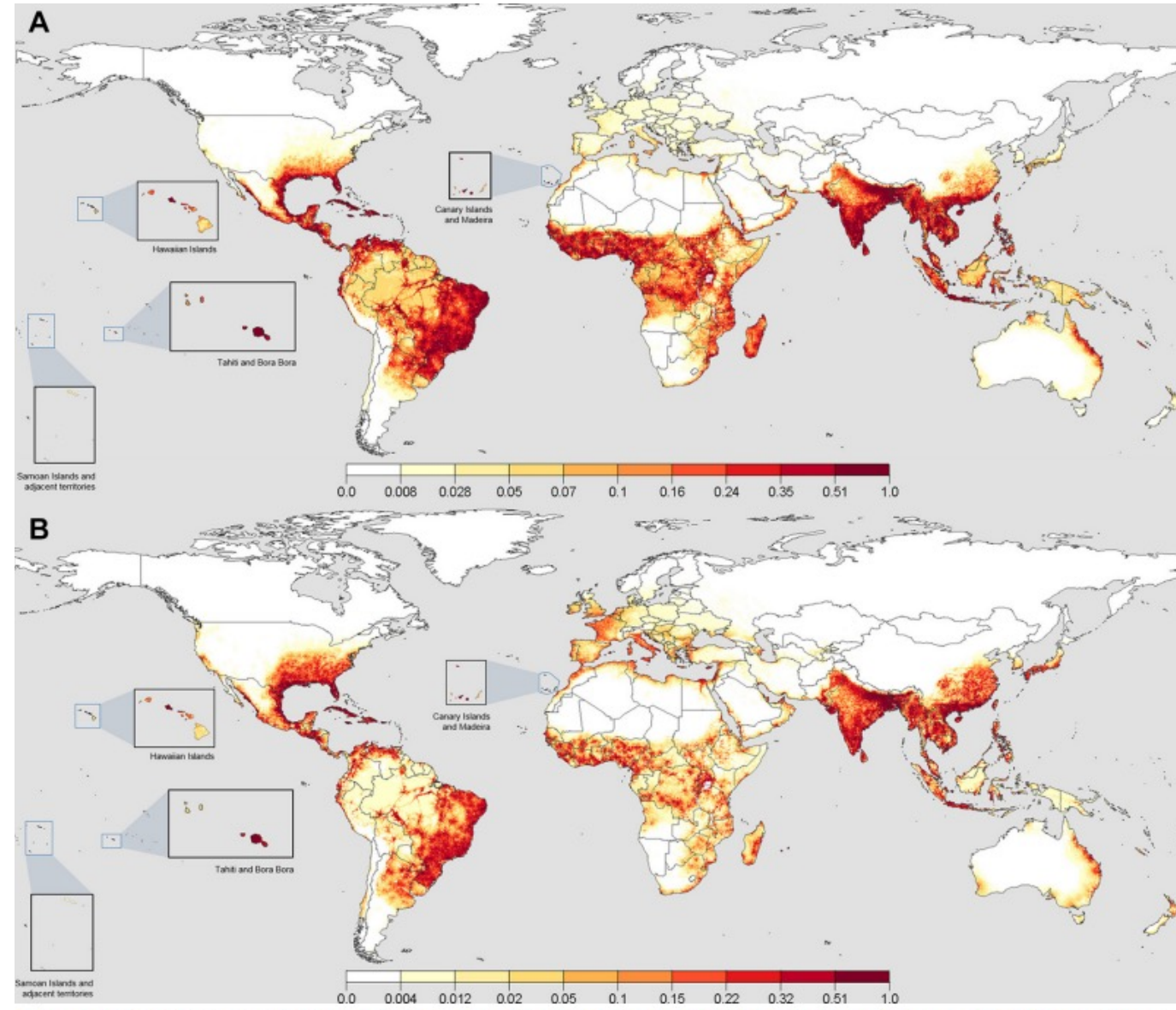
Probabilité de présence :

0,0 (probabilité minimale : aucune présence) **0,5** (probabilité médiane : égalité des chances, absent/présent)

1,0 (probabilité maximale : présence certaine)

Aedes Albopictus

Figure 1 Suitability maps for *Aedes aegypti* and *Ae. albopictus* at the 50th percentile from 250 boosted regression trees. When converted to binary presence/absence, values greater than a median threshold of 0.24 for *Ae. aegypti* and 0.22 for *Ae. albopictus* indicated the presence across all fits. Panel (A) shows the results for *Ae. aegypti*, where the Indian subcontinent, South-East Asia, Eastern South America, Mid-Africa, Caribbean and Southern North America have the highest projected suitability. Notably, East Australia, Madagascar and the coastal regions of the Middle East show areas of high suitability. Europe, the heavily forested areas of the Amazon and latitudinal fringes of the distributions show sharp waning to areas of no suitability. Panel (B) shows the results for *Ae. albopictus*, where considerable similarities exist across the greatest areas of suitability for *Ae. aegypti*. Greater northward suitability exists in North America, Europe, China and the southern coast of Korea and Japan.



DYNAMIQUE EPIDEMIOLOGIQUE / DENGUE ZIKA CHIKUNGUNYA FIEVRE JAUNE

DYNAMIQUE DU VECTEUR AEDES / SA LOCALISATION

Aedes Aegypti

Probabilité de présence :

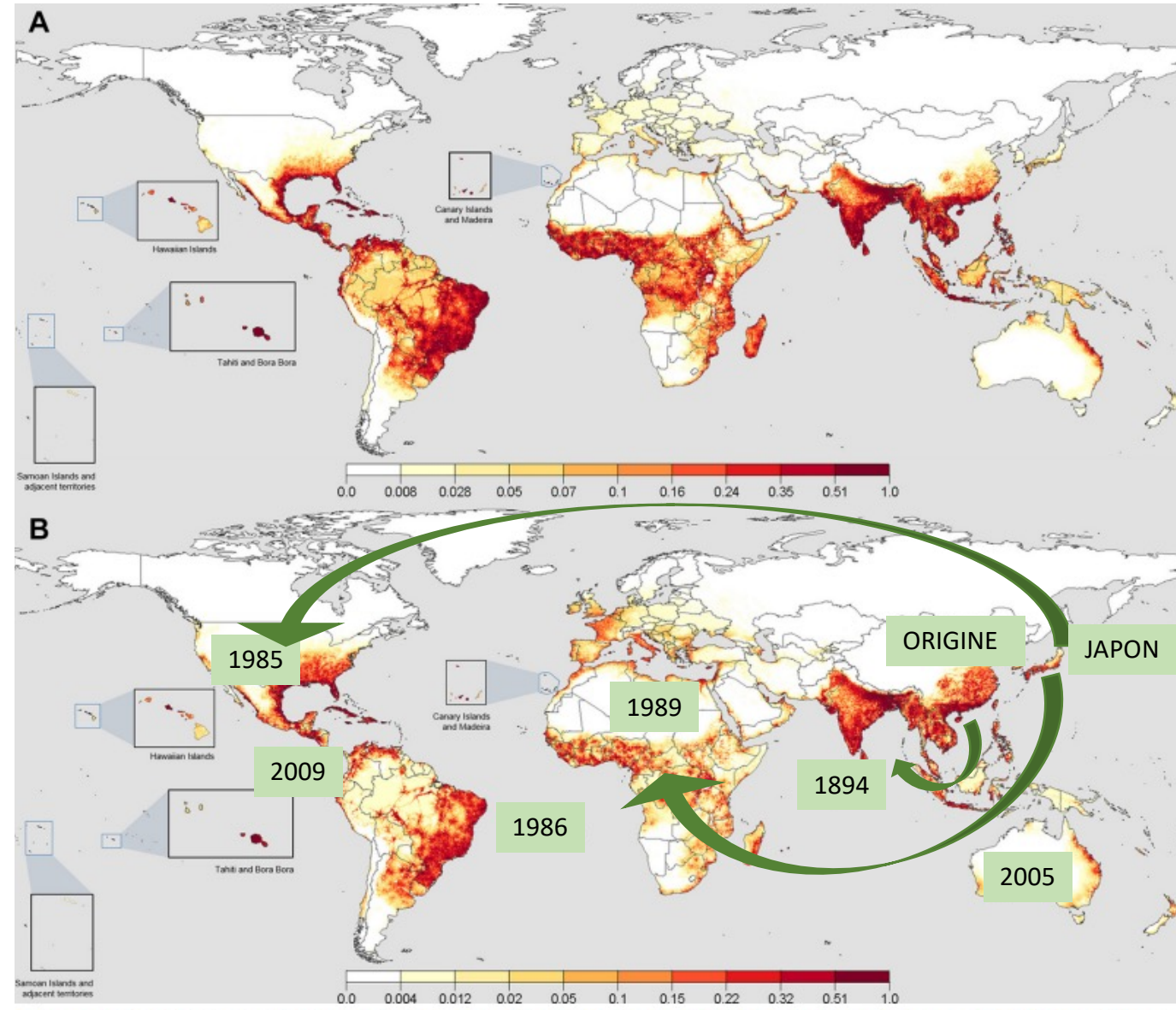
0,0 (probabilité minimale : aucune présence) **0,5** (probabilité médiane : égalité des chances, absent/présent)
1,0 (probabilité maximale : présence certaine)

1970



Aedes Albopictus

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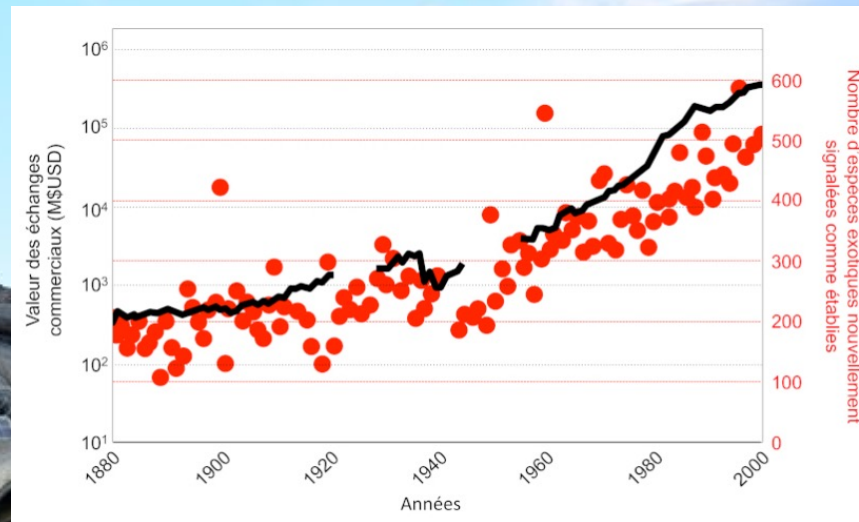


