



# Emergence de nouvelles maladies infectieuses

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## Emerging viruses since 1970 (non exhaustive)

1973	Rotavirus	1997	Influenza A H5N1 (1er)
1977	Ebola virus		Virus Menangle
	Hantaan virus	1999	Virus Nipah
	Influenza A H1N1		Influenza A H9N2
1980	HTLV-1		Virus West Nile (Amériques)
1982	HTLV-2		Metapneumovirus humain
1983	HIV-1	2003	Influenza A H5N1 (2 <sup>e</sup> )
1986	HIV-2		Sars-Co
1988	Virus de l'Hépatite E		Influenza A H7N7
	HHV6	2004	Influenza A H5N1 (suite)
1990	Virus Guanarito		other Influenza A viruses
1993	Virus Sin Nombre		NL coronavirus
		2005	Chikungunya virus (Ocean Indien)
1994	Virus Sabia	2009	Influenza A H1N1pdm
	Virus Hendra	2011	Influenza A H3N2v
1995	Virus de l'Hépatite G	2012	Mers CoV
	HHV8	2013	Influenza A H10N7s
1996	ESB (variant UK)		Influenza A H6N1
	Austrian Bat Lyssavirus	2014	Ebolavirus (Afrique de l'Ouest)
		2015	Zikavirus
			Influenza H5N1/N2/N8 (France)
			Influenza H7N9 (Chine)

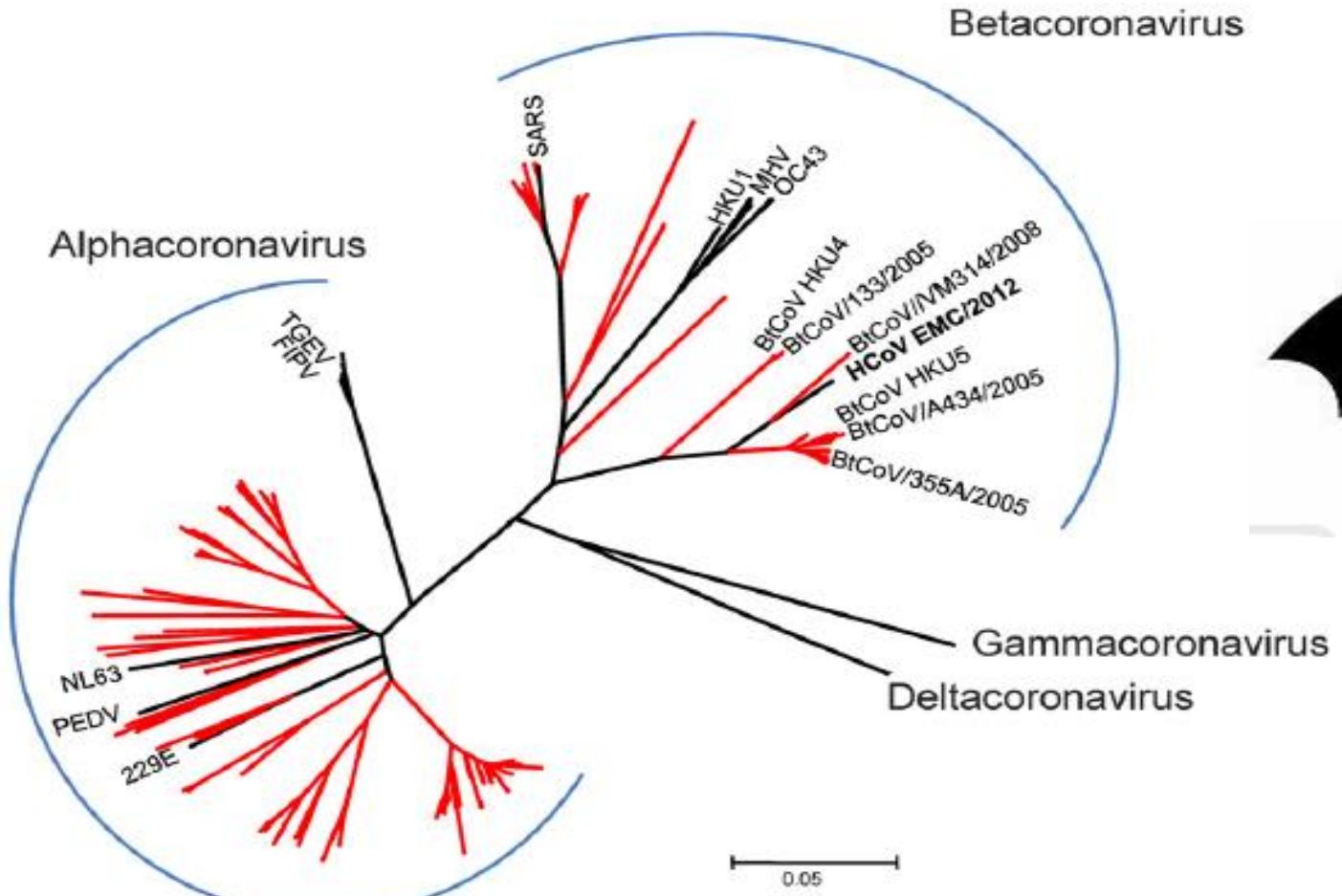
***Et Caetera...***

# Animal sources

- Rongeurs
  - Hantaan virus (inclus Dobrava et Pumalaa)
- Volailles, Oiseaux
  - Influenza A,
  - Virus West Nile
- Cochons
  - Influenza A,
  - Virus Nipah
- Chauve-souris
  - Australian bat lyssavirus,
  - Virus Hendra,
  - Virus Menangle,
  - Ebola virus,
  - Sars-Co
- Camelidés
  - MersCoV
- Singes
  - HIV-1

# Epidémiologie des virus émergents

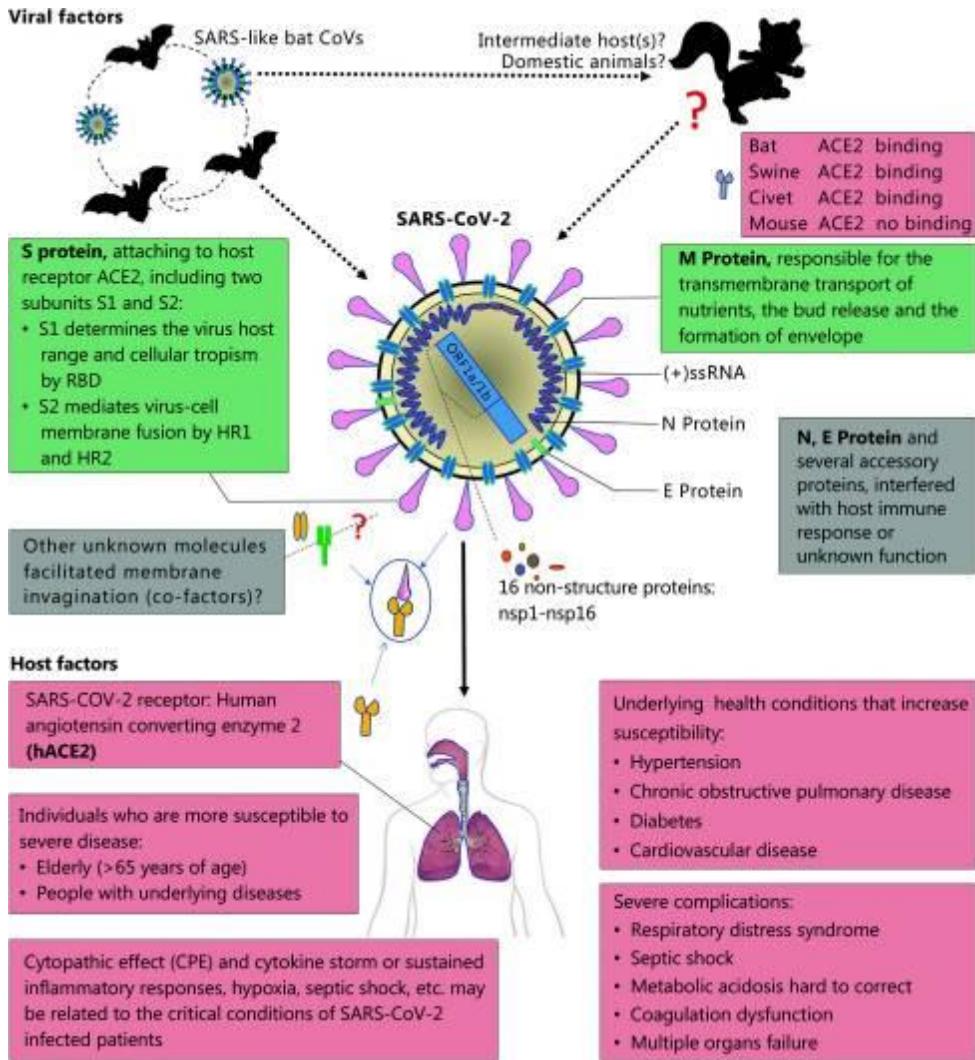
- Afrique
  - Ebola, West Nile, Influenza, ...
- Amériques
  - Guanarito, Sin Nombre, Sabia, West Nile, Zika, Influenza, ...
- Asie & Océanie
  - Influenza, SARS-Co, Encéphalite Japonaise, Hendra, Nipah, Menangle, Hantaan virus, ...
- Moyen Orient
  - MERs CoV, ...
- Europe
  - Influenza, Encephalite à tique, Pumalaa, Dobrava, ...