DYNAMIQUE EPIDEMIOLOGIQUE / DENGUE ZIKA CHIKUNGUNYA

DYNAMIQUE MONDIALE DU VECTEUR MOUSTIQUE TIGRE

transport passif des œufs supportant la dessiccation

COMMERCE INTERNATIONAL DE PNEUS USES



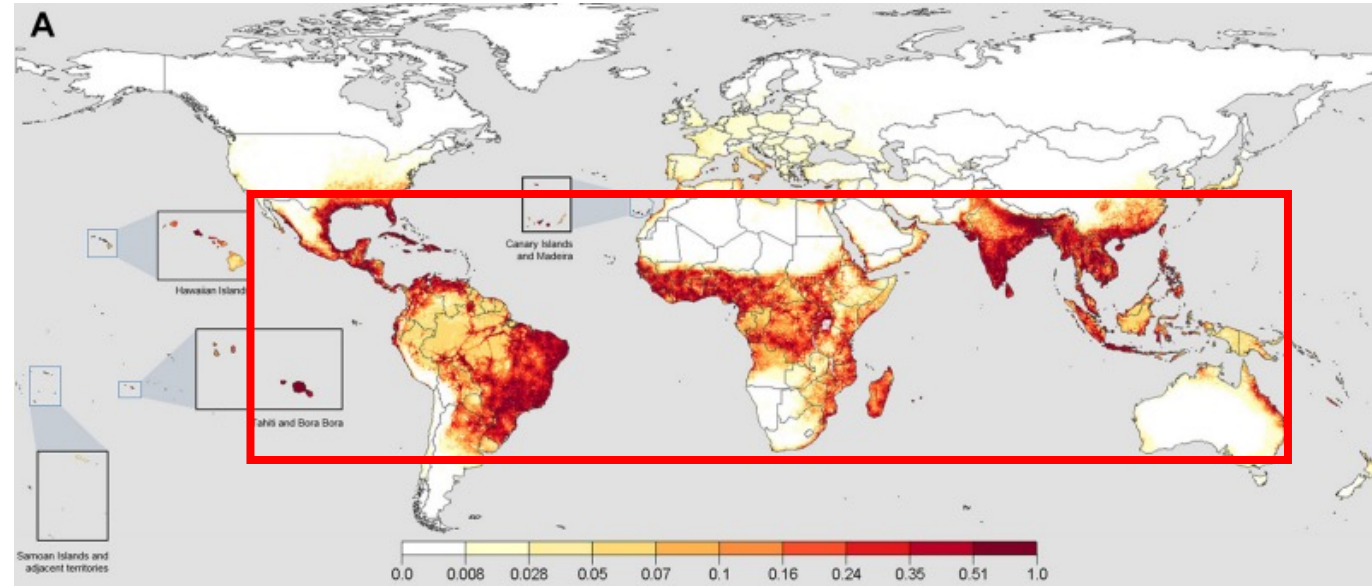
Lucky bamboo *Dracaena sanderiana*



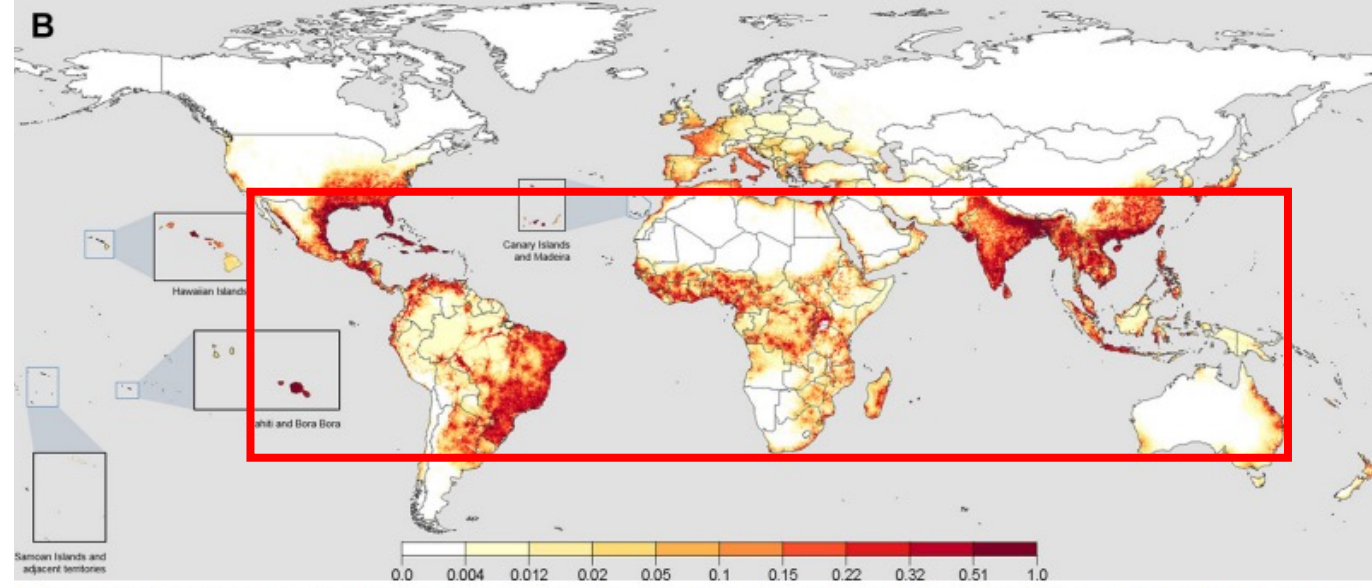
DYNAMIQUE EPIDEMIOLOGIQUE / DENGUE ZIKA CHIKUNGUNYA FIEVRE JAUNE

DYNAMIQUE DU VECTEUR AEDES / ZONE TROPICALE

Aedes Aegypti



Aedes Albopictus



DYNAMIQUE EPIDEMIOLOGIQUE / ZIKA

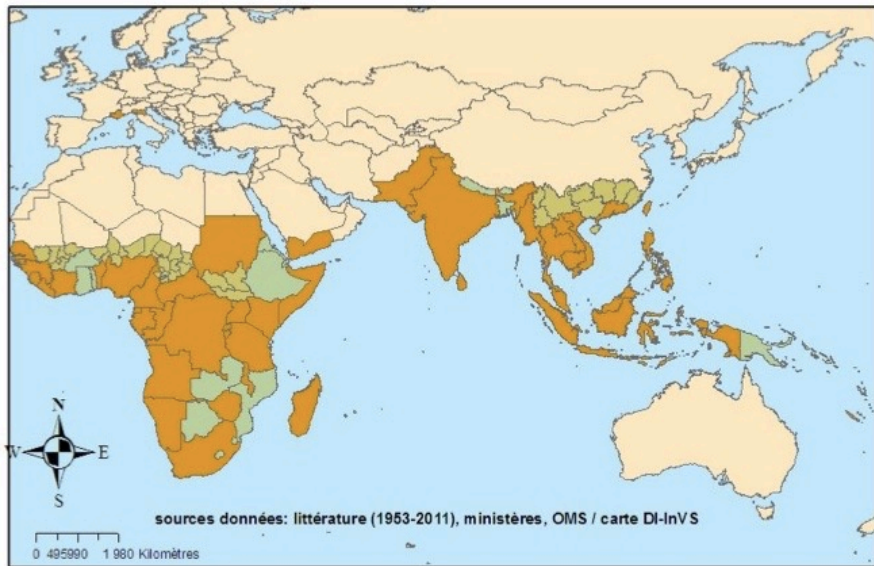


DYNAMIQUE EPIDEMIOLOGIQUE / CHIKUNGUNYA

- In **December 2013, the first local** transmission of chikungunya virus in the Western Hemisphere was reported in Saint Martin.
- Aout 2014 : a total of 576,535 suspected and laboratory-confirmed chikungunya cases had been reported in the Americas, a case count that had nearly doubled over the previous month
- **25 Nov 2014 : 875 000 cas**

Staples NEJM 2014

Carte 1 – Circulation du chikungunya dans le monde, bilan fin 2011 (Carte DI/InVS)

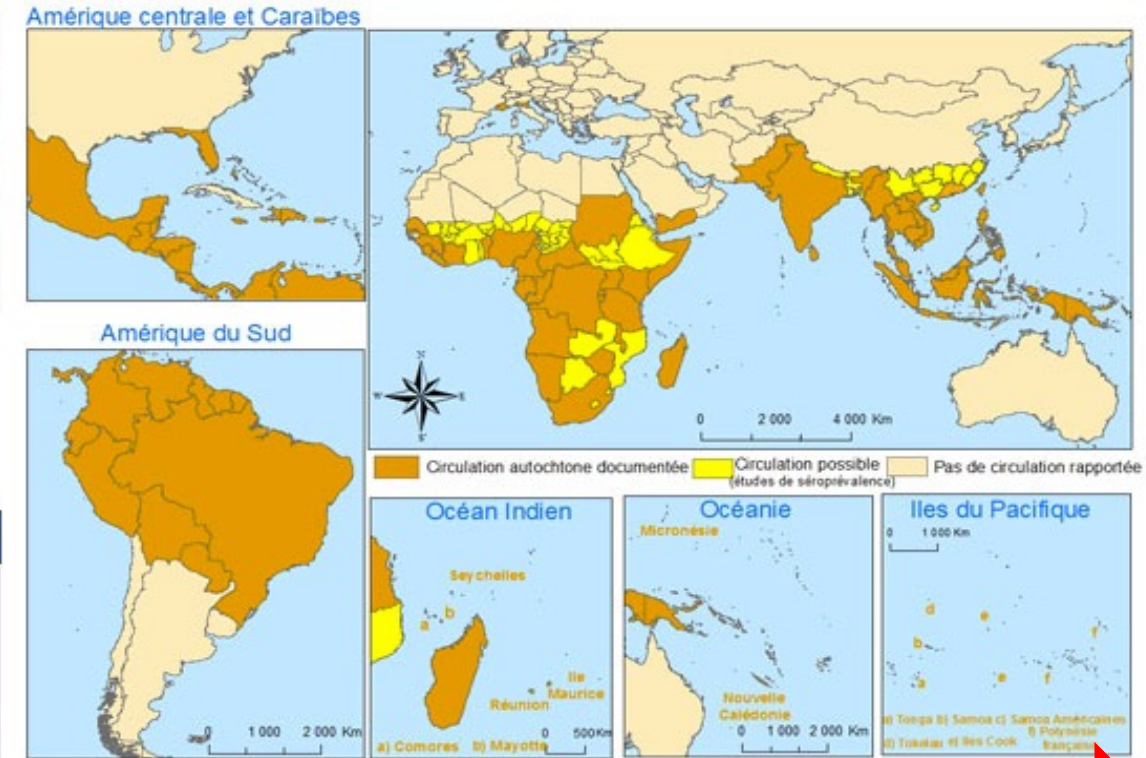


CIRCULATION du CHIKUNGUNYA

■ Circulation autochtone documentée ■ Circulation possible ■ Pas de circulation rapportée

Les systèmes de surveillance sont très hétérogènes et ces données doivent être utilisées avec précautions. De nombreux pays aux ressources limitées ne disposent pas d'une surveillance spécifique du chikungunya. Dans certaines zones de l'ancien monde, la circulation du virus chikungunya ne peut donc être formellement exclue même dans les pays où n'a pas été documentée à ce jour.

Carte 1 - Circulation du chikungunya dans le Monde, bilan juin 2015



TIME LINE

EPIDEMIOLOGIE GEOGRAPHIQUE / DENGUE



MICROEPIDEMIOLOGIE GEOGRAPHIQUE / DENGUE

CDC Centers for Disease Control and Prevention
CDC 24/7: Saving Lives, Protecting People™

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Saudi Arabia: Hajj & Umrah Pilgrimages

CDC Yellow Book 2024

Middle East Respiratory Syndrome

MERS, caused by the Middle East respiratory syndrome coronavirus (MERS-CoV), was identified in Saudi Arabia in 2012 (see Sec. 5, Part 2, Ch. 14, [Middle East Respiratory Syndrome / MERS](#)). Domestic cases in and around the Arabian Peninsula and exported cases, including in the United States, have ranged from mild to severe; ≈35% of reported cases have been fatal. Close contact with someone who has confirmed MERS-CoV infection, exposure to camels, and consuming raw or undercooked camel products (e.g., milk, urine, meat) are all considered risk factors for human infection with MERS-CoV.

Skin Infections

Chafing caused by long periods of standing and walking in the heat can lead to bacterial or fungal skin infections. Advise travelers to keep their skin dry, use talcum powder, and to be aware of any pain or irritation caused by garments. Travelers should disinfect open sores and blisters and keep them covered. As a sign of respect, pilgrims enter the Grand Mosque with the tops of their feet uncovered; while most hajjis perform tawaf in their bare feet, encourage travelers with diabetes to wear appropriate, protective footwear.

Vectorborne Diseases

Aedes mosquitoes, vectors for dengue, and *Anopheles* mosquitoes, vectors for malaria, are present in Saudi Arabia. Travelers should follow mosquito bite prevention measures outlined in Sec. 4, Ch. 6, [Mosquitoes, Ticks & Other Arthropods](#). Dengue has been documented in Mecca and Jeddah, but not in association with Hajj. KSA conducts extensive spraying campaigns before Hajj, and especially targets the housing units of pilgrims from malaria- and dengue-endemic areas. The cities of Jeddah, Mecca, Medina, Riyadh (the capital of KSA), and Ta'if have no malaria transmission, and prophylaxis against malaria is neither recommended nor required for pilgrims.



MICROEPIDEMIOLOGIE GEOGRAPHIQUE / DENGUE



Mapa 1. Casos de dengue autóctonos y en investigación según localidad de residencia. Argentina. SE 31/2022 a SE 18/2023.