Bat coronavirus	Host	Location	Accession number
BtCoV/V/M314/2008	<i>Pipistrellus</i> bat	Netherlands	GQ259977
BtCoV/133/2005	<i>Tylonycteris</i> bat	China	DQ648794.1
BtCoV/ 355A/2005	<i>Pipistrellus</i> bat	China	DQ648809.1
BtCoV/A434/2005	<i>Pipistrellus</i> bat	China	DQ648819.1
HKU4	<i>Pipistrellus</i> bat	China (HK)	DQ249214.1
HKU5	<i>Tylonycteris</i> bat	China (HK)	DQ249217.1

# The path to humans

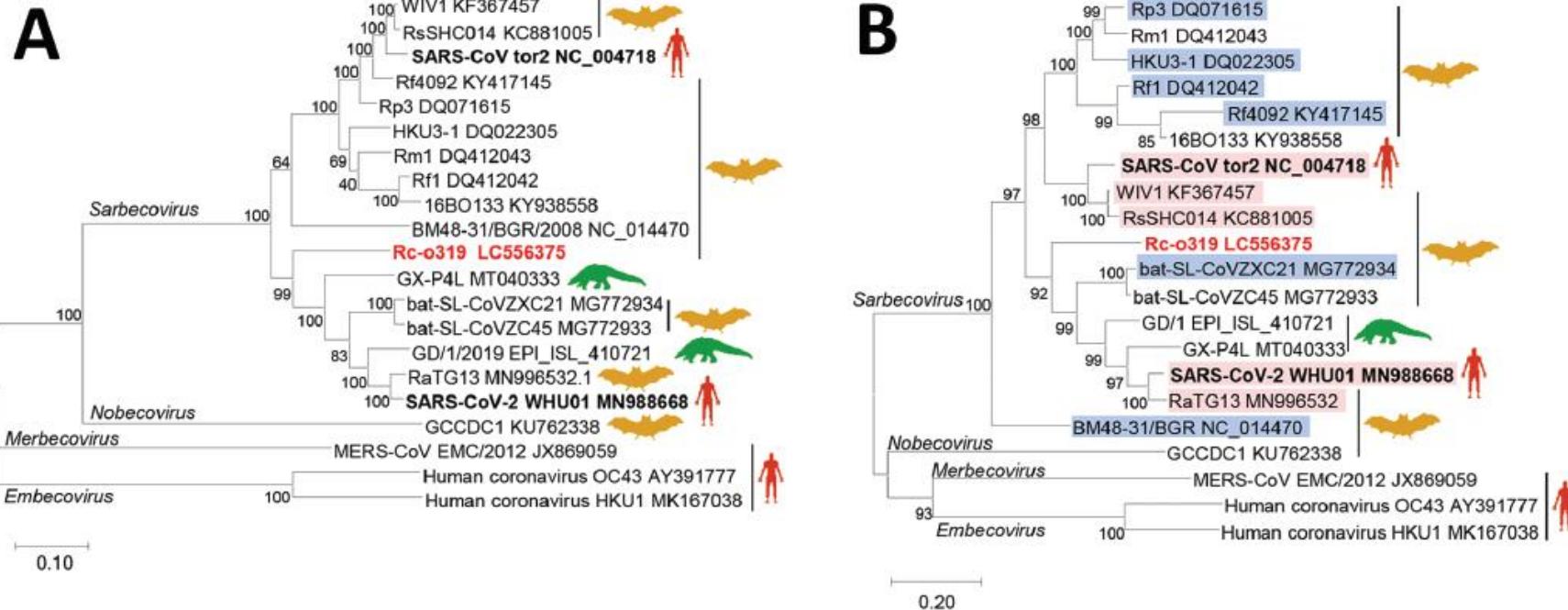
A WHO team is on its way to China  
to decipher the early events and the  
missing link



# Coronaviruses: the other pandemic virus?

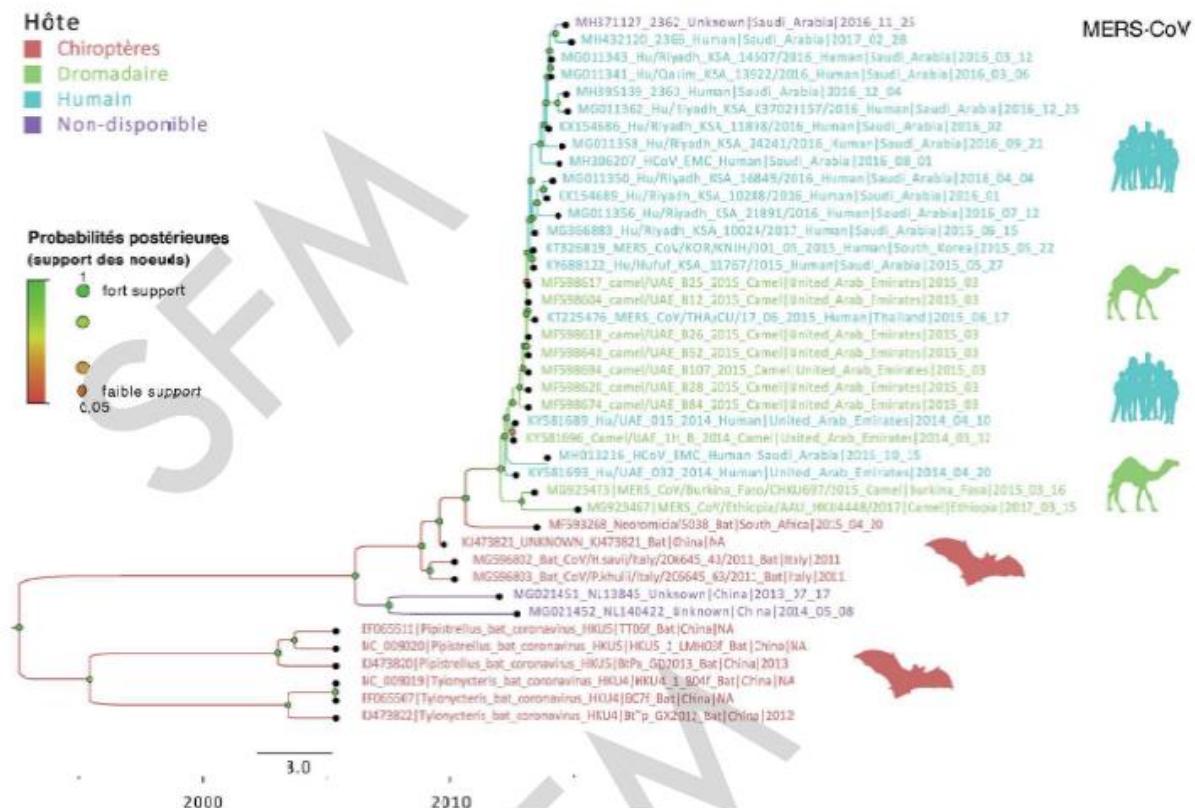
Coronavirus humain (HCoV)	Origine possible (hypothèse)	Hôte intermédiaire identifié	Date d'émergence (détermination du MRCA)	Circulation chez l'humain
HCoV-229E <i>Alphacoronavirus</i>		 Camelidae, <i>Alpaca</i> sp.	Début XIX <sup>e</sup> siècle	Ubiquitaire, saisonnier
HCoV-NL63 <i>Alphacoronavirus</i>		?	XIII <sup>e</sup> siècle	Ubiquitaire, saisonnier
HCoV-OC43 <i>Betacoronavirus</i> Clade A		 Bovidae	Fin XIX <sup>e</sup> siècle	Ubiquitaire, saisonnier
HCoV-HKU1 <i>Betacoronavirus</i> Clade A			?	Ubiquitaire, saisonnier
SARS-CoV <i>Betacoronavirus</i> Clade B		 <i>Paguma larvata</i> (civette)	2002	Pandémie décembre 2002 – juillet 2003 Arrêt de la circulation
MERS-CoV <i>Betacoronavirus</i> Clade C		 <i>Camelus dromedarius</i>	2012	Circulation péninsule arabique. Risque pandémique lié aux voyages

# Which viruses were precursors?



Murakami S et al, EID 2020

# For MERS - CoV



# SARS-CoV 2 emergence and reservoirs



- New nearest bat precursor from Yunnan 2019 (high identity in Orf1ab, greatest difference in Spike protein, recombination or mixed viruses in metagenomic sample, not yet peer-reviewed)
- Nearest pangolin precursors from Guangdong (Southern China)
- Previous closest bat precursor also from Yunnan (Southern China) but sample from 2013

Light Orange ... previous bat CoVs

Orange ... previous closest bat precursor (Yunnan 2013)

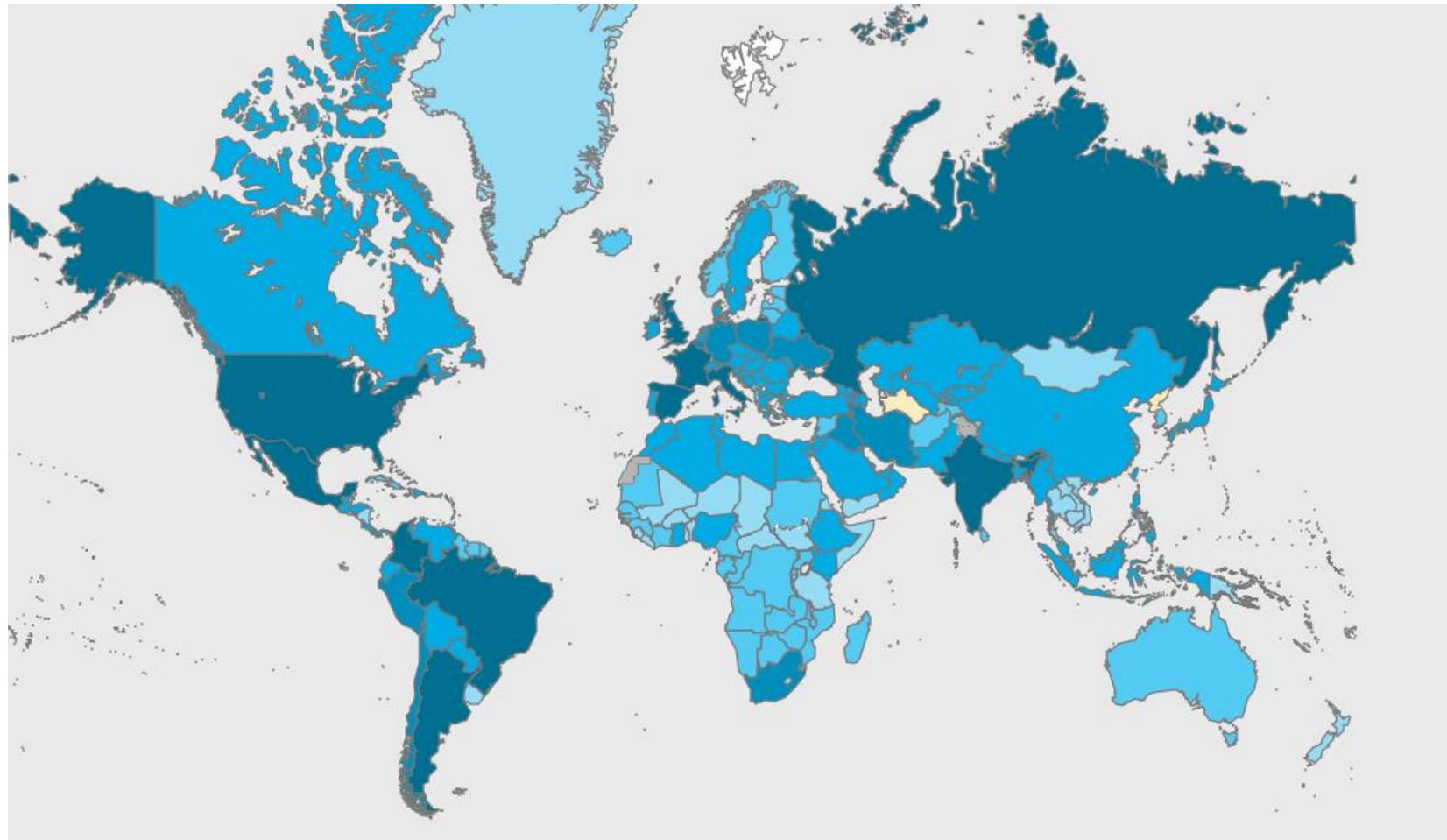
Red ... new bat CoVs (Yunnan 2019)

Light blue ... hCoV-19 2019-2020

Green ... pangolin CoV (Southern China 2019)

Blue ... SARS CoV

## Impact- SARS-CoV-2



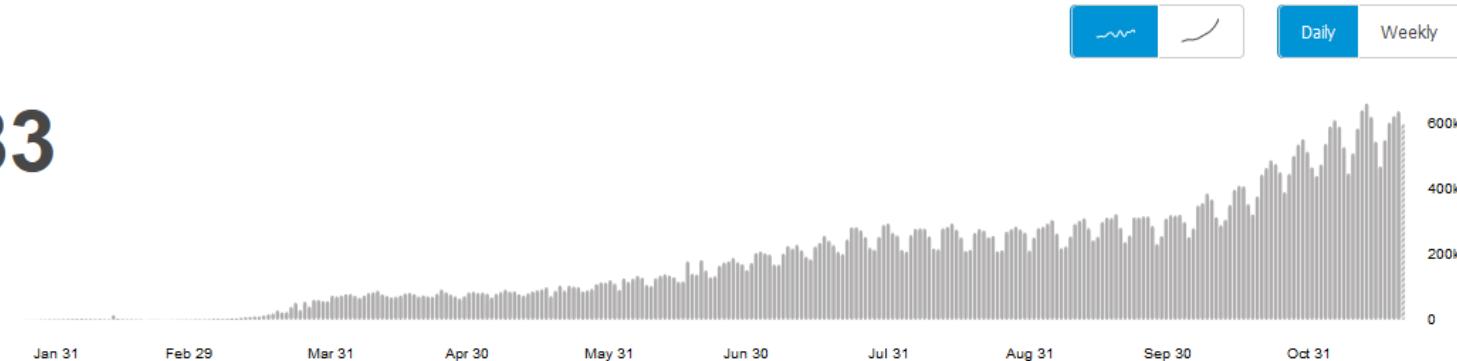
# Impact- SARS-CoV-2

SARS-CoV-2 situation au 23 novembre 2020

## Global Situation

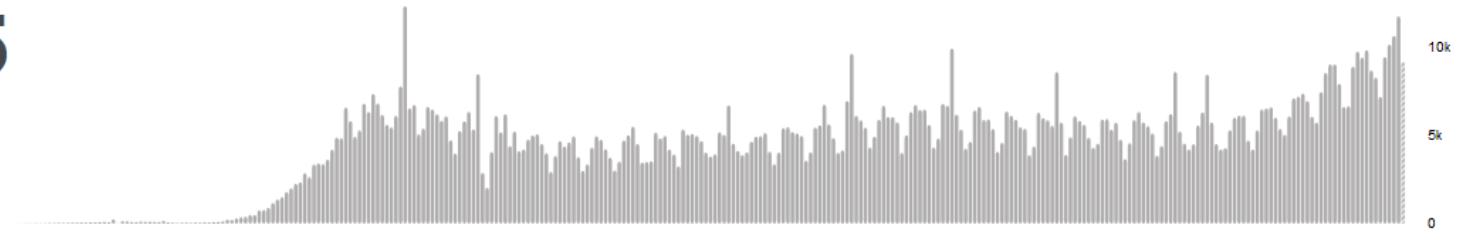
**57,882,183**

confirmed cases



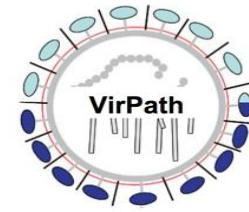
**1,377,395**

deaths



Source: World Health Organization

Data may be incomplete for the current day or week.