CYCLE URBAIN
Densité population
Absence d'immunité
Gîtes larvaires/pontes
anthropiques

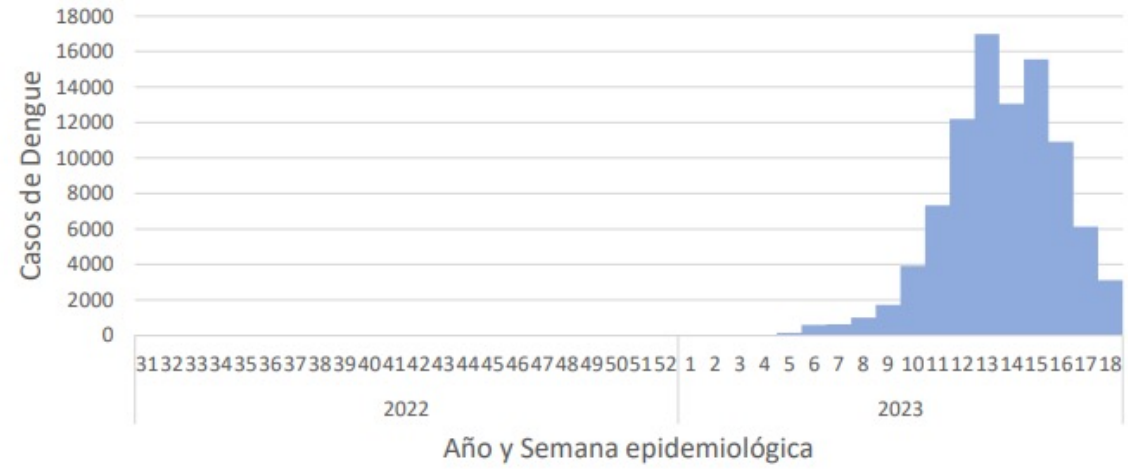
SITUACIÓN DE DENGUE EN ARGENTINA

El período de análisis de esta edición es el comprendido entre la SE 31/2022 (31 de julio) hasta la SE 18/2023 de la temporada 2022-2023.

Hasta la SE 18/2023 se registraron en Argentina **93.694** casos de dengue de los cuales **87.405** son autóctonos, 5.104 se encuentran en investigación⁷ y 1.185 presentan antecedentes de viaje (importados).

En cuanto a la curva de casos por semana epidemiológica a nivel país (Gráfico 1) se registra la cuarta semana con menos casos que en la semana 13 (sin contar la última semana)⁸, consolidando la tendencia al descenso, que se corrobora a su vez en la mayoría de las jurisdicciones (Gráfico 6).

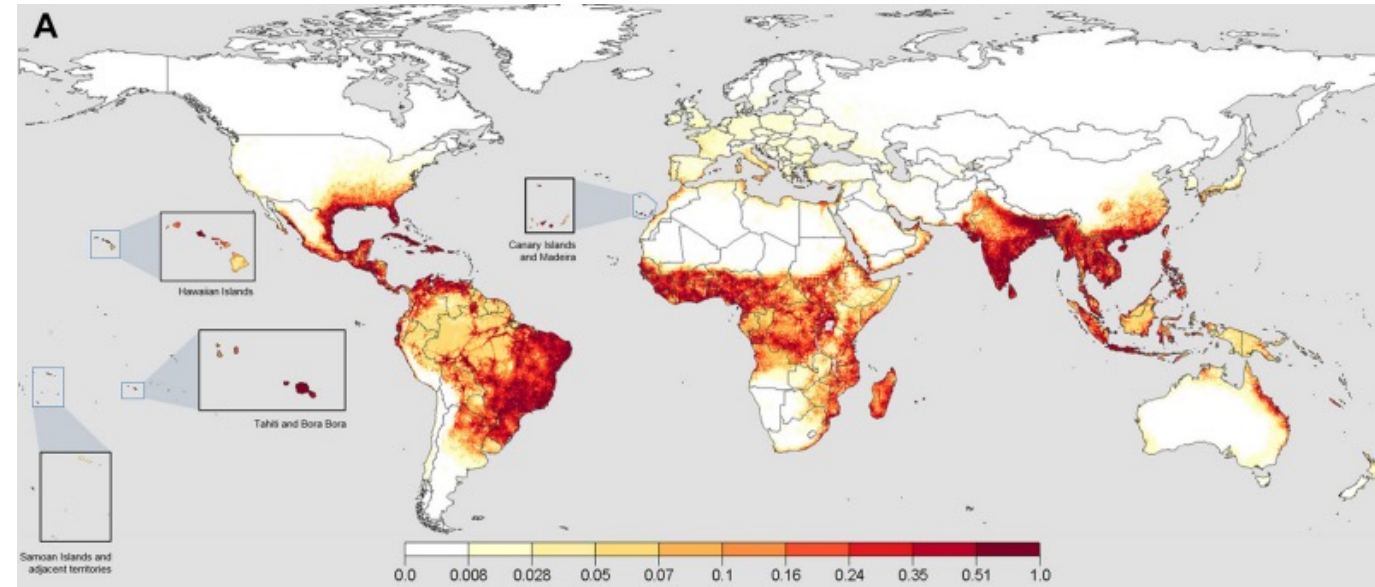
Gráfico 1. Casos de Dengue por SE epidemiológica. SE 31/2022 a SE 18/2023, Argentina.



DYNAMIQUE EPIDEMIOLOGIQUE / DENGUE ZIKA CHIKUNGUNYA

DYNAMIQUE DU VECTEUR AEDES / SA LOCALISATION

Aedes Aegypti



Aedes Albopictus

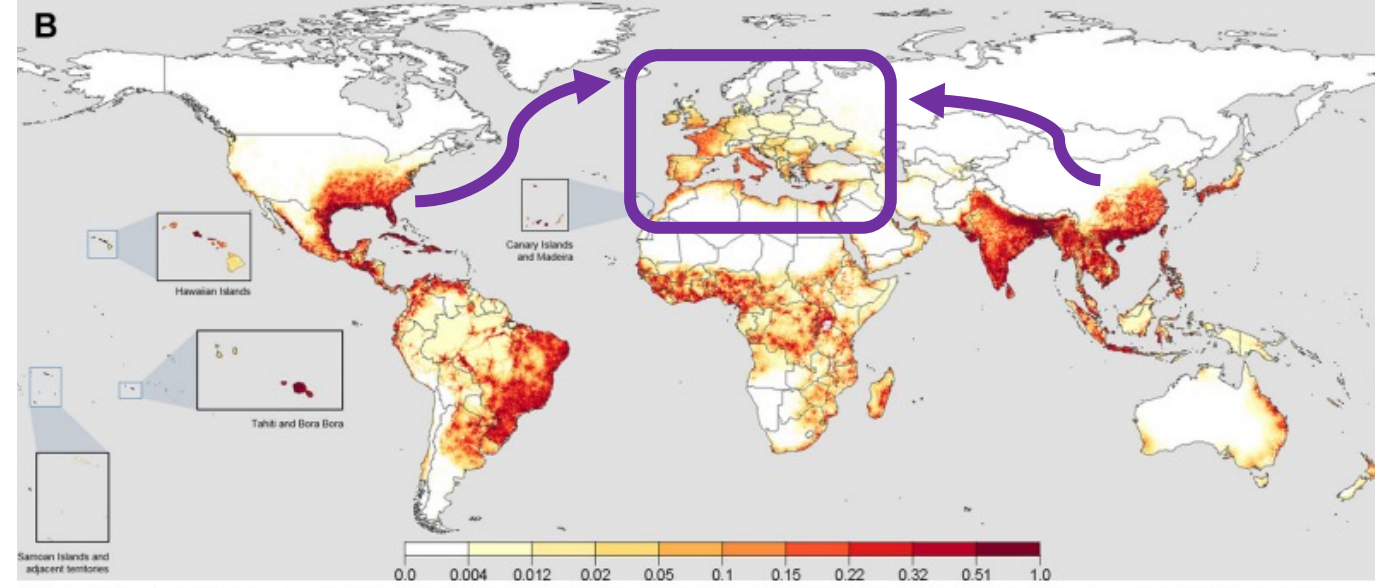
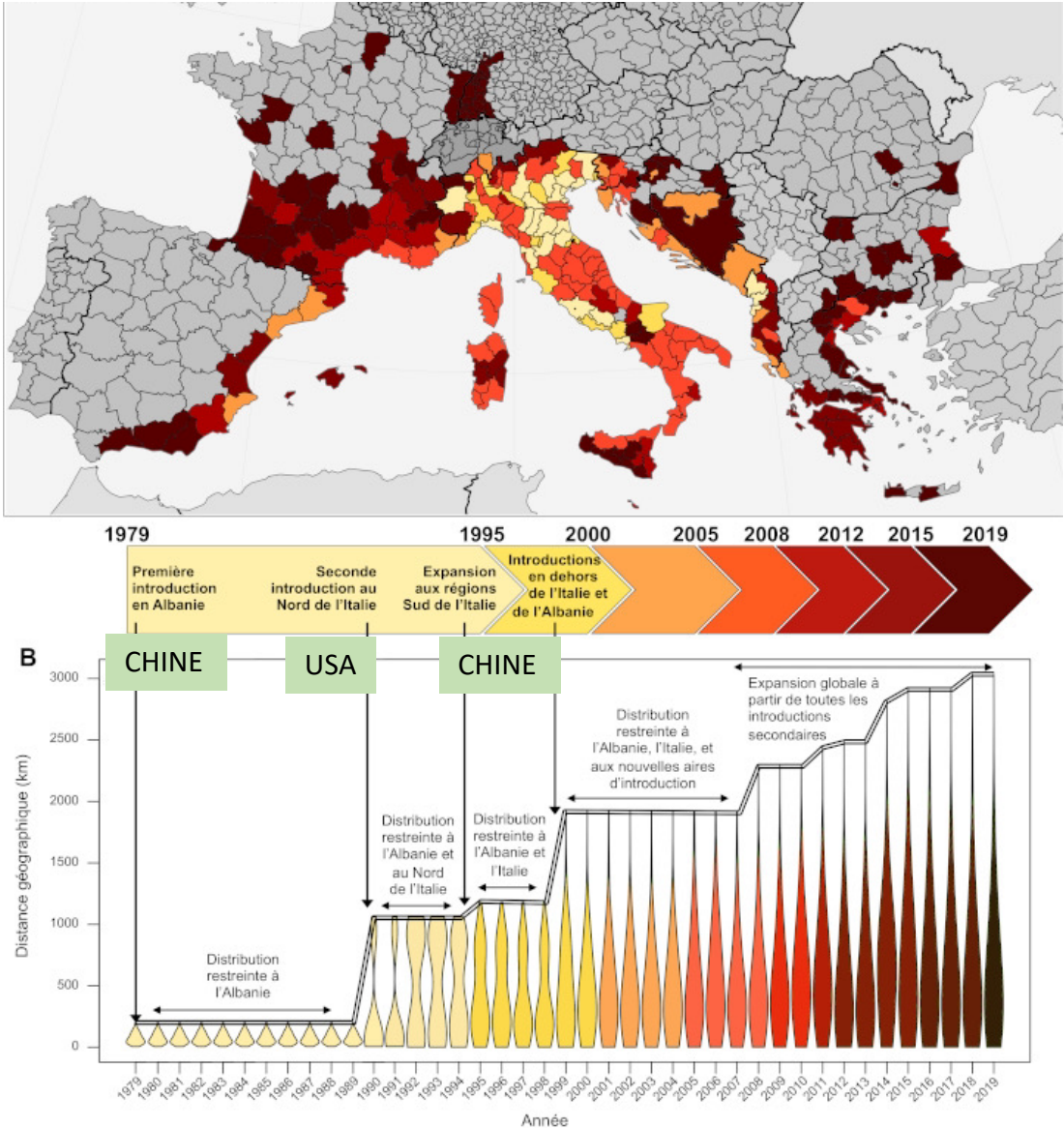
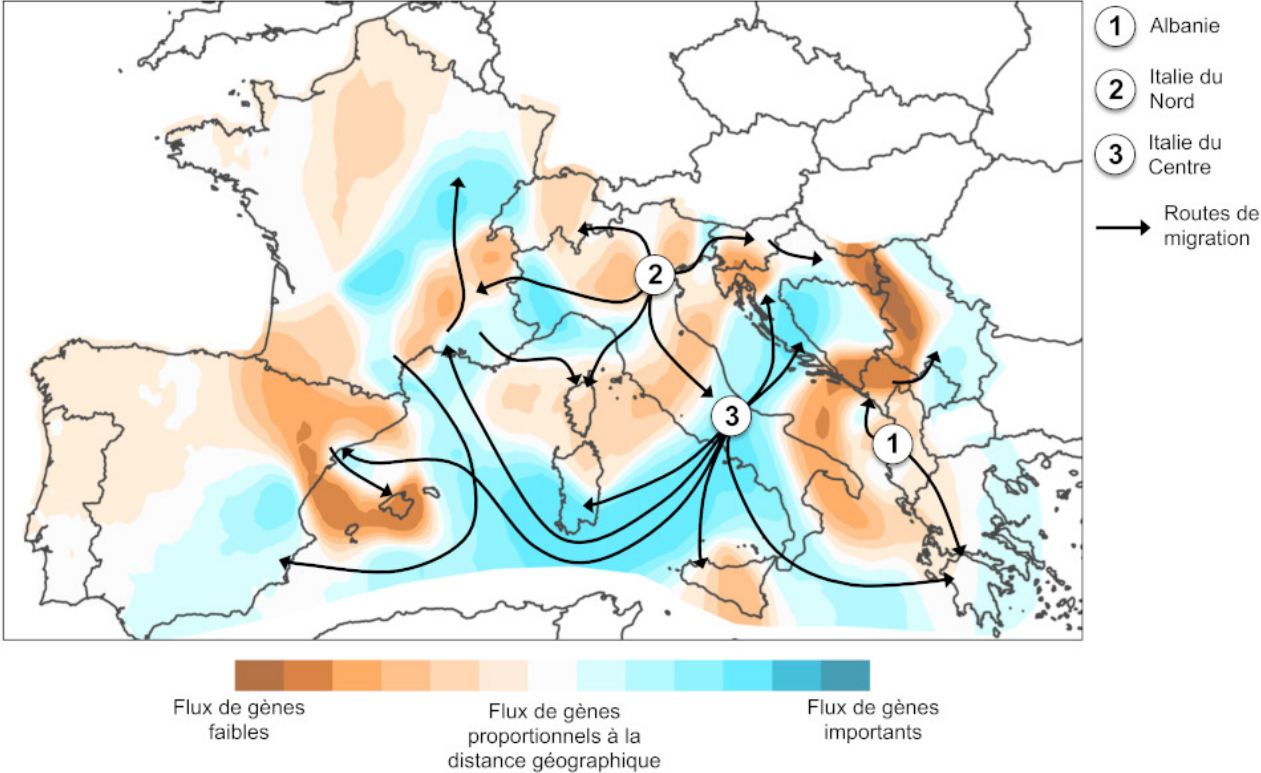