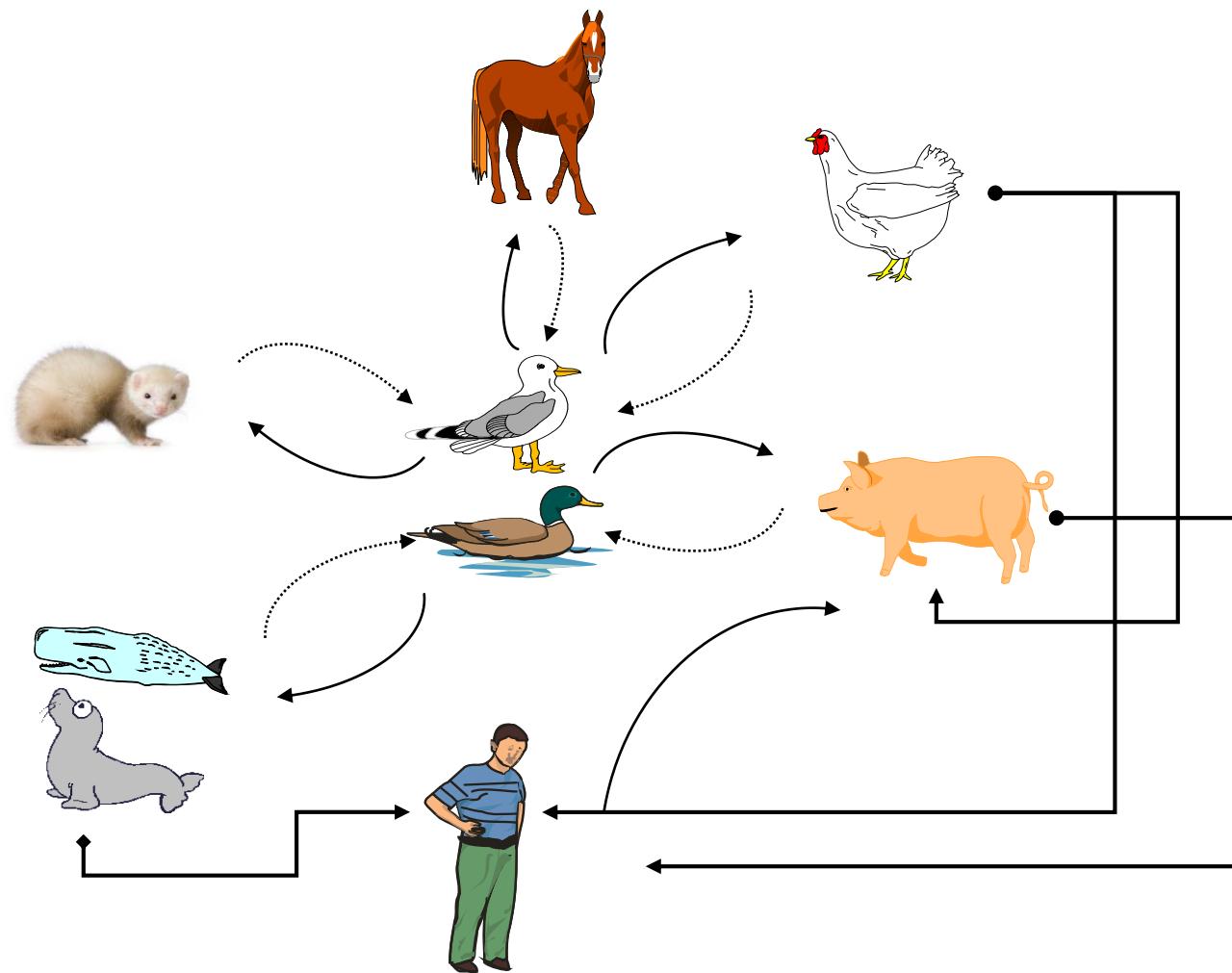
# influenzavirus emergents

**Bruno Lina**

Hospices Civils de Lyon, CNR des virus influenza (Sud), F69677, Bron

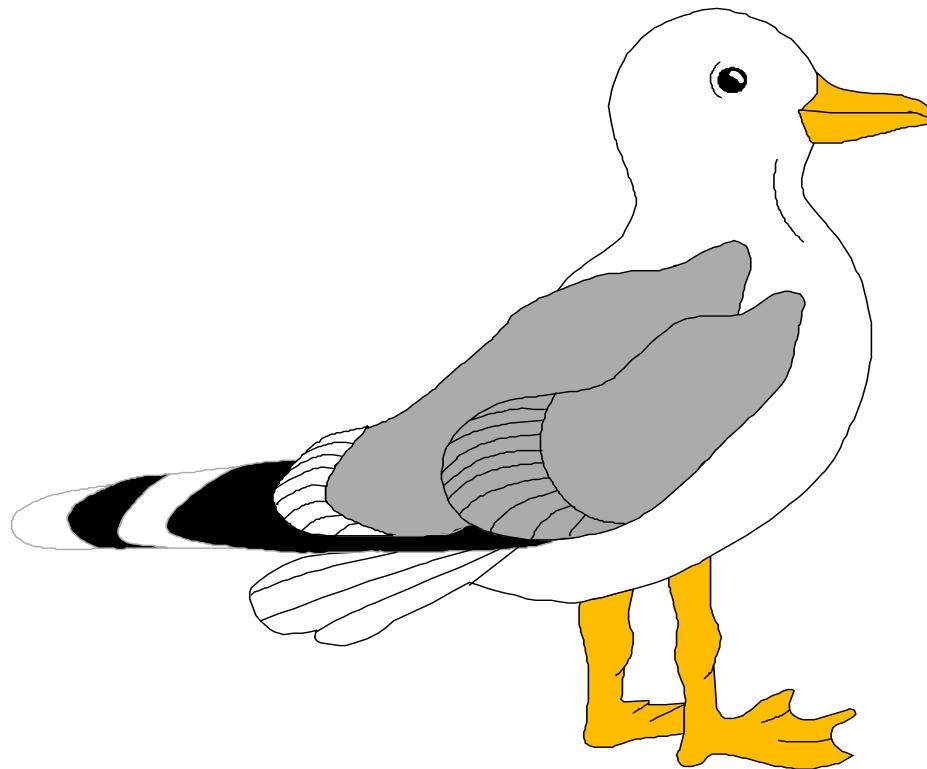
VirPatH, EMR 4610, Université de Lyon, F69372, Lyon

# The path to humans

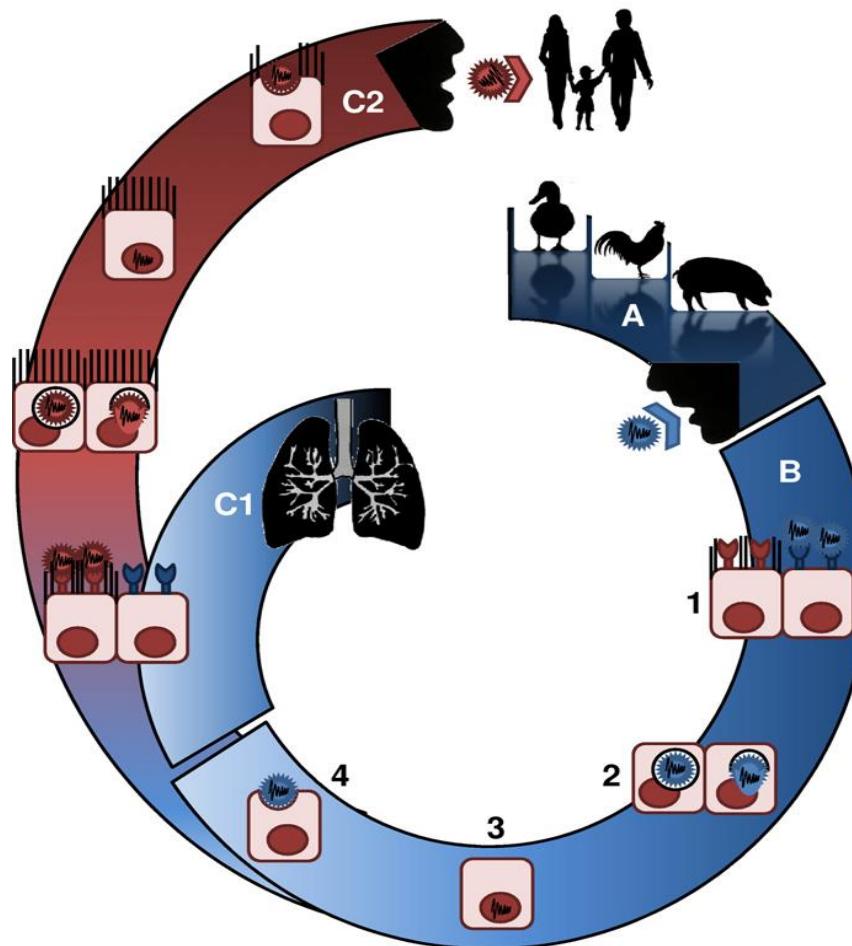


\* Uniquement pour les pandémies

# Transmission of an avian influenza virus?



# What are the barriers



# Influenza pandemics



**1918: “Spanish Flu”**

***H1N1***

***40-50 million***

**1957: “Asian Flu”**

***H2N2***

***1-4 million***

**1968: “Hong Kong Flu”**

***H3N2***

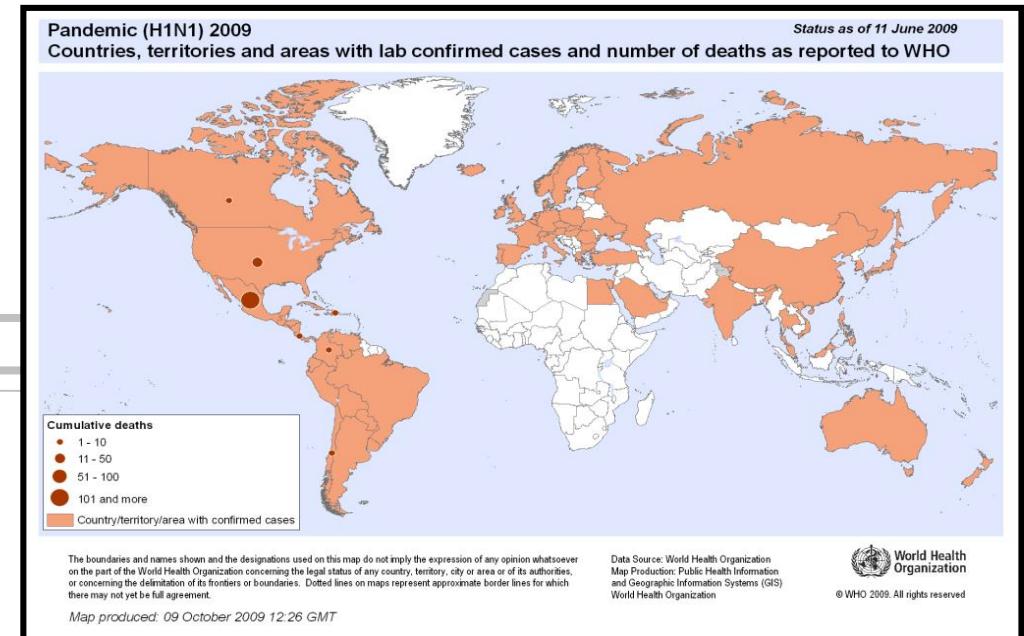
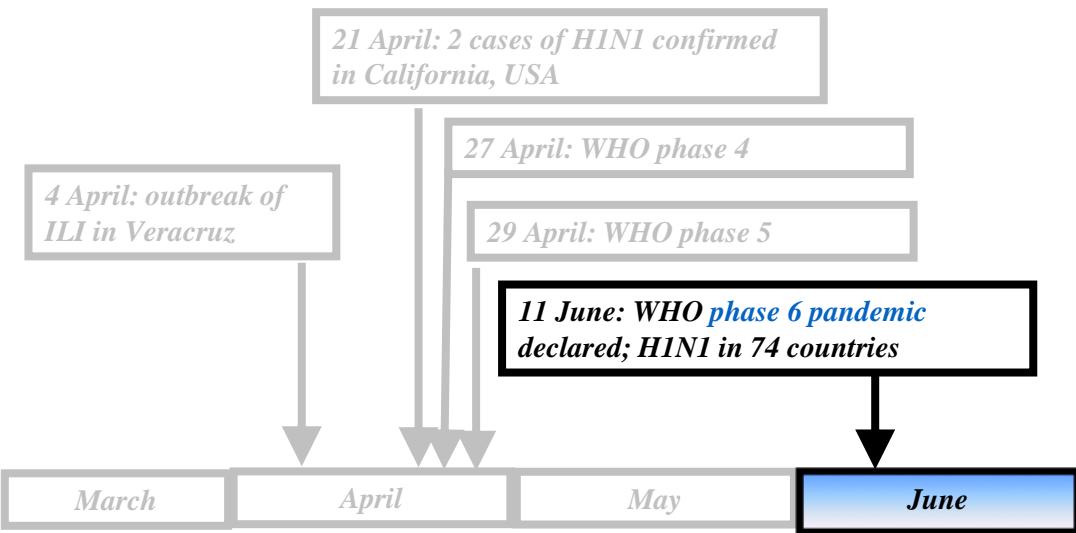
***1 million***

**2009: “Swine Flu”**

***H1N1***

***0.7 million***

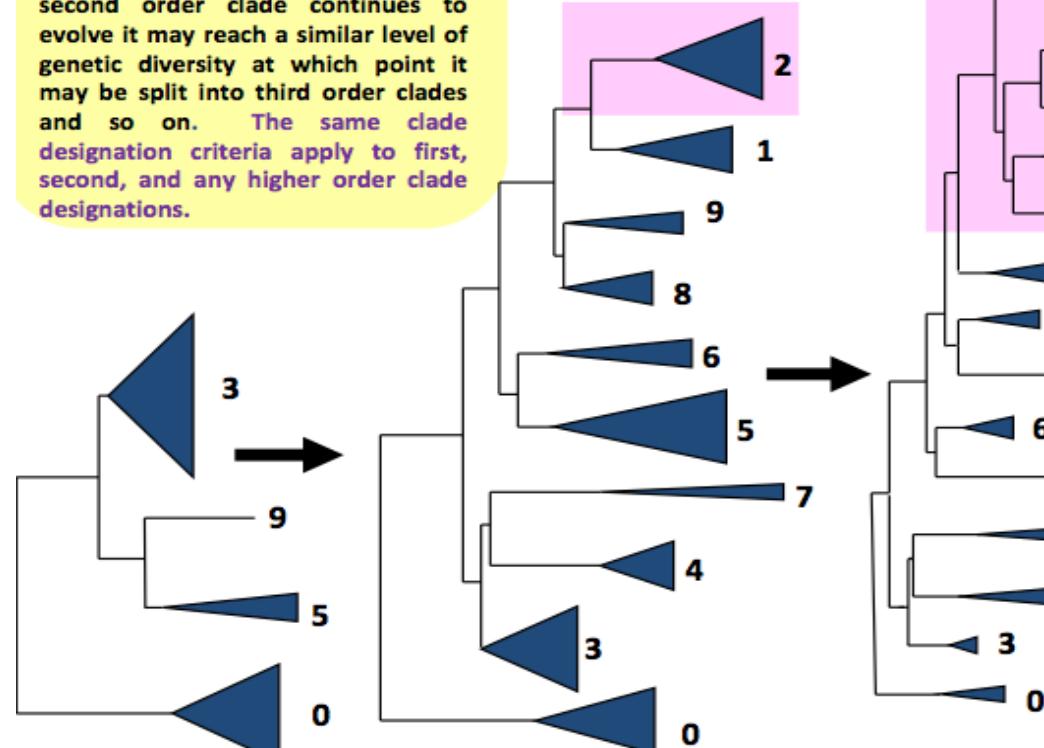
# Pandemic H1N1 2009 Timeline



*It took 6 weeks to reach 3 continents as compared to 3 months in 1957*

# Evolution of the Asian H5 Hemagglutinin

When discrete monophyletic groups begin to appear within a specific clade and those groups meet the nucleotide divergence criteria (as well as having bootstrap values >60), they are split into second order clades (but still considered part of the original first order clade). As a second order clade continues to evolve it may reach a similar level of genetic diversity at which point it may be split into third order clades and so on. The same clade designation criteria apply to first, second, and any higher order clade designations.