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DYNAMIQUE EPIDEMIOLOGIQUE / DENGUE ZIKA CHIKUNGUNYA

DYNAMIQUE EUROPEENNE DU VECTEUR MOUSTIQUE TIGRE

3 introductions = diversité génétique
Mobilité par transport progressif



Le moustique tigre a une **faible capacité de dispersion naturelle**, dont la moyenne estimée à partir des taux de recapture des individus est d'environ 200 m par génération [26]. Le temps de génération [27] est d'environ trois semaines chez le moustique tigre. Les conditions environnementales dans la région de Grenoble étant favorables à la reproduction de Mai à Octobre, l'espèce peut théoriquement accomplir jusqu'à sept générations par an. Ainsi, la dispersion naturelle maximale des individus entre 2013 et 2017 se limite à un rayon de 6 km. La distance géographique séparant les populations génétiquement proches de part et d'autre des axes routiers identifiés (Figure 9) pouvant aller jusqu'à 25 km, cette étude confirme que **le principal facteur expliquant la connectivité entre les populations distantes chez le moustique tigre est le transport humain le long des axes routiers**.

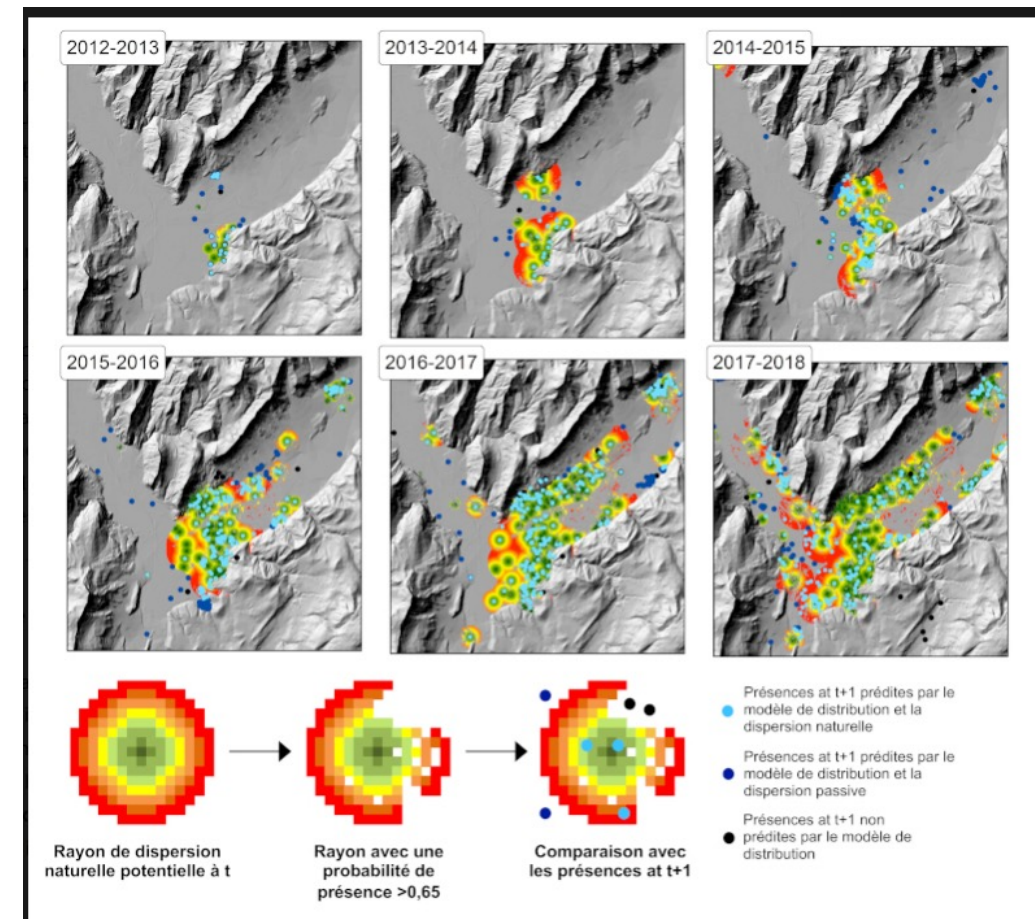
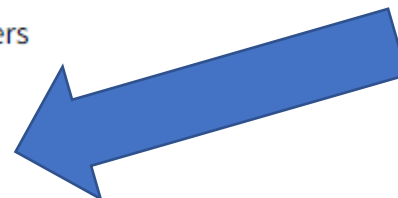
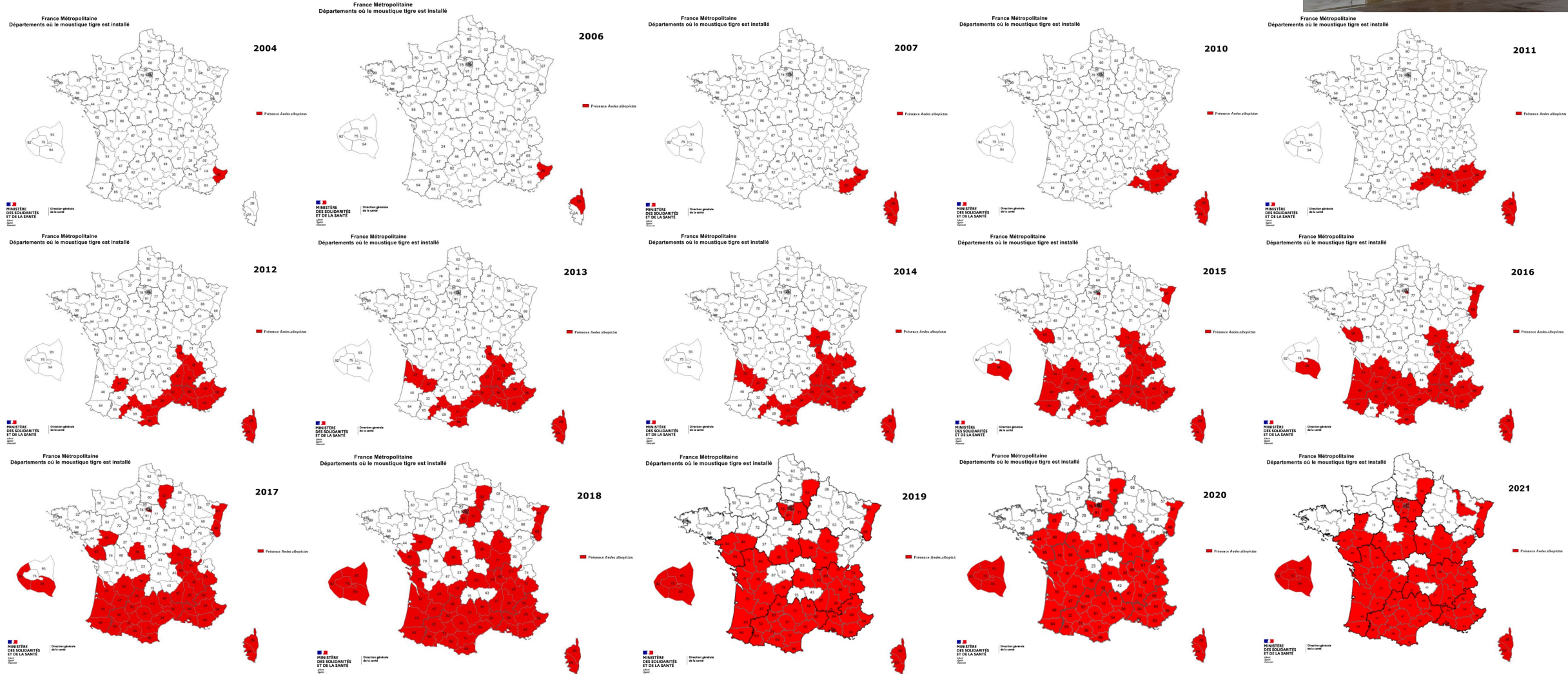


Figure 11. Modélisation des rôles de la dispersion naturelle et passive dans l'expansion du moustique tigre depuis son introduction dans la région de Grenoble. Les cartes montrent l'aire de dispersion naturelle potentielle pour chaque comparaison de deux années consécutives. Le rayon théorique représente le nombre de génération possible de dispersion naturelle (7 générations par ans représentées par 7 couleurs), résultant en une dispersion potentielle allant de 0 à 1 500 m (dispersion maximale de 200m par génération) en fonction de la date de détection, avec un temps de génération de 3 semaines. Les couleurs des points indiquent la catégorie de dispersion. Bleu clair : dispersion naturelle (l'occurrence enregistrée à $t+1$ est située dans le rayon construit avec les occurrences à t), bleu foncé : dispersion assistée par l'homme (l'occurrence enregistrée à $t+1$ est située en dehors du rayon construit avec les occurrences à t). [Source : © Stéphanie Sherpa, modifié depuis ref. 25]