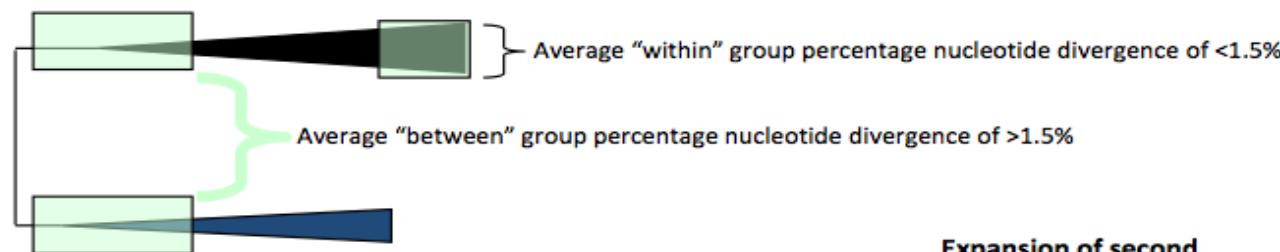
0.002

0.005

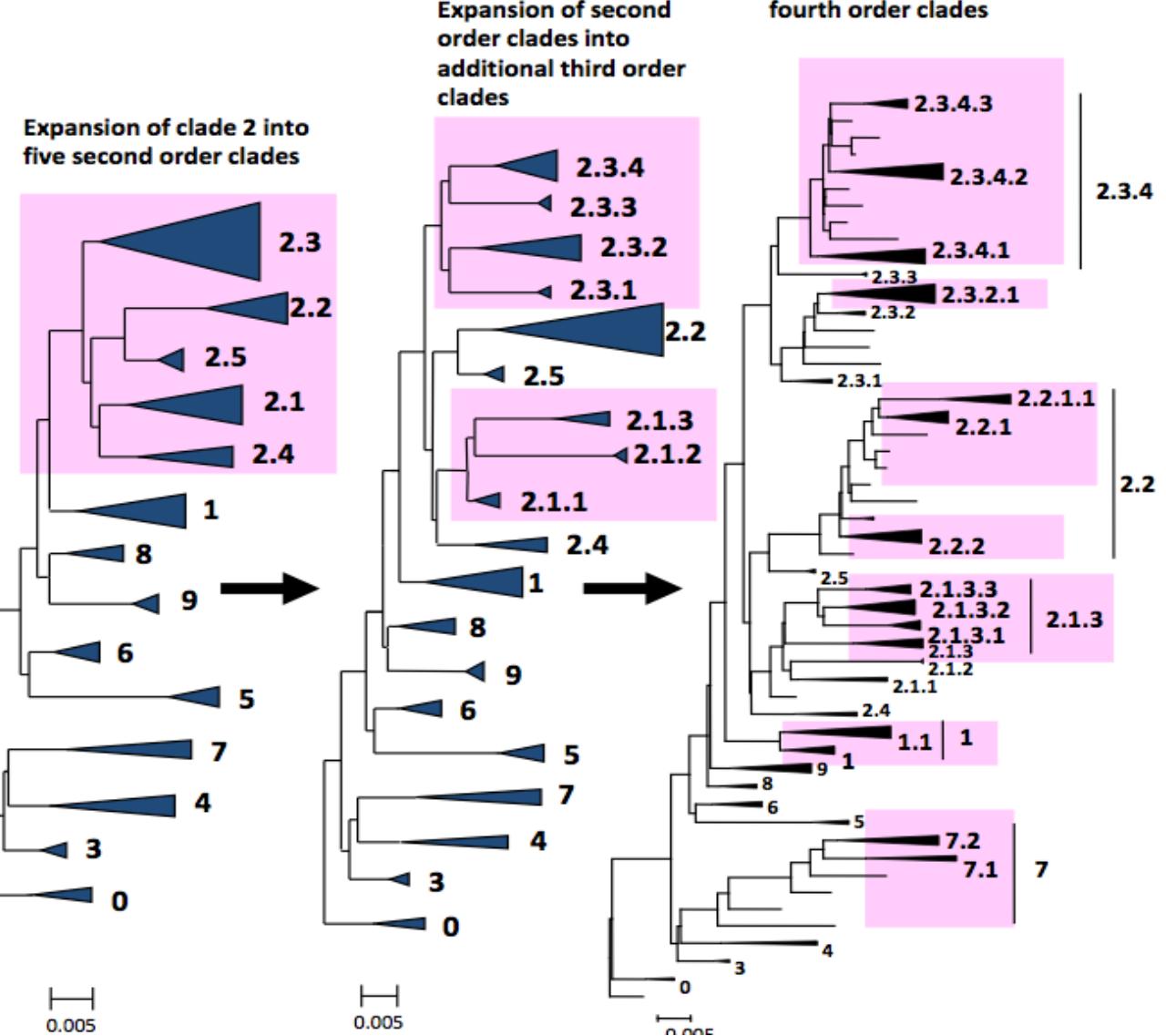
0.005

0.005

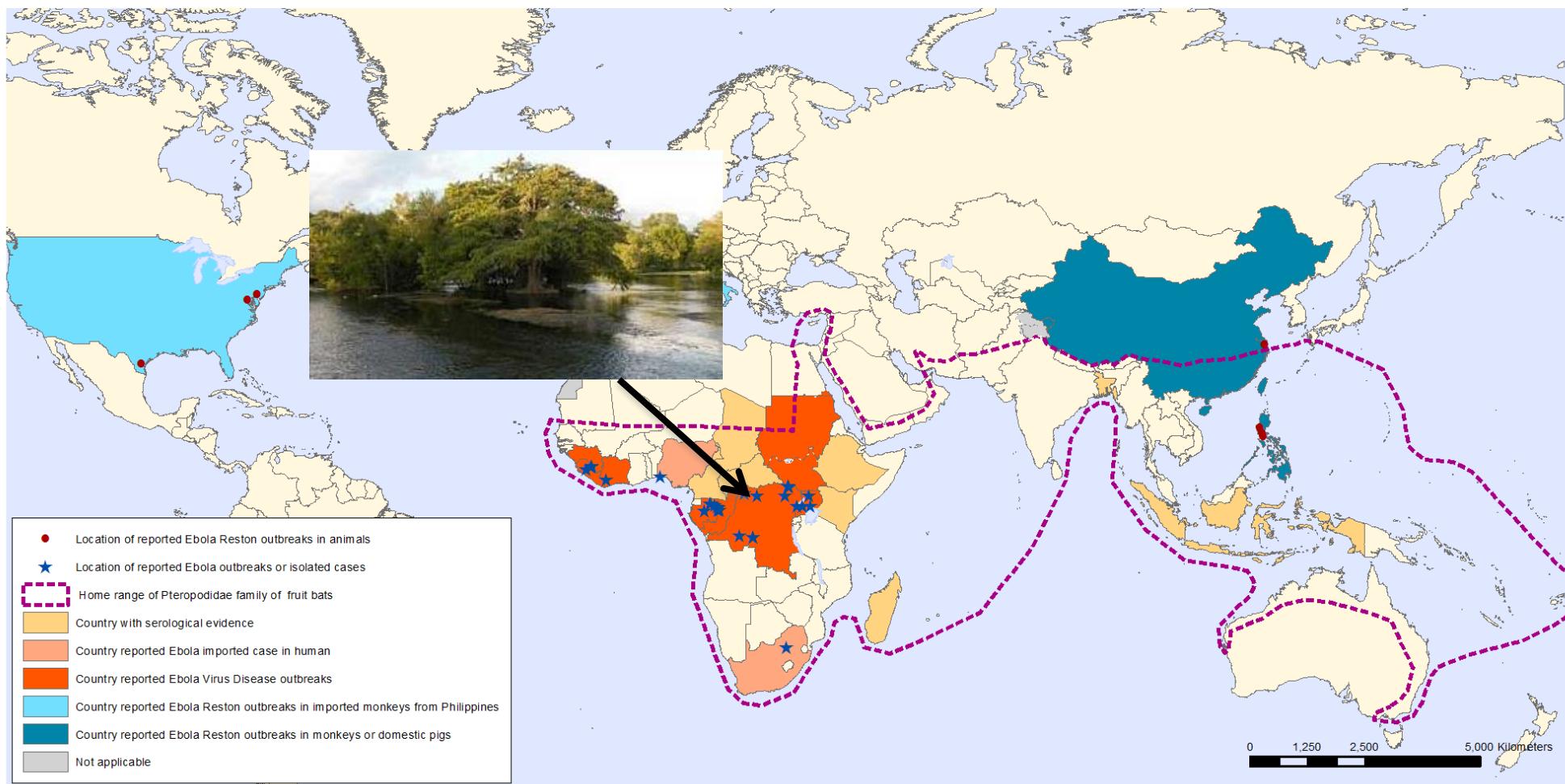
0.005



Expansion of first, second and third order clades into additional second, third and fourth order clades



# Geographic distribution



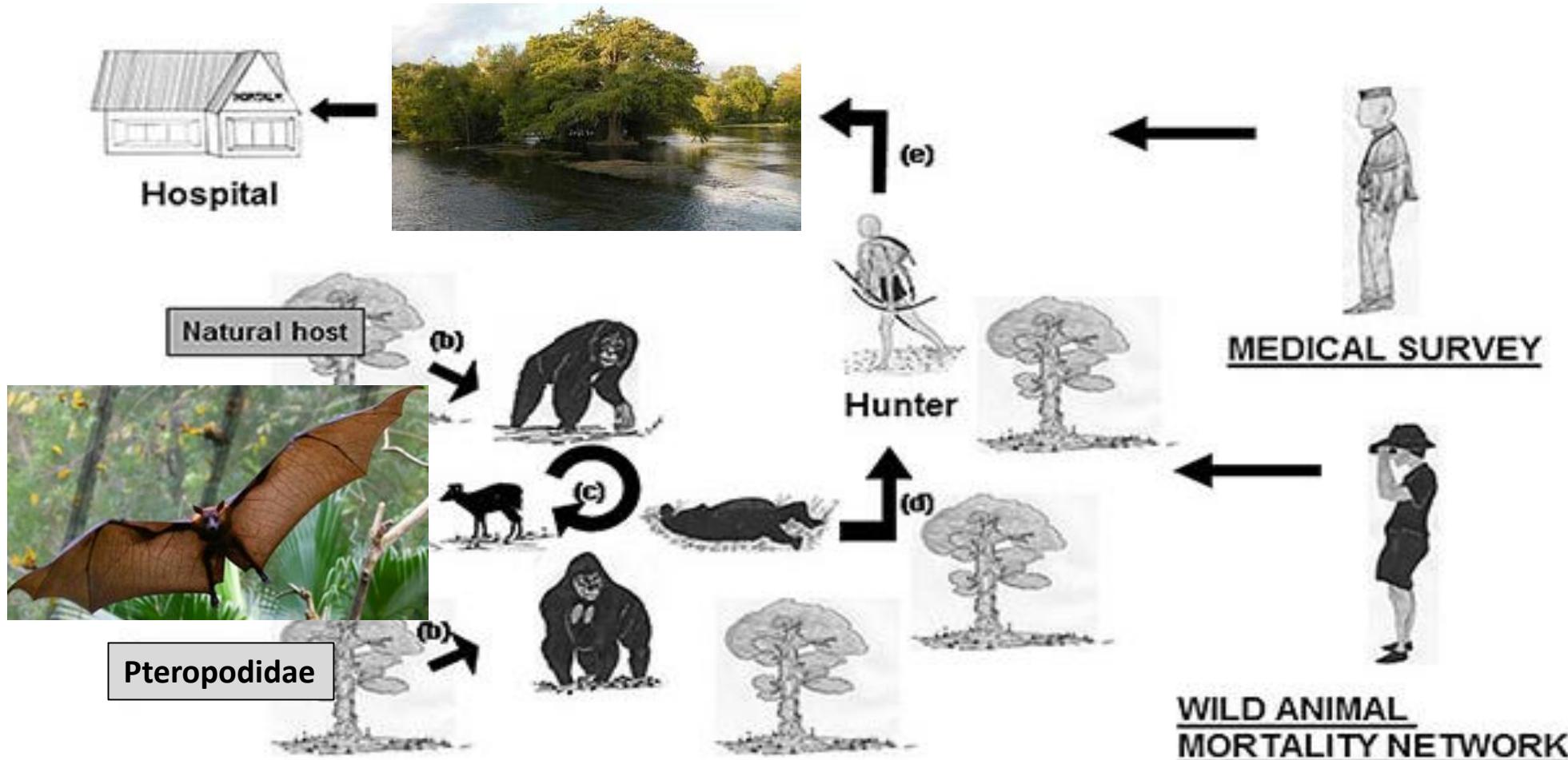
The boundaries and names shown and the designations used on this map do not imply the expression of any opinion whatsoever on the part of the World Health Organization concerning the legal status of any country, territory, city or area or of its authorities, or concerning the delimitation of its frontiers or boundaries. Dotted and dashed lines on maps represent approximate border lines for which there may not yet be full agreement.