DYNAMIQUE EPIDEMIOLOGIQUE / DENGUE ZIKA CHIKUNGUNYA

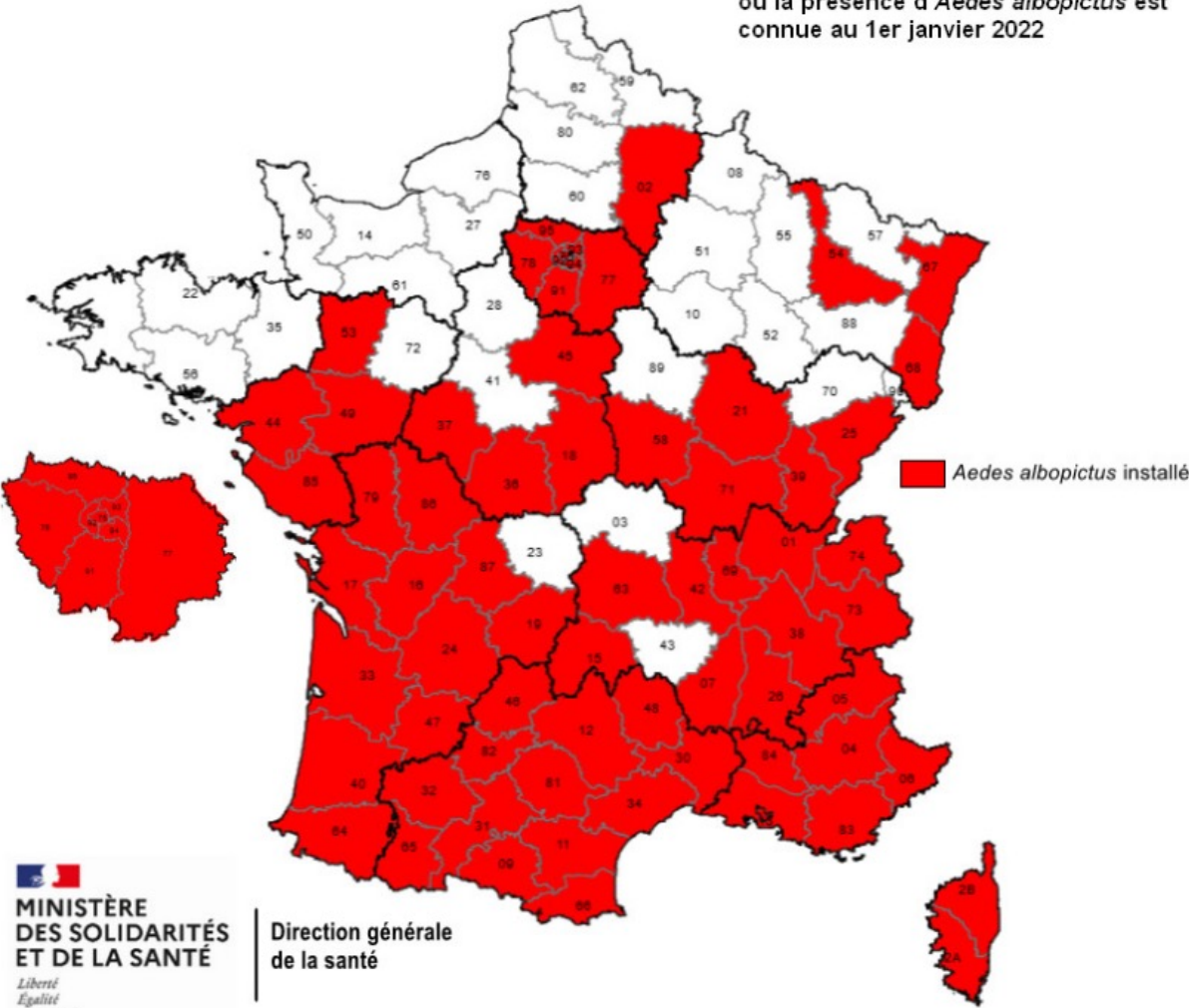
DYNAMIQUE FRANCAISE DU VECTEUR MOUSTIQUE TIGRE



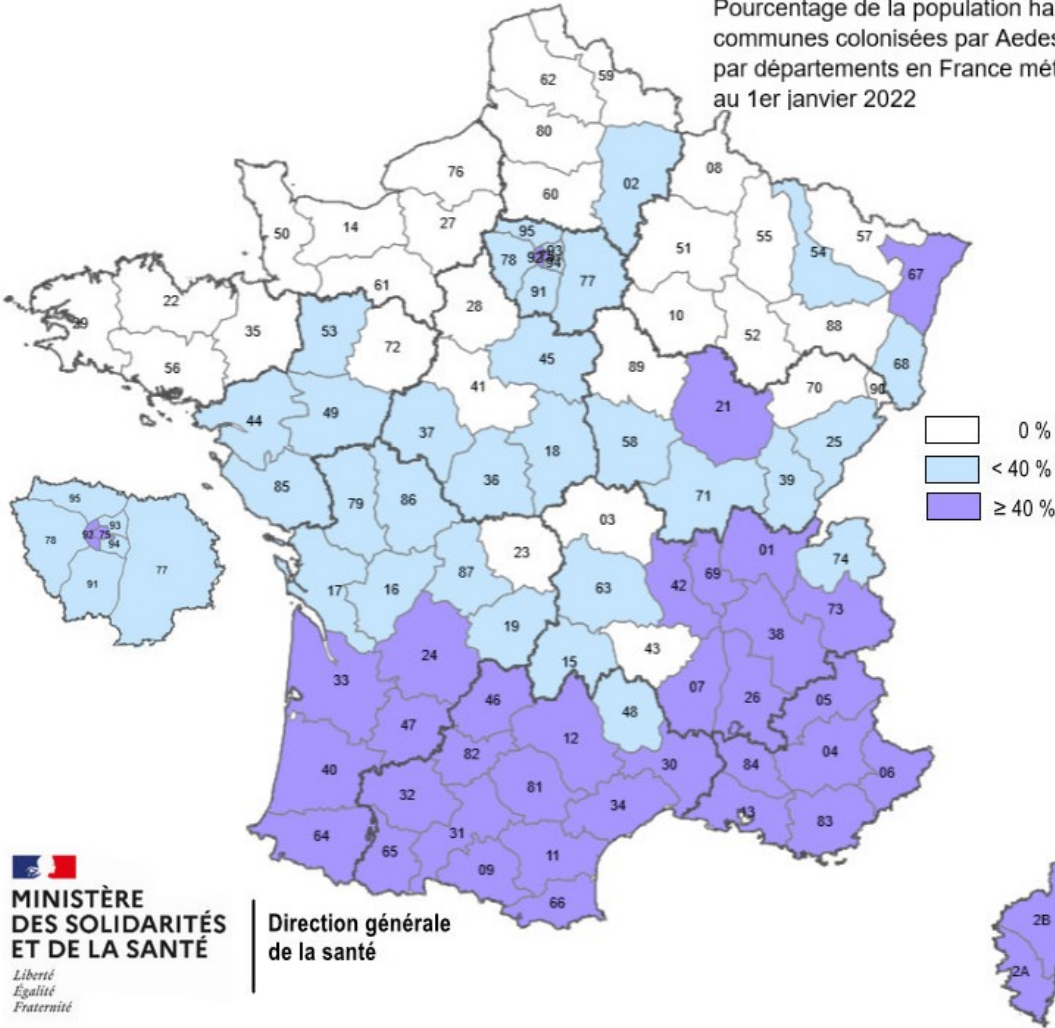
DYNAMIQUE EPIDEMIOLOGIQUE / DENGUE ZIKA CHIKUNGUNYA

DYNAMIQUE FRANCAISE DU VECTEUR MOUSTIQUE TIGRE

Carte des départements de métropole où la présence d'*Aedes albopictus* est connue au 1er janvier 2022



Pourcentage de la population habitant des communes colonisées par *Aedes albopictus* par départements en France métropolitaine au 1er janvier 2022



DYNAMIQUE EPIDEMIOLOGIQUE / DENGUE ZIKA CHIKUNGUNYA

ARBOVIROSE EN CLIMAT TEMPERE

Infection with chikungunya virus in Italy: an outbreak in a temperate region

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Summary

Background Chikungunya virus (CHIKV), which is transmitted by *Aedes* spp mosquitoes, has recently caused several outbreaks on islands in the Indian Ocean and on the Indian subcontinent. We report on an outbreak in Italy.

Methods After reports of a large number of cases of febrile illness of unknown origin in two contiguous villages in northeastern Italy, an outbreak investigation was done to identify the primary source of infection and modes of transmission. An active surveillance system was also implemented. The clinical case definition was presentation with fever and joint pain. Blood samples were gathered and analysed by PCR and serological assays to identify the causal agent. Locally captured mosquitoes were also tested by PCR. Phylogenetic analysis of the CHIKV E1 region was done.

Findings Analysis of samples from human beings and from mosquitoes showed that the outbreak was caused by CHIKV. We identified 205 cases of infection with CHIKV between July 4 and Sept 27, 2007. The presumed index case was a man from India who developed symptoms while visiting relatives in one of the villages. Phylogenetic analysis showed a high similarity between the strains found in Italy and those identified during an earlier outbreak on islands in the Indian Ocean. The disease was fairly mild in nearly all cases, with only one reported death.

Interpretation This outbreak of CHIKV disease in a non-tropical area was to some extent unexpected and emphasises the need for preparedness and response to emerging infectious threats in the era of globalisation.

2007 première fois en Europe



Figure 2: Geographical origin and spatial-temporal diffusion of CHIKV cases. Number of cases in Castiglione di Cervia and Castiglione di Ravenna between days 0-15 (A), between days 0-45 (B), cumulatively (C), and in the province of Ravenna (D).

DYNAMIQUE EPIDEMIOLOGIQUE / DENGUE ZIKA CHIKUNGUNYA

ARBOVIROSE EN CLIMAT TEMPERE

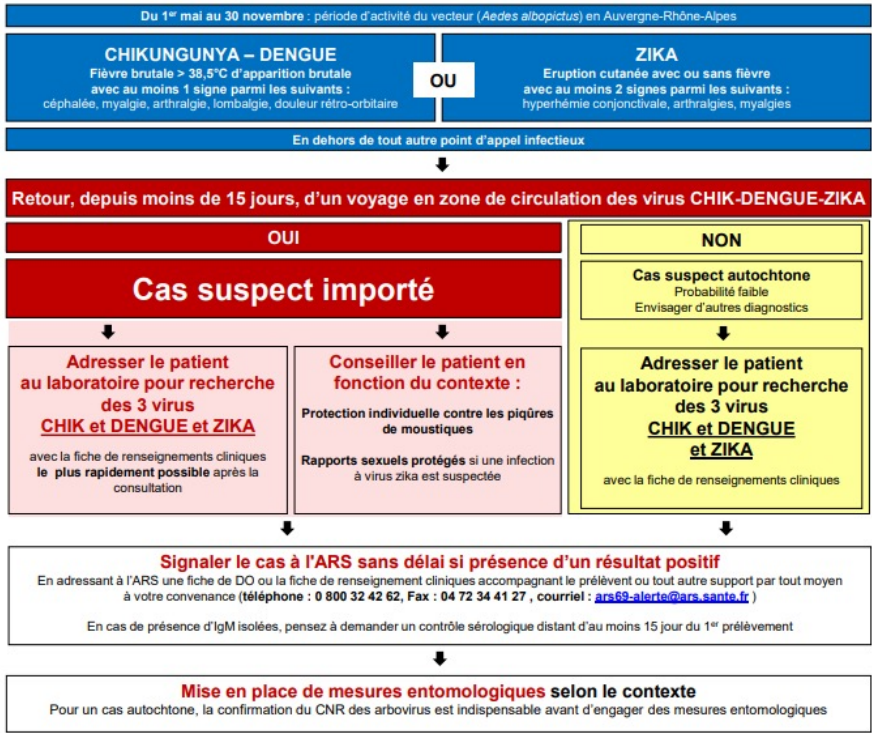


2023 Poster JNI

ZOOM SUR LES EPISODES DE CAS AUTOCHTONES DE DENGUE EN FRANCE METROPOLITAINE EN 2022

Neuf foyers de transmission de dengue, totalisant 65 cas autochtones de dengue ont été identifiés en PACA, Occitanie et Corse au cours de la saison de surveillance 2022. Aucun foyer n'a été identifié en Auvergne-Rhône-Alpes.