Data Source: World Health Organization  
Map Production: Health Statistics and Information Systems (HSI)  
World Health Organization



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# Ebola



# Ebola virus disease - tenth outbreak - Democratic Republic of the Congo - 2018 - 2019

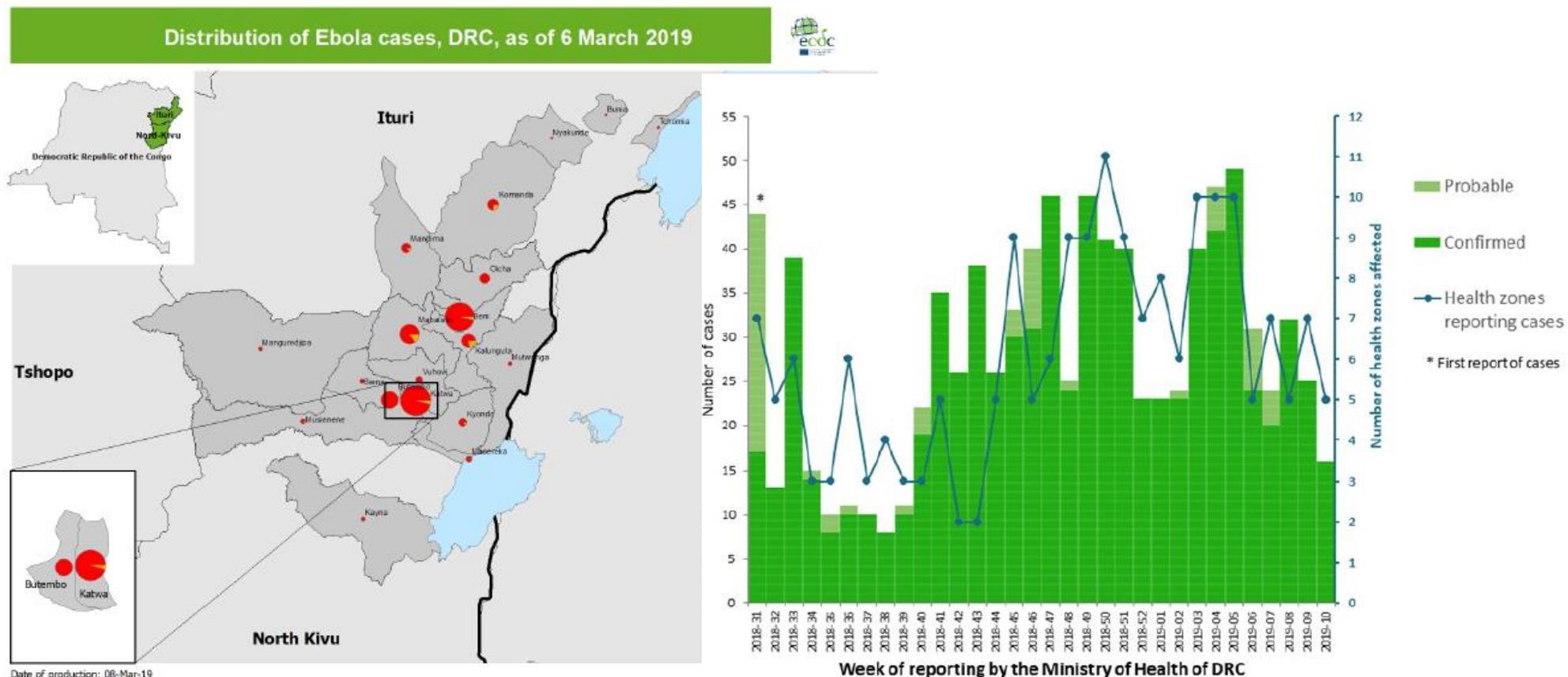
Opening date: 1 August 2018

Latest update: 8 March 2019

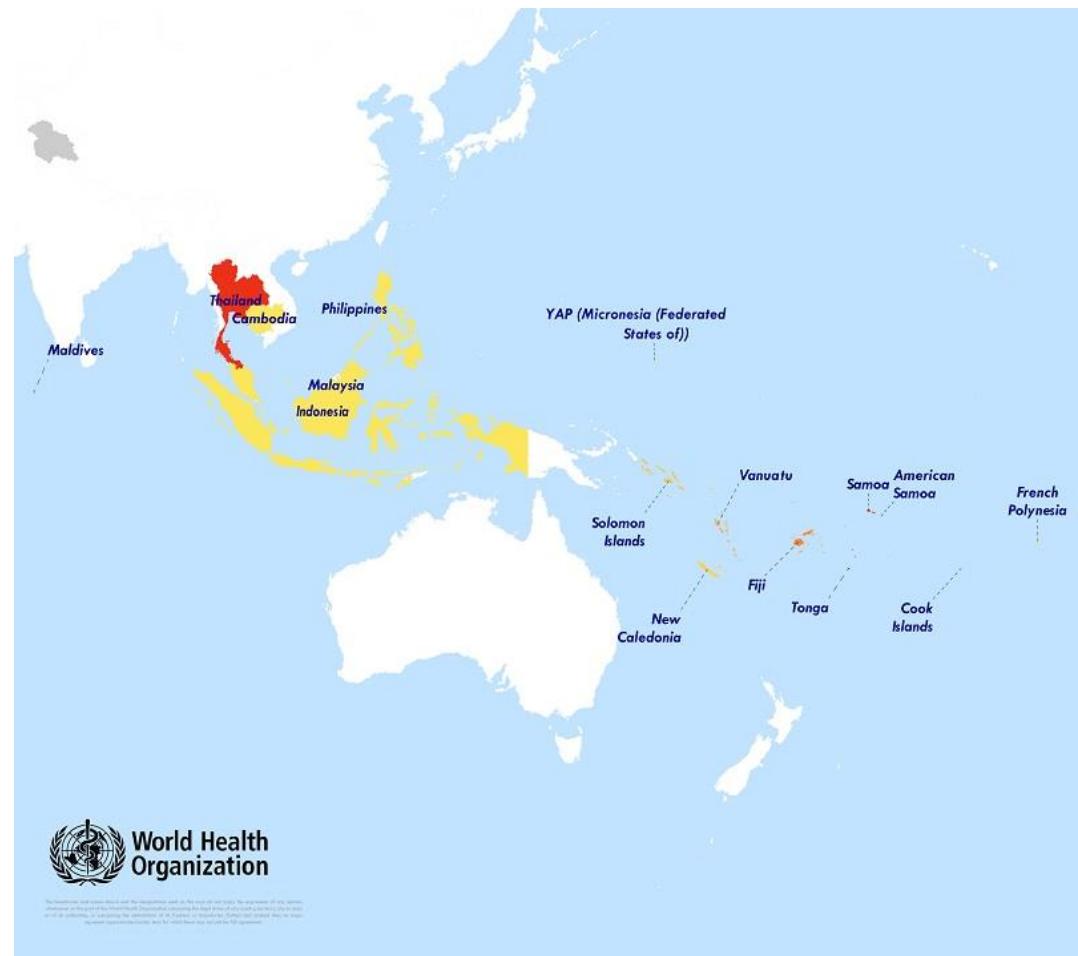
## Epidemiological summary

Since the beginning of the outbreak and as of 6 March 2019, there have been 913 cases (848 confirmed, 65 probable), including 574 deaths (509 confirmed, 65 probable), according to the Ministry of Health of the Democratic Republic of the Congo.