CONDUITE A TENIR DEVANT DES CAS CONFIRMES DE CHIKUNGUNYA, DE DENGUE ET DE ZIKA, 2023

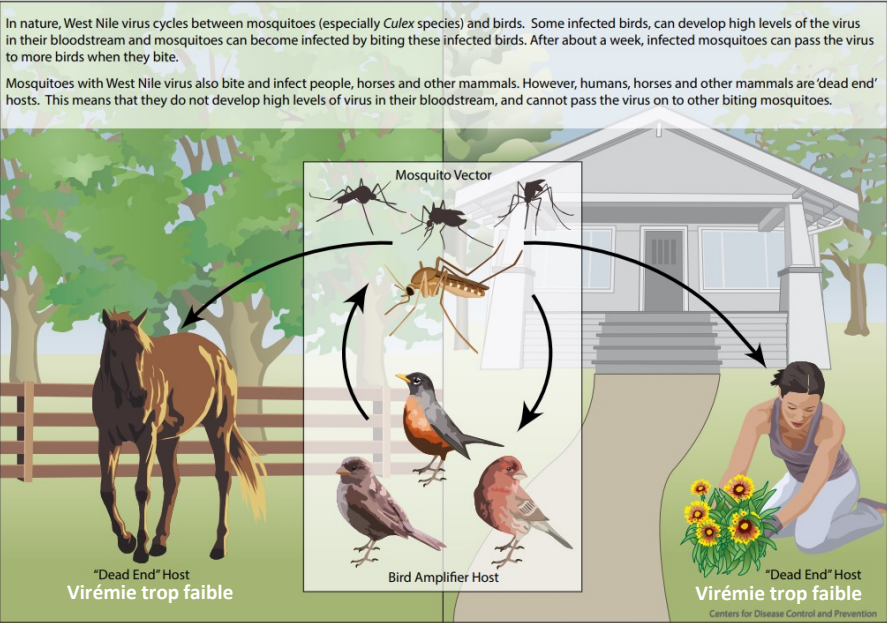


CAS DE DENGUE AUTOCHTONE EN EUROPE

Year	Country	Department or regions affected	Number of autochthonous cases	Probable period of virus circulation	References
2010	Croatia	Korčula Island and the Pelješac peninsula	10	August–October	[1-3]
2010	France	Alpes-Maritimes department	2	August–September	[4-6]
2013	France	Bouches–du-Rhône department	1	September–October	[6,7]
2014	France	Var and Bouches-du-Rhône departments	4	July–September	[6,8]
2015	France	Gard department	8	July–September	[6,9,10]
2018	France	Alpes Maritimes, Hérault, and Gard departments	8	September–October	[6,11]
2018	Spain	Catalonia region, Murcia region or province of Cádiz	6	August–October	[11-13]
2019	Spain	Catalonia region	1	September	[14,15]
2019	France	Alpes-Maritimes and Rhône departments	9	July–September	[15-17]
2020	France	Hérault, Var, Alpes-Maritime, and Gard departments	13	July–October	[18-20]
2020	Italy	Veneto region	10	August	[21]
2021	France	Var and Hérault departments	2	July and September	[22, 23]
2022	France	Pyrénées-Orientales, Hautes-Pyrénées, Haute-Garonne, Tarn et Garonne, Var, Alpes-Maritime, and Corsica departments	65	June– September	[24,25]
2022	Spain	Ibiza	6	August–October	[26]

DYNAMIQUE EPIDEMIOLOGIQUE / WEST NILE

ARBOVIROSE EN CLIMAT TEMPERE



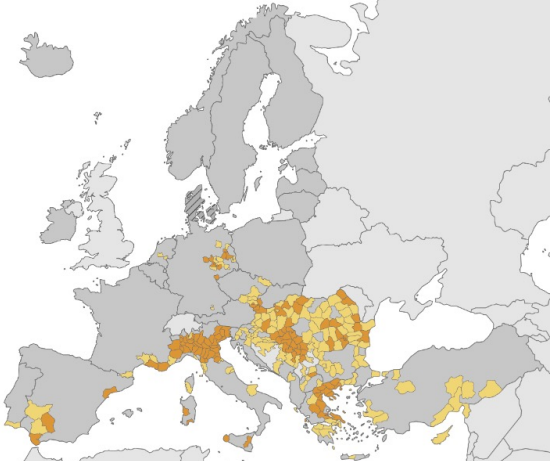
585 cas Italie / 27 France en 2018

Distribution of human West Nile virus infections in NUTS 3 or GAUL 1 regions in the EU/EEA and neighbouring countries during 2013–2022, as of 31 May 2023

- Human infections reported, current season (2023)
- Human infections reported, 2022
- Human infections reported, 2013–2021
- No data reported
- No infections reported
- Not included

Countries not visible in the main map extent

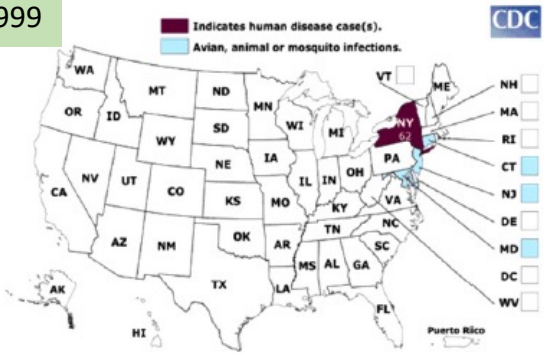
- Malta
- Liechtenstein



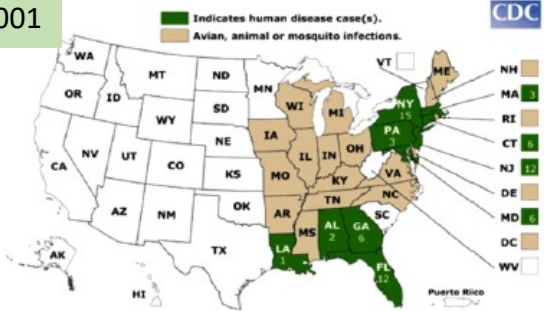
Factors influencing emerging arbovirus diseases

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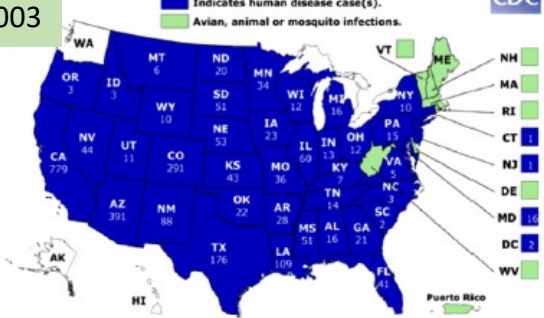
1999



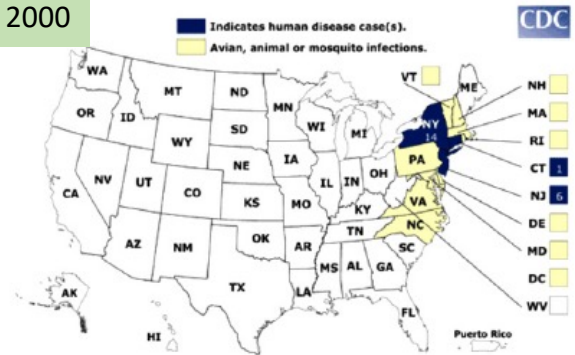
2001



2003



2000



2002

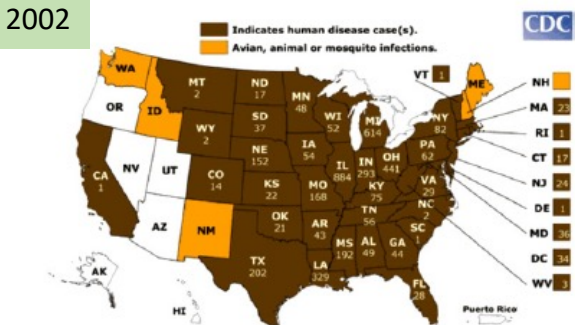


Figure 4 Dispersal of West Nile virus in the USA during: (A) 1999; (B) 2000; (C) 2001; (D) 2002; (E) 2003 (source: <http://www.cdc.gov/ncidod/dvbid/westnile/background.htm>).

DYNAMIQUE EPIDEMIOLOGIQUE / FH CRIMEE CONGO

ARBOVIROSE EN CLIMAT TEMPERE

Retrospective Identification of Early Autochthonous Case of Crimean-Congo Hemorrhagic Fever, Spain, 2013

Before this report, 7 autochthonous human cases of Crimean-Congo hemorrhagic fever had been reported in Spain, all occurring since 2016. We describe the retrospective identification of an eighth case dating back to 2013. This study highlights that the earliest cases of an emerging disease are often difficult to recognize.

Expansion au delà du 50^{ième} parallèle?

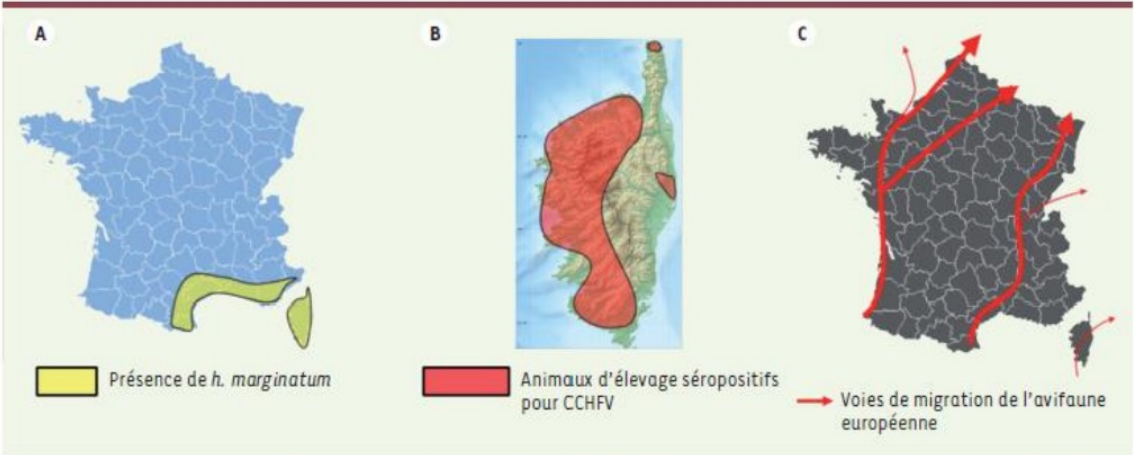
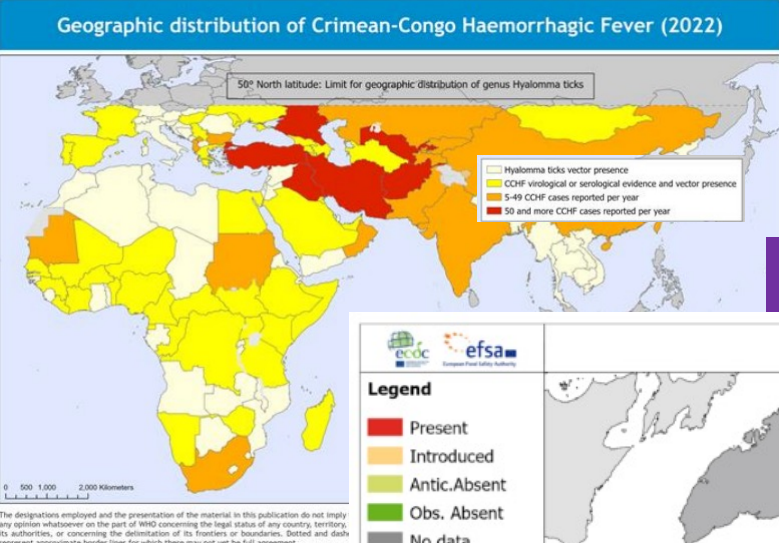
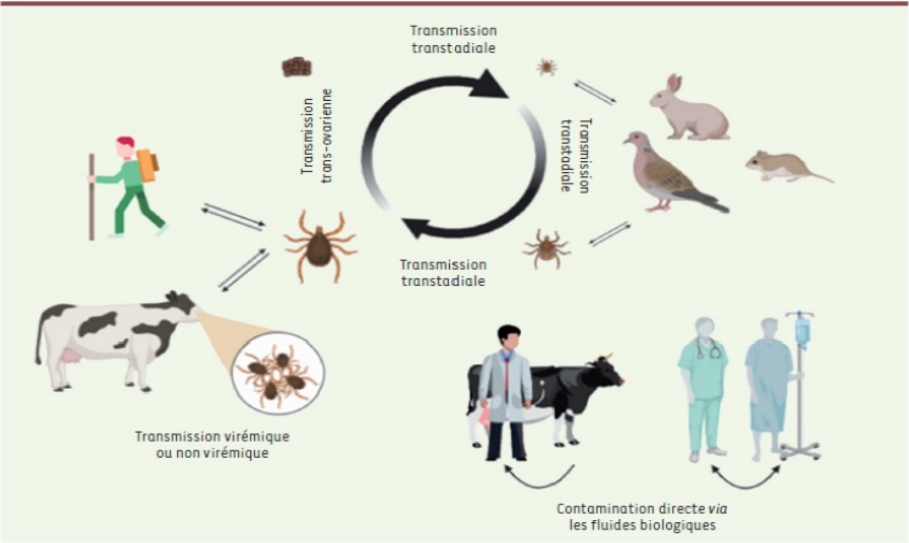
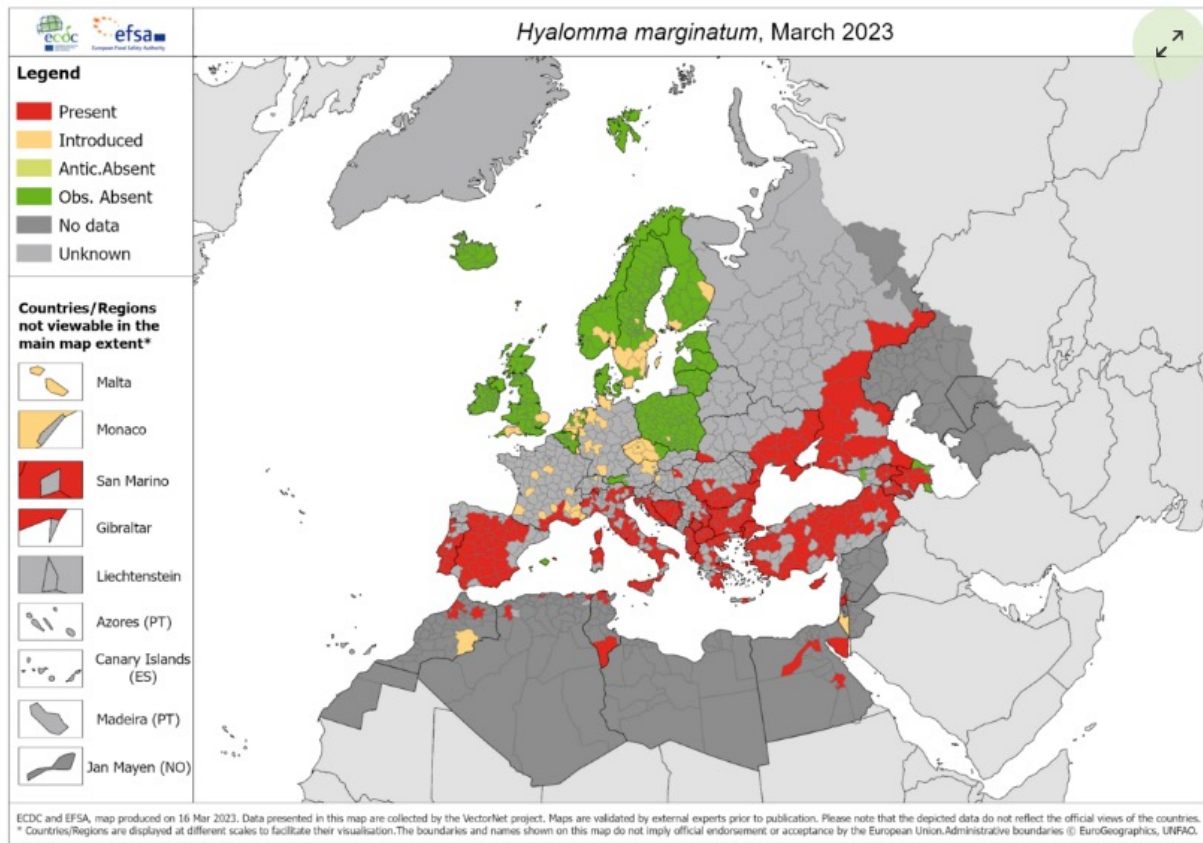


Figure 3. Distribution du vecteur et d'une sérologie positive pour le CCHFV en France. A. Les tiques *Hyalomma marginatum* sont connues depuis de très nombreuses années en Corse où elles constituent la deuxième espèce la plus importante sur ce territoire [40]. Des mentions de leur présence ont été faites dès 1965 dans les Bouches-du-Rhône, mais leur installation pérenne dans le pourtour méditerranéen est plus récente. B. Une étude parue en 2020 indique la présence étendue en Corse d'animaux d'élevage ayant une sérologie positive pour le virus CCHFV (9 % de l'ensemble des animaux testés) [39]. C. Principales voies de migration printanière des oiseaux (d'après *The Scottish wildlife trust*).



DYNAMIQUE EPIDEMIOLOGIQUE / L'AVENIR / ROLE DU CLIMAT

Dickens BL, et al. BMJ
Glob Health 2018

BMJ Global Health Determining environmental and anthropogenic factors which explain the global distribution of *Aedes aegypti* and *Ae. albopictus*

Borame Lee Dickens,¹ Haoyang Sun,¹ Mark Jit,^{2,3} Alex R Cook,¹
Luis Roman Carrasco¹

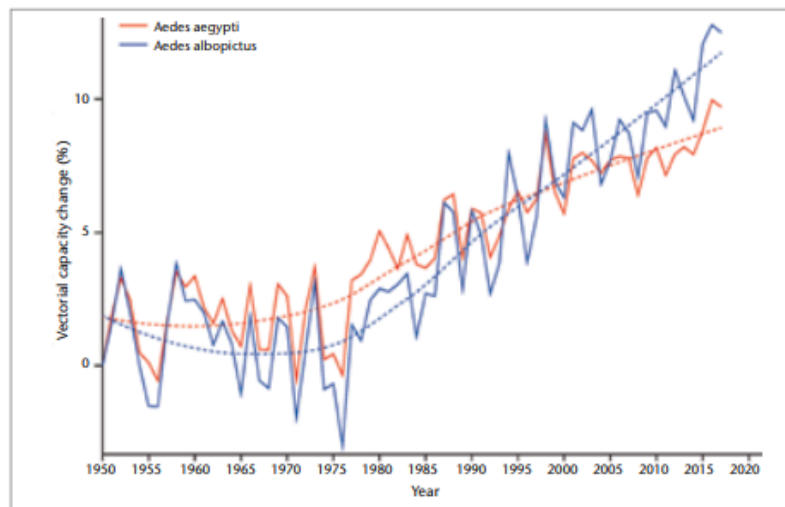
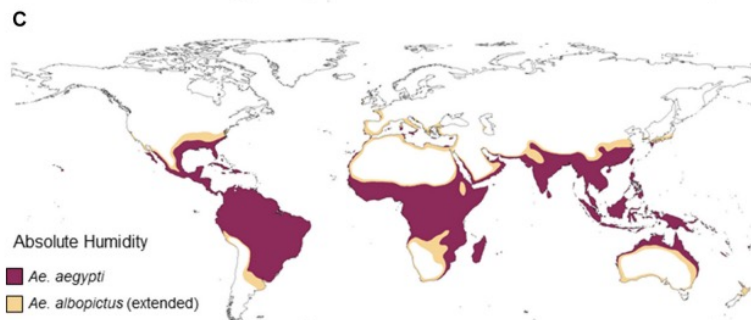
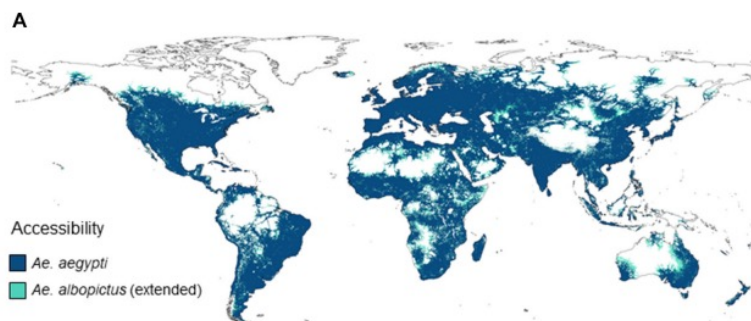
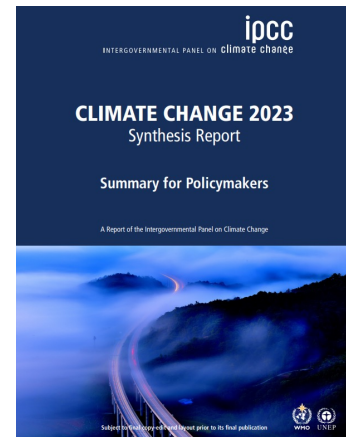


Figure 22. Changes in global vectorial capacity for the dengue virus vectors *Aedes aegypti* and *Aedes albopictus* since 1950. Vectorial capacity depends on temperature and is calculated using historical climate data.⁵⁹

Tout va plus vite chez le moustique par temps chaud

- ## 3 grands phénomènes climatiques
- El niño
 - Augmentation des températures
 - Rivières atmosphériques



Climate change and the increased burden of dengue fever in Pakistan

Climate change is often discussed in terms of its consequences 50 or 100 years from now. But recent events have shown that the devastation is already happening, much sooner than anticipated. Pakistan has been a recipient of the worst consequences of climate change in the form of heavy rainfall resulting in widespread flooding across the country. As of June 2022, Pakistan had experienced rainfall equivalent to 2.9 times its national 30-year average since the beginning of 2022. August 2022 was recorded as the wettest August in Pakistan since 1961. The province of Sindh, the most affected province, had 726% more rain than its August average.¹ The resulting floods have affected 33 million people, which includes 16 million children, and left around 2000 dead and 13 000 injured. 800 000 houses were destroyed and another 1.3 million damaged. More than 2 million people were rendered homeless.²

www.thelancet.com/infection Vol 23 January 2023

Earth's Future

RESEARCH ARTICLE

10.1029/2022EF003230

The Pakistan Flood of August 2022: Causes and Implications

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¹Civil Engineering, Indian Institute of Technology Gandhinagar, Gandhinagar, India; ²Earth Science, Indian Institute of Technology Gandhinagar, Gandhinagar, India

Abstract The risk of floods has increased in South Asia due to high vulnerability and exposure. The August 2022 Pakistan flood shows a difference of 10 times in rainfall compared to the 30-year average, which is the primary driver of floods.

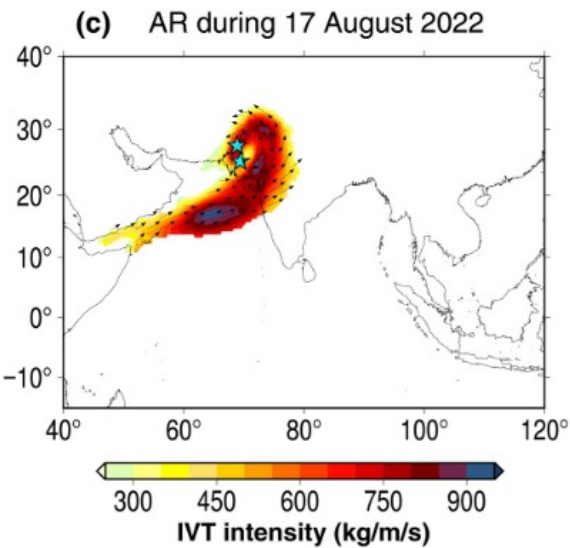


Figure 4. Atmospheric river (AR) during August 2022 flood in Pakistan. (a) Frequ

Global risk model for vector-borne transmission of Zika virus reveals the role of El Niño 2015

Cyril Caminade^{a,b,1}, Joanne Turner^a, Soeren Metelmann^{b,c}, Jenny C. Hesson^{a,d}, Marcus S. C. Blagrove^{a,b}, Tom Solomon^{b,e}, Andrew P. Morse^{b,c}, and Matthew Baylis^{a,b}

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Edited by Anthony A. James, University of California, Irvine, CA, and approved November 14, 2016 (received for review September 2, 2016)

Zika, a mosquito-borne viral disease that emerged in South America in 2015, was declared a Public Health Emergency of International Concern by the WHO in February of 2016. We developed a climate-driven R_0 mathematical model for the transmission risk of Zika virus (ZIKV) that explicitly includes two key mosquito vector species: *Aedes aegypti* and *Aedes albopictus*. The model was parameterized and calibrated using the most up to date information from the available literature. It was then driven by observed gridded temperature and rainfall datasets for the period 1950–2015. We find that the transmission risk in South America in 2015 was the highest since 1950. This maximum is related to favoring temperature conditions that caused the simulated biting rates to be largest and mosquito mortality rates and extrinsic incubation periods to be smallest in 2015. This event followed the suspected introduction of ZIKV in Brazil in 2013. The ZIKV outbreak in Latin America has very likely been fueled by the 2015–2016 El Niño climate phenomenon affecting the region. The highest transmission risk globally is in South America and tropical countries where *Ae. aegypti* is abundant. Transmission risk is strongly seasonal in temperate regions where *Ae. albopictus* is present, with significant risk of ZIKV transmission in the southeastern states of the United States, in southern China, and to a lesser extent, over southern Europe during the boreal summer season.

otherwise fully susceptible population. R_0 has an important threshold value: a value above one indicates that the pathogen could spread if it were introduced, resulting in a minor or major outbreak depending on the size of R_0 , whereas a value below one indicates that pathogen transmission would be insufficient to produce a major outbreak. Mathematical formulations of R_0 exist for several vector-borne diseases (VBDs), including those with one host and one vector [such as malaria (10)] and those with two hosts and one vector [such as zoonotic sleeping sickness (11) and African horse sickness (12)]. Relatively little attention has been paid to developing mathematical formulations of R_0 where there are two vector species and either one or multiple host species (13). Consideration of two vector species in the R_0 formulation is essential where two vectors have different epidemiological parameters. It also allows for the estimation of R_0 where the two species co-occur and primary infections in one species can lead to secondary infections in the second.