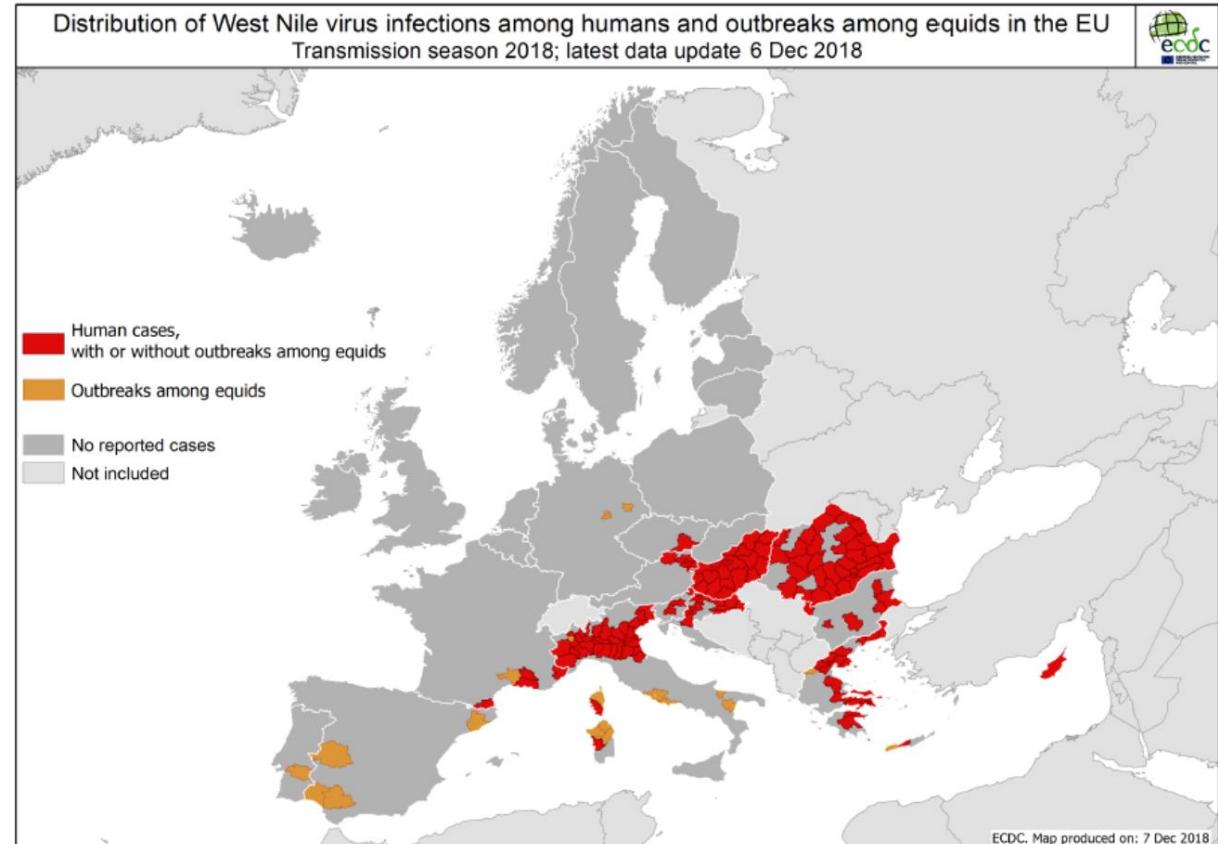
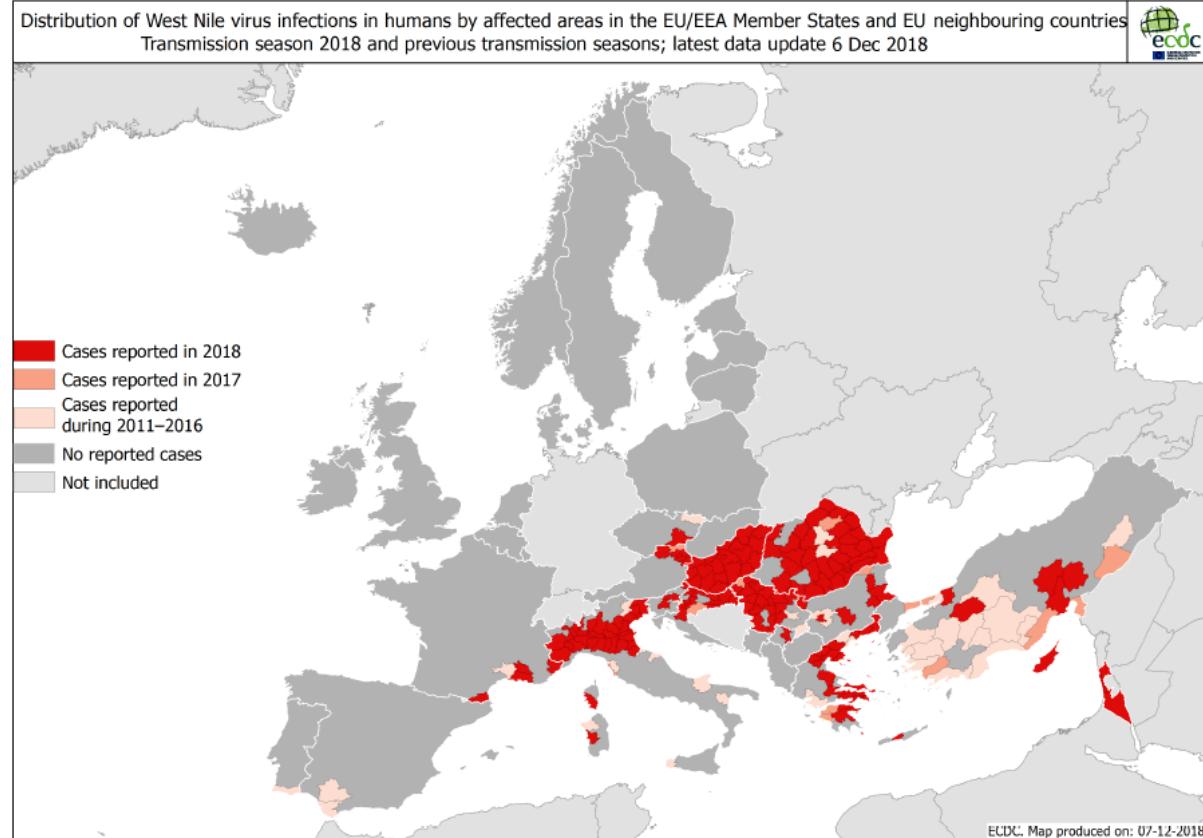
As of 2 March 2019 and according to the [WHO Regional Office for Africa External Situation Report 30](#), 72 healthcare workers have been infected, including 24 deaths.



# And Zikavirus



# And West Nile in Europe



# Summary

- Pandemic respiratory viruses: influenza and coronaviruses
  - Similar trends of introduction
  - Different reservoirs
  - Others?
- Pandemic vector borne-diseases
  - Zika and chik share vectors
  - Dengue and west-nile can expand
  - Others to be identified
- Animal borne viruses
  - Hantaan
  - Ebolaviruses
  - Other viruses



# MERCI

## Respiratory virus National Reference Center (NRC) :

NGS team

Antonin Bal (PhD Student)

Grégory Destras (PhD Student)

Grégory Quéromès (PhD Student)

Hadrien Regue (Bioinformatician)

Gwendolyne Burfin (technician)

Solenne Brun (technician)

Pr Florence Morfin

Dr Antonin Bal

Dr Maude Bouscambert

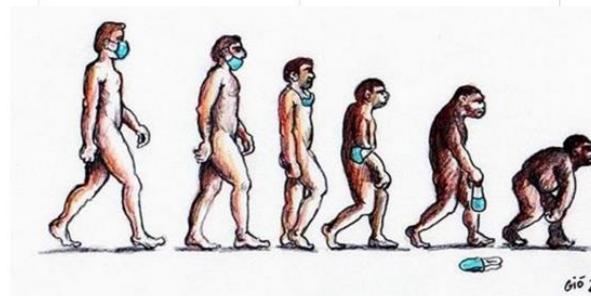
Dr Alexandre Gaymard

Dr Emilie Frobert

Dr Martine Valette

## Public resources for SARS-CoV-2 genome analysis :

- GISAID
- NextStrain
- COV-GLUE



## Virpath lab (Université de Lyon)

Dr Olivier Terrier

Dr Manuel Rosa-Calatrava

Mario Andres Pizzorno (Post-Doc)

[www](#) Claire Nicolas de Lamballerie (Post-Doc)

Aurelien Traversier (technician)

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