Ae. aegypti and *Ae. albopictus* seem to have different susceptibilities to ZIKV (7, 14–16), feeding rates, and feeding preferences (17, 18). *Ae. aegypti* feeds more often and almost exclusively on humans, and it is, therefore, an extremely efficient transmitter of human viruses. *Ae. albopictus* feeds less frequently and on a broader range of hosts, and it is, therefore, less likely to both ac-

Fischer et al. International Journal of Health Geographics 2013, 12:51
http://www.ij-healthgeographics.com/content/12/1/51



RESEARCH Open Access

Climate change effects on Chikungunya transmission in Europe: geospatial analysis of vector's climatic suitability and virus' temperature requirements

Dominik Fischer^{1,2}, Stephanie M Thomas¹, Jonathan E Suk³, Bertrand Sudre³, Andrea Hess¹, Nils B Tjaden¹, Carl Beierkuhnlein¹ and Jan C Semenza^{3*}

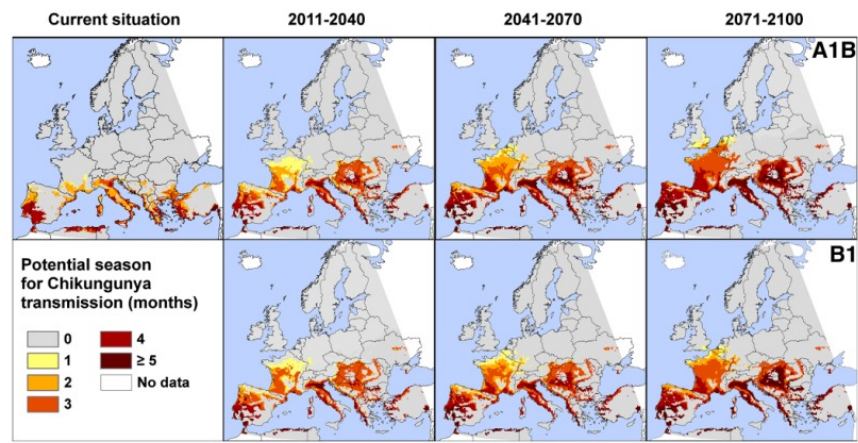


Figure 5 Length of transmission season for Chikungunya (in months), but filtered by areas, where the presence of the vector *Aedes albopictus* can be expected. The threshold for occurrences from continuous values of suitability was obtained by minimising the absolute difference between the sensitivity and specificity, resulting in a specific value (0.371) as threshold for vector occurrences. Projections for different time-frames are based on two emission scenarios (A1B and B1) from the Intergovernmental Panel on Climate Change, implemented in the regional climate model COSMO-CLM.

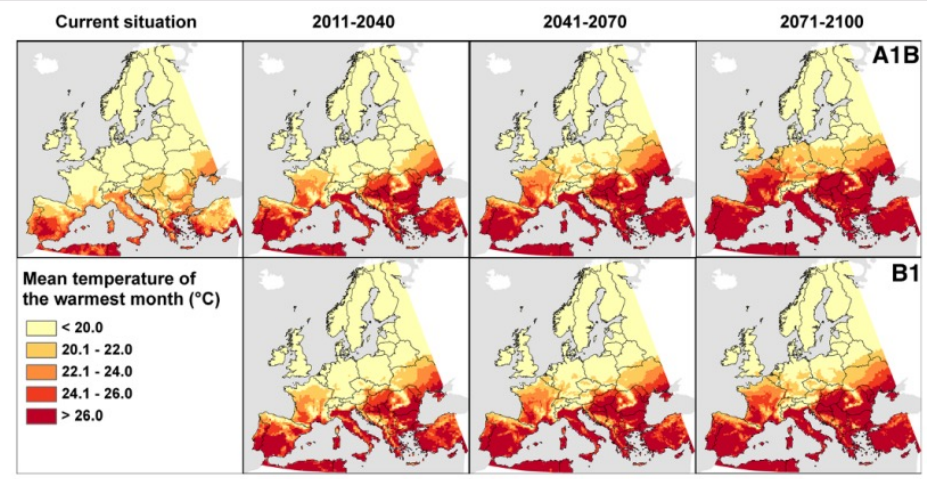


Figure 2 Fulfilling of temperature requirements for the Chikungunya virus in Europe. Projections for different time-frames are based on two emission scenarios (A1B and B1) from the Intergovernmental Panel on Climate Change, implemented in the regional climate model COSMO-CLM.

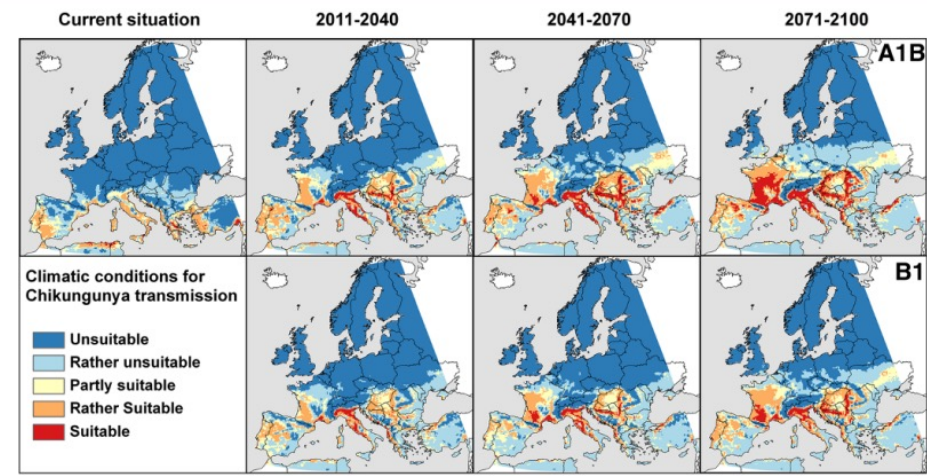


Figure 3 Risk map for Chikungunya transmission in Europe generated by combining temperature requirements of the Chikungunya virus with the climatic suitability of the vector *Aedes albopictus*. Projections for different time-frames are based on two emission scenarios (A1B and B1) from the Intergovernmental Panel on Climate Change, implemented in the regional climate model COSMO-CLM.

AU TOTAL

CONVAINCUS DU DYNAMISME?

Réchauffement + Humidité + Précipitation
= Expansion futur des Vecteurs en zone actuellement tempérée

MAIS

Les déterminants de la prolifération des vecteurs et de l'augmentation de l'incidence des arboviroses sont anthropocentrés

- Augmentation des villes imperméables et chaudes
- Surpopulation urbaine, exode rural
- Conditions de vie en ville dégradées, précarités
- accès précaire à l'eau
- défaut d'organisation politique et social pour lutte contre les vecteurs
- Augmentation des déplacements humains

With every increment of global warming, regional changes in mean climate and extremes become more widespread and pronounced

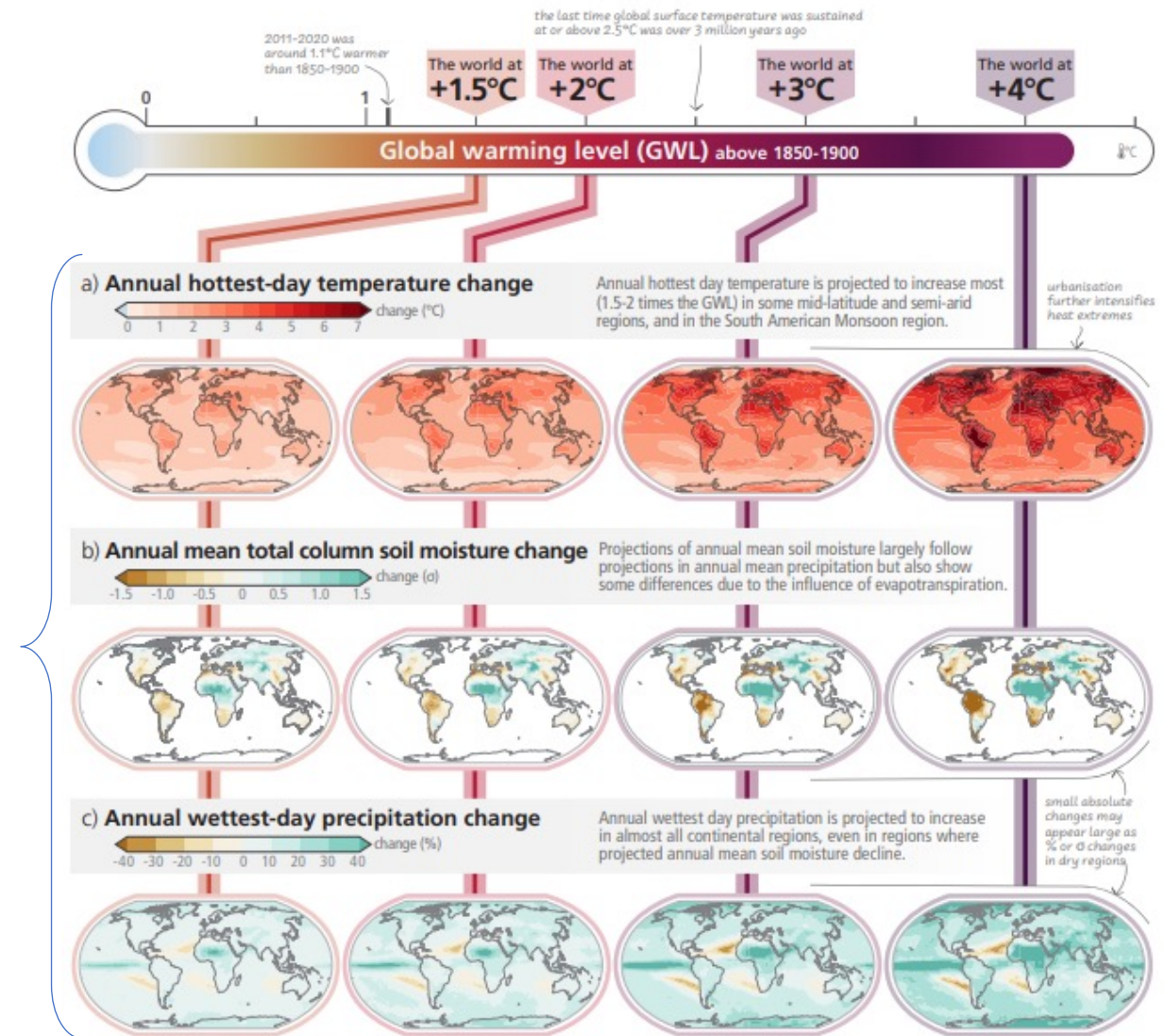


Figure SPM.2: Projected changes of annual maximum daily maximum temperature, annual mean total column soil moisture and annual maximum 1-day precipitation at global warming levels of 1.5°C, 2°C, 3°C, and 4°C relative to 1850-1900. Projected (a) annual maximum daily temperature change (°C), (b) annual mean total column soil moisture (standard deviation), (c) annual maximum 1-day precipitation change (%). The panels show CMIP6 multi-model median changes. In panels (b) and (c), large positive relative changes in dry regions may correspond to small absolute changes. In panel (b), the unit is the standard deviation of interannual variability in soil moisture during 1850-1900. Standard deviation is a widely used metric in characterising drought severity. A projected reduction in mean soil moisture by one standard deviation corresponds to soil moisture conditions typical of droughts that occurred about once every six years during 1850-1900. The WGI Interactive Atlas (<https://interactive-atlas.ipcc.ch/>) can be used to explore additional changes in the climate system across the range of global warming levels presented in this figure. (Figure 3.1, Cross-Section Box.2)



*“There are many examples where disease emergences reflect
our increasing inability to live in harmony with nature”*

Fauci AS

MERCI